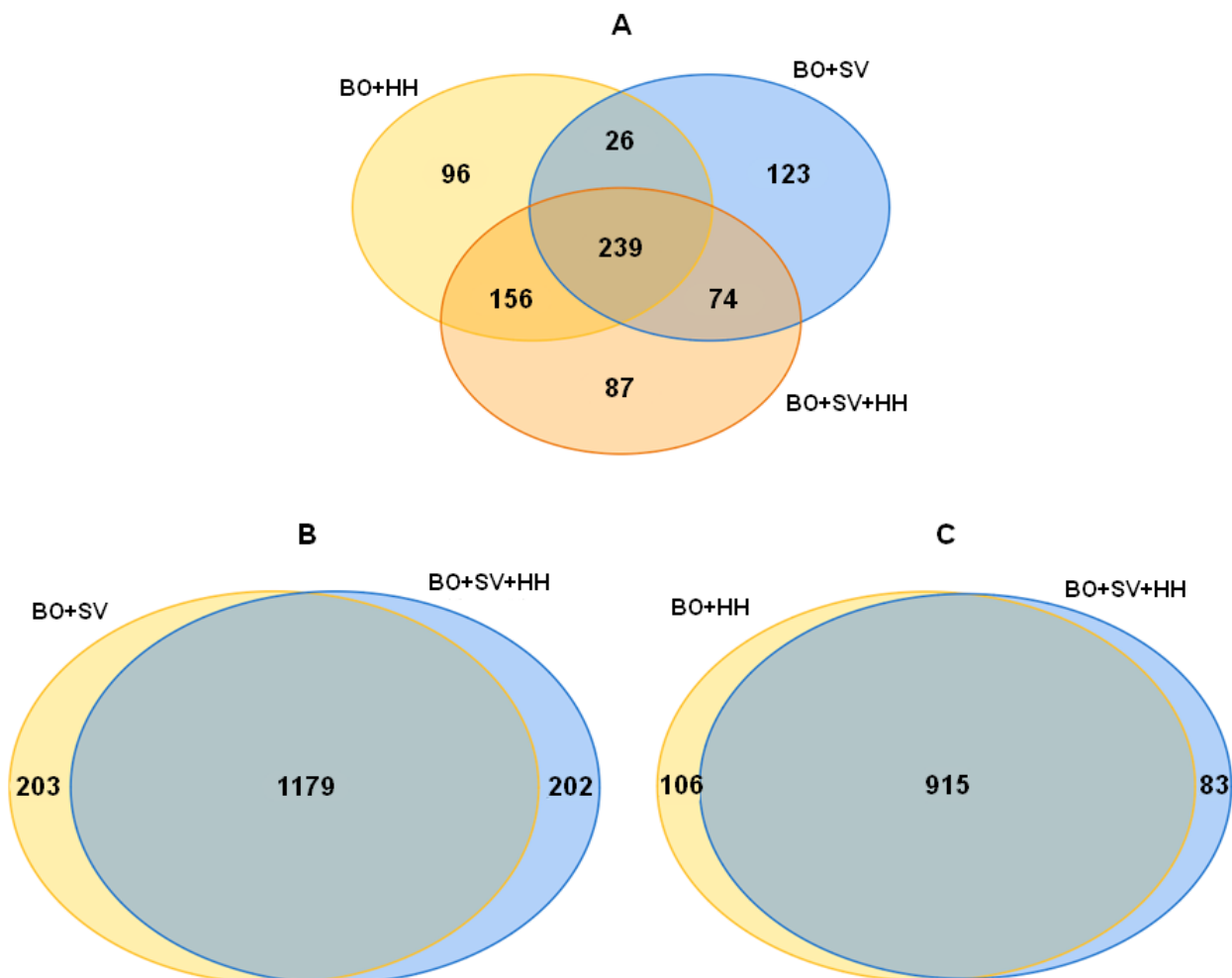


**Figure S1.** Number of differentially transcribed (DT) genes grouped according to Cluster of Orthologous Genes (COG) categories. **A.** *B. ovatus* ATCC 8483<sup>T</sup> DT genes uniquely expressed in co-cultures. *S. variable* DSM 15176<sup>T</sup> (**B**) and *H. hathewayi* DSM 13479<sup>T</sup> (**C**) DT genes uniquely expressed in co-cultures. Genes that

had increased transcription in co-culture compared to pure culture conditions are indicated in red bars, genes with decreased transcription in light blue bars. COG categories: [A], RNA processing and modification; [B], Chromatin structure and dynamics; [C], Energy production and conversion; [D], Cell cycle control cell division chromosome partitioning; [E], Amino acid transport and metabolism; [F], Nucleotide transport and metabolism; [G], Carbohydrate transport and metabolism; [H], Coenzyme transport and metabolism; [I], Lipid transport and metabolism; [J], Translation ribosomal structure and biogenesis; [K], Transcription; [L], Replication recombination and repair; [M], Cell wall/membrane/envelope biogenesis; [N], Cell motility; [O], Post-translational modification protein turnover and chaperones; [P], Inorganic ion transport and metabolism; [Q], Secondary metabolites biosynthesis transport and catabolism; [R], General function prediction only; [S], Function unknown; [T], Signal transduction mechanisms; [U], Intracellular trafficking secretion and vesicular transport; [V], Defense mechanisms; [W], Extracellular structures; [Y], Nuclear structure; [Z], Cytoskeleton.



**FIG S2.** Venn diagrams of the number of common and unique differentially transcribed genes of *B. ovatus* ATCC 8483<sup>T</sup> (BO) (**A**), *S. variabile* DSM 15176<sup>T</sup> (SV) (**B**) and *H. hathewayi* DSM 13479<sup>T</sup> (HH) (**C**) in co-cultures.

**Table S1.** Summary of RNA-seq data obtained from all pure and co-culture samples.

BO16, BO20, BO24 and BO26 indicate *B. ovatus* ATCC 8483<sup>T</sup> pure culture samples

at 16, 20, 24 and 26 h, respectively. SV12, SV14, SV16 and SV24 indicate *S.*

*variabile* DSM 15176<sup>T</sup> pure culture samples at 12, 14, 16 and 24 h, respectively.

HH06, HH16, HH18, HH20 and HH24 indicate *H. hathewayi* DSM 13479<sup>T</sup> pure

culture samples at 6, 16, 18, 20 and 24 h, respectively. BO+SV, BO+HH and

BO+SV+HH indicate co-culture samples of *B. ovatus* and *S. variabile*, *B. ovatus* and

*H. hathewayi*, and *B. ovatus*, *S. variabile* and *H. hathewayi*, respectively.

**Pure culture**

Reference genome		<i>B. ovatus</i> ATCC 8483 <sup>T</sup>								
Sample	BO16		BO20		BO24		BO26			
Biological replicate	1	2	1	2	1	2	1	2		
Adapter- and quality-trimmed reads (pair)	6275610	6171428	5672569	5780334	18119414	19225175	6134182	6146063		
Reads mapped to genome (pair)	5834141 (93%)	5640524 (91%)	5275180 (93%)	5239690 (91%)	15315133 (85%)	16358203 (85%)	5607694 (91%)	5738493 (93%)		
Reads aligned (sense) to protein-coding genes	94%	94%	94%	94%	94%	94%	93%	93%		
Reads aligned (antisense) to protein-coding gene	1%	1%	1%	1%	1%	1%	1%	1%		
Reads aligned (sense) to ribosomal RNAs	0%	0%	0%	0%	0%	0%	0%	0%		
Reads aligned (antisense) to ribosomal RNAs	0%	0%	0%	0%	0%	0%	0%	0%		
Reads aligned (sense) to transfer RNAs	0%	0%	0%	0%	0%	0%	0%	0%		
Reads aligned (antisense) to transfer RNAs	0%	0%	0%	0%	0%	0%	0%	0%		
Reads aligned (sense) to miscellaneous RNAs	1%	0%	1%	1%	1%	1%	1%	1%		
Reads aligned (antisense) to miscellaneous RNAs	0%	0%	0%	0%	0%	0%	0%	0%		
Reads aligned to unannotated regions	4%	5%	5%	5%	4%	5%	5%	5%		
Reference genome		<i>S. variabile</i> DSM 15176 <sup>T</sup>								
Sample	SV12		SV14		SV16			SV24		
Biological replicate	1	2	1	2	3	1	2	3	1	2
Adapter- and quality-trimmed reads (pair)	5296033	4899087	5395150	5872683	4050882	5027329	5260404	4947739	16503690	16046974
Reads mapped to genome (pair)	4803047 (91%)	4740926 (97%)	4963869 (92%)	5326185 (91%)	3412214 (84%)	4651029 (93%)	4798418 (91%)	4750547 (96%)	13545113 (82%)	13296521 (83%)
Reads aligned (sense) to protein-coding genes	87%	81%	90%	89%	86%	88%	89%	90%	64%	50%
Reads aligned (antisense) to protein-coding gene	1%	2%	1%	1%	1%	1%	1%	1%	4%	5%
Reads aligned (sense) to ribosomal RNAs	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Reads aligned (antisense) to ribosomal RNAs	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Reads aligned (sense) to transfer RNAs	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Reads aligned (antisense) to transfer RNAs	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Reads aligned (sense) to miscellaneous RNAs	1%	2%	1%	2%	2%	2%	2%	1%	3%	3%
Reads aligned (antisense) to miscellaneous RNAs	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Reads aligned to unannotated regions	10%	16%	7%	8%	11%	9%	8%	8%	29%	42%

Reference genome	<i>H. hathewayi</i> DSM 13479 <sup>T</sup>									
Sample	HH06		HH16		HH18		HH20		HH24	
Biological replicate	1	2	1	2	1	2	1	2	1	2
Adapter- and quality-trimmed reads (pair)	5673589	5437765	5659507	5376647	5203979	5455634	5742994	5545527	16039801	18032570
Reads mapped to genome (pair)	4533453 (80%)	4371695 (80%)	4580845 (81%)	4422405 (82%)	4407666 (85%)	4613236 (85%)	4888885 (85%)	2748512 (50%)	11533717 (72%)	13561227 (75%)
Reads aligned (sense) to protein-coding genes	77%	77%	76%	84%	84%	83%	84%	82%	48%	67%
Reads aligned (antisense) to protein-coding gene	2%	3%	3%	3%	3%	3%	3%	3%	2%	3%
Reads aligned (sense) to ribosomal RNAs	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Reads aligned (antisense) to ribosomal RNAs	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Reads aligned (sense) to transfer RNAs	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Reads aligned (antisense) to transfer RNAs	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Reads aligned (sense) to miscellaneous RNAs	1%	1%	1%	1%	0%	0%	0%	1%	2%	1%
Reads aligned (antisense) to miscellaneous RNAs	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Reads aligned to unannotated regions	20%	20%	20%	13%	12%	13%	12%	14%	48%	40%

## Co-culture

Sample	BO+SV				BO+HH				BO+SV+HH					
	<i>B.ovatus</i> ATCC 8483 <sup>T</sup>		<i>S. variable</i> DSM 15176 <sup>T</sup>		<i>B.ovatus</i> ATCC 8483 <sup>T</sup>		<i>H. hathewayi</i> DSM 13479 <sup>T</sup>		<i>B.ovatus</i> ATCC 8483 <sup>T</sup>		<i>S. variable</i> DSM 15176 <sup>T</sup>		<i>H. hathewayi</i> DSM 13479 <sup>T</sup>	
Biological replicate	1	2	1	2	1	2	1	2	1	2	1	2	1	2
Adapter- and quality-trimmed reads (pair)	5563190	7185843	5563190	7185843	5310034	5463546	5310034	5463546	5664614	5625551	5664614	5625551	5664614	5625551
Reads mapped to genome (pair)	2541504 (46%)	3477039 (48%)	959115 (17%)	1067613 (15%)	2879519 (54%)	2988344 (55%)	541846 (10%)	507501 (9%)	2873130 (51%)	2814112 (50%)	50819 (1%)	28326 (1%)	619989 (11%)	611988 (11%)
Reads aligned (sense) to protein-coding genes	94%	94%	89%	89%	94%	94%	71%	67%	94%	94%	84%	78%	80%	76%
Reads aligned (antisense) to protein-coding gene	1%	1%	1%	1%	1%	1%	3%	3%	1%	1%	1%	2%	3%	3%
Reads aligned (sense) to ribosomal RNAs	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Reads aligned (antisense) to ribosomal RNAs	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Reads aligned (sense) to transfer RNAs	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Reads aligned (antisense) to transfer RNAs	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Reads aligned (sense) to miscellaneous RNAs	1%	1%	2%	2%	0%	1%	1%	1%	0%	0%	2%	3%	1%	1%
Reads aligned (antisense) to miscellaneous RNAs	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Reads aligned to unannotated regions	5%	5%	8%	8%	5%	5%	25%	29%	5%	5%	12%	17%	16%	20%

**Table S2.** List of enriched and depleted GO terms and their category number for each individual species in each co-culture condition.

<i>B. ovatus</i> ATCC 8483 <sup>T</sup> perspective				
	Enriched GO terms		Depleted GO terms	
<b>Common between BO+SV+HH, BO+SV and BO+HH</b>	-	-	GO:0046872	metal ion binding
			GO:0030001	metal ion transport
<b>Common between BO+SV+HH and BO+HH</b>	GO:0020037	heme binding	GO:0006568	tryptophan metabolic process
	GO:0017004	cytochrome complex assembly	GO:0046373	L-arabinose metabolic process
	GO:0006814	sodium ion transport	GO:0046556	alpha-L-arabinofuranosidase activity
	GO:0008565	protein transporter activity	GO:0003697	single-stranded DNA binding
<b>Unique to BO+HH</b>	GO:0016887	ATPase activity	GO:0005215	transporter activity
	GO:0005622	intracellular	GO:0016491	oxidoreductase activity
<b>Common between BO+SV+HH and BO+SV</b>	-	-	GO:0015655	alanine:sodium symporter activity
			GO:0032328	alanine transport
			GO:0043565	sequence-specific DNA binding
<b>Unique to BO+SV</b>	GO:0016861	intramolecular oxidoreductase activity, interconverting aldoses and ketoses	GO:0007165	signal transduction
	GO:0016310	phosphorylation	GO:0006310	DNA recombination
	GO:0030599	pectinesterase activity	GO:0005515	protein binding
	GO:0042545	cell wall modification	GO:0004565	beta-galactosidase activity
	GO:0006457	protein folding	GO:0009341	beta-galactosidase complex
	GO:0004872	receptor activity	GO:0052855	ADP-dependent NAD(P)H-hydrate dehydratase activity
	GO:0005618	cell wall	GO:0042279	nitrite reductase (cytochrome, ammonia-forming) activity
			GO:0004673	protein histidine kinase activity
			GO:0051536	iron-sulfur cluster binding
			GO:0006270	DNA replication initiation
			GO:0019288	isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway
			GO:0050992	dimethylallyl diphosphate biosynthetic process
			GO:0051745	4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase activity
			GO:0004594	pantothenate kinase activity
			GO:0015074	DNA integration
			GO:0004784	superoxide dismutase activity
			GO:0006801	superoxide metabolic process
<b>Unique to BO+SV+HH</b>	GO:0008948	oxaloacetate decarboxylase activity	GO:0046873	metal ion transmembrane transporter activity
	GO:0015081	sodium ion transmembrane transporter activity	GO:0005506	iron ion binding
	GO:0071436	sodium ion export		
	GO:0016829	lyase activity		
	GO:0008654	phospholipid biosynthetic process		
<i>S. variabile</i> DSM 15176 <sup>T</sup> perspective				
	Enriched GO terms		Depleted GO terms	
<b>Common between BO+SV+HH and BO+SV</b>	GO:0003735	structural constituent of ribosome	GO:0043565	sequence-specific DNA binding
	GO:0006412	translation	GO:0006355	regulation of transcription, DNA-templated
	GO:0005840	ribosome	GO:0003700	transcription factor activity, sequence-specific DNA binding
	GO:0005622	intracellular	GO:0005975	carbohydrate metabolic process
	GO:0004812	aminoacyl-tRNA ligase activity	GO:0055114	oxidation-reduction process
	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	GO:0016491	oxidoreductase activity
	GO:0016021	integral component of membrane	GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds
	GO:0055085	transmembrane transport	GO:0006064	glucuronate catabolic process
	GO:0000166	nucleotide binding	GO:0000160	phosphorelay signal transduction system
	GO:0006418	tRNA aminoacylation for protein translation	GO:0045454	cell redox homeostasis
	GO:0030246	carbohydrate binding	GO:0008927	mannonate dehydratase activity
	GO:0042173	regulation of sporulation resulting in formation of a cellular spore		
<b>Unique to BO+SV+HH</b>	GO:0006614	SRP-dependent cotranslational protein targeting to membrane	GO:0006281	DNA repair
	GO:0009116	nucleoside metabolic process		

	GO:0015986	ATP synthesis coupled proton transport		
	GO:0015078	hydrogen ion transmembrane transporter activity		
	GO:0008184	glycogen phosphorylase activity		
	GO:0006396	RNA processing		
	GO:0006810	transport		
	GO:0006520	cellular amino acid metabolic process		
<b>Unique to BO+SV</b>	GO:0004356	glutamate-ammonia ligase activity	GO:0050662	coenzyme binding
	GO:0003924	GTPase activity	GO:0030288	outer membrane-bounded periplasmic space
	GO:0000049	tRNA binding		
	GO:0009086	methionine biosynthetic process		
	GO:0019888	protein phosphatase regulator activity		
	GO:0030289	protein phosphatase 4 complex		
	GO:0015031	protein transport		
<hr/>				
<b>H. hathewayi DSM 13479<sup>T</sup> perspective</b>				
	Enriched GO terms		Depleted GO terms	
<b>Common between BO+SV+HH and BO+HH</b>	GO:0003735	structural constituent of ribosome	GO:0006810	transport
	GO:0005840	ribosome	GO:0055114	oxidation-reduction process
	GO:0006412	translation	GO:0006777	Mo-molybdopterin cofactor biosynthetic process
	GO:0005622	intracellular	GO:0004134	4-alpha-glucanotransferase activity
	GO:0005525	GTP binding	GO:0016491	oxidoreductase activity
	GO:0004812	aminoacyl-tRNA ligase activity	GO:0045454	cell redox homeostasis
	GO:0015986	ATP synthesis coupled proton transport	GO:0005506	iron ion binding
	GO:0006418	tRNA aminoacylation for protein translation	GO:0008452	RNA ligase activity
	GO:0015078	hydrogen ion transmembrane transporter activity	GO:0009116	nucleoside metabolic process
	GO:0000166	nucleotide binding		
	GO:0045263	proton-transporting ATP synthase complex, coupling factor F(o)		
	GO:0004594	pantothenate kinase activity		
	GO:0016876	ligase activity, forming aminoacyl-tRNA and related compounds		
	GO:0043039	tRNA aminoacylation		
	GO:0016021	integral component of membrane		
	GO:0003924	GTPase activity		
	GO:0006633	fatty acid biosynthetic process		
	GO:0009007	site-specific DNA-methyltransferase (adenine-specific) activity		
	GO:0032775	DNA methylation on adenine		
	GO:0008033	tRNA processing		
<b>Unique to BO+SV+HH</b>	GO:0006400	tRNA modification	GO:0005975	carbohydrate metabolic process
	GO:0015991	ATP hydrolysis coupled proton transport		
	GO:0003899	DNA-directed RNA polymerase activity		
	GO:0006351	transcription, DNA-templated		
	GO:0005328	neurotransmitter:sodium symporter activity		
	GO:0006836	neurotransmitter transport		
	GO:0006855	drug transmembrane transport		
	GO:0015238	drug transmembrane transporter activity		
	GO:0015297	antiporter activity		
	GO:0046933	proton-transporting ATP synthase activity, rotational mechanism		
<b>Unique to BO+HH</b>	GO:0009002	serine-type D-Ala-D-Ala carboxypeptidase activity	GO:0015558	p-aminobenzoyl-glutamate uptake transmembrane transporter activity
	GO:0006164	purine nucleotide biosynthetic process	GO:1902604	p-aminobenzoyl-glutamate transmembrane transport
	GO:0015031	protein transport		

**Table S3.** List of primer sets used for RT-qPCR. All primer sets were designed in this study.

Name	Sequence	Target <sup>a</sup>	
		Gene name	Product
<b><i>B. ovatus</i> ATCC 8483<sup>T</sup></b>			
Bovatus_RS01400_F	CGTTTCTATCTGTGCCGTGG	Bovatus_RS01400	MFS transporter
Bovatus_RS01400_R	TGAGGGCGAACAGGAAGAAT		
Bovatus_RS15290_F	AGACTAACGGCGGACTATGG	Bovatus_RS15290	Glycoside hydrolase family 16 protein
Bovatus_RS15290_R	TCCGCTCTGTTCTCCATTT		
Bovatus_RS15310_F	CTTGTGGCTTCGCTTACTCC	Bovatus_RS15310	Beta-glucosidase
Bovatus_RS15310_R	CCCCTTGTCCAGTACCCAT		
Bovatus_RS21310_F	GTCTTGGAGCGGCAGTAATG	Bovatus_RS21310	PTS sugar transporter subunit IIC
Bovatus_RS21310_R	GAGCAATGCCGTCCTACTG		
Bovatus_RS06075_F	GGGAGCTAATCAAAGGCCGG	Bovatus_RS06075	ABC transporter ATP binding protein
Bovatus_RS06075_R	GGGCAATCGTTGTTTTCCCT		
Bovatus_RS09210_F	AGAGTGCTTATCCTCCCTGC	Bovatus_RS09210	Molecular chaperone GroES
Bovatus_RS09210_R	CCGTGACCTATTGCCACAAC		
Bovatus_RS03700_F	CGAGGTGGACAAAGTTGGTG	Bovatus_RS03700 <sup>b</sup>	DNA polymerase III subunit delta
Bovatus_RS03700_R	TCTGTTCAGGAGTTACGCGT		
<b><i>S. variable</i> DSM 15176<sup>T</sup></b>			
SUBVAR_RS12285_F	CAGCAGAACATCATCACCGG	SUBVAR_RS12285	Carbohydrate ABC transporter permease
SUBVAR_RS12285_R	CCCGBAATGACGTATACCCA		
SUBVAR_RS12505_F	CTCCGGCTCCATCTATGTGT	SUBVAR_RS12505	PTS beta-glucoside transporter subunit IIBCA
SUBVAR_RS12505_R	GAGGTTGGGGTGGATCATCA		
SUBVAR_RS14140_F	CAACGACAATGTGCTACCCC	SUBVAR_RS14140	Beta-glucosidase
SUBVAR_RS14140_R	CAATCTTCGCTGGTCAGGTG		
SUBVAR_RS14155_F	CTCCCGCATTATCAGGACT	SUBVAR_RS14155	Carbohydrate ABC transporter substrate binding protein
SUBVAR_RS14155_R	CCCTGGAAGTAGTCGCTGAA		
SUBVAR_RS14170_F	TTGAGACCAGCCGCATCTA	SUBVAR_RS14170	Cellobiose phosphorylase
SUBVAR_RS14170_R	TTCATCAAAGTTCGGCGG		
SUBVAR_RS02860_F	TTCAATTTGCCGGATCGTG	SUBVAR_RS02860	CidA/LrgA family protein
SUBVAR_RS02860_R	ACCTGTTCCAGTCTGAGCAA		
SUBVAR_RS02935_F	ACCATCCCAACAAGAAGAG	SUBVAR_RS02935	Molecular chaperone DnaK
SUBVAR_RS02935_R	TTGCTCATGTTGGTGAAGC		
SUBVAR_RS15530_F	CCTACTTTGCGGATCTGGC	SUBVAR_RS15530 <sup>b</sup>	Class D sortase
SUBVAR_RS15530_R	CTCCCCAGCGAACCTTATCA		
<b><i>H. hathewayi</i> DSM 13479<sup>T</sup></b>			
CLOSTHATH_RS01805_F	CCAAGTTTTGCCATACCCC	CLOSTHATH_RS01805	Glucan binding protein
CLOSTHATH_RS01805_R	CAGCCGGTAACCAAATAGCC		
CLOSTHATH_RS19270_F	CGACGACACAGATTCAGCAG	CLOSTHATH_RS19270	Carbohydrate ABC transporter permease
CLOSTHATH_RS19270_R	GGCCGTCATTGTGAAAAAGT		
CLOSTHATH_RS02765_F	GGCGGAAATAAGGAAGCAGG	CLOSTHATH_RS02765	Sugar ABC transporter substrate binding protein
CLOSTHATH_RS02765_R	GTCTCCTTCGTGAAATCGGC		
CLOSTHATH_RS07435_F	CCGCTGGTATTTCTGTACGC	CLOSTHATH_RS07435	Iron ABC transporter permease
CLOSTHATH_RS07435_R	CCTTCGCCGATTAACATGGG		
CLOSTHATH_RS09305_F	CTCTTGGCGTGGATCATGTG	CLOSTHATH_RS09305	Stage III sporulation protein J



CLOSTHATH_RS09305_R	TTCCACGATCGTTCCTGAA		
CLOSTHATH_RS16585_F	ATGCAGTCCATCAGCTCAGT	CLOSTHATH_RS16585	MATE family efflux transporter
CLOSTHATH_RS16585_R	GATACAAAAGCTGCTCCGGG		
CLOSTHATH_RS09845_F	GGCGATGCTGGTGAAAATCT	CLOSTHATH_RS09845 <sup>b</sup>	Sigma 70 family RNA polymerase sigma factor
CLOSTHATH_RS09845_R	CGGAATGGTTCTCTGCTCGA		

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<sup>a</sup> *B. ovatus* ATCC 8483<sup>T</sup>, *S. variabile* DSM 15176<sup>T</sup> and *H. hathewayi* DSM 13479<sup>T</sup> reference genome locus tags, respectively.

<sup>b</sup> Reference genes used for gene expression level normalization.

**Table S4.** Transcriptional level of selected gene targets for *B. ovatus* ATCC 8483<sup>T</sup>, *S. variabile* DSM 15176<sup>T</sup> and *H. hathewayi* DSM 13479<sup>T</sup>, measured by RT-qPCR and RNA-seq. Expression levels of DT genes are indicated as log<sub>2</sub> fold change (Log2FC) for comparison between condition 1 and 2, as indicated in the Table. BO16, BO20, BO24 and BO26 indicate *B. ovatus* pure culture samples at 16, 20, 24 and 26 h, respectively. SV12, SV14, SV16 and SV24 indicate *S. variabile* pure culture samples at 12, 14, 16 and 24 h, respectively. HH06, HH16, HH18, HH20 and HH24 indicate *H. hathewayi* pure culture samples at 6, 16, 18, 20 and 24 h, respectively. BO+SV, BO+HH and BO+SV+HH indicate co-culture samples of *B. ovatus* and *S. variabile*, *B. ovatus* and *H. hathewayi*, and *B. ovatus*, *S. variabile* and *H. hathewayi*, respectively. RT-qPCR values are means of all the biological replicates, and for each biological replicate three technical replicates were measured, ± SEM (standard error of the mean).

		<i>Bacteroides ovatus</i> ATCC 8483 <sup>T</sup>														
		Pure culture						Co-culture								
		BO16 vs. BO20		BO16 vs. BO26		BO+HH vs. BO24		BO+SV vs. BO24		BO+SV+HH vs. BO24						
		RT-qPCR		RNA-seq results		RT-qPCR		RNA-seq results		RT-qPCR		RNA-seq results				
Mean Log2FC		SEM		Mean Log2FC		SEM		Mean Log2FC		SEM		Mean Log2FC		SEM		
MFS transporter	Bovatus_RS01400	-1.065	0.093	-1.668	-1.373	0.081	-1.659		0.998	0.241	1.049					
Glycoside hydrolase family 16 protein	Bovatus_RS15290	4.080	0.327	3.786	7.016	0.600	7.074	7.562	0.807	6.695			6.363	0.221	5.395	
Beta glucosidase	Bovatus_RS15310	2.911	0.382	2.542	7.491	0.841	6.996	7.742	0.677	6.862	1.995	1.203	1.345	7.025	0.606	6.159
PTS sugar transporter subunit IIC	Bovatus_RS21310	1.424	0.145	1.203				1.099	0.318	1.069	1.937	0.302	2.006	1.541	0.071	1.886
ABC transporter ATP binding protein	Bovatus_RS06075							1.688	0.050	4.486				2.020	0.139	4.892
Molecular chaperone GroES	Bovatus_RS09210										1.749	0.512	1.919	1.061	0.423	1.389
		<i>Subdoligranulum variabile</i> DSM 15176 <sup>T</sup>														
		Pure culture						Co-culture								
		SV12 vs. SV14		SV12 vs. SV16		BO+SV vs. SV24		BO+SV+HH vs. SV24								
		RT-qPCR		RNA-seq results		RT-qPCR		RNA-seq results		RT-qPCR		RNA-seq results				
Mean Log2FC		SEM		Mean Log2FC		SEM		Mean Log2FC		SEM		Mean Log2FC		SEM		

Carbohydrate ABC transporter permease	SUBVAR_RS12285	1.728	0.184	1.487	1.561	0.076	1.109	-2.169	1.116	-2.595	-1.853	0.384	-2.442
PTS beta glucosidase transporter subunit IIBCA	SUBVAR_RS12505	2.215	0.138	2.126	2.659	0.020	2.497	-6.686	1.059	-7.116	-6.166	0.031	-5.950
Beta glucosidase	SUBVAR_RS14140							2.158	0.954	1.712	2.079	0.295	1.804
Carbohydrate ABC transporter substrate binding protein	SUBVAR_RS14155							2.283	0.321	1.549	2.771	0.268	1.911
Cellobiose phosphorylase	SUBVAR_RS14170							3.220	0.135	2.020	3.590	0.147	2.785
CidA/LrgA family protein	SUBVAR_RS02860							4.123	0.002	4.617	4.260	0.174	3.864
Molecular chaperone DnaK	SUBVAR_RS02935							-3.367	0.216	-3.404	-2.655	0.109	-3.737

***Hungatella hathewayi* DSM 13479<sup>T</sup>**

		Pure culture									Co-culture					
		HH06 vs. HH16			HH06 vs. HH18			HH06 vs. HH20			BO+HH vs. HH24			BO+SV+HH vs. HH24		
		RT-qPCR		RNA-seq results	RT-qPCR		RNA-seq results	RT-qPCR		RNA-seq results	RT-qPCR		RNA-seq results	RT-qPCR		RNA-seq results
		Mean Log2FC	SEM	Log2FC	Mean Log2FC	SEM	Log2FC	Mean Log2FC	SEM	Log2FC	Mean Log2FC	SEM	Log2FC	Mean Log2FC	SEM	Log2FC
Glucan binding protein	CLOSTHATH_RS01805	1.647	0.243	1.643	2.141	0.261	1.805	2.557	0.235	2.099						
Carbohydrate ABC transporter permease	CLOSTHATH_RS19270	-5.370	0.406	-7.013	-5.611	0.006	-7.289	-4.785	0.121	-6.755						
Sugar ABC transporter substrate binding protein	CLOSTHATH_RS02765	4.447	0.503	3.820	5.502	0.271	4.728	5.807	0.550	4.754	3.832	0.876	3.566	3.686	1.340	3.317
Iron ABC transporter permease	CLOSTHATH_RS07435	4.729	0.123	4.872	6.537	0.214	7.646	5.683	0.705	6.126	-2.157	0.156	-4.349	-1.319	0.039	-1.642
Stage III sporulation protein J	CLOSTHATH_RS09305	-1.497	0.029	-1.472	-1.534	0.325	-1.687	-1.227	0.152	-1.583	2.431	0.346	2.339	2.725	0.207	2.469
MATE family efflux transporter	CLOSTHATH_RS16585	-1.051	0.040	-1.405	-1.098	0.123	-1.911	-0.879	0.087	-1.868	1.534	0.987	2.291	1.276	0.698	2.084