

**Supplemental material for Heinken, A. and Thiele, I.**

**Supplemental Results**

**Supplemental Tables S1, S3-S7**

**Supplemental Figures S1-S7**

## Supplemental Results

### Correlation between metabolic distances between microbes and microbe-microbe interactions

Under the expectation that metabolic distance would correlate with giver/consumer interactions and inversely correlate with competitive interactions, we plotted the Jaccard reaction and metabolite distance scores (determined in Ref. <sup>1</sup>) against the percentage of interactions for each pair (Figure S2). However, we found that reaction and metabolite distance could only poorly explain the giver/consumer, mutualistic, or competitive interaction displayed per pair (Figure S2). The correlations between the reaction and metabolite distances and the percentages of giver/consumer relationships were 36% and 32%, respectively (Figure S2a-b). For competitive relationships, the correlation was 35% for the reaction distance and 31% for the metabolite distance (Figure S2c-d). Accordingly, we found differences in the predicted behavior between the *E. coli* MG1655 and the *E. coli* O157:H7 strains despite reaction and metabolite distance scores of 0.03 or less between the three *E. coli* strains (Figure 1c, Figure S2). We conclude that metabolic proximity does not provide an adequate explanation for the capability of certain pairs to engage in commensal, mutualistic, or competitive interactions. The more likely explanation for the observed species-specific differences in interaction type is the metabolic functions encoded in the bacterial genomes. It should be noted, however, that the observed low metabolic proximity between most of the 11 microbes is partly due to reconstruction bias, which leads to the inclusion or omission of certain pathways.

## Supplemental Tables

**Table S1:** Description of the included reconstructions and the reconstructed species. Modifications to the reconstructions are described in Ref. <sup>1</sup>.

Reconstructed Organism	Type	NCBI Taxonomy ID	Reconstruction Version	Reactions	Metabolites	Genes	Ref.
<i>Bacteroides thetaiotaomicron</i> VPI-5482	Commensal	226186	iAH991	1528	1176	993	<sup>2</sup>
<i>Faecalibacterium prausnitzii</i> A2-165	Commensal	411483	iFpraus_v1.0	1030	833	602	<sup>3</sup>
<i>Escherichia coli</i> str. K-12 substr. MG1655	Commensal	511145	iEco1339_Mg1655	2428	1705	1338	<sup>4</sup>
<i>Lactobacillus plantarum</i> WCFS1	Probiotic	220668	Unnamed	777	662	724	<sup>5</sup>
<i>Lactococcus lactis</i> subsp. cremoris MG1363	Probiotic	416870	Unnamed	751	650	518	<sup>6</sup>
<i>Streptococcus thermophilus</i> LMG 18311	Probiotic	264199	Unnamed	556	549	422*	<sup>7</sup>
<i>Helicobacter pylori</i> 26695	Opportunistic Pathogen	85962	iIT341	555	485	339	<sup>8</sup>
<i>Klebsiella pneumoniae</i> MGH 78578	Opportunistic Pathogen	1328388	iYL1228	2262	1658	1229	<sup>9</sup>
<i>Salmonella enterica</i> subsp. typhimurium LT2	Pathogen	99287	STM_v1.0	2623	1864	1288	<sup>10</sup>
<i>Escherichia coli</i> O157:H7 strain Sakai	Pathogen	386585	iEco1345_Sakai	2372	1688	1345	<sup>4</sup>
<i>Escherichia coli</i> O157:H7 strain EDL933	Pathogen	155864	iEco1344_EDL933	2376	1686	1344	<sup>4</sup>
Homo sapiens (small intestinal enterocyte)	Host	9606	hs_sIEC611	1282	844	611	<sup>11</sup>

**Table S3:** Uptake constraints on external exchanges in the framework implemented to simulate the three *in silico* dietary regimes (Figure 2b).

Metabolite type/ BiGG ID	Metabolite	Uptake rate (mmol*gDW <sup>-1</sup> * hr <sup>-1</sup> )		
		Adjusted to carbons per molecule		
Simple sugars and starch		Western diet	High fiber diet	Protein diet
fru	Fructose	0.29486781	0.0625	0.15625
glc	Glucose	0.29486781	0.0625	0.15625
gal	Galactose	0.29486781	0.0625	0.15625
man	Mannose	0.29486781	0.0625	0.15625
lcts	Lactose	0.14743391	0.03125	0.078125
malt	Maltose	0.14743391	0.03125	0.078125
sucr	Sucrose	0.14743391	0.03125	0.078125
melib	Melibiose	0.14743391	0.03125	0.078125
strch1	Soluble starch	0.21444932	0.04545455	0.11363636
Fiber		Western diet	High fiber diet	Protein diet
inulin	Inulin	0.00078365	0.01527778	0.00694444
levan1000	Levan	2.351E-05	0.00045833	0.00020833
starch1200	Insoluble starch	1.9591E-05	0.00038194	0.00017361
arabinogal	Arabinogalactan	3.6528E-05	0.00071214	0.0003237
pect	Pectins	5.5644E-05	0.00108481	0.0004931
pullulan1200	Pullulan	1.9591E-05	0.00038194	0.00017361
amylose300	Amylose	7.8365E-05	0.00152778	0.00069444
lmn30	Laminarin	0.00078365	0.01527778	0.00694444
raffin	Raffinose	0.00783653	0.15277778	0.06944444
stys	Stachyose	0.0058774	0.11458333	0.05208333
oligofru4	Oligofructose	0.0058774	0.11458333	0.05208333
dextran40	Dextran	0.00029387	0.00572917	0.00260417
Fat		Western diet	High fiber diet	Protein diet
arachd	Arachidonic acid	0.00386729	0.00220988	0.00220988
chsterol	Cholesterol	0.00575975	0.00329129	0.00329129
glyc	Glycerol	2.09119895	1.19497083	1.19497083
hdca	Hexadecanoic acid	0.46058299	0.26319028	0.26319028
hdcea	Hexadecenoic acid	0.04243272	0.02424727	0.02424727
lnlc	linoleic acid (all cis C18:2) n-6	0.41728993	0.23845139	0.23845139

lnlnca	alpha-Linolenic acid, C18:3, n-3	0.02041092	0.01166338	0.01166338
lnlncg	gamma-linolenic acid	0.02041092	0.01166338	0.01166338
ocdca	octadecanoate (n-C18:0)	0.19670876	0.112405	0.112405
ocdcea	octadecenoate (n-C18:1)	0.79184823	0.4524847	0.4524847
octa	octanoate (n-C8:0)	0.01503944	0.00859397	0.00859397
ttдца	tetradecanoate (n-C14:0)	0.07979793	0.04559882	0.04559882
<b>Protein</b>		<b>Western diet</b>	<b>High fiber diet</b>	<b>Protein diet</b>
ala-L	L-alanine	0.3	0.3	0.6
arg-L	L-arginine	0.15	0.15	0.3
glu-L	L-glutamate	0.18	0.18	0.36
gly	Glycine	0.45	0.45	0.9
ile-L	L-isoleucine	0.15	0.15	0.3
leu-L	L-leucine	0.15	0.15	0.3
lys-L	L-lysine	0.15	0.15	0.3
met-L	L-methionine	0.18	0.18	0.36
pro-L	L-proline	0.18	0.18	0.36
asn-L	L-asparagine	0.225	0.225	0.45
asp-L	L-aspartate	0.225	0.225	0.45
his-L	L-histidine	0.15	0.15	0.3
phe-L	L-phenylalanine	0.099	0.099	0.198
ser-L	L-serine	0.3	0.3	0.6
thr-L	L-threonine	0.225	0.225	0.45
trp-L	L-tryptophan	0.081	0.081	0.162
tyr-L	L-tyrosine	0.099	0.099	0.198
gln-L	L-glutamine	0.18	0.18	0.36
val-L	L-valine	0.18	0.18	0.36
cys-L	L-cysteine	0.3	0.3	0.6
<b>Vitamins/ minerals/ other</b>		<b>Western diet</b>	<b>High fiber diet</b>	<b>Protein diet</b>
adocbl	Adenosylcobalamin	1	1	1
avite1	alpha-Tocopherol	1	1	1
ca2	Calcium	1	1	1
cbl1	Cob(I)alamin	1	1	1
chol	Choline	1	1	1

cl	Chloride	1	1	1
cobalt2	Co <sup>2+</sup>	1	1	1
cu2	Cu <sup>2+</sup>	1	1	1
fe2	Fe <sup>2+</sup>	1	1	1
fe3	Fe <sup>3+</sup>	1	1	1
fe3dcit	Fe(III)dicitrate	1	1	1
fol	Folate	1	1	1
h2s	Hydrogen sulfide	1	1	1
k	potassium	1	1	1
mg2	magnesium	1	1	1
mn2	Mn <sup>2+</sup>	1	1	1
mobd	Molybdate	1	1	1
mqn8	Menaquinone 8	1	1	1
na1	Sodium	1	1	1
nac	Nicotinate	1	1	1
orot	Orotate	1	1	1
pHEME	Protoheme	1	1	1
phyQ	Phylloquinone	1	1	1
pime	Pimelate	1	1	1
pnto-R	(R)-Pantothenate	1	1	1
pydam	Pyridoxamine	1	1	1
pydx	Pyridoxal	1	1	1
pydxn	Pyridoxine	1	1	1
retinol	Retinol	1	1	1
ribflv	Riboflavin	1	1	1
sel	Selenate	1	1	1
so4	Sulfate	1	1	1
spmd	Spermidine	1	1	1
thf	5,6,7,8-Tetrahydrofolate	1	1	1
thm	Thiamin	1	1	1
vitd3	Vitamin D3	1	1	1
zn2	Zinc	1	1	1

**Table S4:** Pareto frontiers for 55 pairs on 12 scenarios grouped into four types (total n = 600). Type 1: Microbes benefit the other microbe at low growth rates but compete at higher growth rates; Type 2: Microbe benefit each other even at highest possible growth rates; Type 3: Only one microbe benefits the other at low growth rates but competes at high growth rates; Type 4: The microbes compete at every possible growth tradeoff. Examples for the four types are shown in Figure 2. WD = Western diet, HFD = high fiber diet, PD = protein diet, sIEC = small intestinal enterocyte.

Scenario		Type 1	Type 2	Type 3	Type 4	Total	
- O <sub>2</sub>	- sIEC	WD	16	5	16	8	45
		HFD	9	5	21	10	45
		PD	18	5	13	9	45
	+ sIEC	WD	18	0	10	17	45
		HFD	8	5	20	12	45
		PD	14	5	12	14	45
+ O <sub>2</sub>	- sIEC	WD	6	0	34	15	55
		HFD	8	0	38	9	55
		PD	24	0	27	4	55
	+ sIEC	WD	5	0	34	16	55
		HFD	6	0	34	15	55
		PD	12	0	32	11	55
<b>Western diet total</b>		45	5	94	56	200	
<b>High fiber diet total</b>		31	10	113	46	200	
<b>Protein diet total</b>		68	10	84	38	200	
<b>Without oxygen total</b>		83	25	92	70	270	
<b>With oxygen total</b>		61	0	199	70	330	
<b>Without sIEC total</b>		81	15	149	55	300	
<b>With sIEC total</b>		63	10	142	85	300	
<b>Total</b>		144	25	291	140	600	

**Table S5:** Growth rates achieved when each microbe is grown alone and linked with enterocyte, as well as simultaneously optimized growth of each microbe-microbe pair with and without the enterocyte.

Scenario	BT	FP	LP	LL	ST	HP	KP	STy	EC	ECs	ECe
<b>Western diet, no oxygen</b>											
Single	0.22	0.13	0.13	0.11	0.07	N/A	0.11	0.10	0.16	0.14	0.14
With IEC	0.26	0.18	0.29	0.21	0.26	N/A	0.22	0.22	0.28	0.26	0.26
With BT	N/A	0.04	0.58	0.19	0.19	N/A	0.08	0.14	0.03	0.03	0.03
With FP	0.31	N/A	0.29	0.19	0.14	N/A	0.21	0.35	0.46	0.42	0.42
With LP	0.18	0.04	N/A	0.01	0.14	N/A	0.22	0.23	0.32	0.28	0.28
With LL	0.10	0.03	0.14	N/A	0.10	N/A	0.09	0.12	0.15	0.13	0.13
With ST	0.09	0.08	0.01	0.04	N/A	N/A	0.01	0.01	0.02	0.04	0.04
With KP	0.21	0.05	0.22	0.09	0.17	N/A	N/A	0.12	0.14	0.12	0.12
With STy	0.18	0.07	0.23	0.02	0.15	N/A	0.01	N/A	0.16	0.13	0.13
With EC	0.34	0.03	0.32	0.02	0.29	N/A	0.001	0.004	N/A	0.01	0.03
With ECs	0.32	0.05	0.28	0.02	0.15	N/A	0.01	0.01	0.14	N/A	0.06
With ECe	0.32	0.05	0.28	0.02	0.15	N/A	0.01	0.01	0.14	0.07	N/A
With BT/ IEC	N/A	0.05	0.59	0.20	0.25	N/A	0.07	0.13	0.02	0.03	0.03
With FP/ IEC	0.37	N/A	0.37	0.24	0.31	N/A	0.18	0.44	0.55	0.48	0.48
With LP/ IEC	0.17	0.05	N/A	0.003	0.21	N/A	0.35	0.37	0.35	0.28	0.28
With LL/ IEC	0.15	0.03	0.30	N/A	0.25	N/A	0.18	0.24	0.27	0.25	0.25
With ST/ IEC	0.11	0.04	0.11	0.05	N/A	N/A	0.04	0.01	0.08	0.07	0.07
With KP/ IEC	0.28	0.14	0.38	0.16	0.29	N/A	N/A	0.22	0.27	0.25	0.25
With STy/ IEC	0.23	0.08	0.39	0.04	0.31	N/A	0.02	N/A	0.28	0.25	0.25
With EC/ IEC	0.39	0.05	0.45	0.04	0.29	N/A	0.001	0.004	N/A	0.01	0.03
With ECs/ IEC	0.36	0.04	0.44	0.04	0.27	N/A	0.001	0.001	0.27	N/A	0.13
With ECe/ IEC	0.36	0.04	0.44	0.04	0.27	N/A	0.001	0.001	0.25	0.13	N/A
Scenario	BT	FP	LP	LL	ST	HP	KP	STy	EC	ECs	ECe
<b>High fiber diet, no oxygen</b>											
Single	0.44	0.07	0.04	0.04	0.02	N/A	0.04	0.04	0.06	0.05	0.05
With IEC	0.45	0.11	0.10	0.09	0.11	N/A	0.08	0.09	0.12	0.10	0.10
With BT	N/A	0.38	0.71	0.28	0.35	N/A	0.13	0.19	0.44	0.42	0.42
With FP	0.12	N/A	0.13	0.06	0.06	N/A	0.06	0.19	0.41	0.21	0.21
With LP	0.11	0.02	N/A	0.01	0.04	N/A	0.08	0.10	0.14	0.10	0.10
With LL	0.23	0.05	0.04	N/A	0.05	N/A	0.03	0.05	0.06	0.05	0.05
With ST	0.20	0.04	0.01	0.01	N/A	N/A	0.01	0.01	0.02	0.01	0.01
With KP	0.38	0.06	0.08	0.03	0.05	N/A	N/A	0.04	0.05	0.03	0.03
With STy	0.31	0.02	0.10	0.01	0.06	N/A	0.01	N/A	0.06	0.04	0.04
With EC	0.08	0.07	0.14	0.01	0.17	N/A	0.001	0.01	N/A	0.01	0.001
With ECs	0.10	0.03	0.10	0.01	0.06	N/A	0.01	0.01	0.05	N/A	0.02
With ECe	0.10	0.03	0.10	0.01	0.06	N/A	0.01	0.01	0.05	0.02	N/A



Scenario	BT	FP	LP	LL	ST	HP	KP	STy	EC	ECs	ECe
With BT/ IEC	N/A	0.27	0.73	0.31	0.39	N/A	0.10	0.16	0.24	0.05	0.05
With FP/ IEC	0.30	N/A	0.18	0.09	0.17	N/A	0.09	0.28	0.50	0.28	0.28
With LP/ IEC	0.10	0.03	N/A	0.004	0.11	N/A	0.18	0.21	0.27	0.22	0.22
With LL/ IEC	0.24	0.06	0.11	N/A	0.12	N/A	0.07	0.10	0.12	0.10	0.10
With ST/ IEC	0.21	0.03	0.01	0.003	N/A	N/A	0.01	0.01	0.01	0.01	0.01
With KP/ IEC	0.43	0.08	0.18	0.06	0.13	N/A	N/A	0.09	0.12	0.10	0.10
With STy/ IEC	0.40	0.05	0.21	0.01	0.13	N/A	0.01	N/A	0.12	0.10	0.10
With EC/ IEC	0.34	0.09	0.27	0.01	0.17	N/A	0.001	0.01	N/A	0.01	0.001
With ECs/ IEC	0.51	0.04	0.22	0.01	0.13	N/A	0.001	0.001	0.11	N/A	0.09
With ECe/ IEC	0.51	0.04	0.22	0.01	0.13	N/A	0.001	0.001	0.12	0.01	N/A
Scenario	BT	FP	LP	LL	ST	HP	KP	STy	EC	ECs	ECe
<b>Protein diet, no oxygen</b>											
Single	0.24	0.10	0.08	0.07	0.05	N/A	0.07	0.07	0.10	0.09	0.09
With IEC	0.29	0.14	0.18	0.14	0.19	N/A	0.14	0.15	0.19	0.17	0.17
With BT	N/A	0.03	0.88	0.11	0.24	N/A	0.03	0.04	0.03	0.02	0.02
With FP	0.33	N/A	0.19	0.09	0.12	N/A	0.08	0.28	0.77	0.31	0.31
With LP	0.50	0.03	N/A	0.01	0.09	N/A	0.15	0.18	0.22	0.19	0.19
With LL	0.17	0.07	0.09	N/A	0.10	N/A	0.06	0.09	0.10	0.09	0.09
With ST	0.06	0.05	0.01	0.01	N/A	N/A	0.01	0.05	0.02	0.01	0.01
With KP	0.27	0.10	0.15	0.06	0.10	N/A	N/A	0.08	0.08	0.07	0.07
With STy	0.28	0.02	0.18	0.02	0.06	N/A	0.01	N/A	0.11	0.08	0.08
With EC	0.33	0.20	0.22	0.02	0.27	N/A	0.001	0.01	N/A	0.02	0.001
With ECs	0.31	0.04	0.19	0.02	0.12	N/A	0.01	0.01	0.08	N/A	0.01
With ECe	0.31	0.04	0.19	0.02	0.12	N/A	0.01	0.01	0.09	0.07	N/A
With BT/ IEC	N/A	0.05	0.95	0.11	0.25	N/A	0.03	0.03	0.03	0.03	0.03
With FP/ IEC	0.40	N/A	0.26	0.14	0.25	N/A	0.12	0.38	0.88	0.37	0.37
With LP/ IEC	0.46	0.05	N/A	0.01	0.21	N/A	0.30	0.37	0.42	0.38	0.38
With LL/ IEC	0.22	0.07	0.19	N/A	0.21	N/A	0.12	0.17	0.19	0.17	0.17
With ST/ IEC	0.12	0.03	0.01	0.01	N/A	N/A	0.01	0.02	0.01	0.01	0.01
With KP/ IEC	0.32	0.13	0.30	0.11	0.22	N/A	N/A	0.15	0.19	0.16	0.16
With STy/ IEC	0.34	0.07	0.37	0.02	0.21	N/A	0.01	N/A	0.20	0.17	0.17
With EC/ IEC	0.38	0.22	0.42	0.02	0.27	N/A	0.001	0.01	N/A	0.02	0.001
With ECs/ IEC	0.36	0.05	0.38	0.02	0.23	N/A	0.001	0.004	0.17	N/A	0.16
With ECe/ IEC	0.36	0.05	0.38	0.02	0.23	N/A	0.001	0.004	0.19	0.001	N/A
Scenario	BT	FP	LP	LL	ST	HP	KP	STy	EC	ECs	ECe
<b>Western diet, with oxygen</b>											
Single	0.44	0.17	0.47	0.11	0.09	0.20	0.51	0.43	0.49	0.49	0.49
With IEC	0.45	0.25	0.70	0.21	0.39	0.34	0.51	0.55	0.60	0.51	0.51
With BT	N/A	0.22	0.79	0.33	0.24	0.46	0.57	0.19	0.52	0.52	0.52
With FP	0.28	N/A	0.66	0.12	0.15	0.25	0.53	0.16	0.48	0.48	0.48

Scenario	BT	FP	LP	LL	ST	HP	KP	STy	EC	ECs	ECe
With LP	0.08	0.04	N/A	0.01	0.26	0.13	0.17	0.17	0.08	0.08	0.08
With LL	0.24	0.14	0.52	N/A	0.22	0.07	0.10	0.22	0.09	0.11	0.11
With ST	0.35	0.09	0.27	0.02	N/A	0.31	0.44	0.31	0.28	0.29	0.29
With HP	0.04	0.18	0.50	0.32	0.09	N/A	0.53	0.01	0.48	0.48	0.48
With KP	0.01	0.01	0.70	0.55	0.17	0.01	N/A	0.01	0.01	0.01	0.01
With STy	0.31	0.30	0.60	0.33	0.22	0.45	0.56	N/A	0.48	0.48	0.48
With EC	0.01	0.01	0.79	0.52	0.36	0.01	0.57	0.01	N/A	0.05	0.24
With ECs	0.01	0.01	0.78	0.49	0.34	0.01	0.57	0.01	0.43	N/A	0.24
With ECe	0.01	0.01	0.78	0.49	0.34	0.01	0.57	0.01	0.25	0.25	N/A
With BT/ IEC	N/A	0.12	0.84	0.43	0.36	0.46	0.66	0.29	0.60	0.60	0.60
With FP/ IEC	0.44	N/A	0.74	0.16	0.45	0.21	0.55	0.22	0.60	0.51	0.51
With LP/ IEC	0.05	0.05	N/A	0.002	0.51	0.02	0.06	0.11	0.08	0.04	0.04
With LL/ IEC	0.15	0.15	0.72	N/A	0.45	0.02	0.07	0.22	0.11	0.07	0.07
With ST/ IEC	0.27	0.03	0.29	0.02	N/A	0.20	0.24	0.36	0.31	0.18	0.18
With HP/ IEC	0.02	0.25	0.72	0.36	0.46	N/A	0.54	0.05	0.60	0.51	0.51
With KP/ IEC	0.002	0.001	0.84	0.57	0.49	0.001	N/A	0.001	0.001	0.001	0.001
With STy/ IEC	0.28	0.35	0.88	0.45	0.34	0.52	0.65	N/A	0.60	0.60	0.60
With EC/ IEC	0.001	0.001	0.94	0.63	0.53	0.001	0.65	0.001	N/A	0.27	0.30
With ECs/ IEC	0.002	0.001	0.86	0.56	0.59	0.001	0.57	0.001	0.33	N/A	0.26
With ECe/ IEC	0.002	0.001	0.86	0.56	0.59	0.001	0.57	0.001	0.30	0.26	N/A
Scenario	BT	FP	LP	LL	ST	HP	KP	STy	EC	ECs	ECe
<b>High fiber diet, with oxygen</b>											
Single	0.44	0.08	0.26	0.04	0.02	0.13	0.44	0.33	0.49	0.49	0.49
With IEC	0.45	0.14	0.46	0.09	0.15	0.34	0.51	0.53	0.60	0.51	0.51
With BT	N/A	0.49	0.93	0.60	0.76	0.46	0.57	0.19	0.52	0.52	0.52
With FP	0.01	N/A	0.44	0.05	0.06	0.37	0.53	0.32	0.48	0.48	0.48
With LP	0.01	0.03	N/A	0.01	0.13	0.21	0.33	0.26	0.12	0.13	0.13
With LL	0.05	0.08	0.29	N/A	0.08	0.19	0.29	0.35	0.23	0.32	0.32
With ST	0.09	0.04	0.15	0.01	N/A	0.16	0.42	0.33	0.44	0.44	0.44
With HP	0.04	0.01	0.21	0.19	0.04	N/A	0.07	0.21	0.48	0.48	0.48
With KP	0.01	0.01	0.45	0.29	0.04	0.40	N/A	0.40	0.01	0.05	0.05
With STy	0.31	0.13	0.26	0.01	0.01	0.24	0.07	N/A	0.48	0.48	0.48
With EC	0.01	0.01	0.71	0.34	0.08	0.01	0.57	0.01	N/A	0.24	0.24
With ECs	0.01	0.01	0.69	0.23	0.08	0.01	0.53	0.01	0.25		0.24
With ECe	0.01	0.01	0.69	0.23	0.08	0.01	0.53	0.01	0.25	0.24	
With BT/ IEC	N/A	0.53	0.93	0.60	0.85	0.46	0.66	0.29	0.60	0.60	0.60
With FP/ IEC	0.04	N/A	0.56	0.10	0.22	0.35	0.55	0.40	0.60	0.51	0.51
With LP/ IEC	0.01	0.02		0.003	0.22	0.13	0.18	0.28	0.18	0.10	0.10
With LL/ IEC	0.04	0.08	0.48	N/A	0.20	0.07	0.10	0.48	0.45	0.16	0.16
With ST/ IEC	0.03	0.02	0.28	0.01	N/A	0.38	0.46	0.46	0.49	0.37	0.37

Scenario	BT	FP	LP	LL	ST	HP	KP	STy	EC	ECs	ECe
With HP/ IEC	0.02	0.12	0.47	0.31	0.14	N/A	0.54	0.09	0.60	0.51	0.51
With KP/ IEC	0.002	0.001	0.65	0.53	0.13	0.001	N/A	0.22	0.08	0.001	0.001
With STy/ IEC	0.28	0.17	0.50	0.06	0.10	0.48	0.36	N/A	0.60	0.60	0.60
With EC/ IEC	0.001	0.001	0.77	0.19	0.18	0.001	0.56	0.001	N/A	0.30	0.26
With ECs/ IEC	0.002	0.001	0.75	0.45	0.25	0.001	0.57	0.002	0.30	N/A	0.26
With ECe/ IEC	0.002	0.001	0.75	0.45	0.25	0.001	0.57	0.002	0.33	0.26	N/A
Scenario	BT	FP	LP	LL	ST	HP	KP	STy	EC	ECs	ECe
<b>Protein diet, with oxygen</b>											
Single	0.58	0.12	0.42	0.07	0.06	0.26	0.55	0.53	0.69	0.67	0.67
With IEC	0.63	0.19	0.62	0.14	0.26	0.61	0.69	0.71	0.82	0.79	0.79
With BT	N/A	0.04	0.89	0.25	0.25	0.93	0.56	0.71	0.58	0.69	0.69
With FP	0.59	N/A	0.58	0.09	0.12	0.60	0.62	0.66	0.93	0.80	0.80
With LP	0.50	0.03	N/A	0.01	0.28	0.39	0.63	0.48	0.53	0.55	0.55
With LL	0.40	0.10	0.46	N/A	0.15	0.34	0.40	0.55	0.69	0.67	0.67
With ST	0.40	0.06	0.19	0.01	N/A	0.36	0.50	0.49	0.64	0.62	0.62
With HP	0.07	0.02	0.39	0.34	0.09	N/A	0.08	0.41	0.05	0.05	0.05
With KP	0.21	0.03	0.63	0.40	0.08	0.56	N/A	0.53	0.65	0.63	0.63
With STy	0.10	0.03	0.48	0.02	0.06	0.41	0.08	N/A	0.70	0.67	0.67
With EC	0.32	0.04	0.89	0.02	0.07	0.76	0.09	0.01	N/A	0.01	0.08
With ECs	0.18	0.02	0.85	0.02	0.07	0.73	0.09	0.01	0.68	N/A	0.22
With ECe	0.18	0.02	0.85	0.02	0.07	0.73	0.09	0.01	0.61	0.45	N/A
With BT/ IEC	N/A	0.04	1.08	0.31	0.30	0.93	0.68	0.75	0.51	0.70	0.70
With FP/ IEC	0.69	N/A	0.67	0.13	0.33	0.73	0.68	0.77	1.04	0.88	0.88
With LP/ IEC	0.40	0.03	N/A	0.01	0.46	0.39	0.68	0.64	0.57	0.51	0.51
With LL/ IEC	0.42	0.12	0.62	N/A	0.33	0.28	0.50	0.69	0.81	0.79	0.79
With ST/ IEC	0.42	0.03	0.24	0.02	N/A	0.76	0.57	0.61	0.70	0.68	0.68
With HP/ IEC	0.06	0.01	0.67	0.47	0.23	N/A	0.09	0.31	0.05	0.05	0.05
With KP/ IEC	0.15	0.06	0.82	0.50	0.18	0.73	N/A	0.66	0.77	0.75	0.75
With STy/ IEC	0.13	0.05	0.79	0.03	0.14	0.72	0.10	N/A	0.83	0.80	0.80
With EC/ IEC	0.46	0.07	1.00	0.04	0.17	0.90	0.09	0.01	N/A	0.02	0.001
With ECs/ IEC	0.23	0.03	0.98	0.03	0.16	0.87	0.09	0.002	0.80	N/A	0.26
With ECe/ IEC	0.23	0.03	0.98	0.03	0.16	0.87	0.09	0.002	0.82	0.53	N/A

**Table S6:** Description of the ten recurring metabolite exchanges between pairs predicted for the microbe-microbe pairs, and occurrence by pair. Pairs that did not display any reoccurring exchanges are not shown.

- i) pyruvate/ D-lactate shuttling coupled to NAD<sup>+</sup>/NADH interconversion
- ii) ethanol/ acetaldehyde shuttling coupled to NAD<sup>+</sup>/NADH interconversion
- iii) L-alanine/ L-lactate exchange with pyruvate as an intermediate
- iv) fumarate/ succinate exchange depending on quinol and NAD<sup>+</sup>/NADH
- v) succinate/ malate exchange depending on quinol and FAD/ FADH<sub>2</sub> or NAD<sup>+</sup>/NADH
- vi) glutamate/ citrate exchange depending on transamination
- vii) acetate/ butyrate exchange depending on acetyl-CoA and butyryl-CoA
- viii) acetate/ dihydroxyacetone exchange via pyruvate and acetyl-CoA as intermediates
- ix) threonine/ glycine interconversion via acetaldehyde
- x) 2,3-butandiol/ diacetyl interconversion via R-acetoin

Pair	# scenarios containing crossfeeding exchanges per pair										
	(i) Pyruvate/ D-lactate	(ii) Acetaldehyde/ Ethanol	(iii) L-alanine/ L-lactate	(iv) Fumarate/ Succinate	(v) Malate/ Succinate	(vi) Citrate/ Glutamate	(vii) Acetate/ Butyrate	(viii) Acetate/ Dihydroxyacetone	(ix) Glycine/ Threonine	(x) 2,3-butandiol/ Diacetyl	Total # of scenarios
BTFP				8					7		12
BTLP	8		8						4		12
BTLL			1						1		12
BTST			1								12
BTSTy	5										12
BTEC	1			2							12
BTECs	1			2							12
BTECe	1			2							12
FPLP					12				9		12
FPLL									1		12
FPST						12					12
FPKP					2	1					12
FPSTy				6		7					12
FPEC				8		8	7				12
FPECs				8		8					12



**Table S7:** Co-occurrences of the ten metabolite exchanges described in Table S6 in all 600 pairs grouped by type of interaction. Co-occurring exchanges that were not computed in any pairs are not shown.

Exchange co-occurrences summed up for predicted interactions	Parasitism (n=299)	Commensalism (n=22)	Neutralism (n=1)	Amensalism (n=175)	Competition (n=66)	Mutualism (n=37)
Average # of exchange co-occurrences/ pair	0.29	0.38	0	0.03	0.09	1.05
Pyruvate/ D-lactate + Acetaldehyde/ Ethanol	10	4		2		29
Pyruvate/ D-lactate + L-alanine/ L-lactate	6					1
Pyruvate/ D-lactate + Fumarate/ Succinate	2					
Pyruvate/ D-lactate + Glycine/ Threonine	2					1
Acetaldehyde/ Ethanol + Fumarate/ Succinate	8					
Acetaldehyde/ Ethanol + Malate/ Succinate	3					1
Acetaldehyde/ Ethanol + 2,3-butandiol/ Diacetyl	6				6	
L-alanine/ L-lactate + Acetate/ Dihydroxyacetone	1					
L-alanine/ L-lactate + Glycine/ Threonine	3					1
Fumarate/ Succinate + Citrate/ Glutamate	26	1				2
Fumarate/ Succinate + Acetate/ Butyrate	4	1				2
Fumarate/ Succinate + Glycine/ Threonine	4	1				
Malate/ Succinate + Glycine/ Threonine	7			2		
Citrate/ Glutamate + Acetate/ Butyrate	4	1				2
Citrate/ Glutamate + Acetate/ Dihydroxyacetone	1			1		

## Supplemental Figures

Figure S1: Pareto optimality analysis of all possible pairs in every scenario.

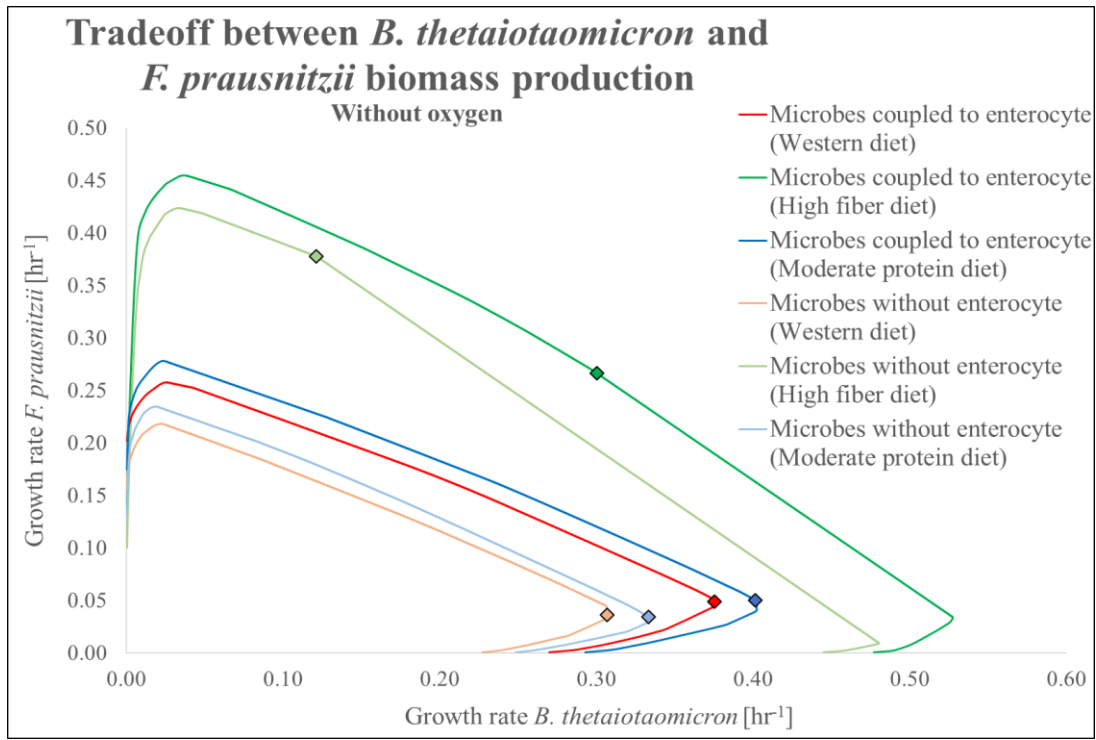


Figure S1.1

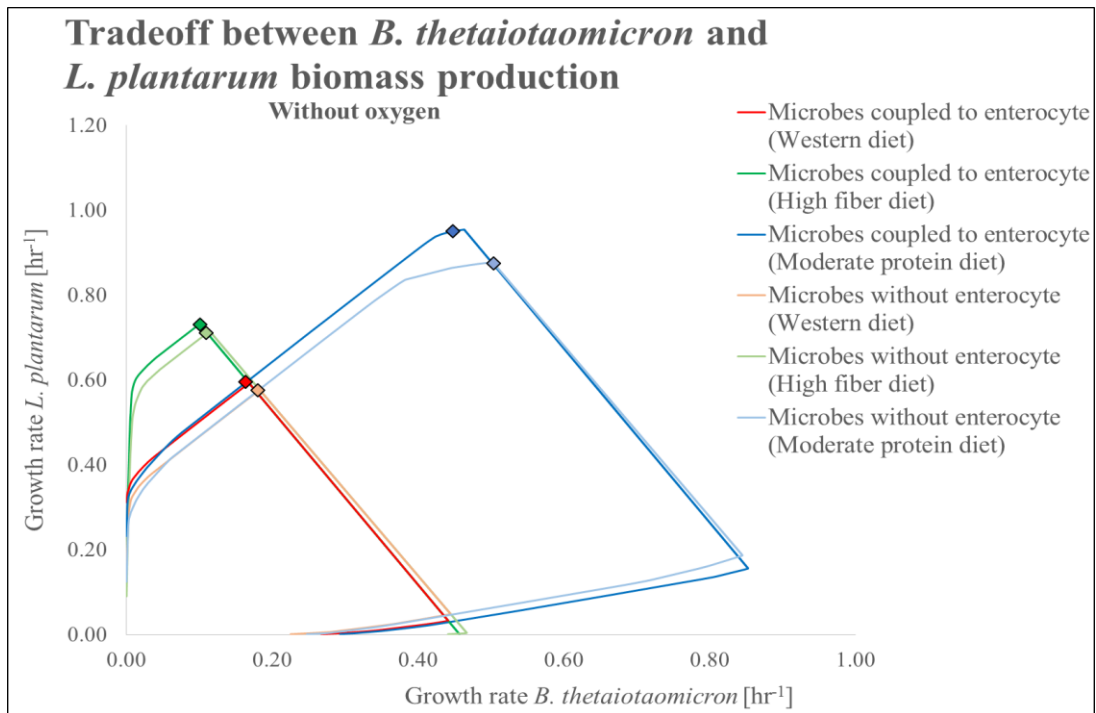


Figure S1.2

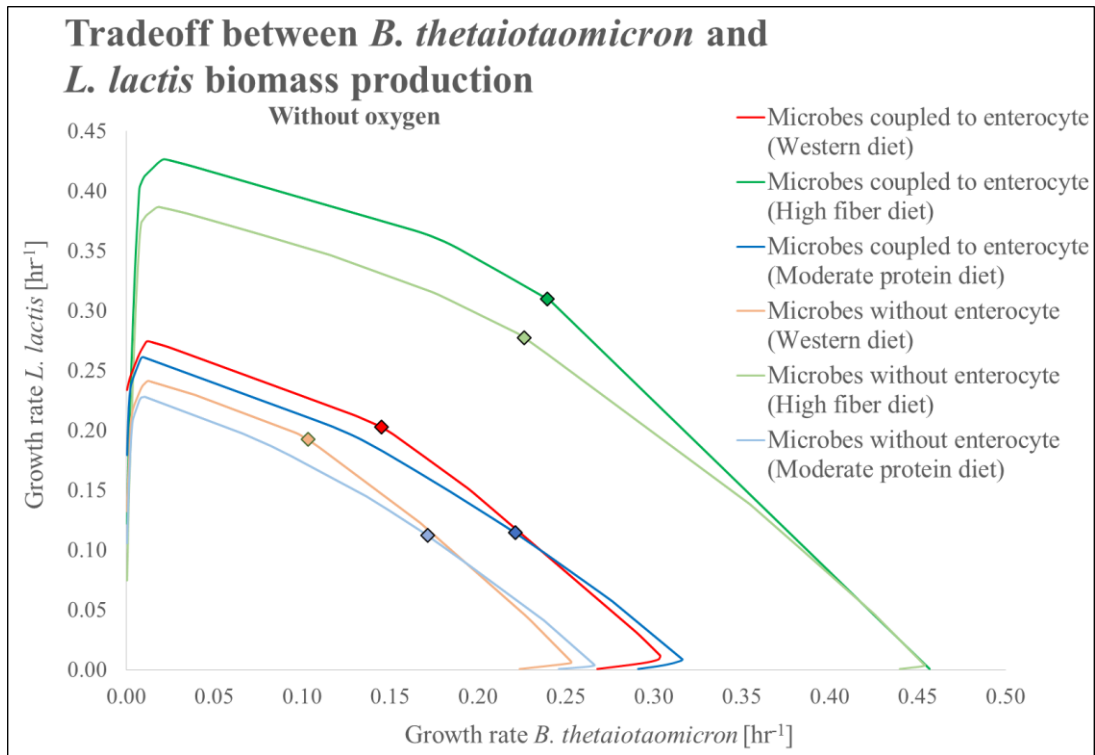


Figure S1.3

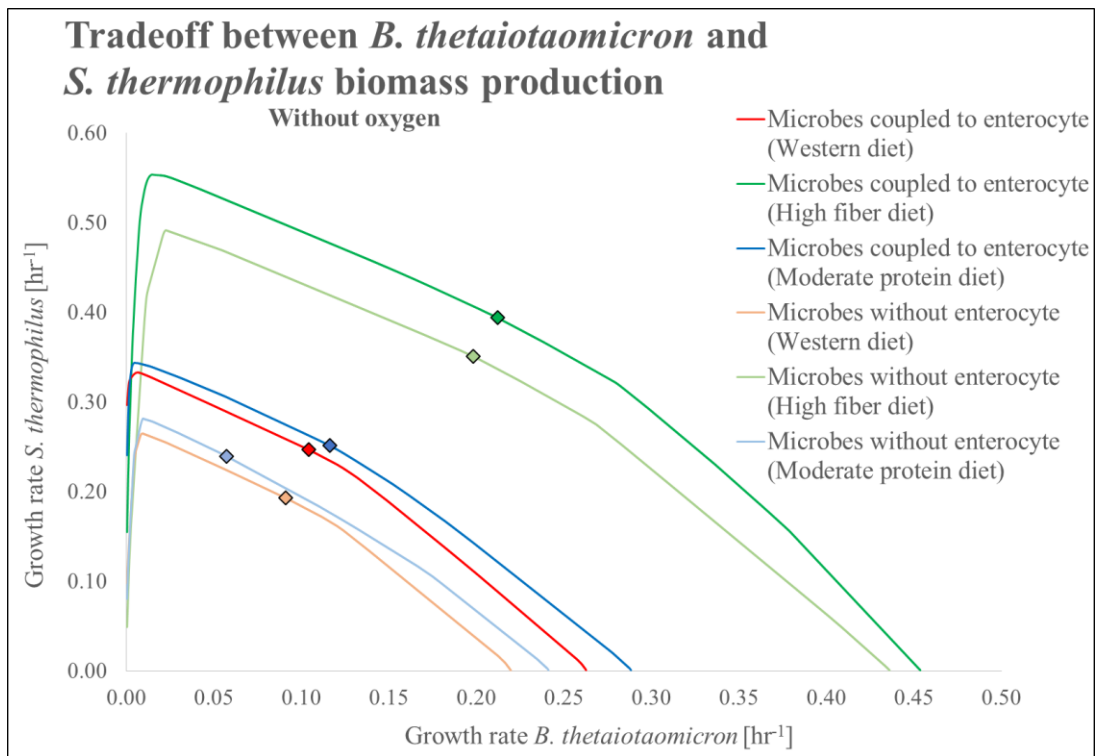


Figure S1.4



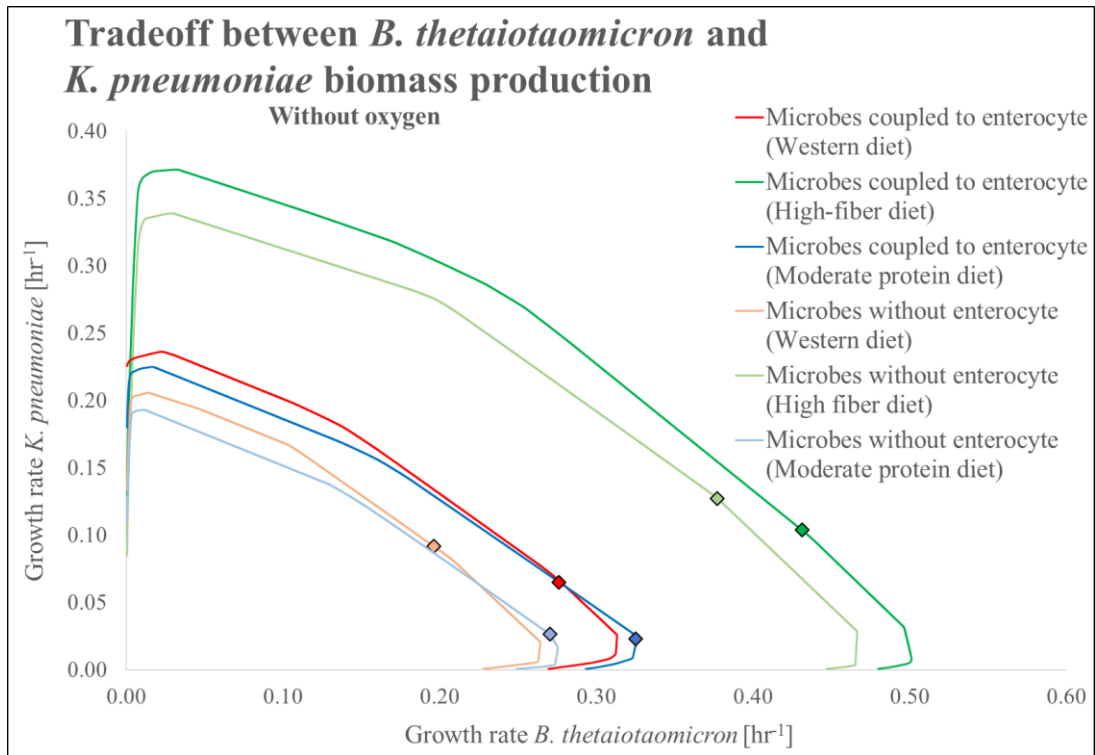


Figure S1.5

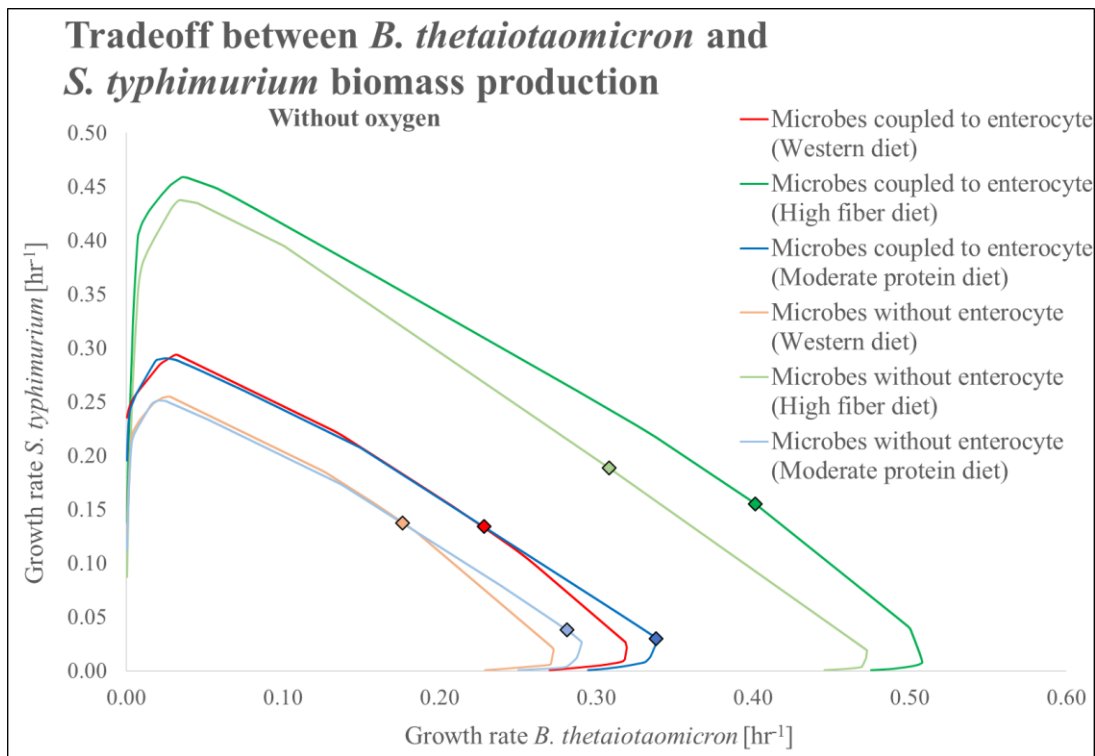


Figure S1.6

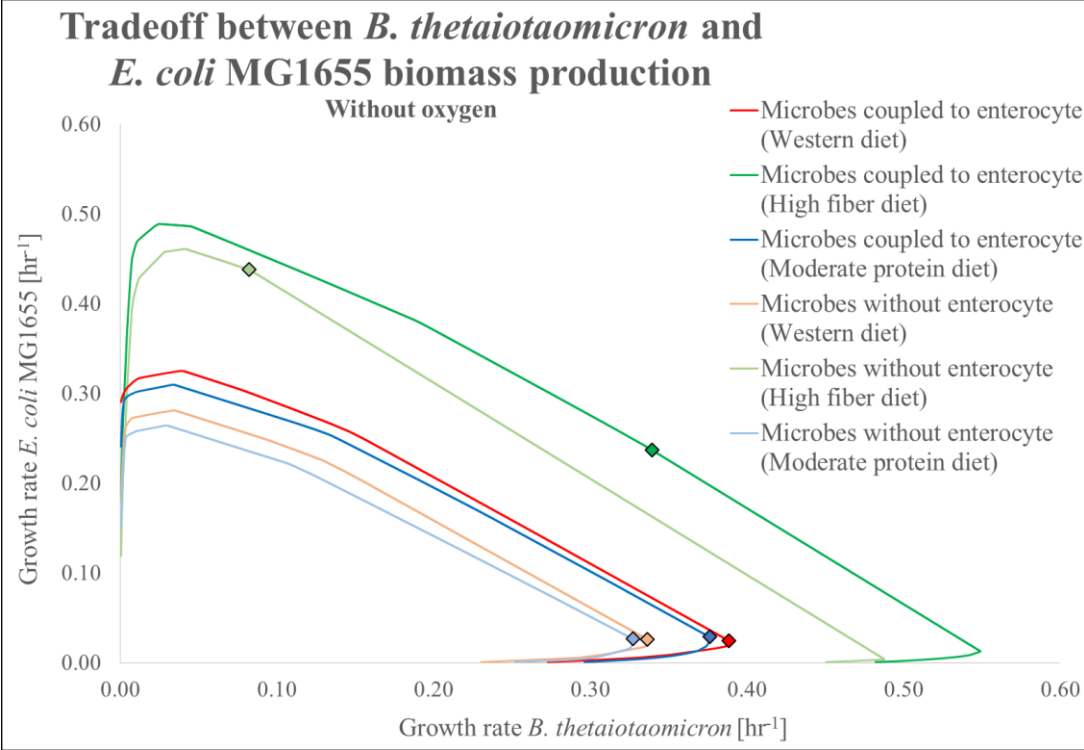


Figure S1.7

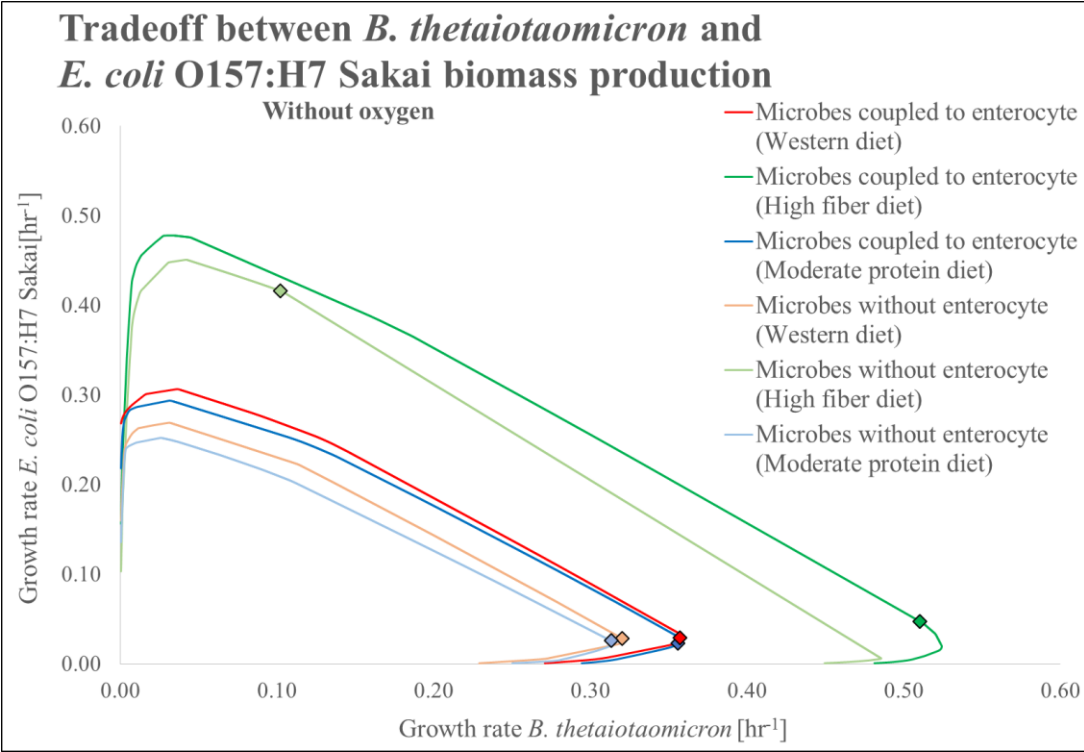


Figure S1.8

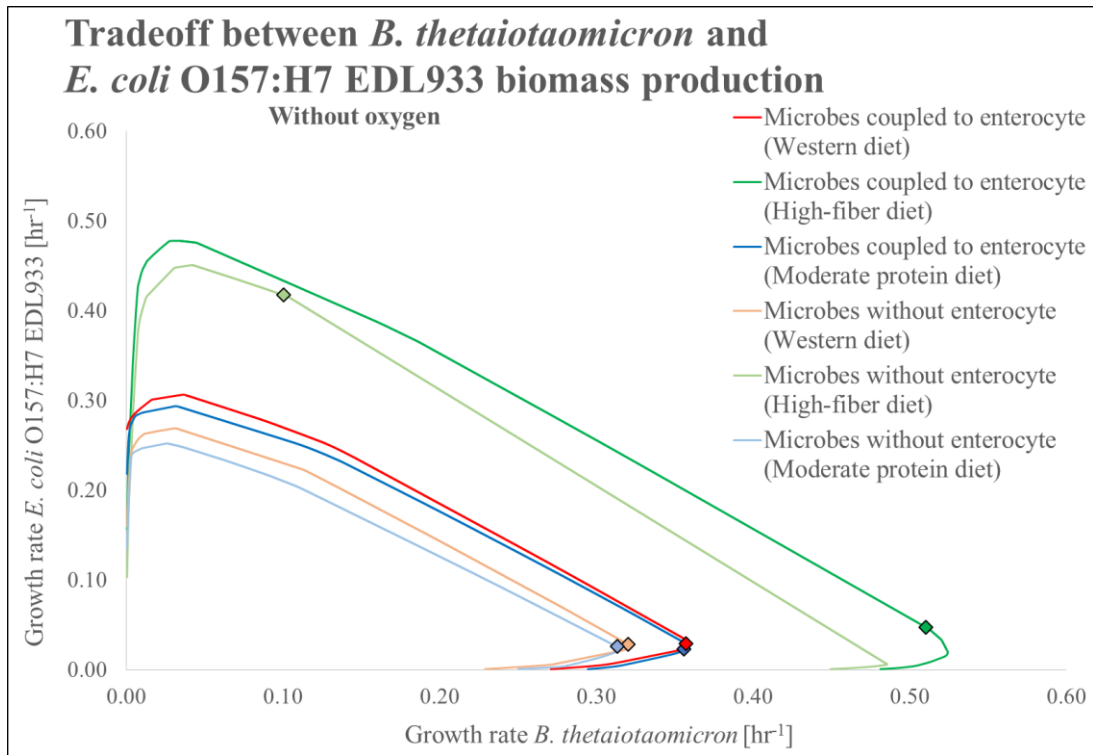


Figure S1.9

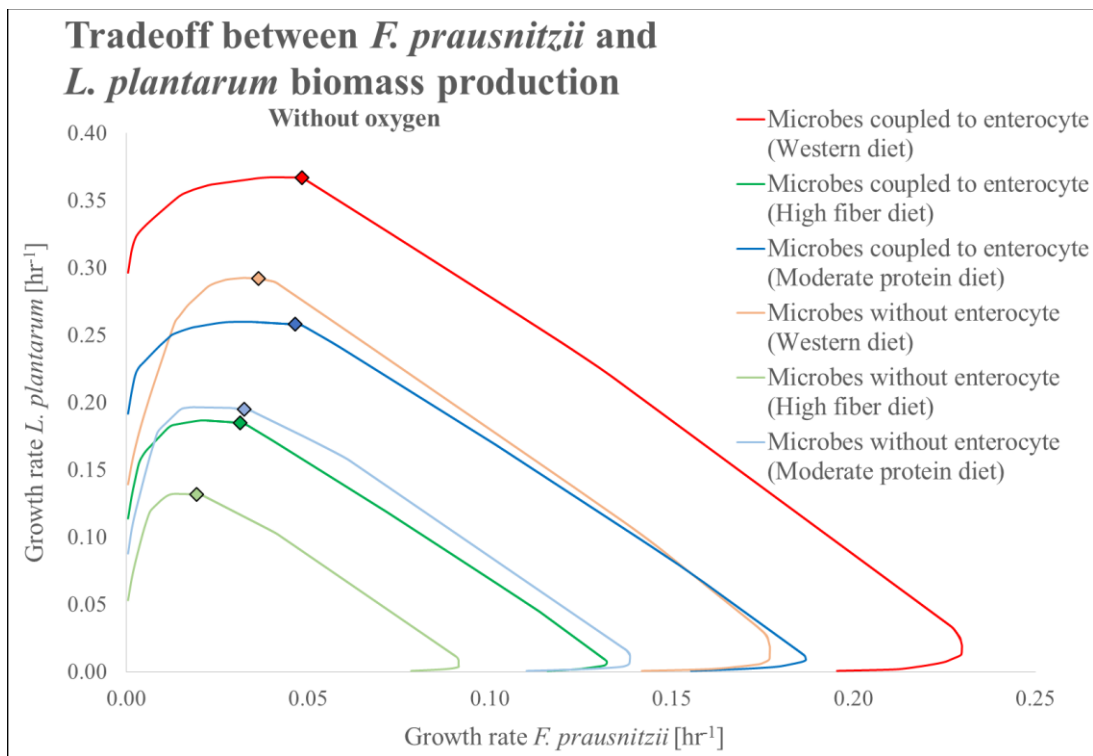


Figure S1.10

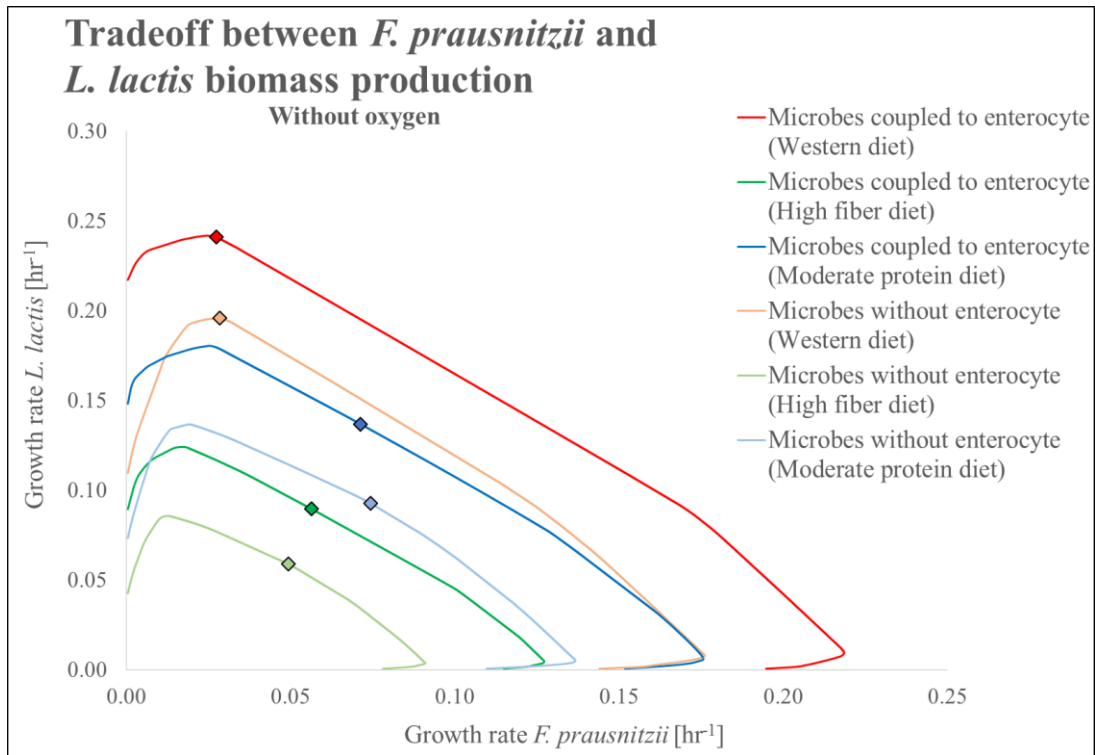


Figure S1.11

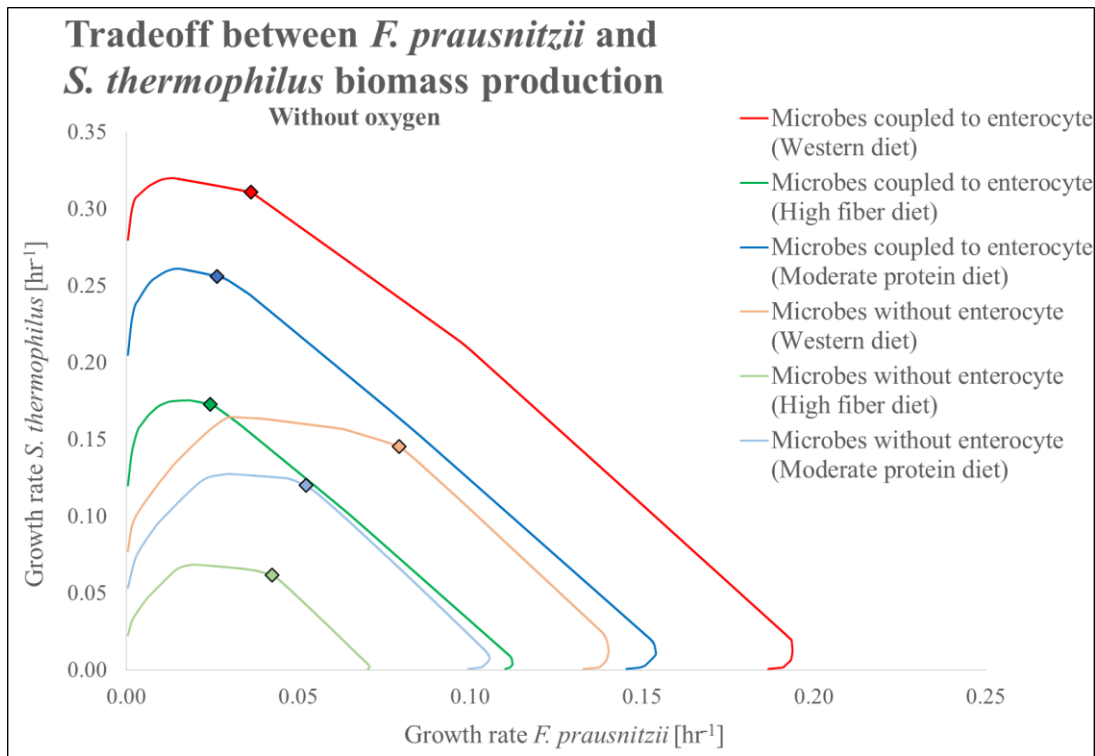


Figure S1.12

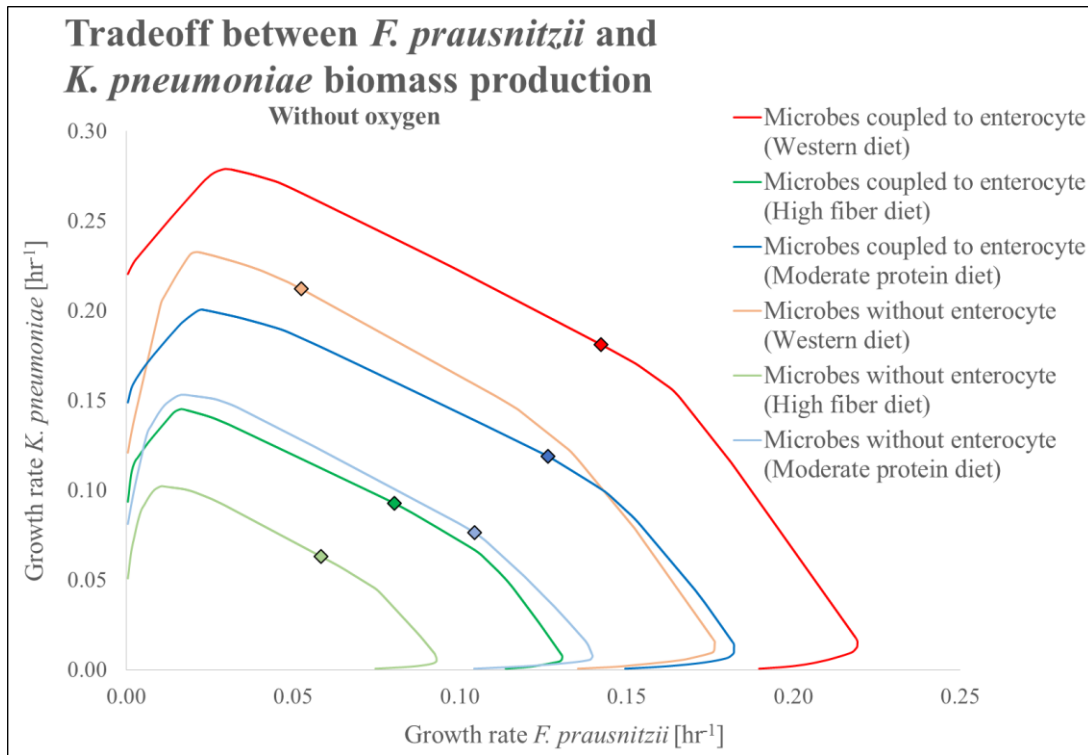


Figure S1.13

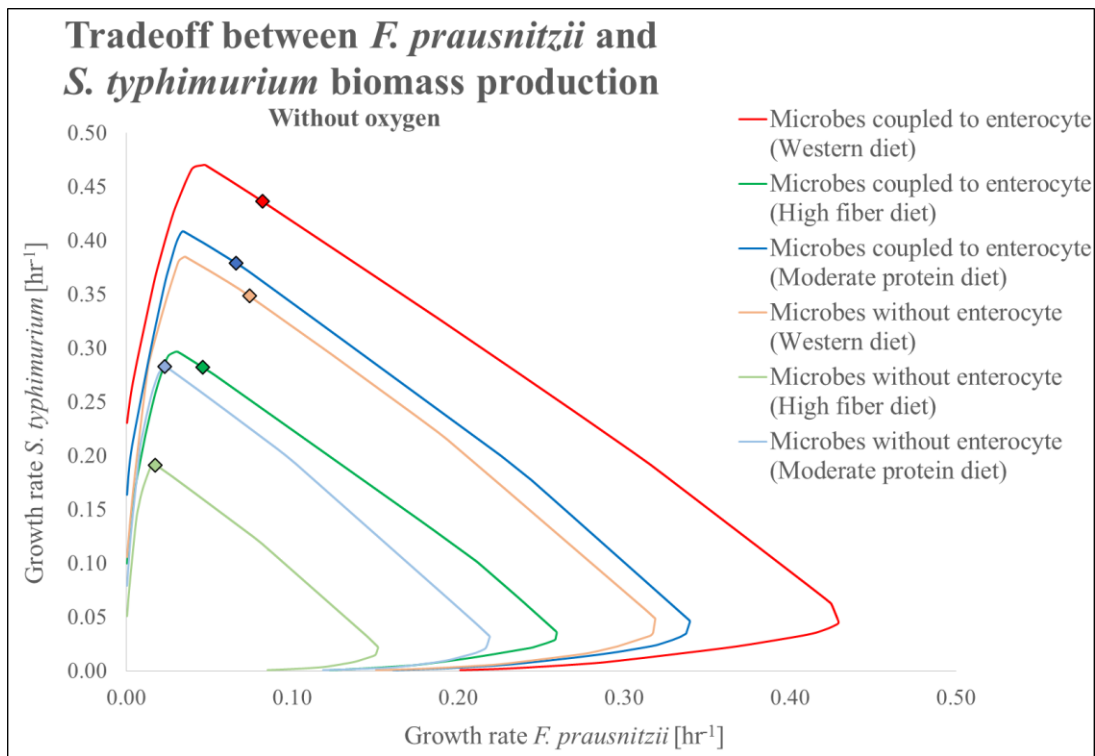


Figure S1.14

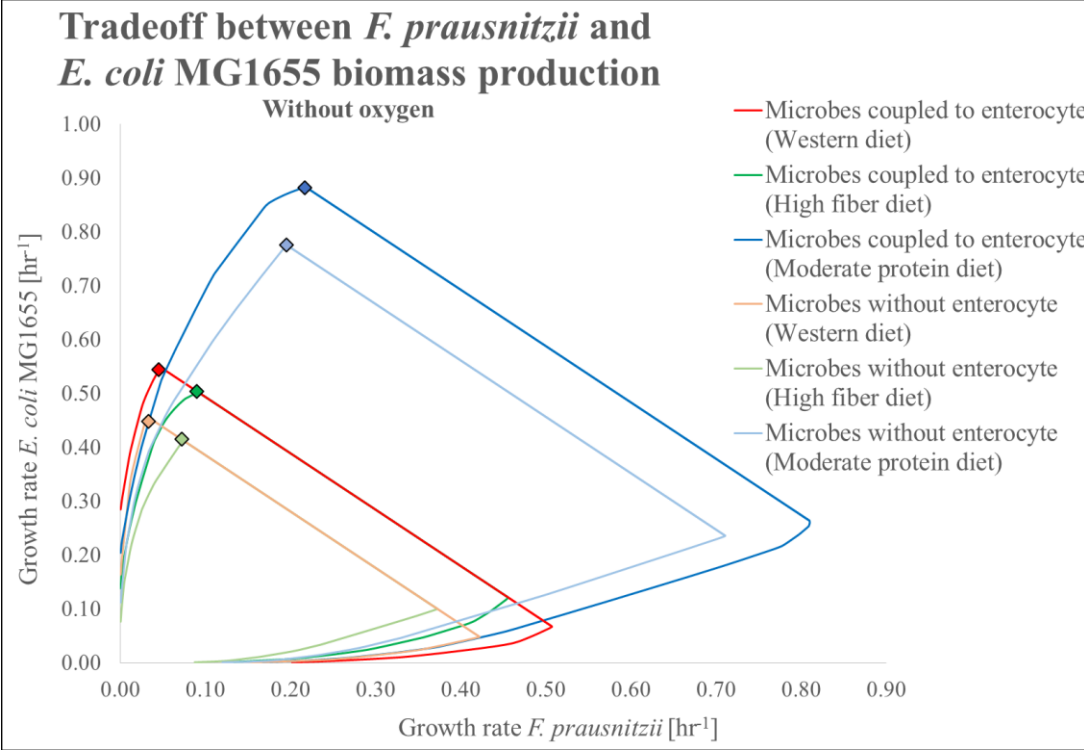


Figure S1.15

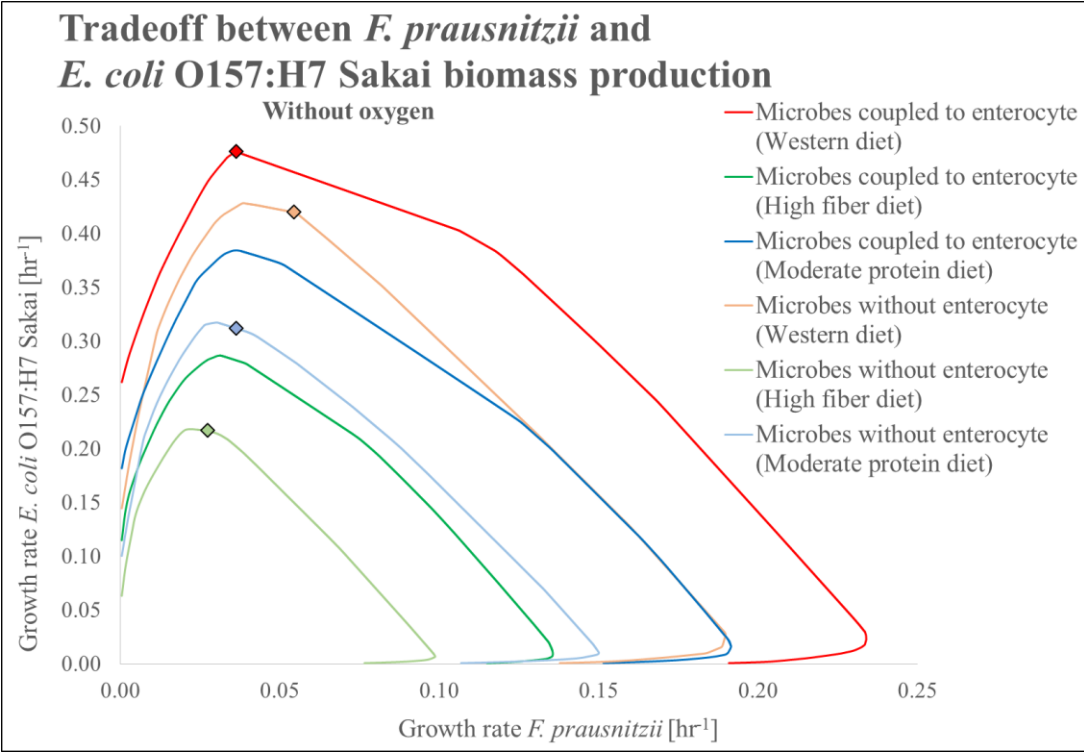


Figure S1.16

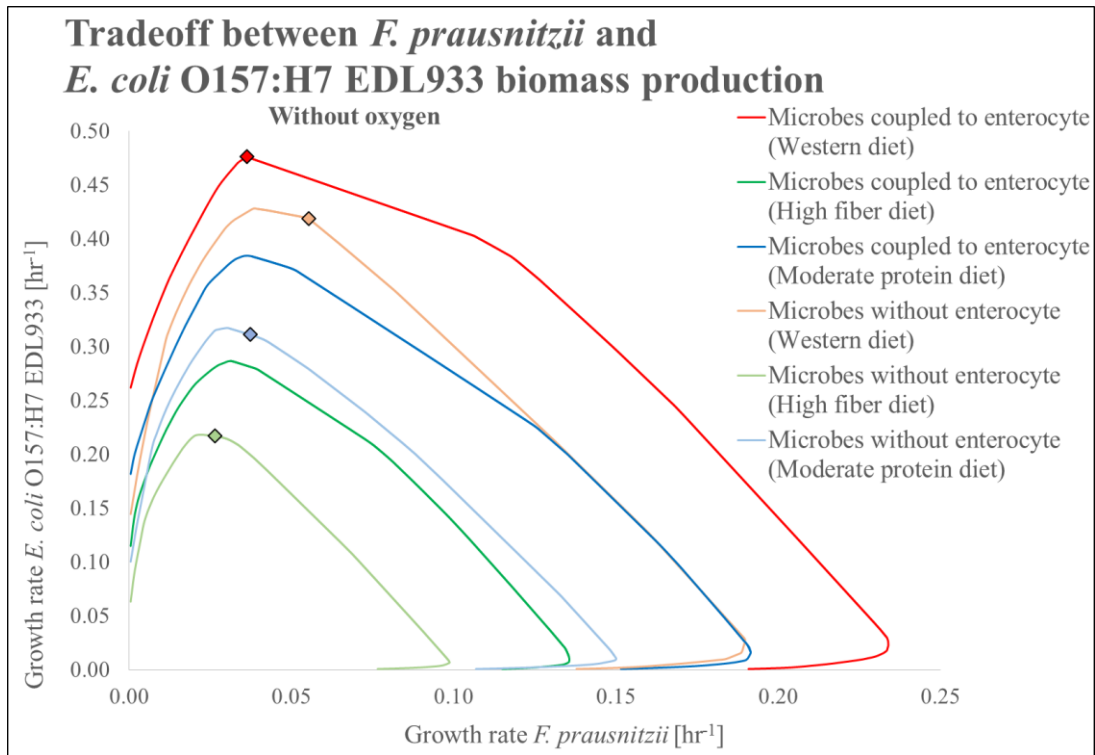


Figure S1.17

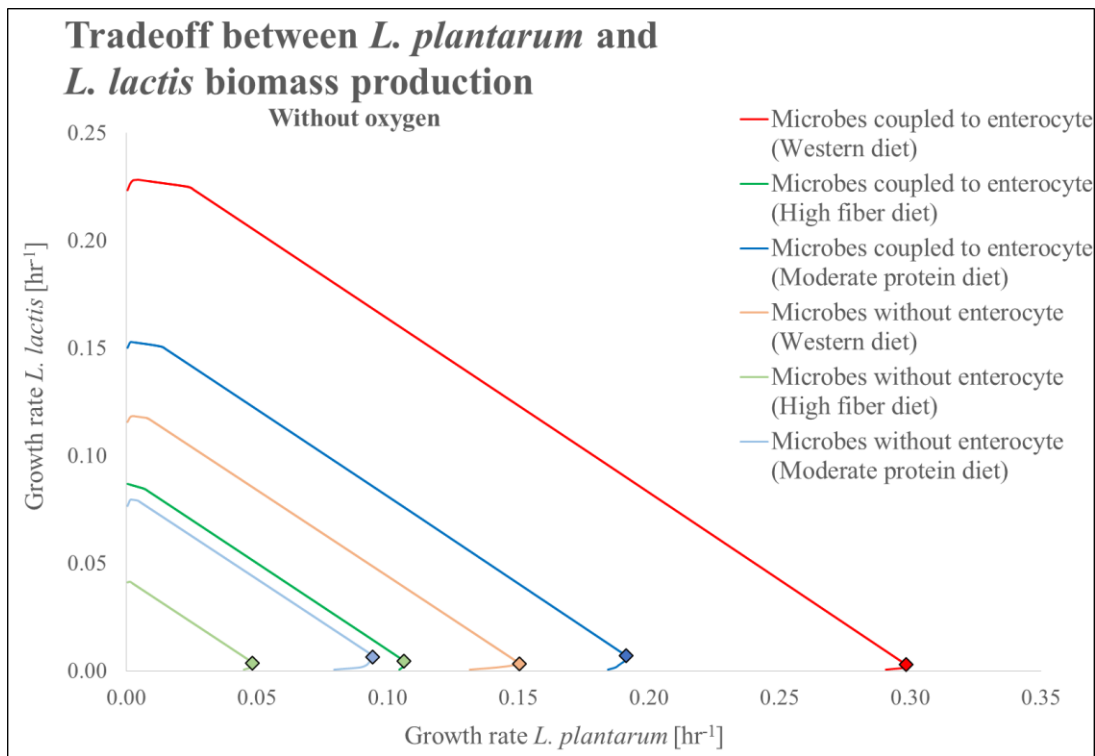


Figure S1.18

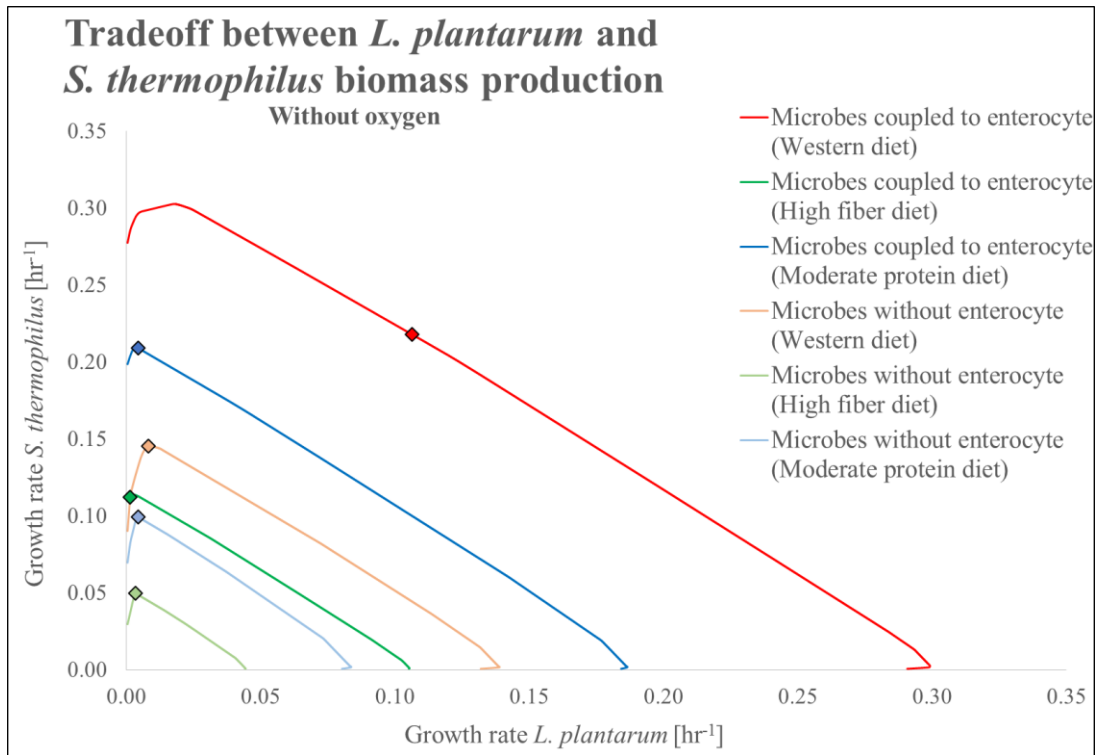


Figure S1.19

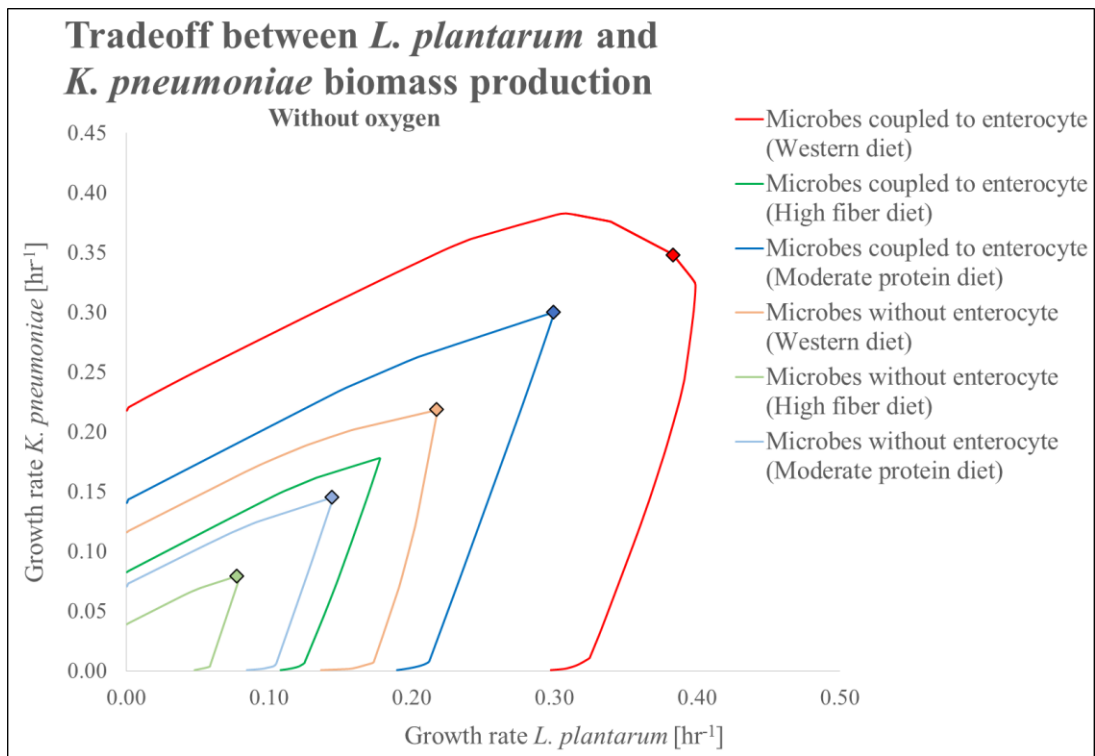


Figure S1.20



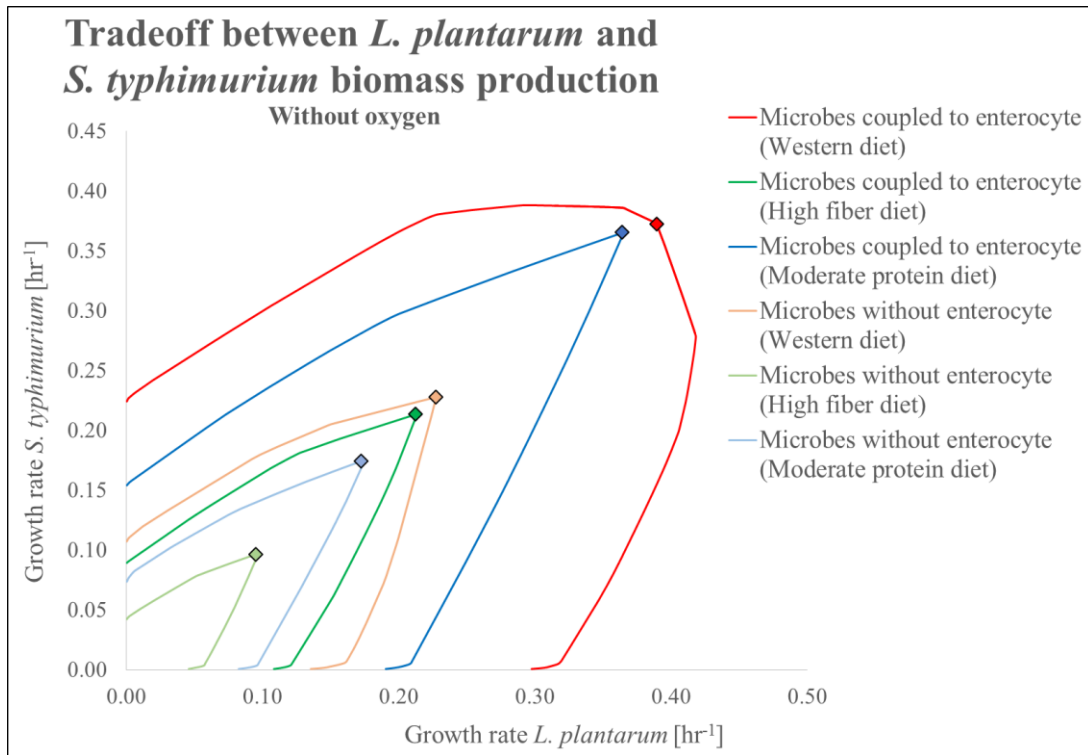


Figure S1.21

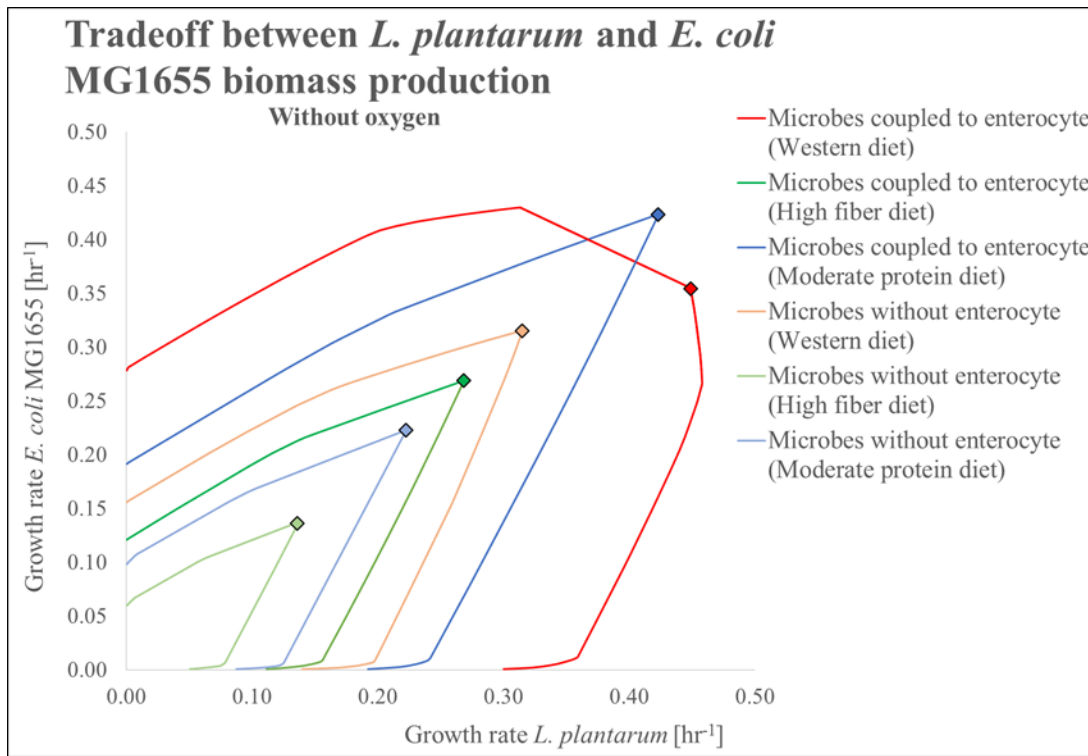


Figure S1.22

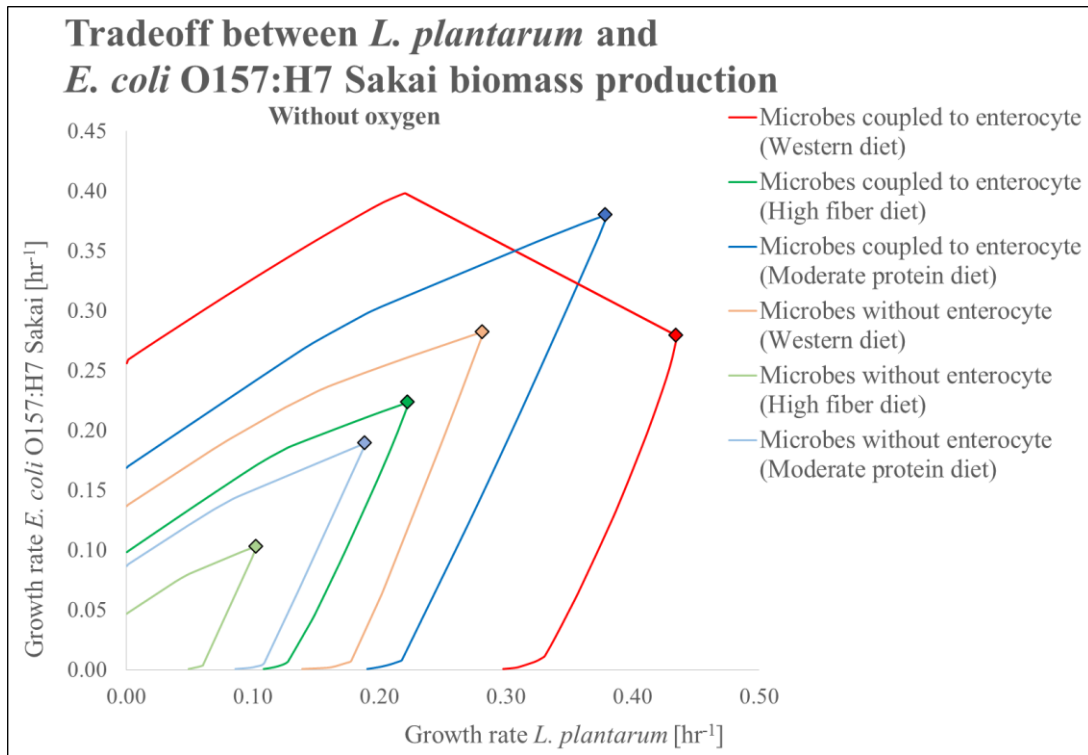


Figure S1.23

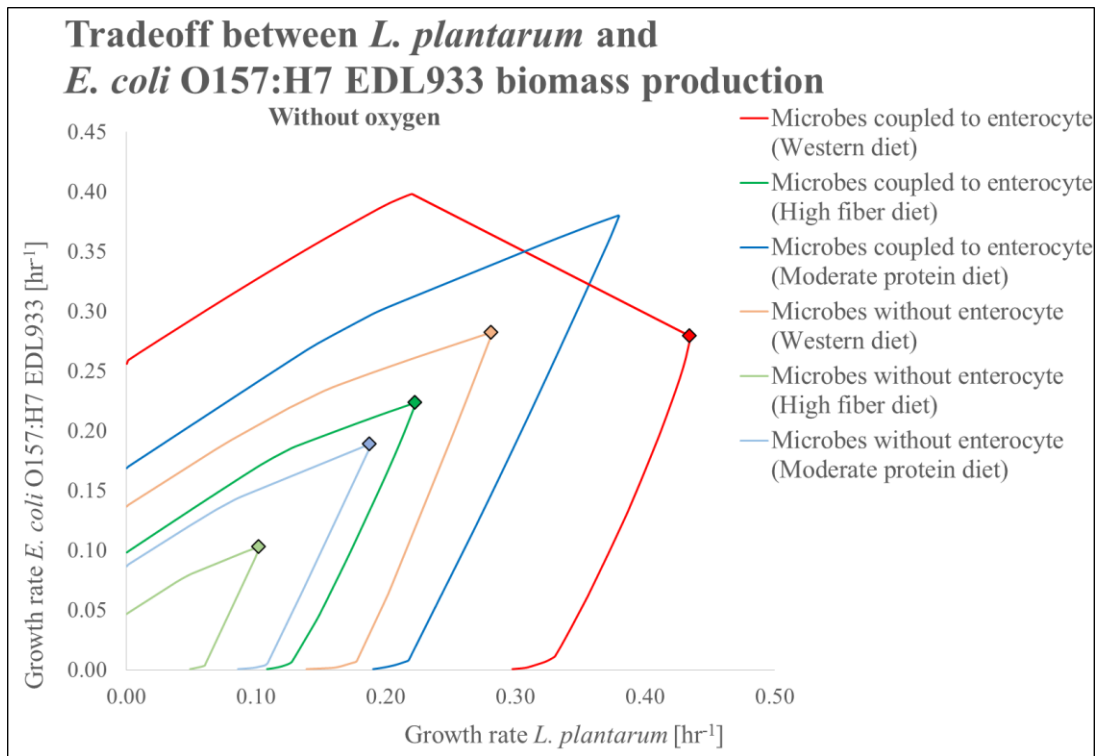


Figure S1.24

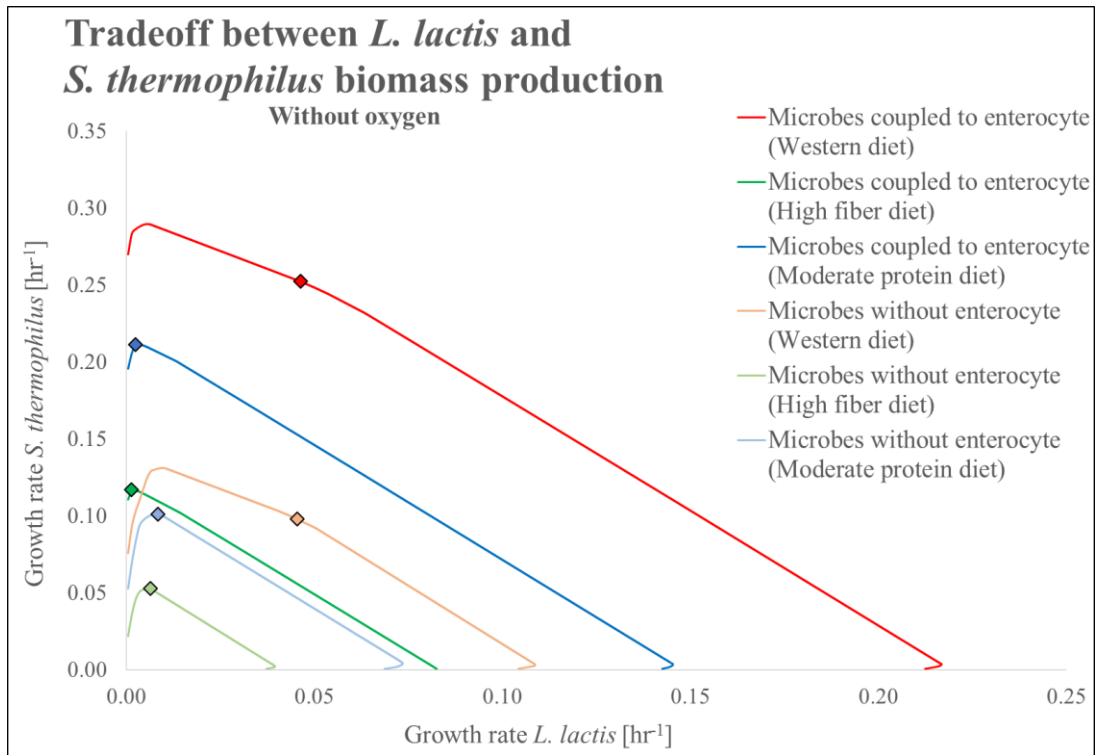


Figure S1.25

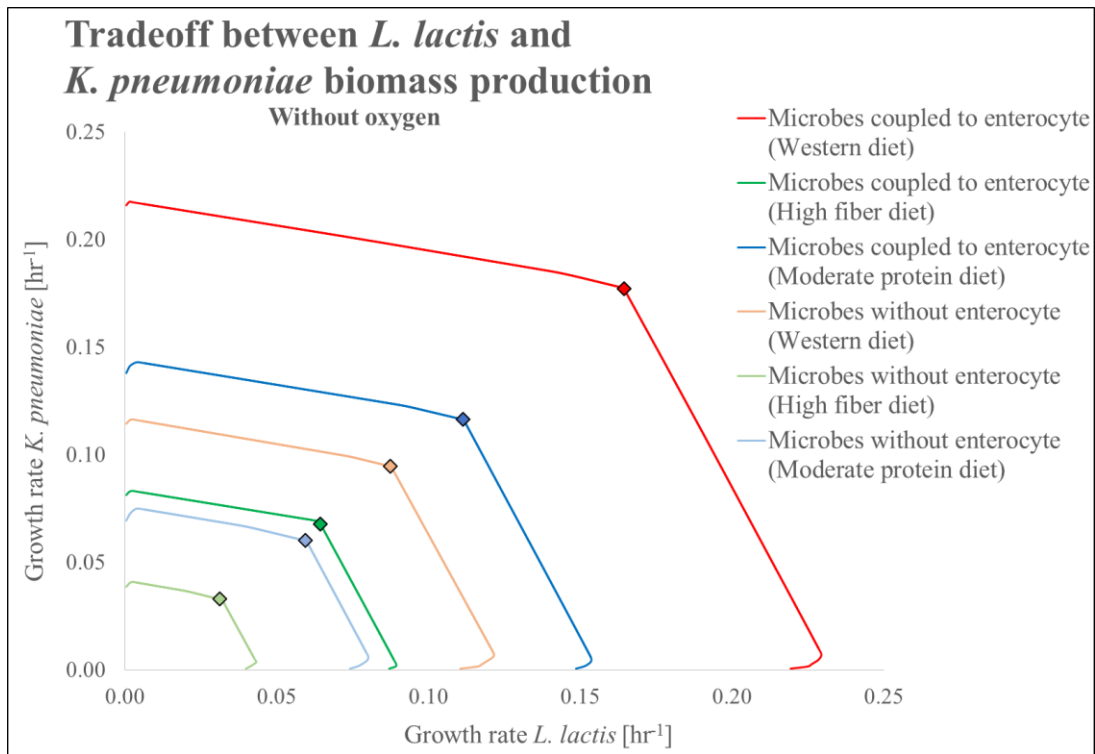


Figure S1.26

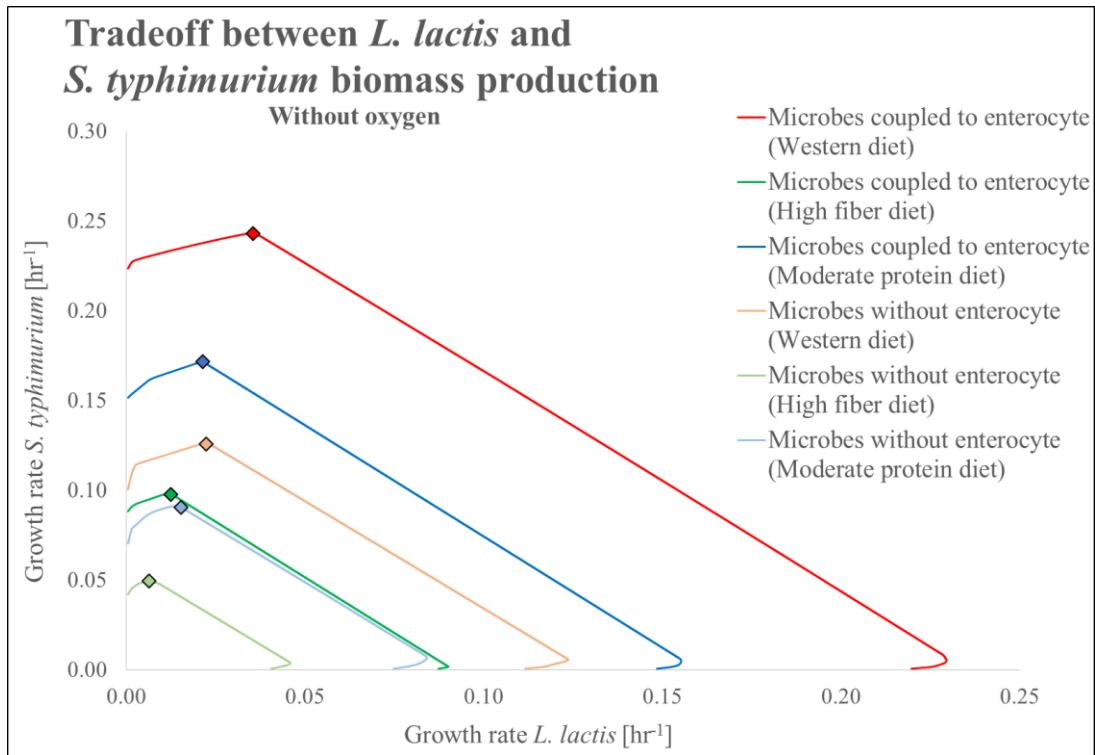


Figure S1.27

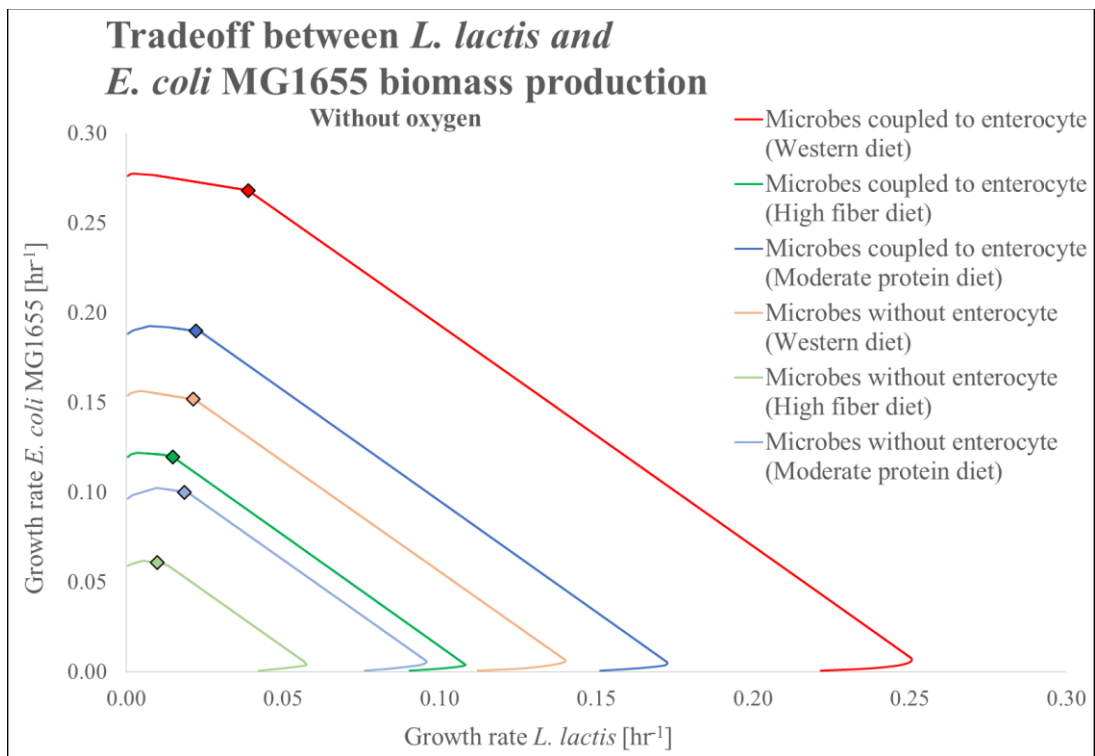


Figure S1.28

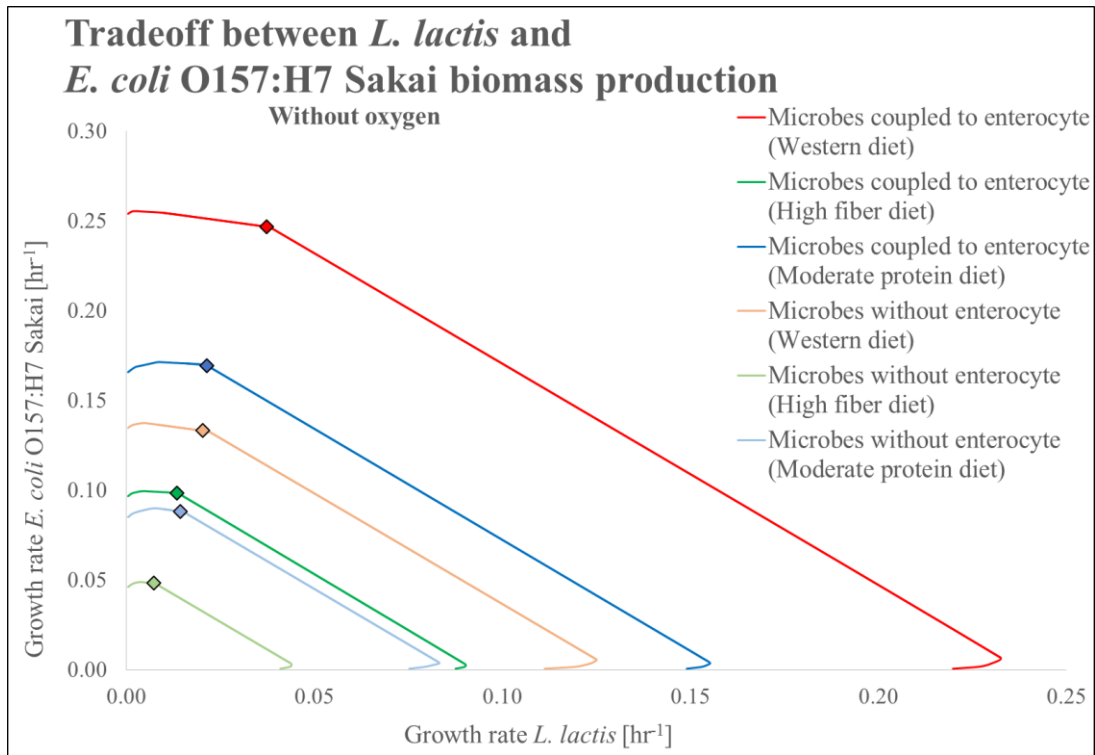


Figure S1.29

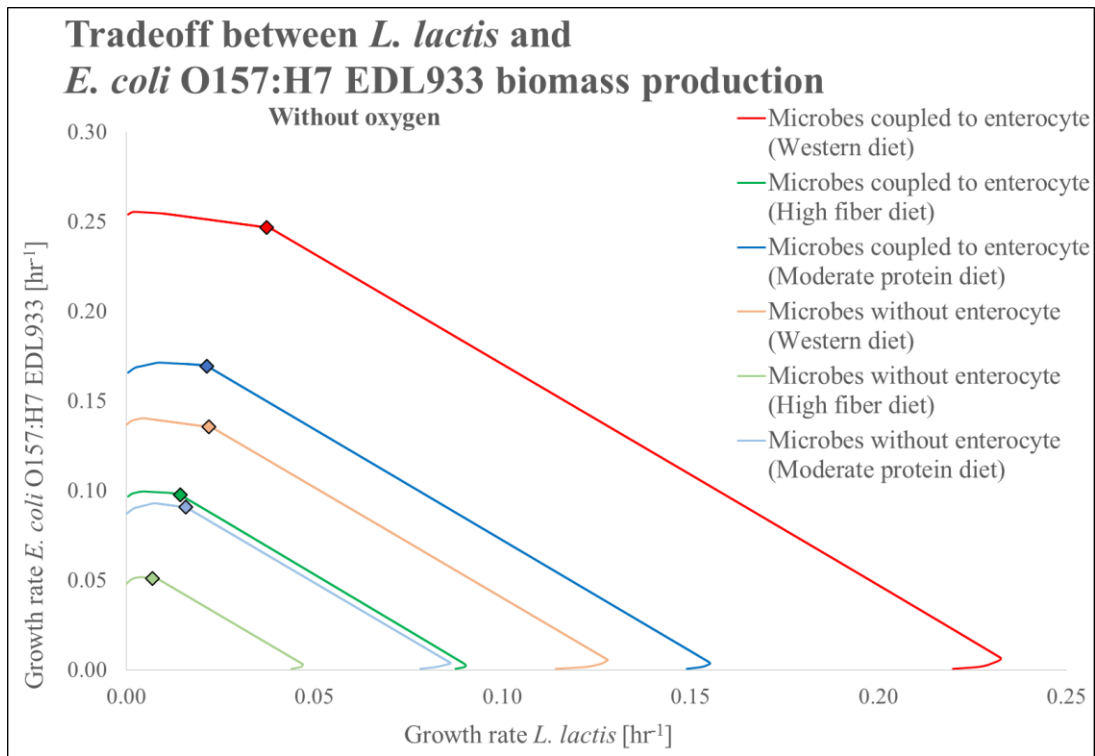


Figure S1.30

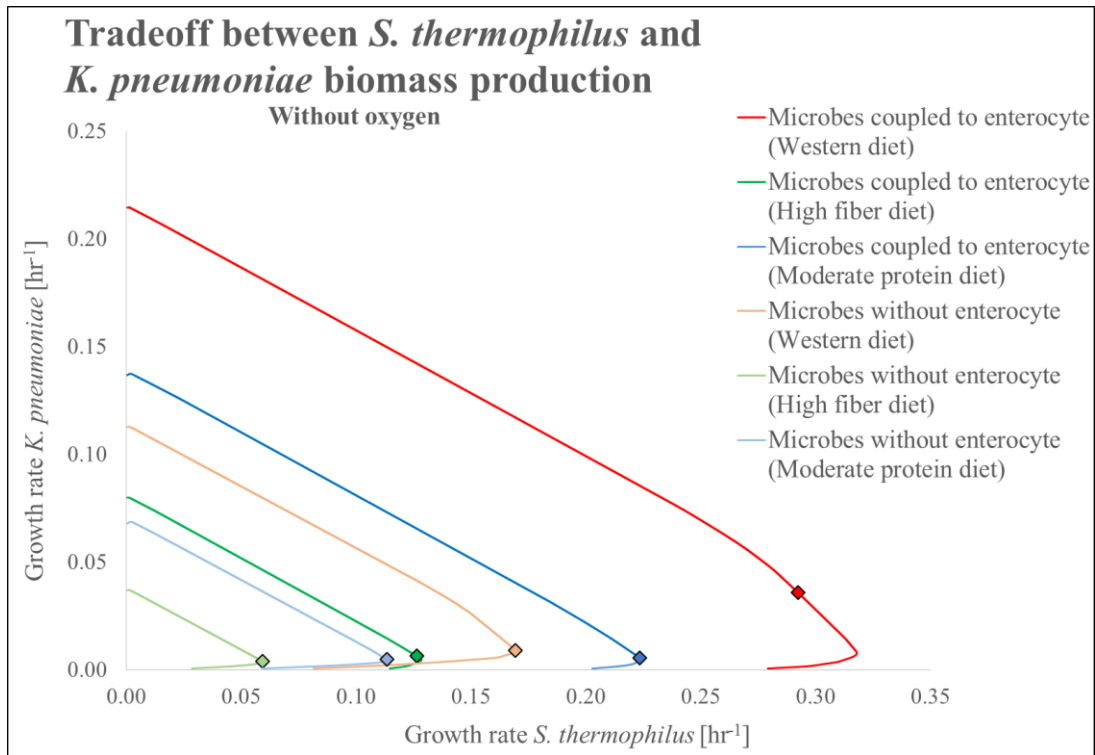


Figure S1.31

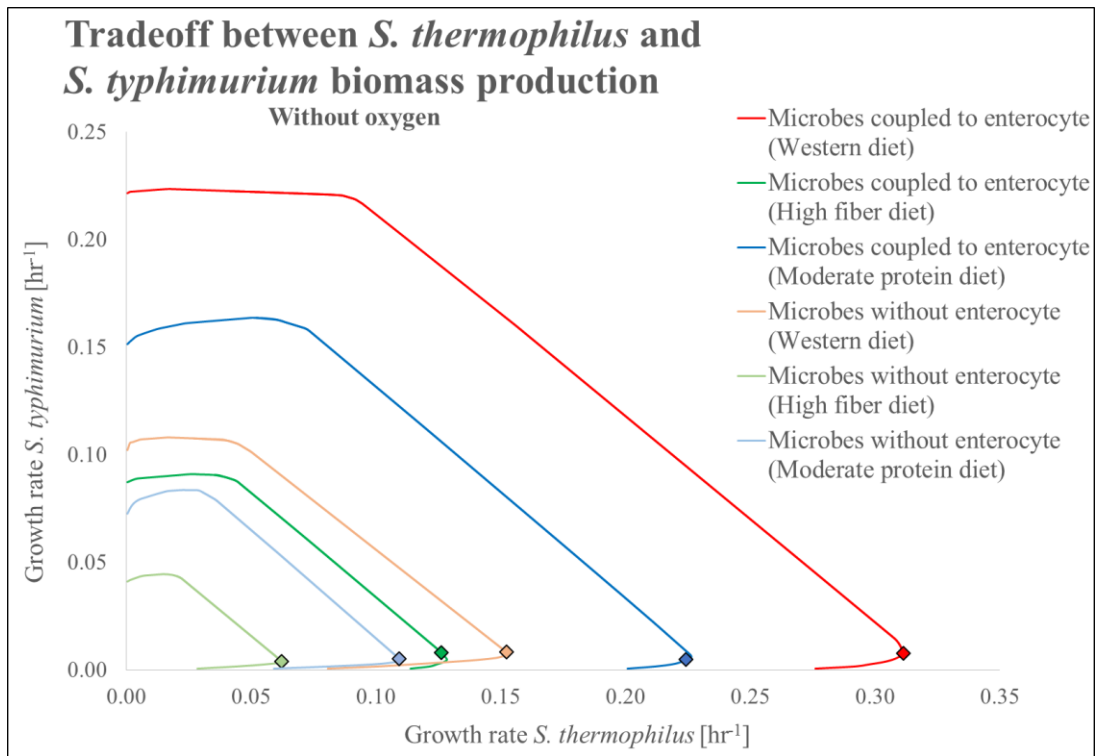


Figure S1.32

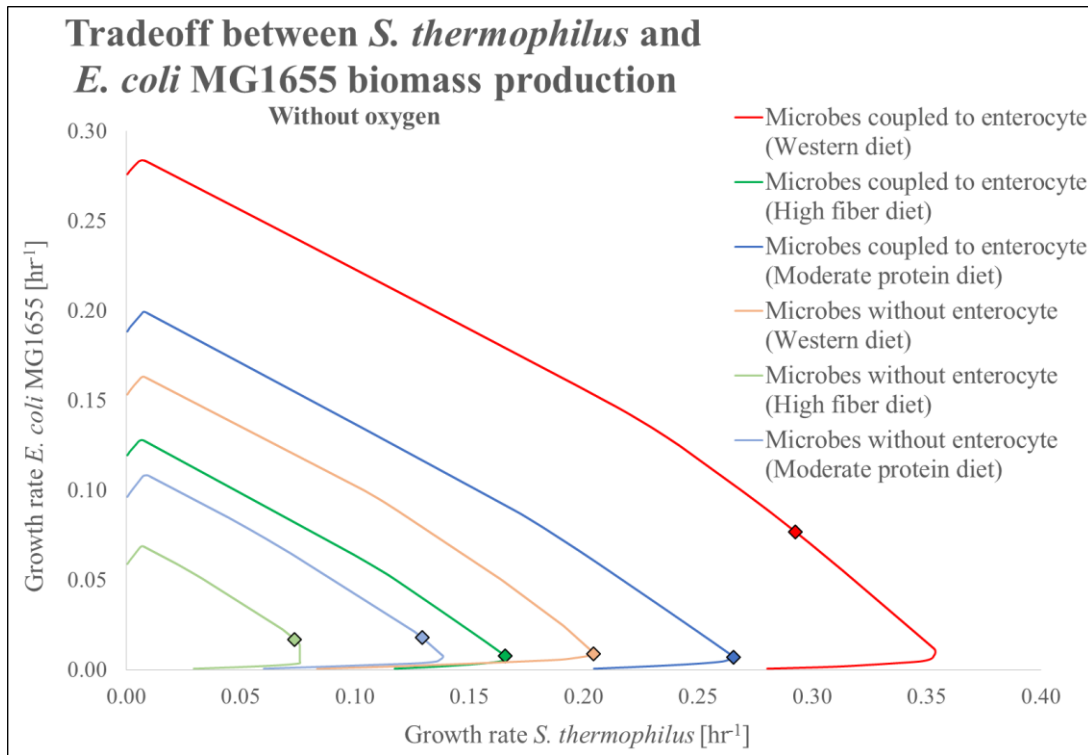


Figure S1.33

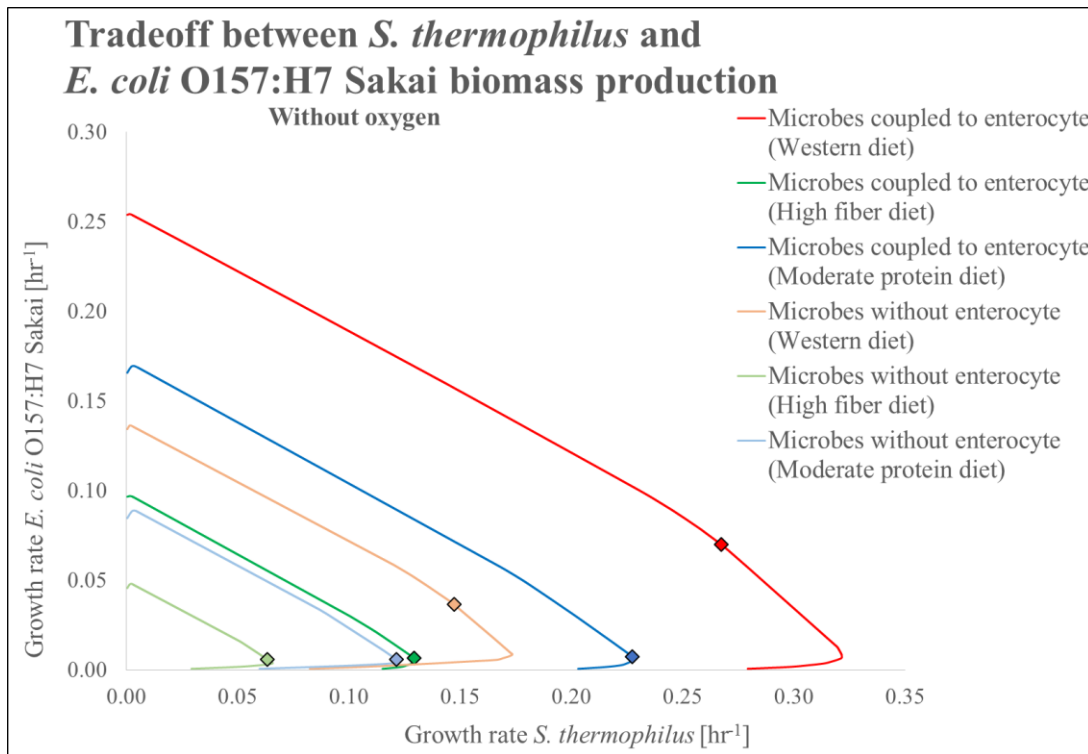


Figure S1.34

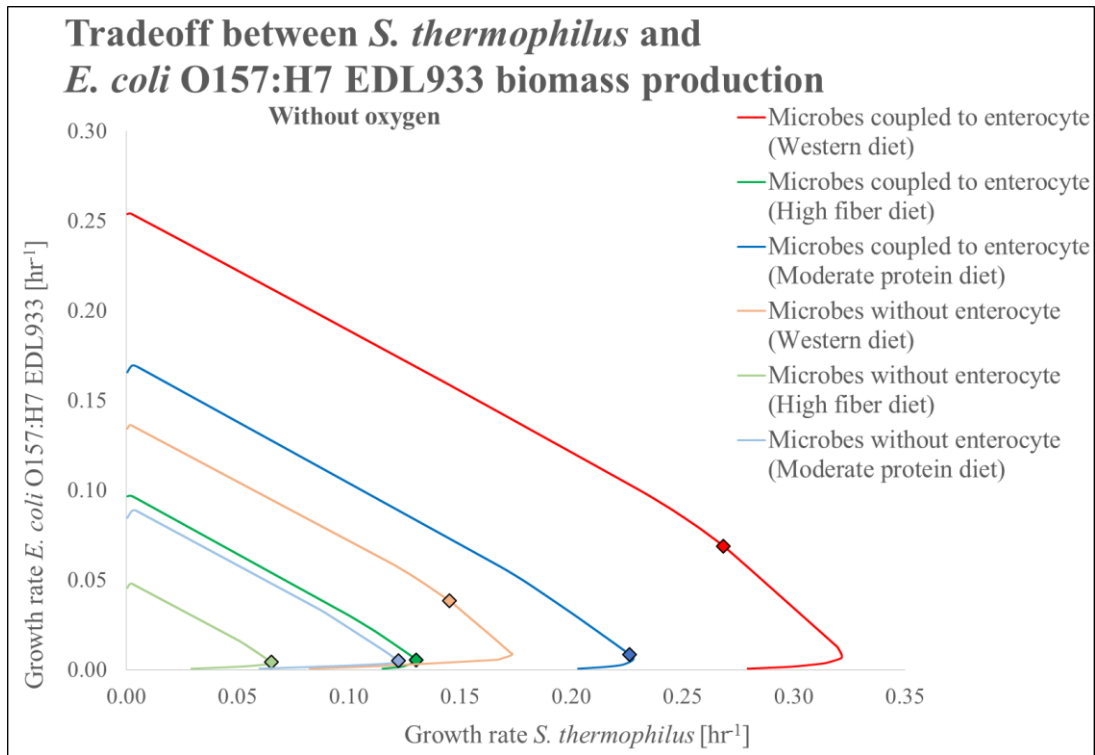


Figure S1.35

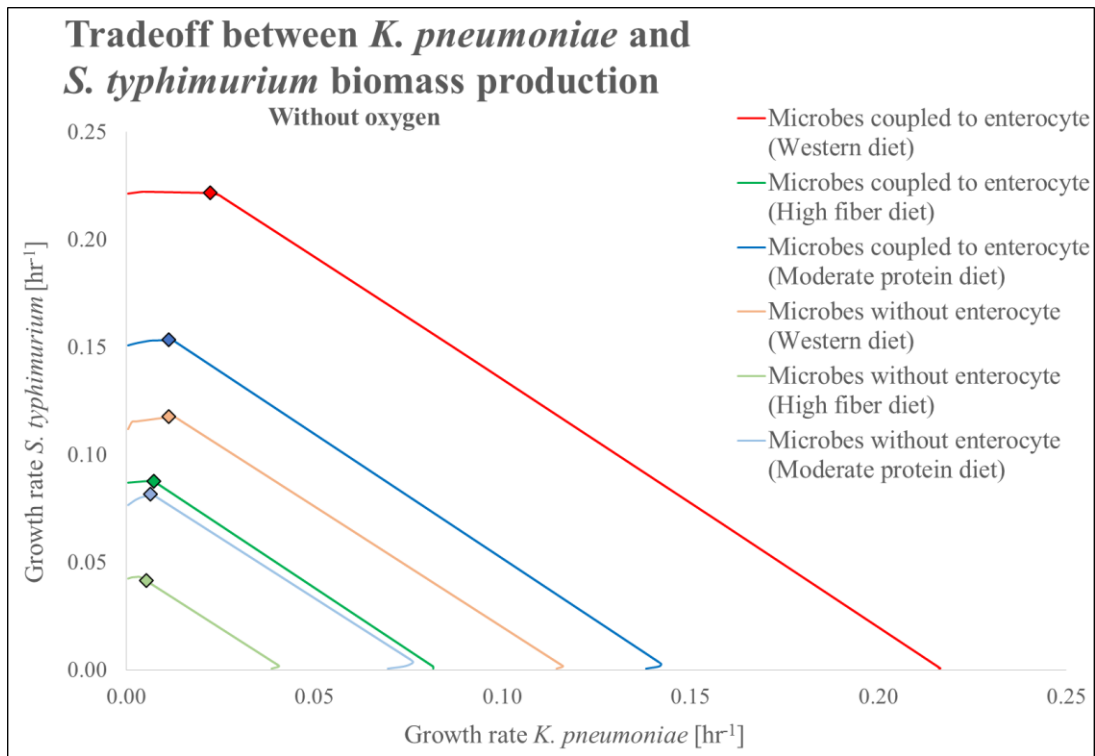


Figure S1.36



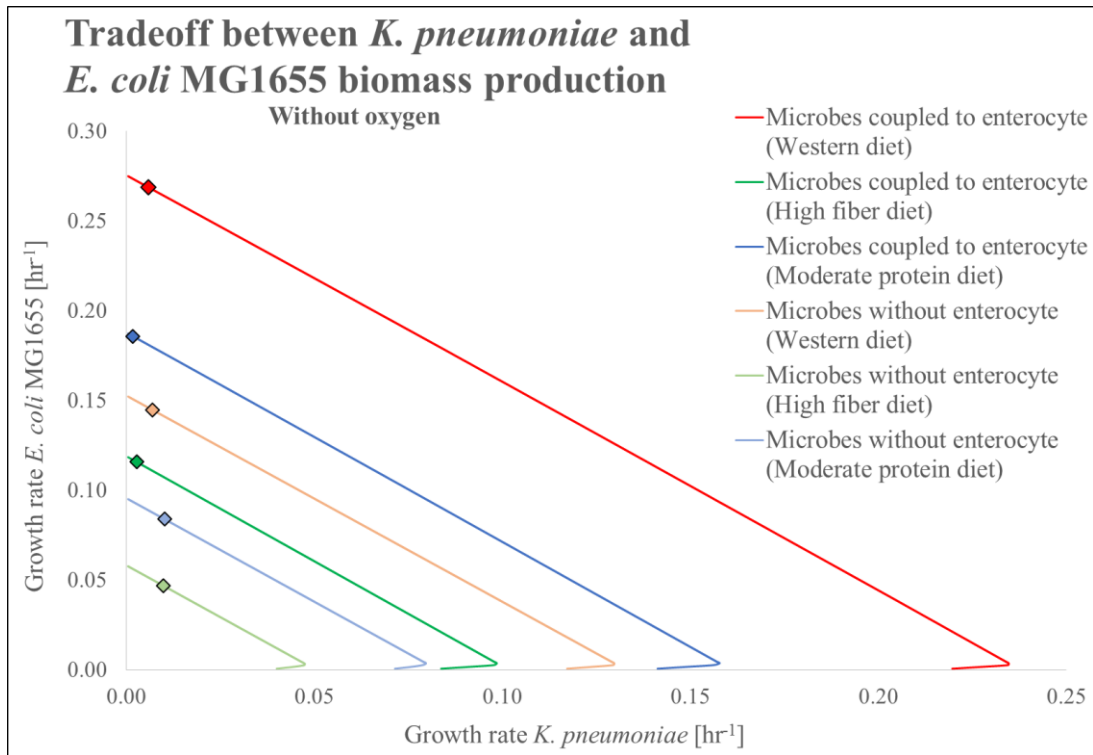


Figure S1.37

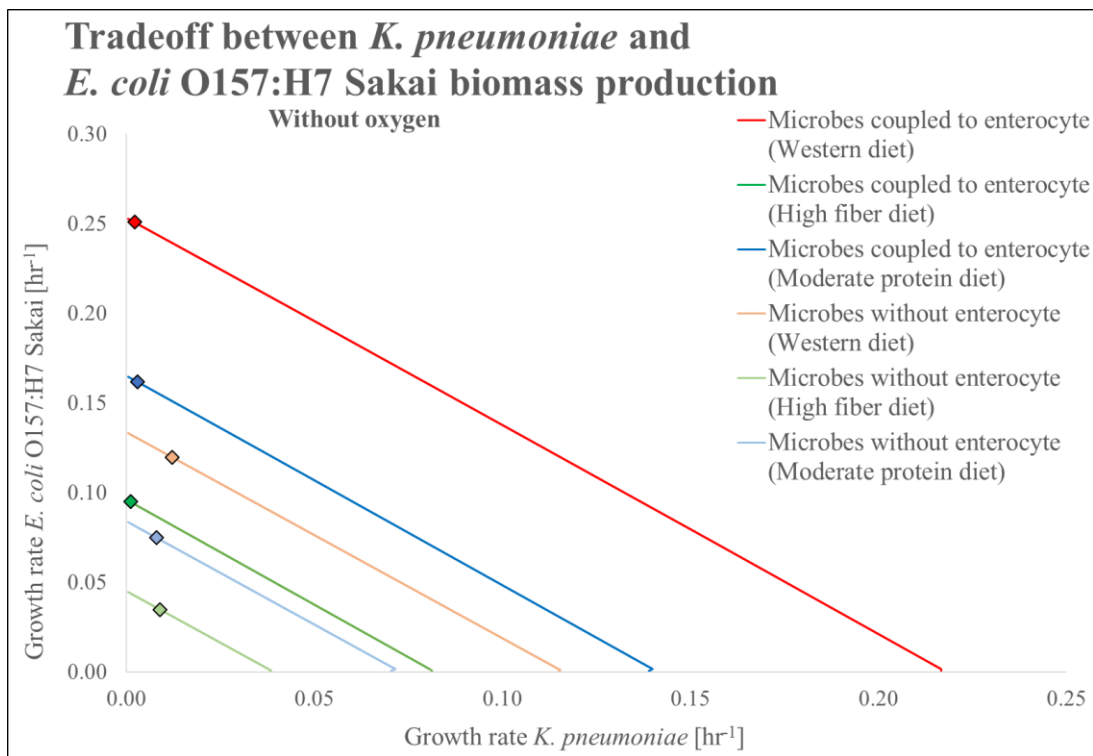


Figure S1.38

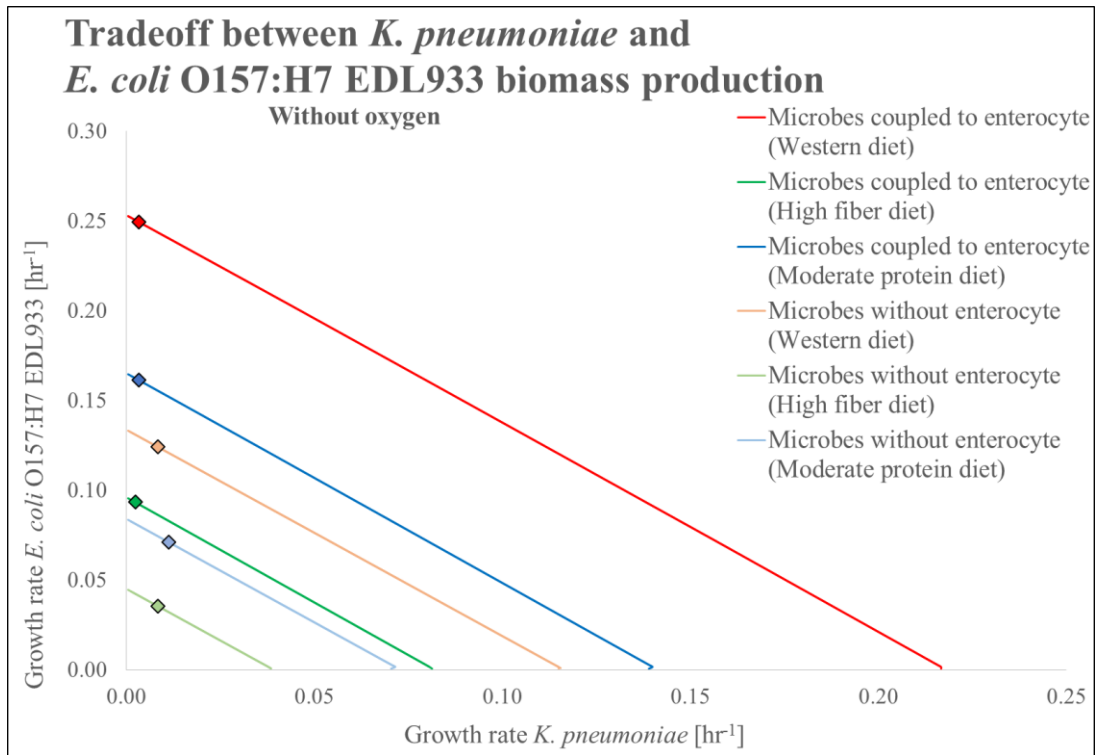


Figure S1.39

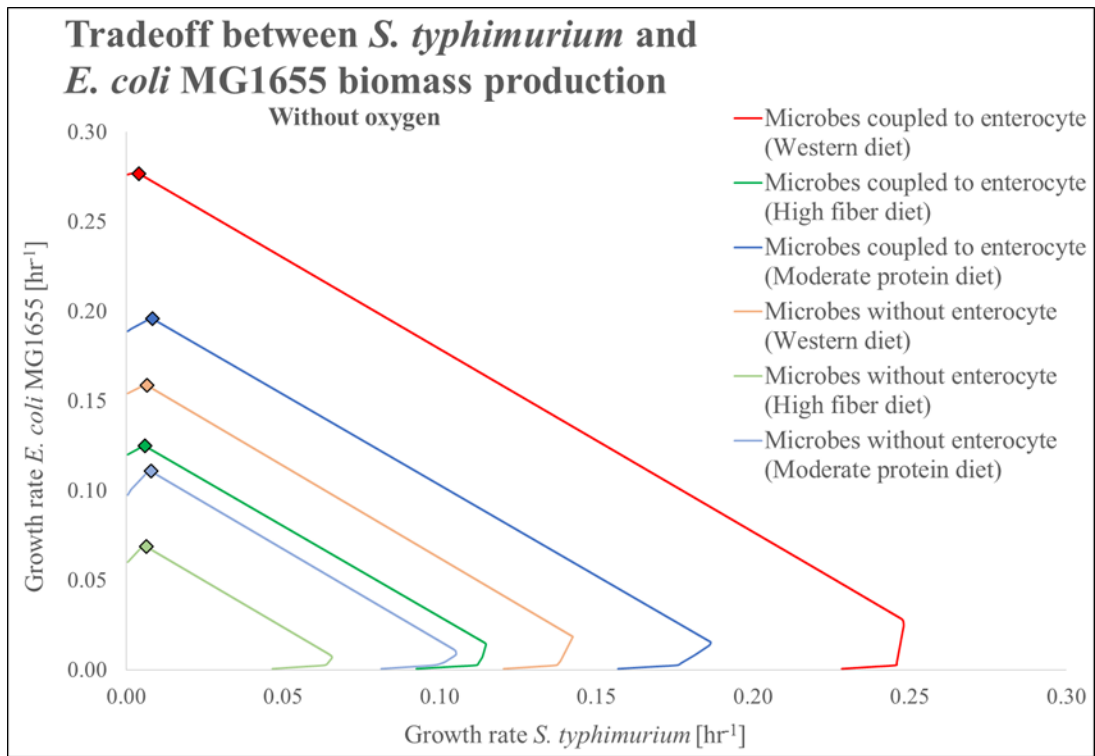


Figure S1.40

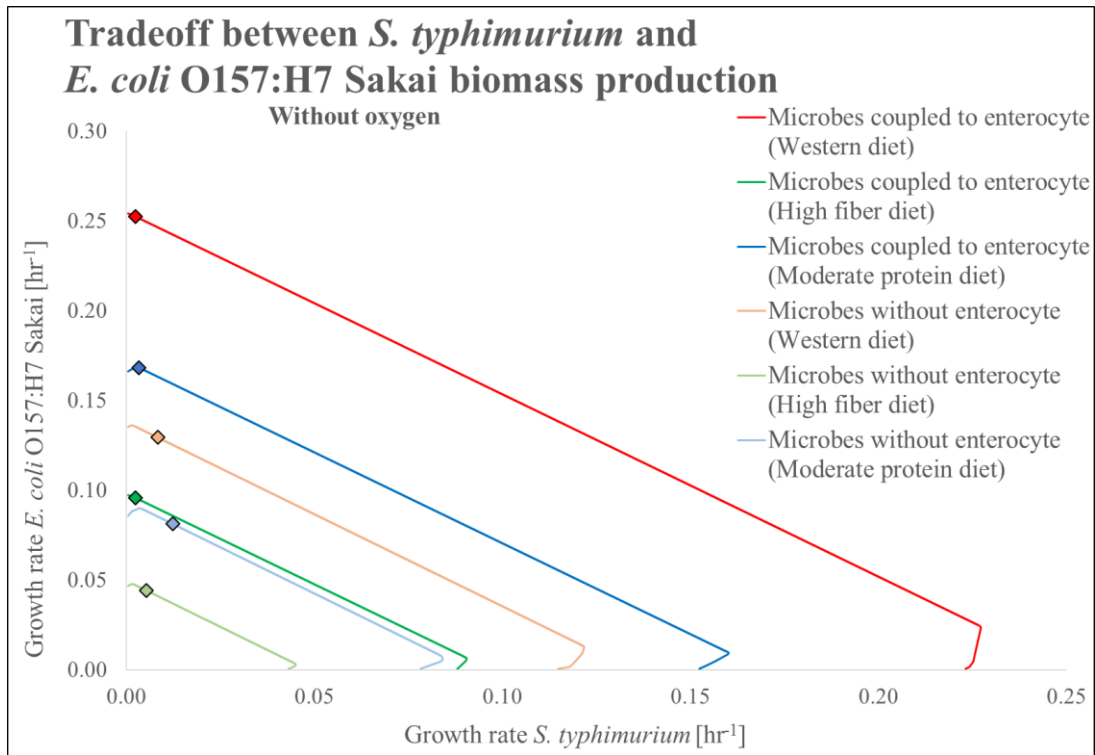


Figure S1.41

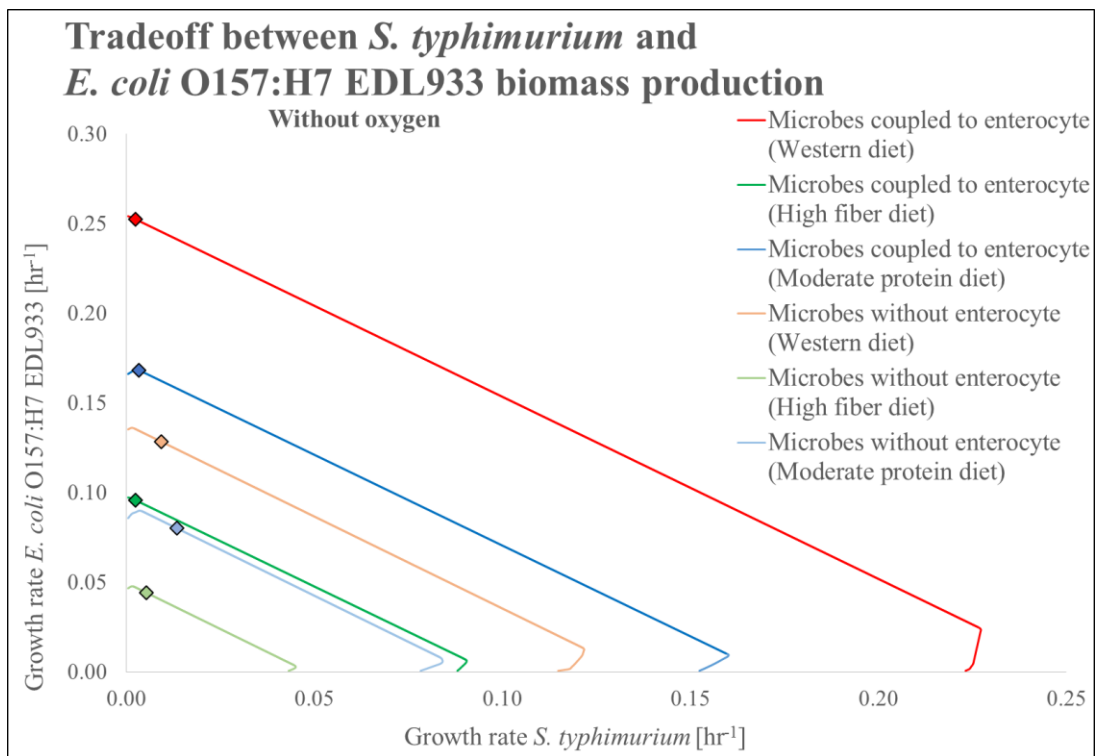


Figure S1.42

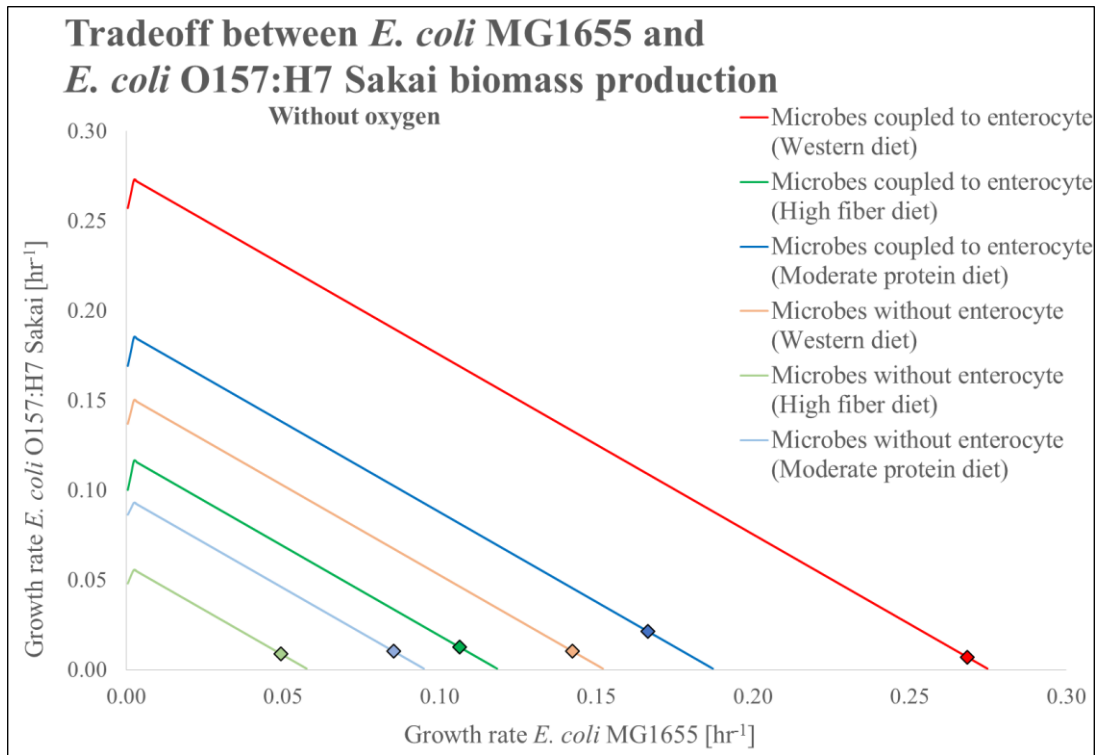


Figure S1.43

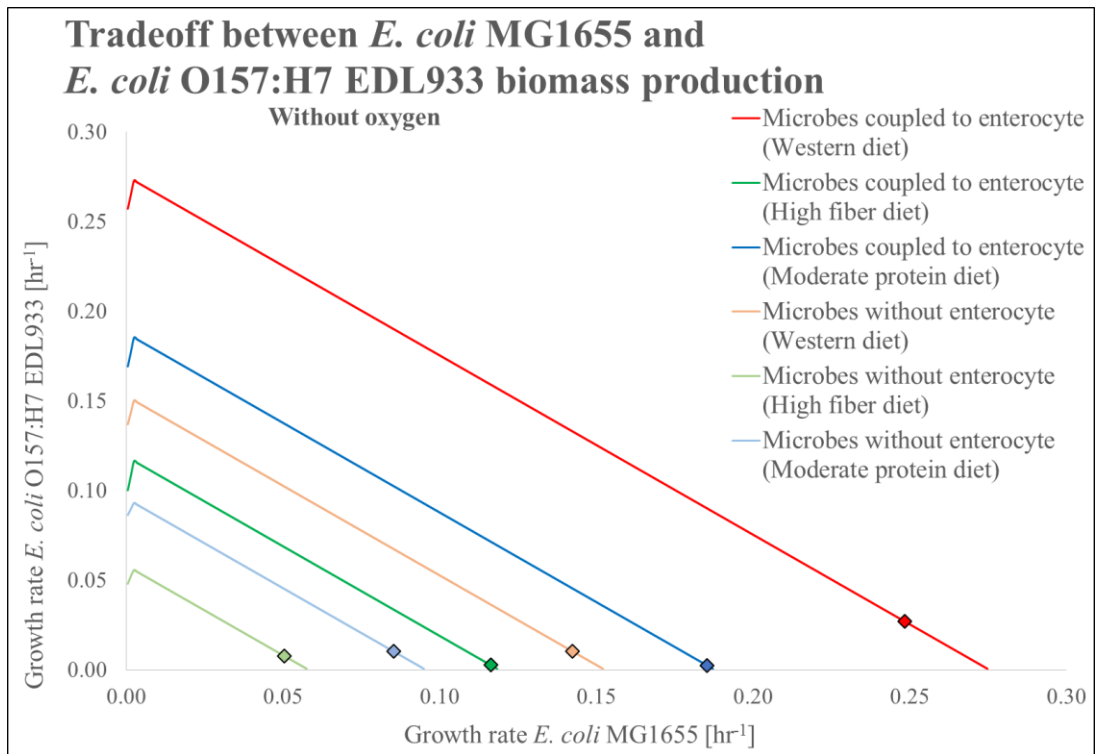


Figure S1.44

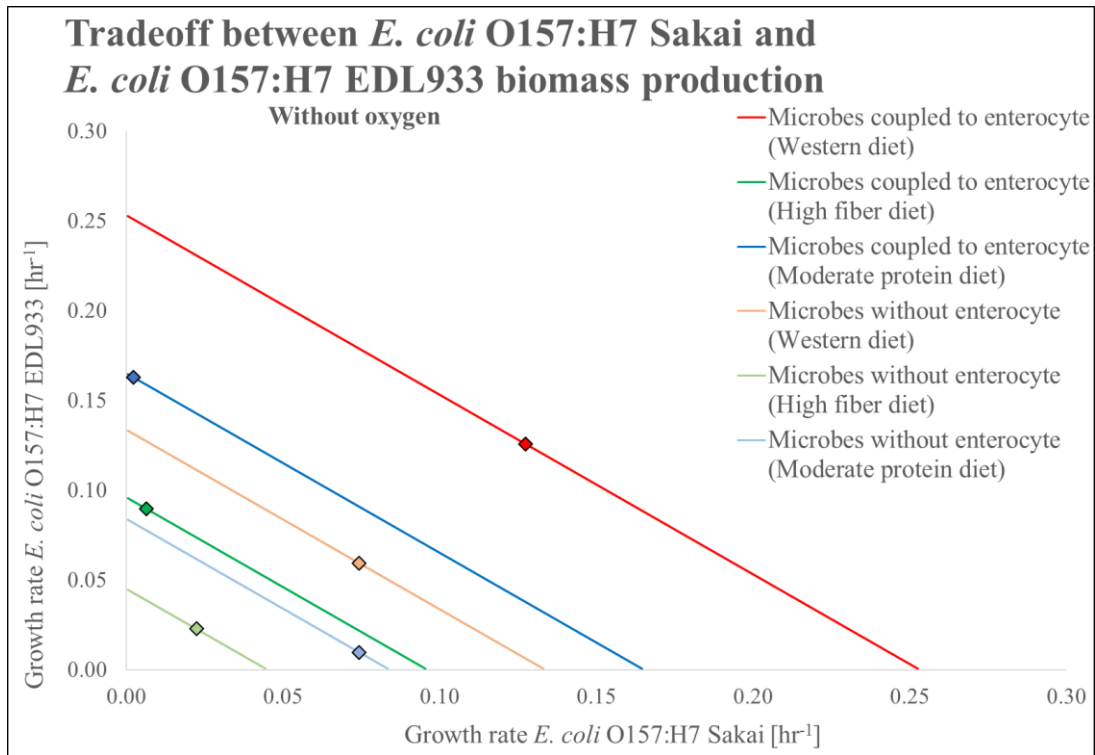


Figure S1.45

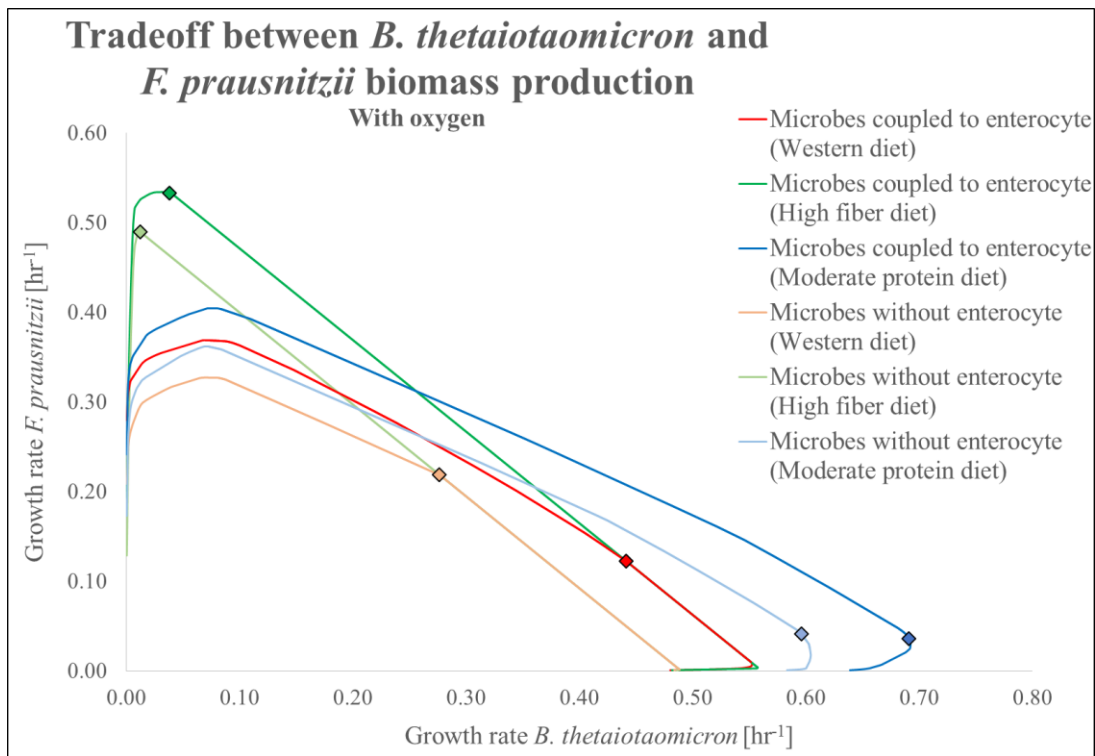


Figure S1.46

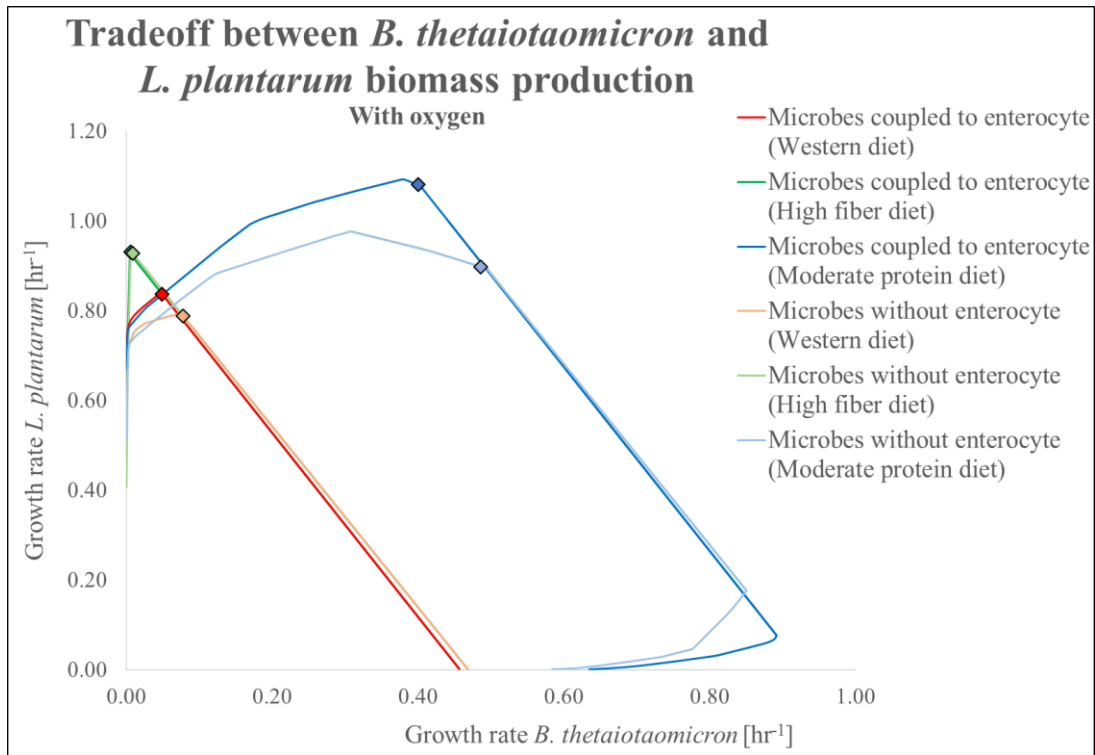


Figure S1.47

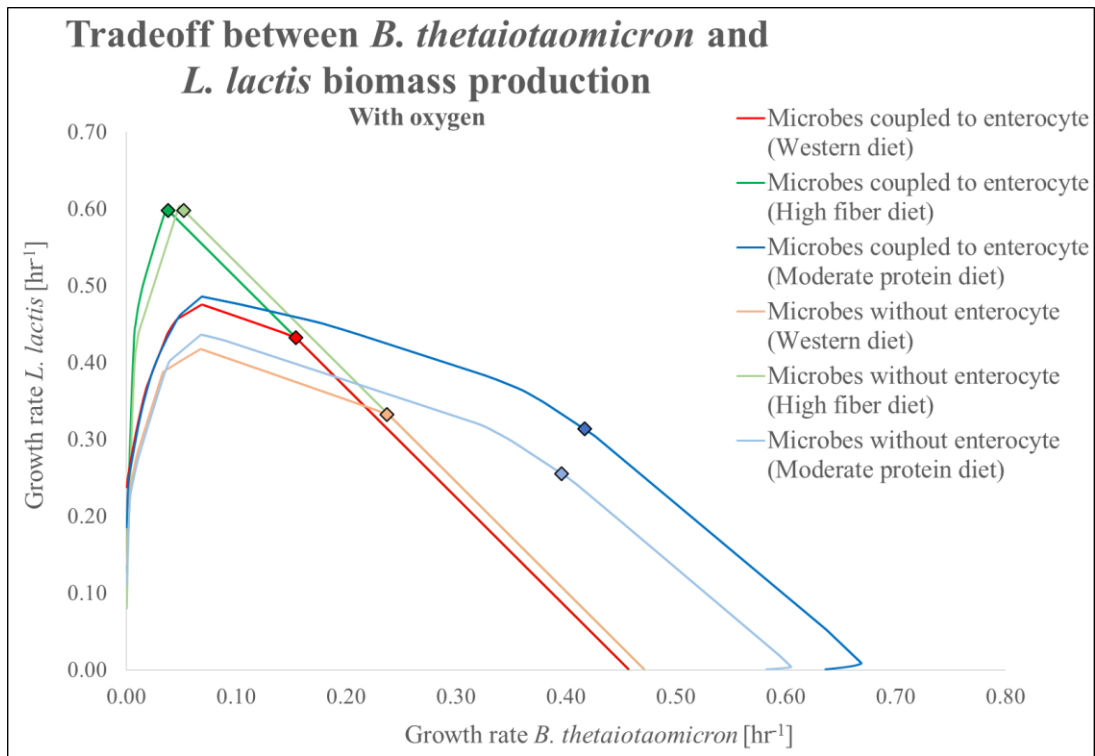
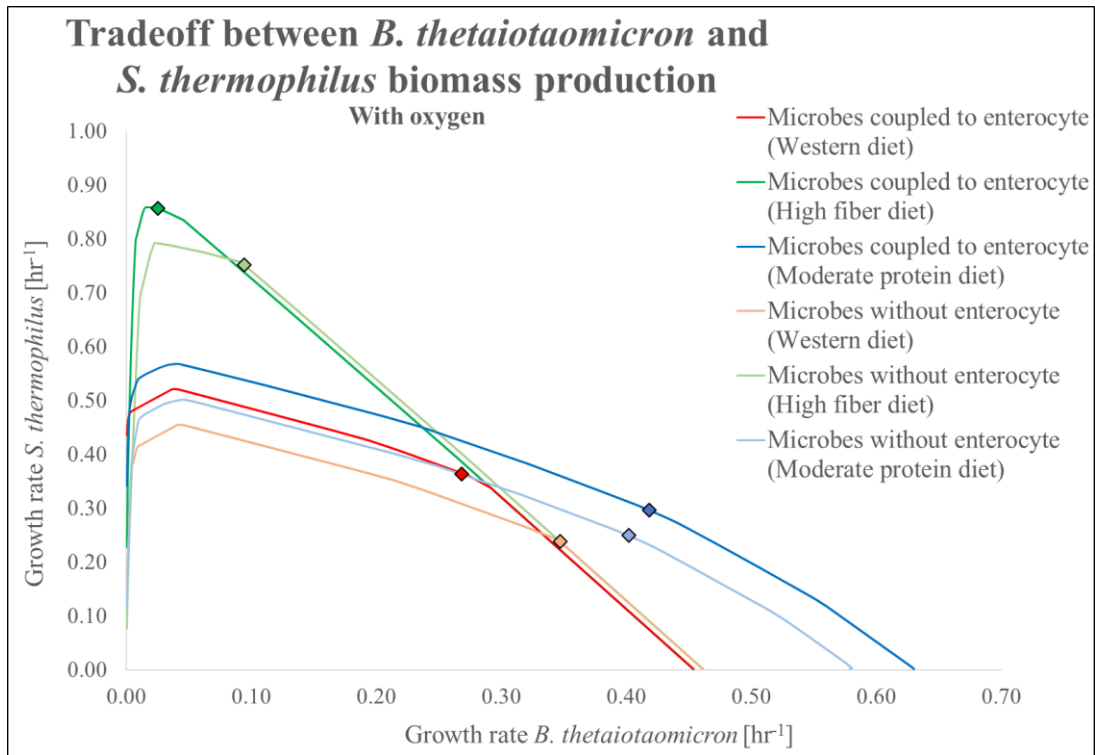
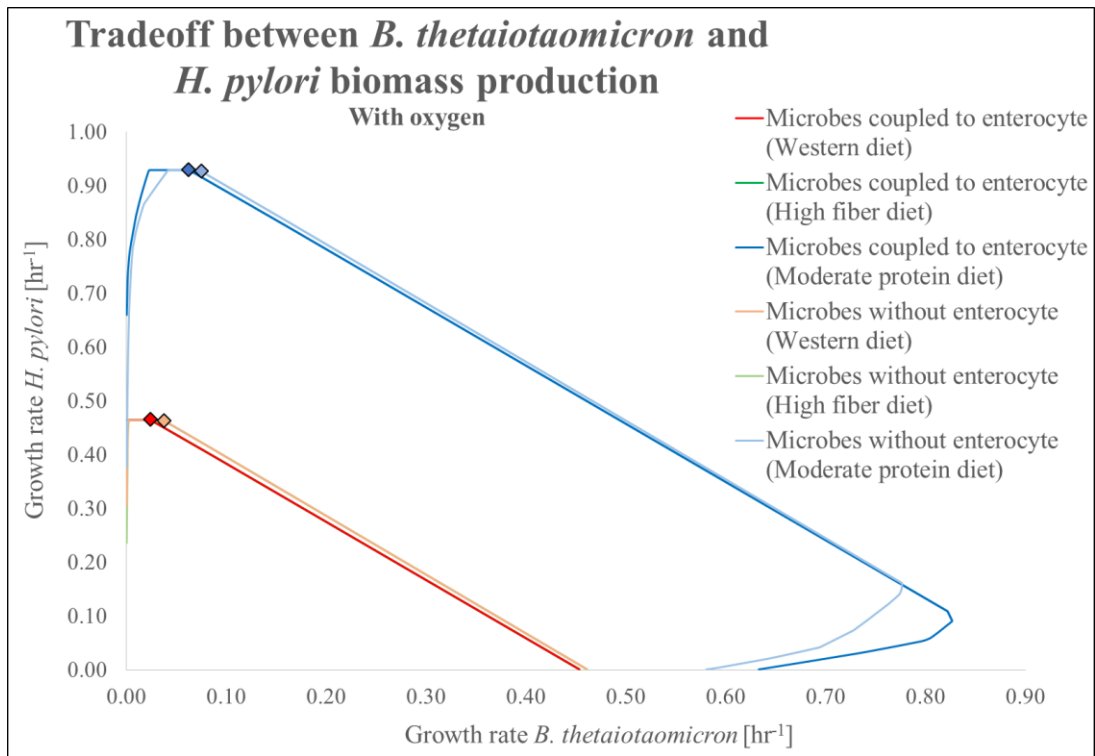


Figure S1.48



**Figure S1.49**



**Figure S1.50**

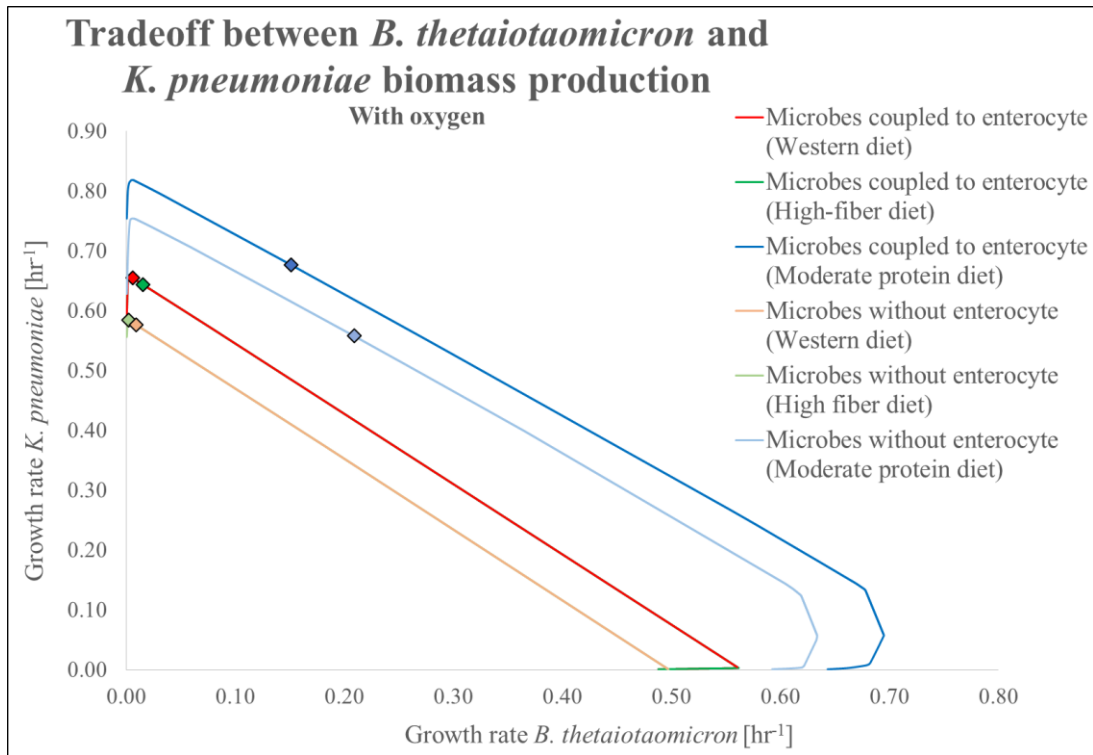


Figure S1.51

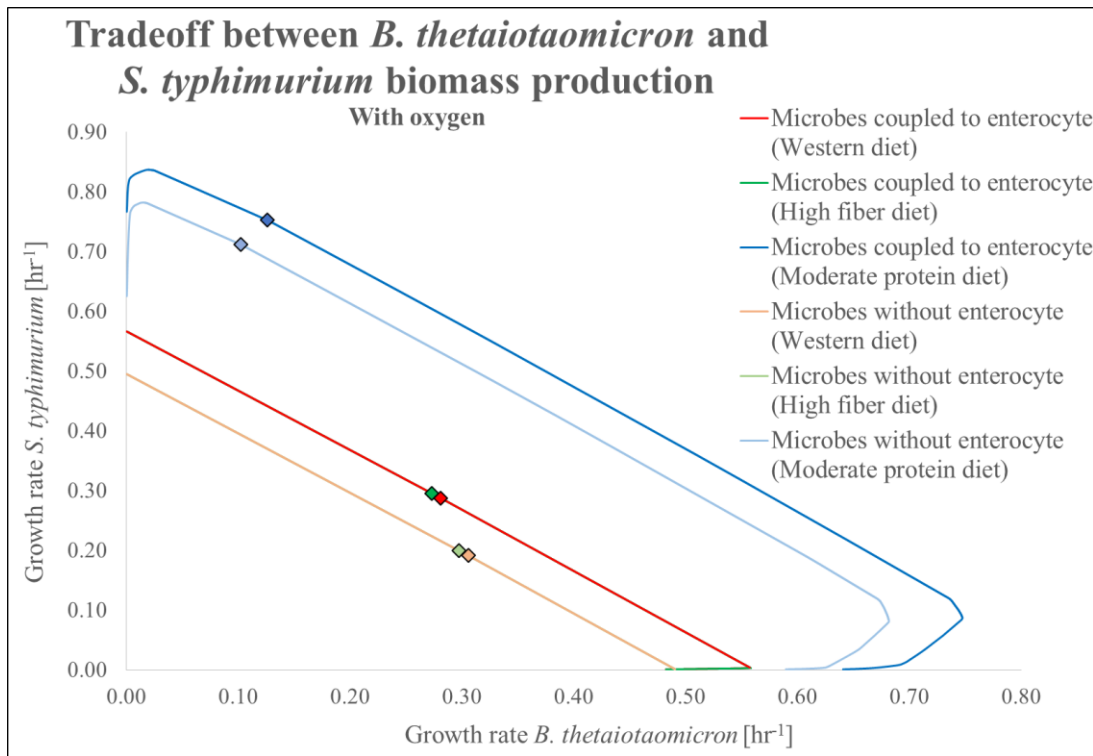


Figure S1.52



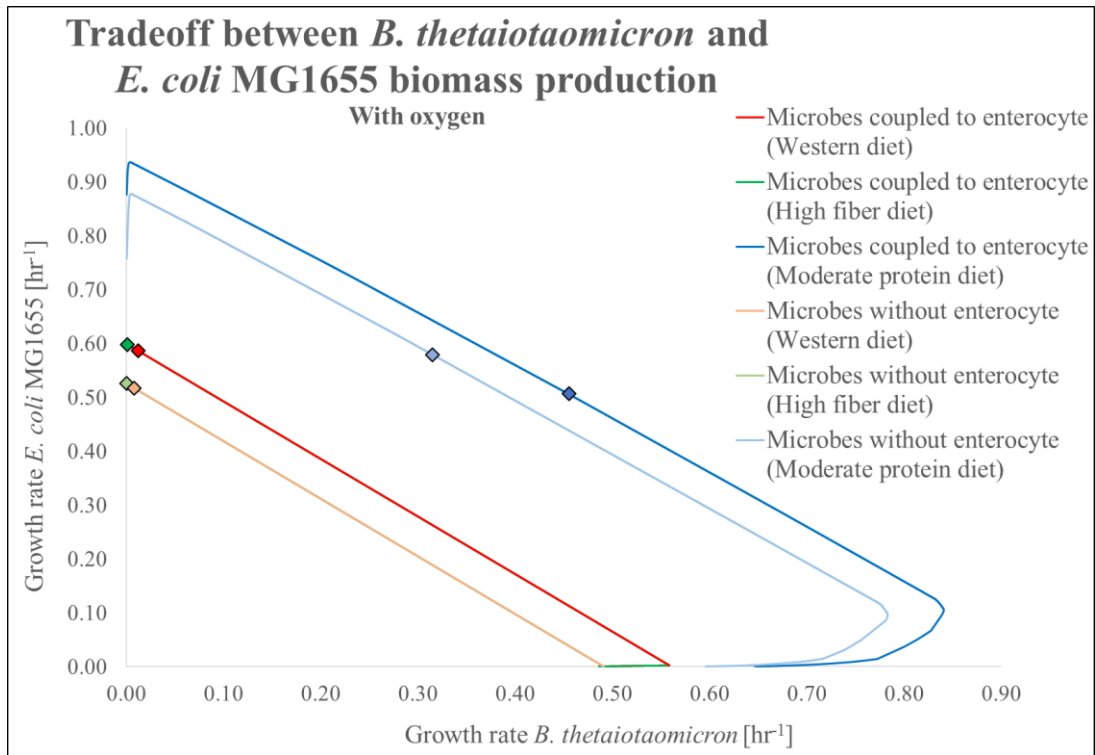


Figure S1.53

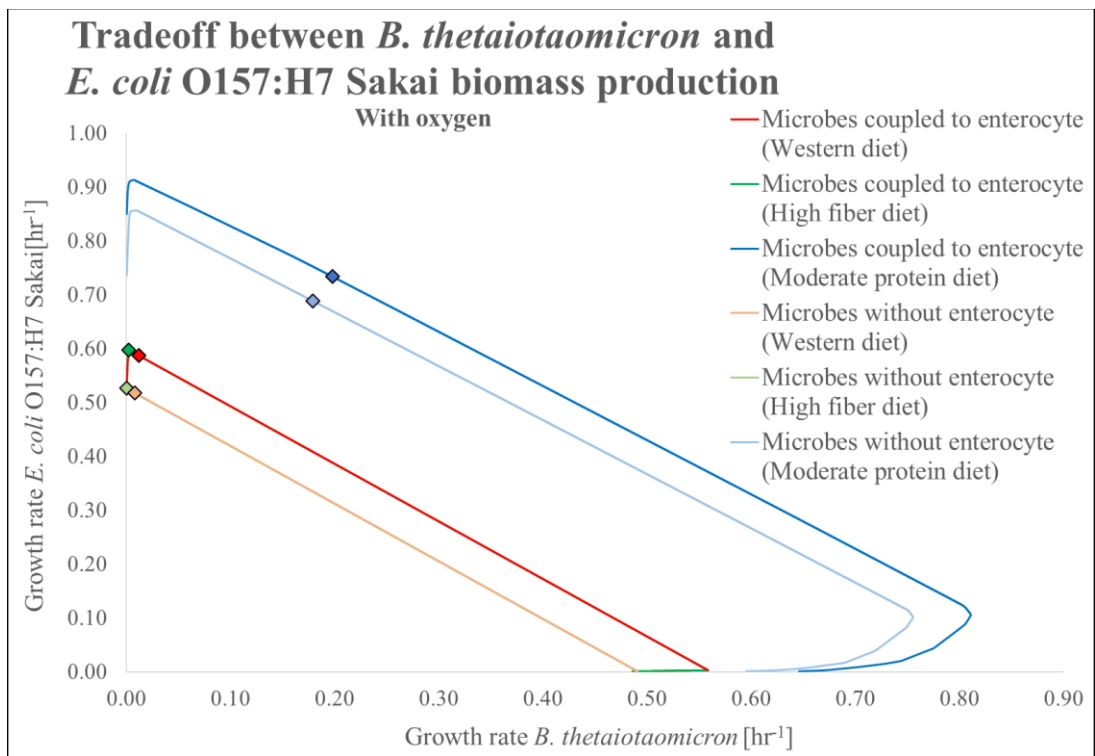
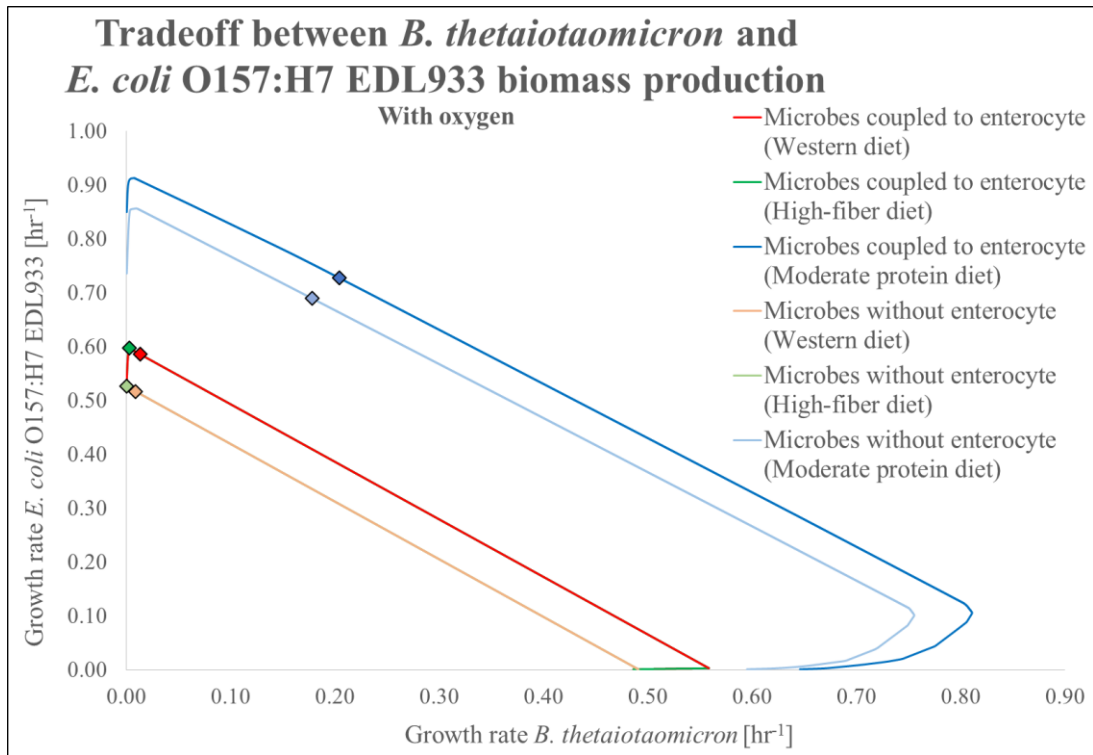
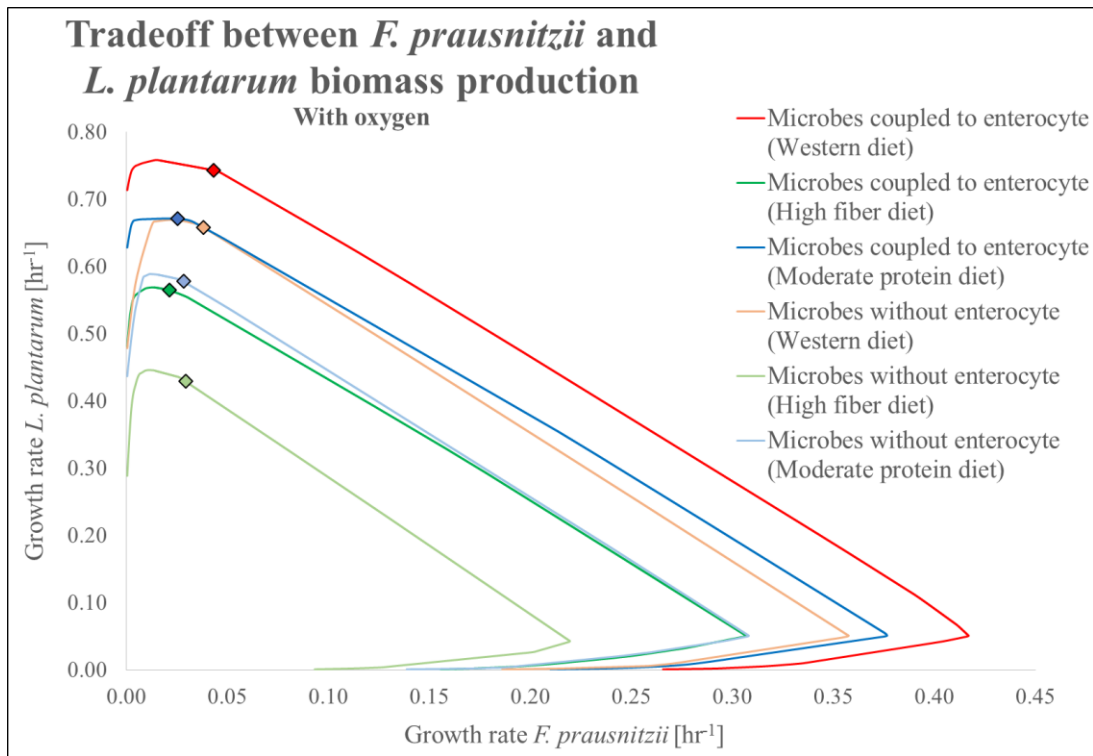


Figure S1.54



**Figure S1.55**



**Figure S1.56**

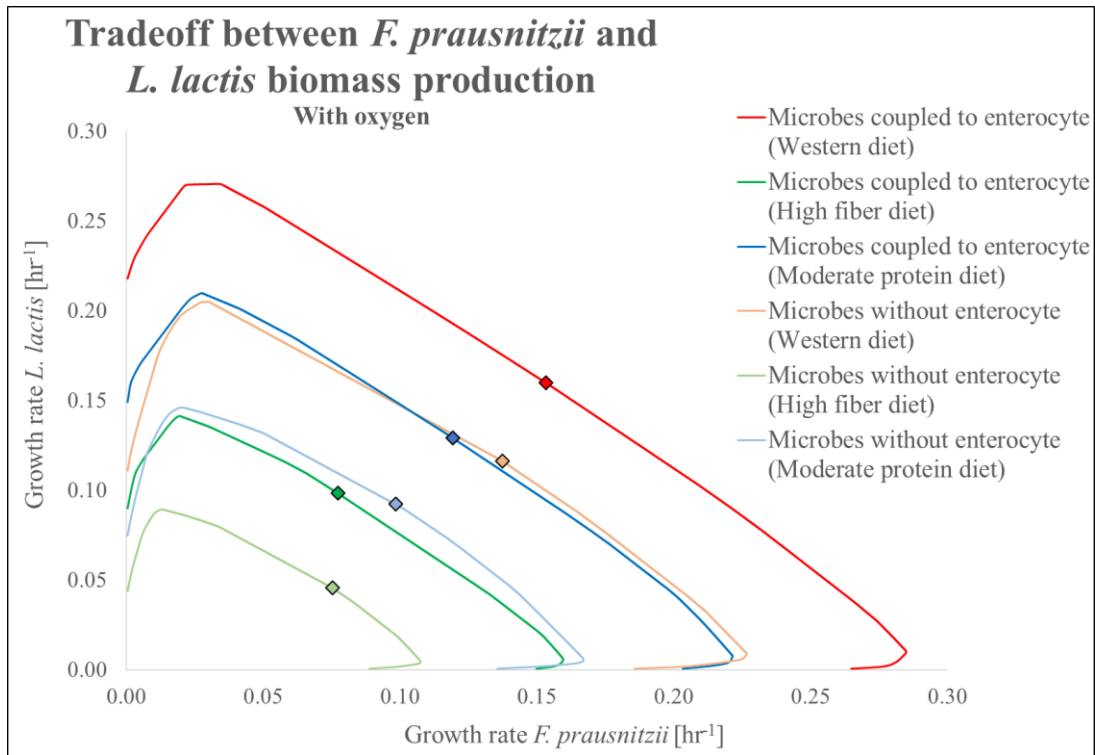


Figure S1.57

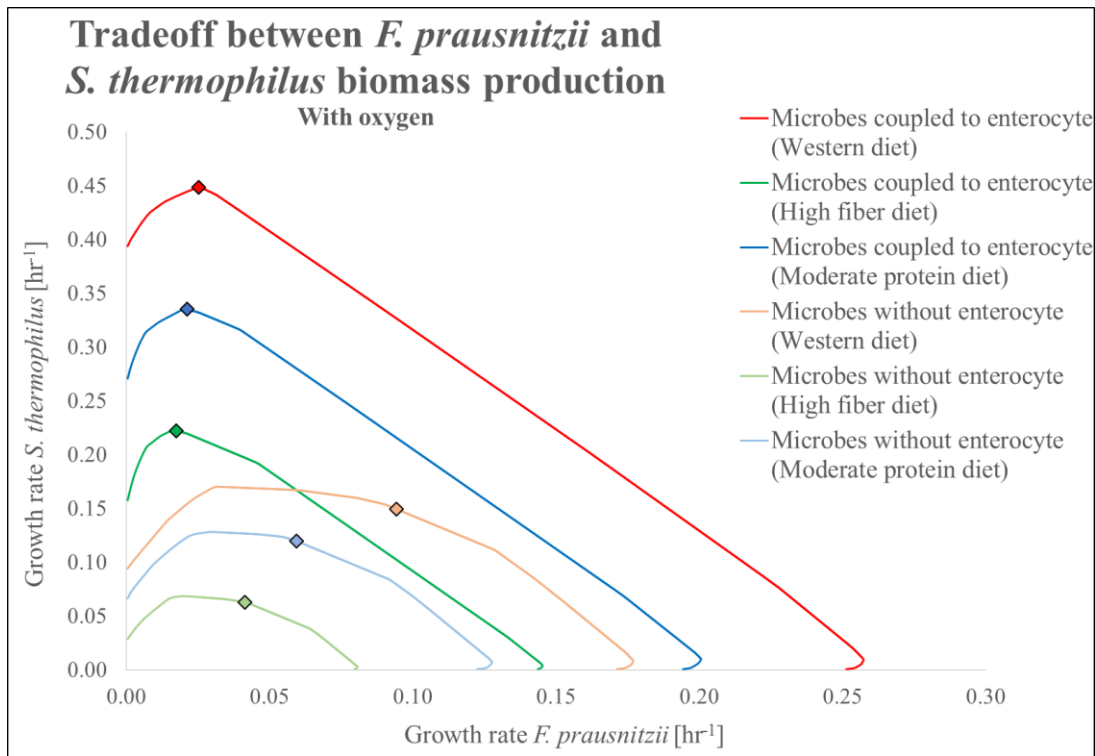


Figure S1.58

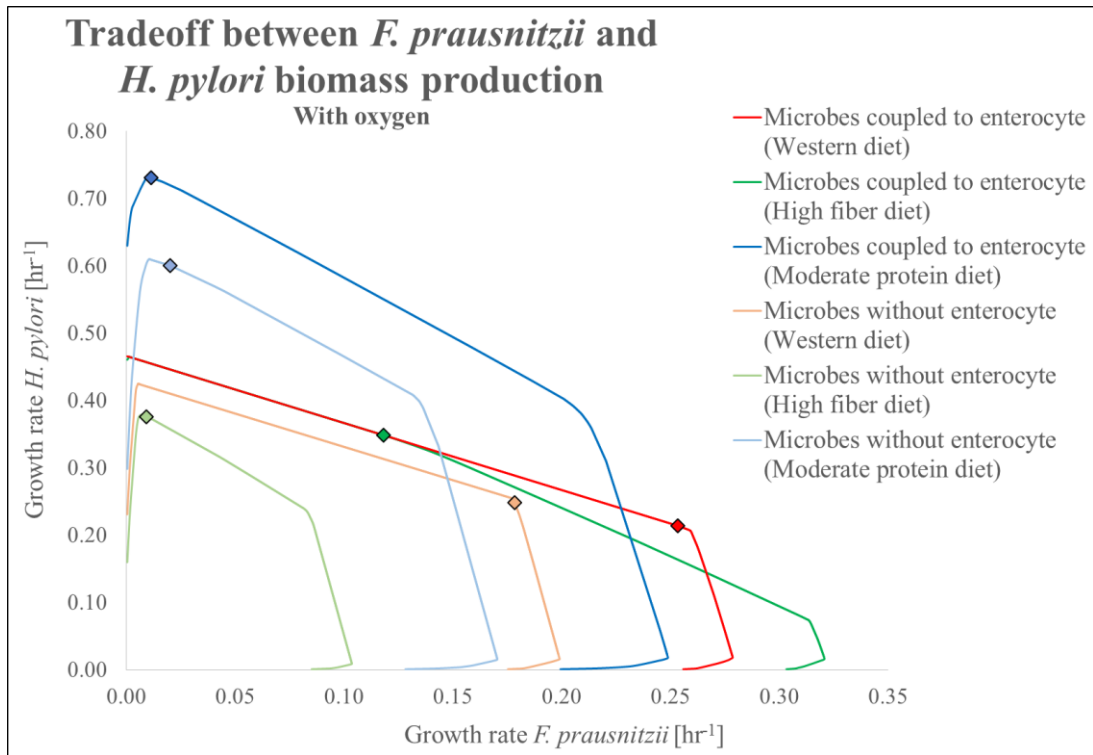


Figure S1.59

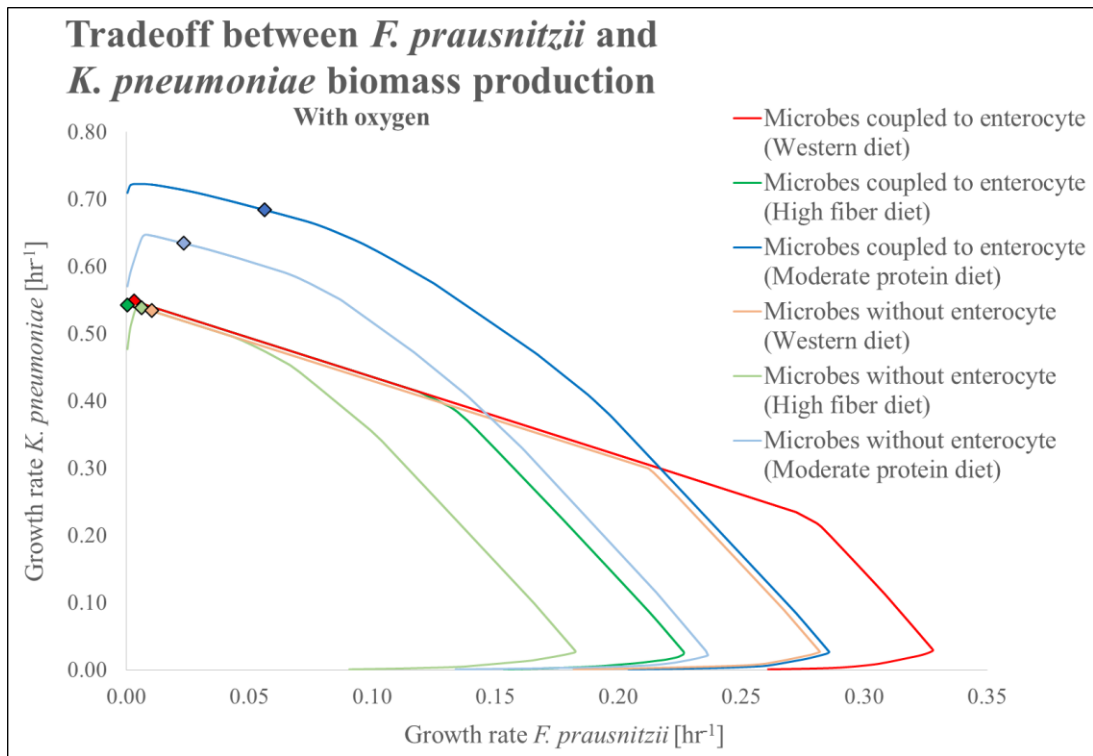


Figure S1.60

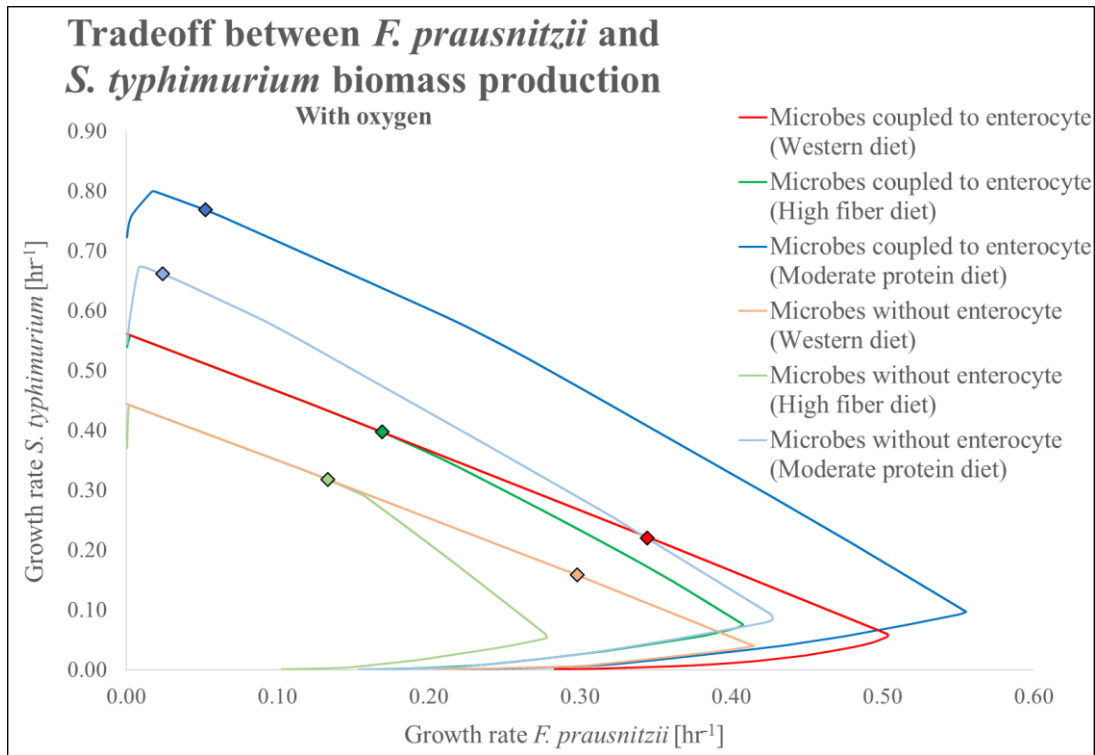


Figure S1.61

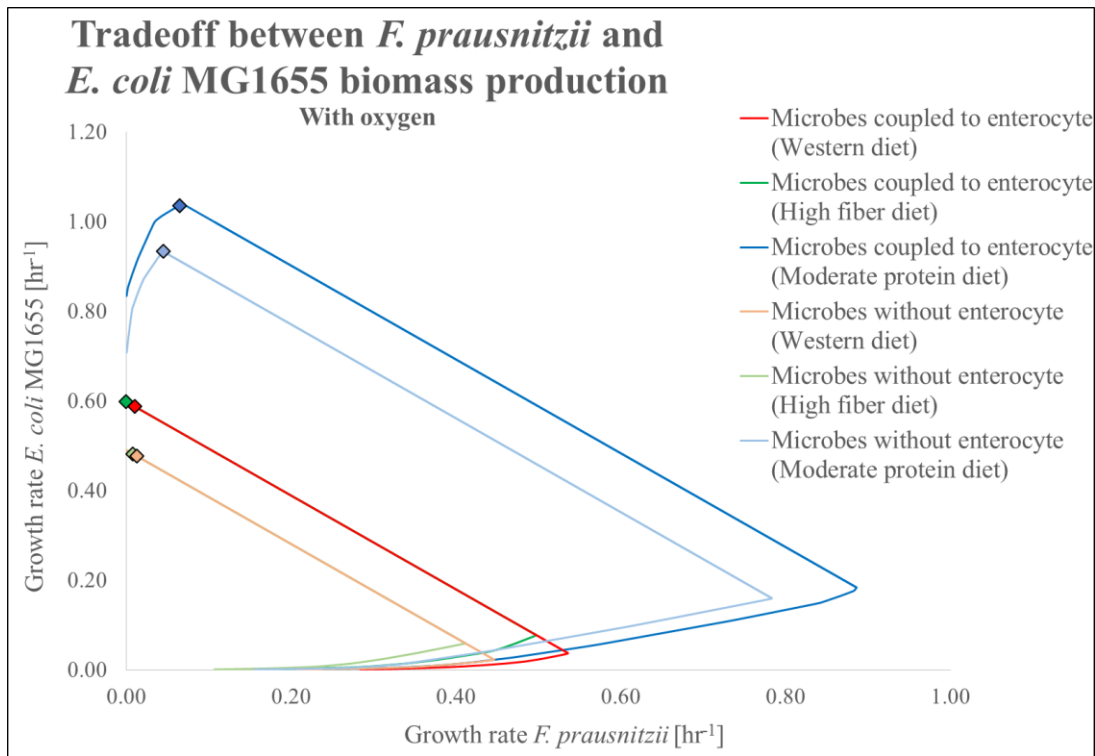
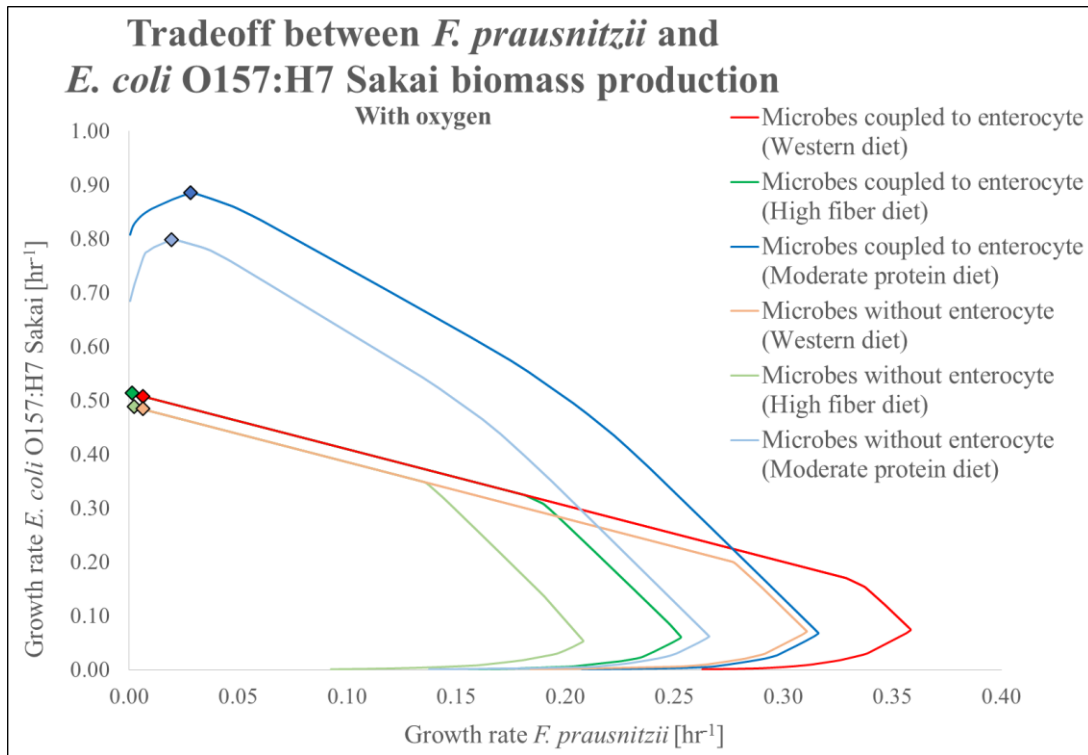
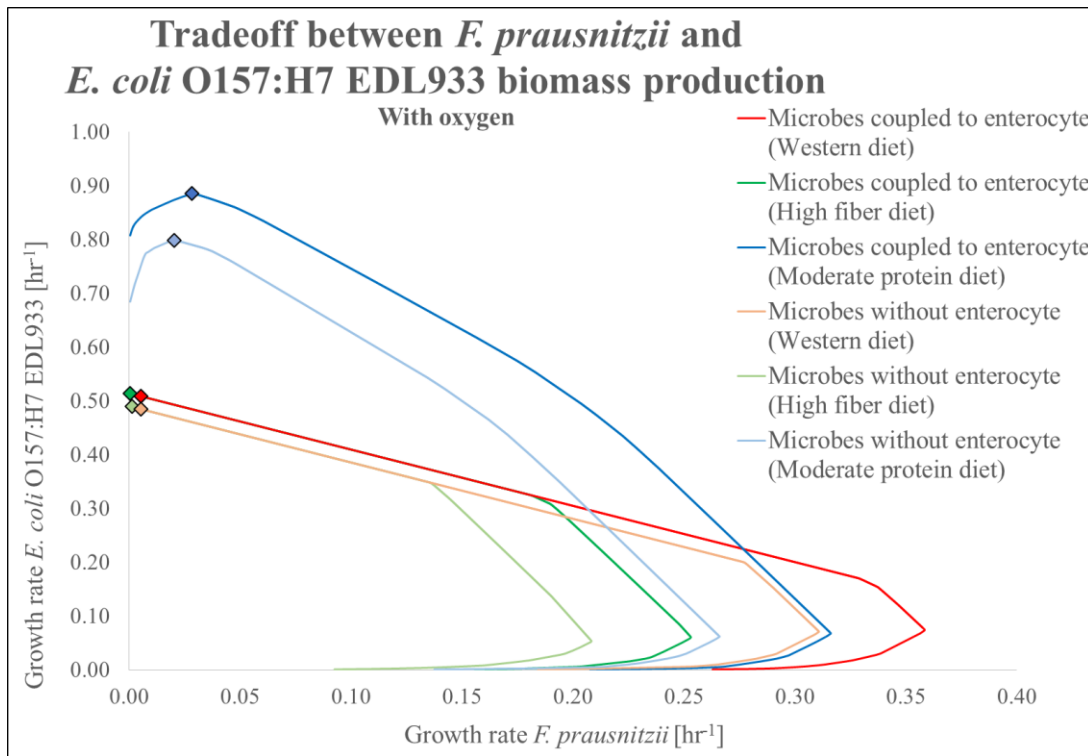


Figure S1.62



**Figure S1.63**



**Figure S1.64**

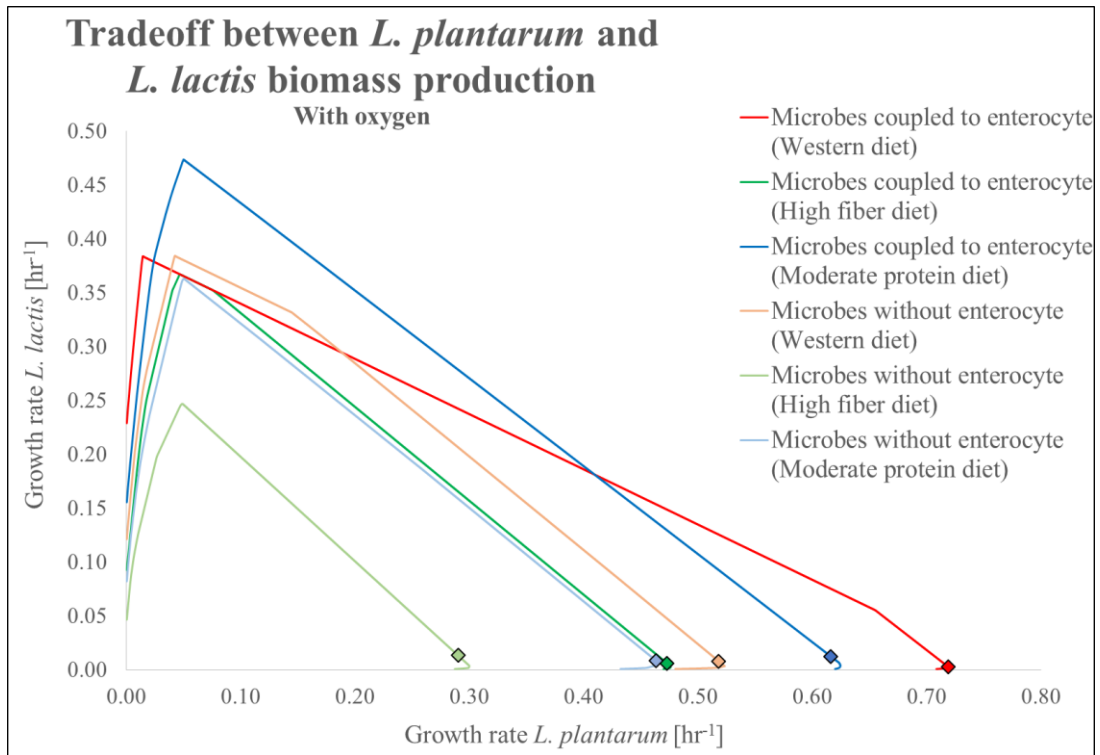


Figure S1.65

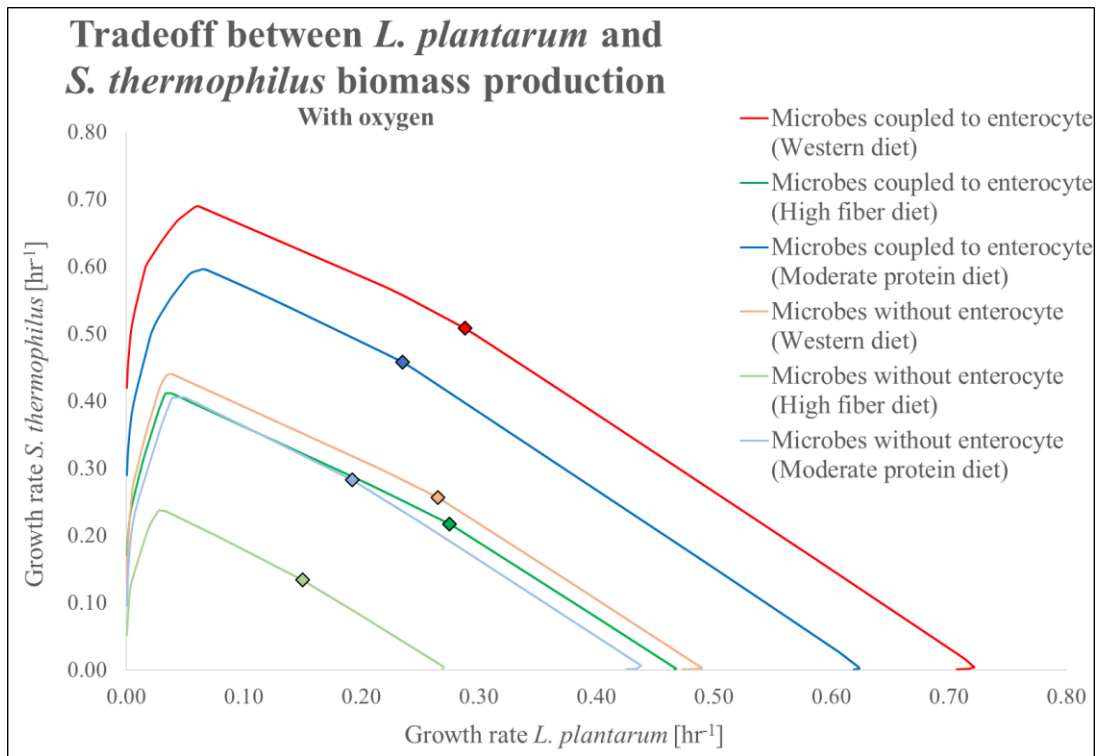


Figure S1.66

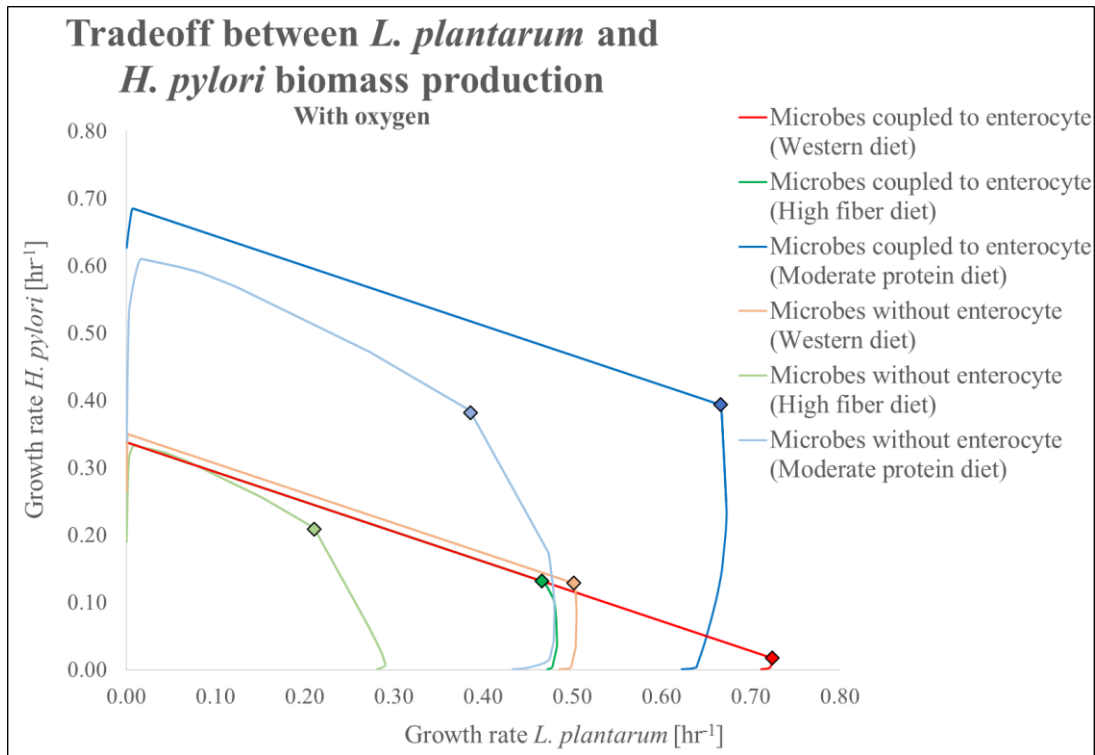


Figure S1.67

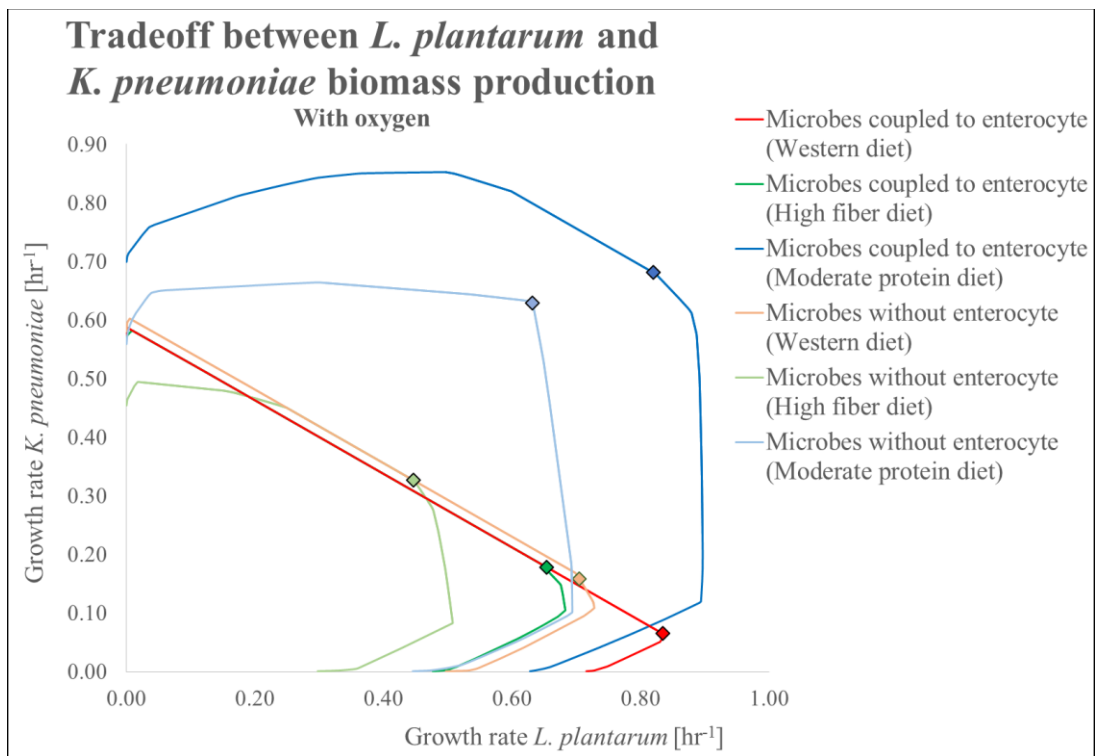


Figure S1.68



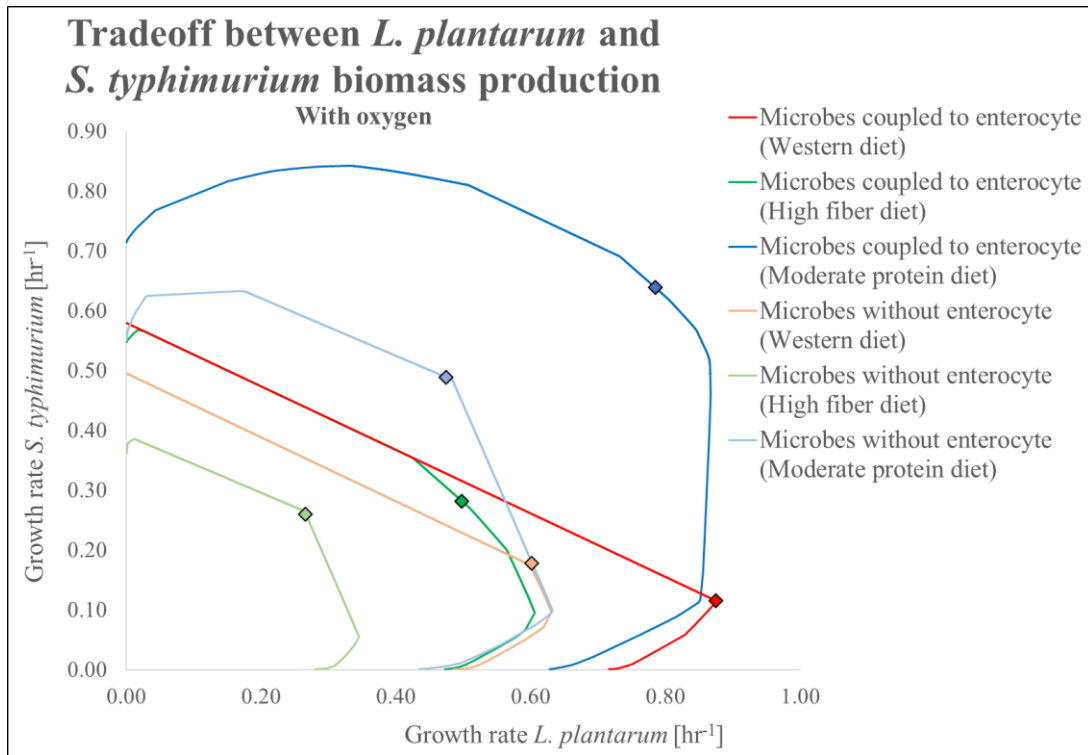


Figure S1.69

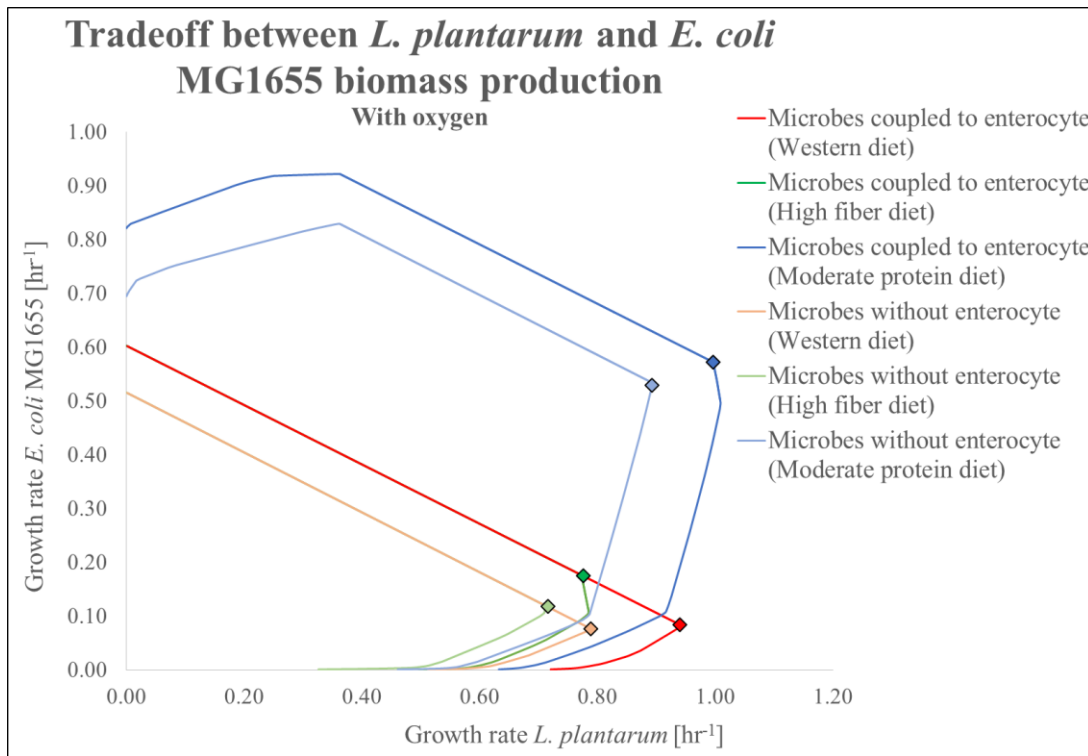
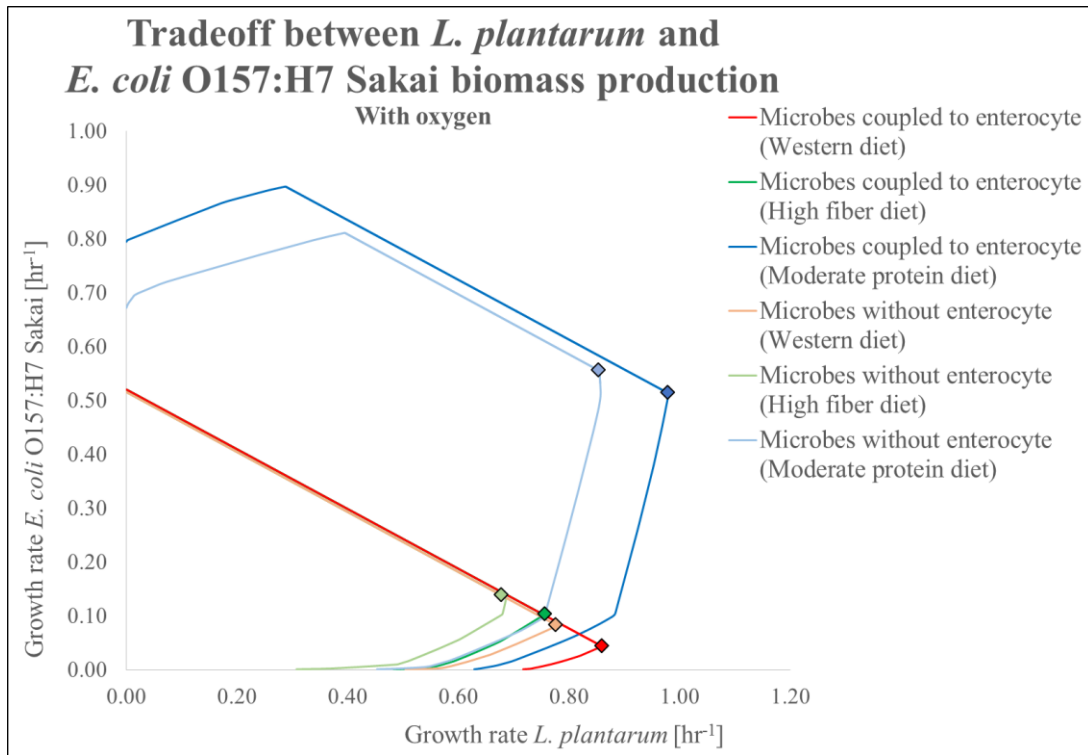
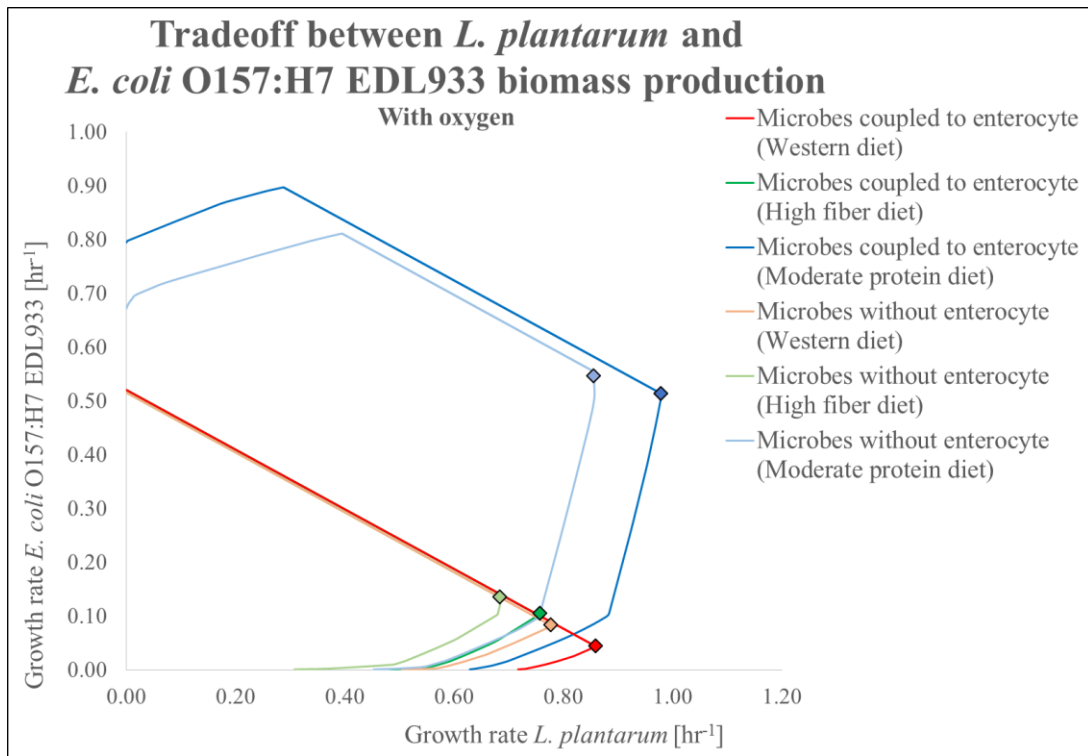


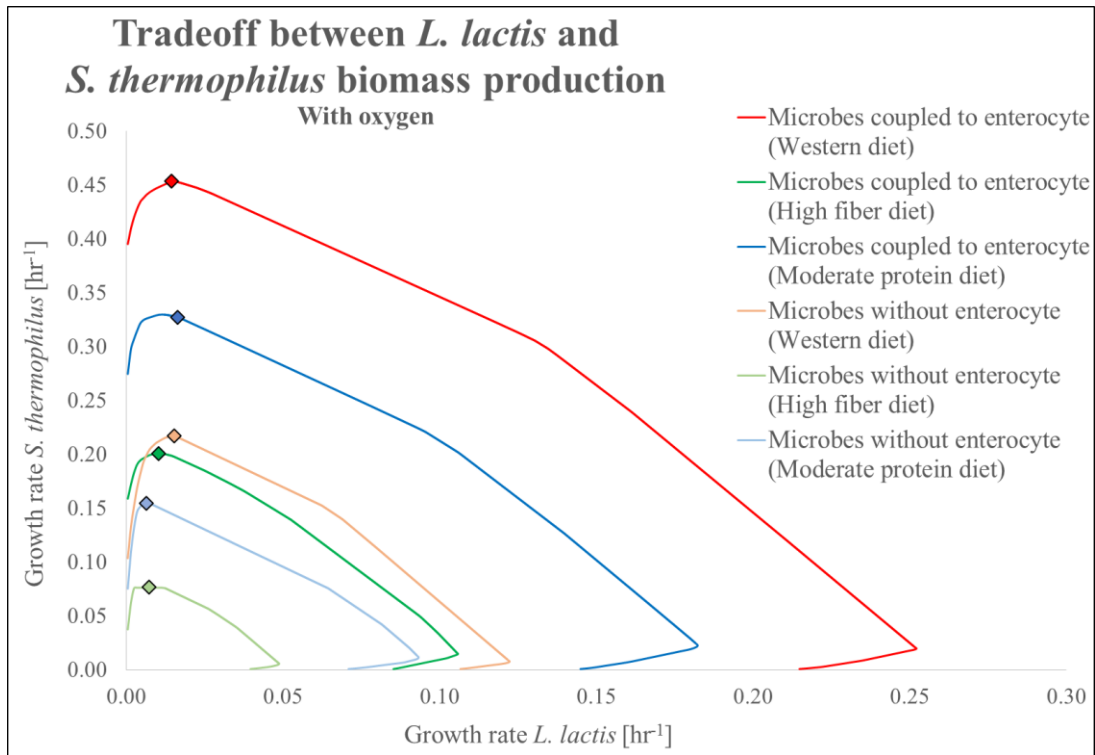
Figure S1.70



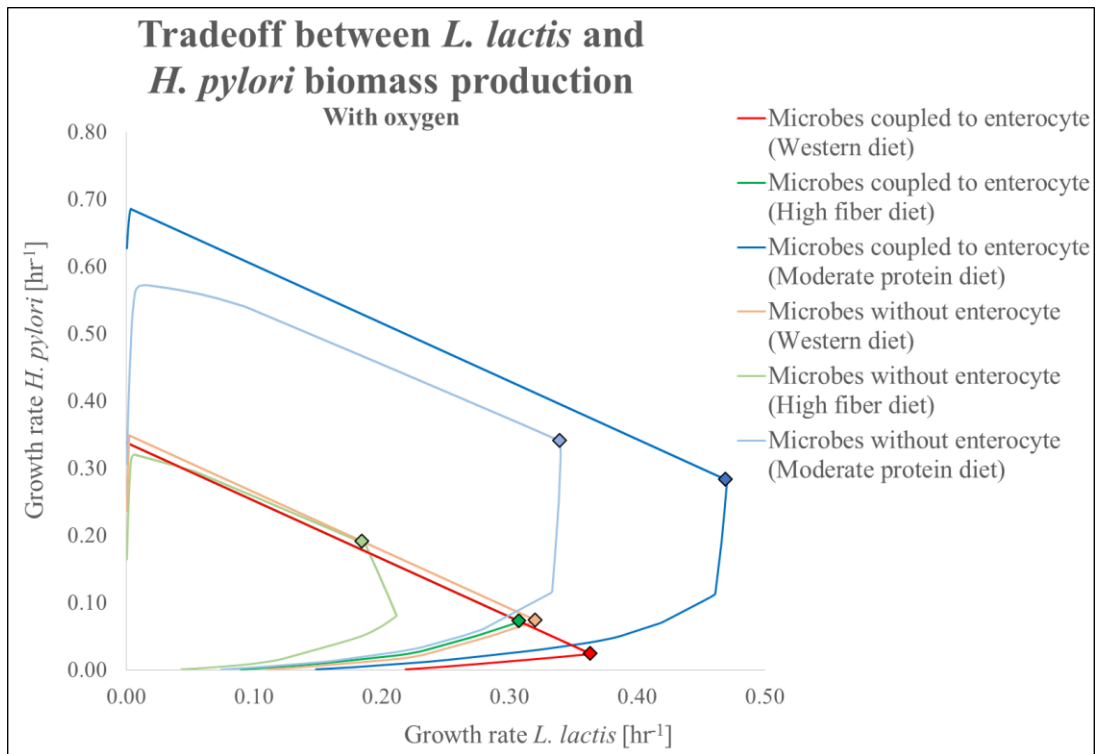
**Figure S1.71**



**Figure S1.72**



**Figure S1.73**



**Figure S1.74**

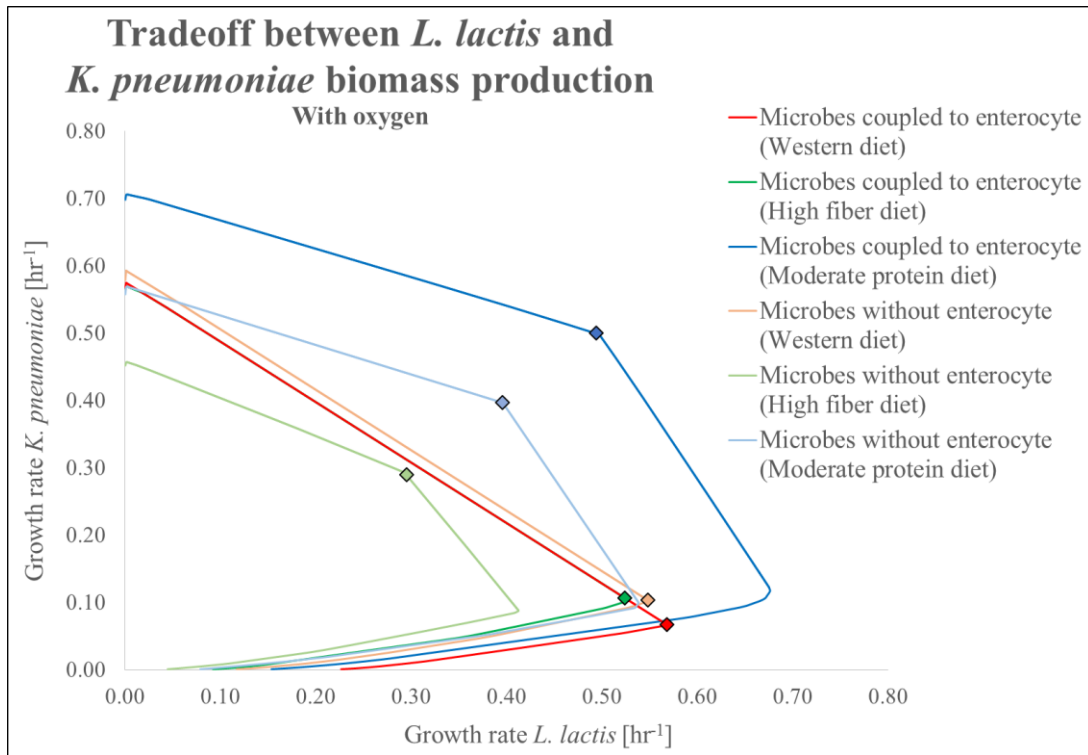


Figure S1.75

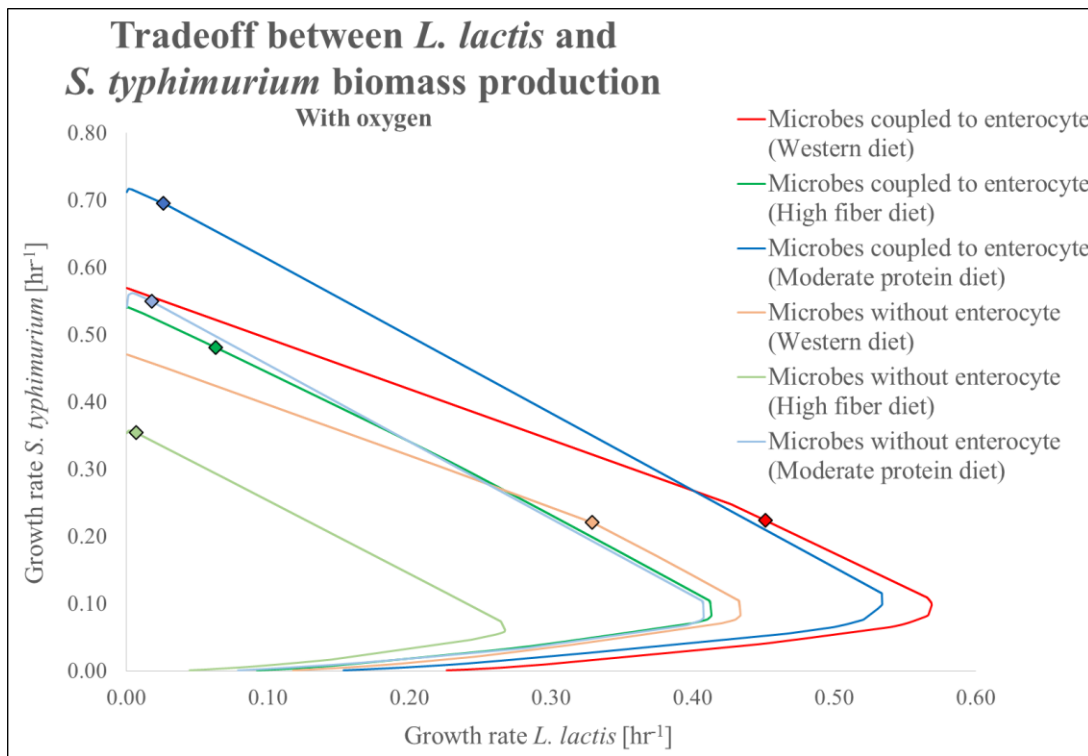
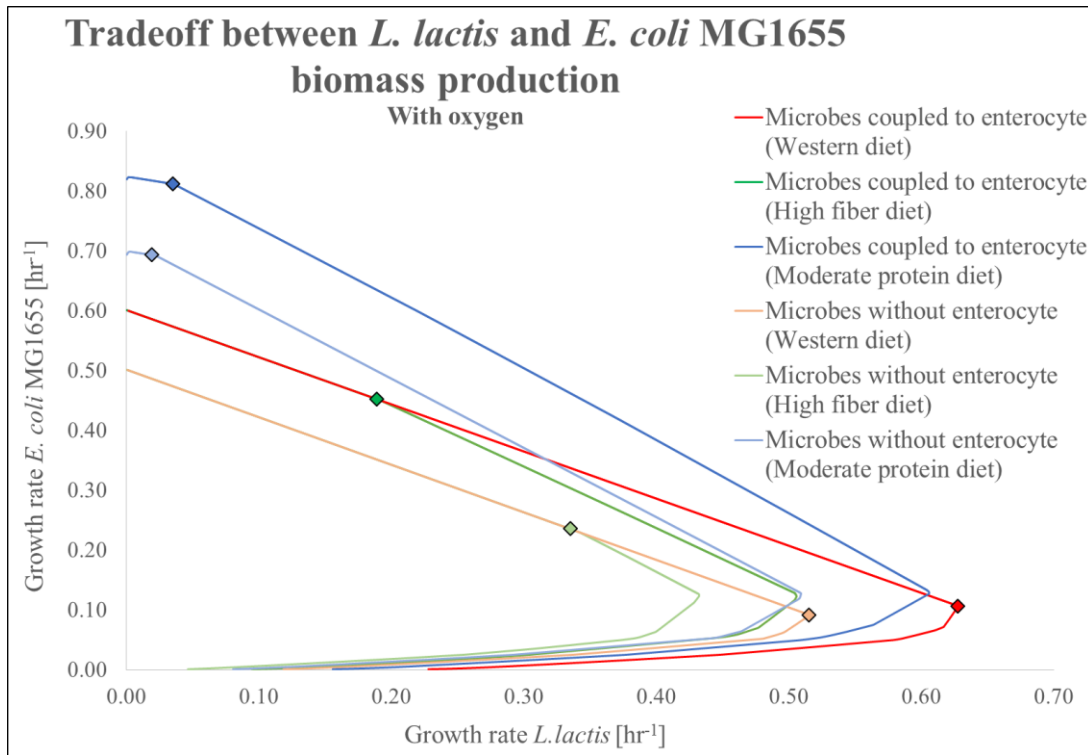
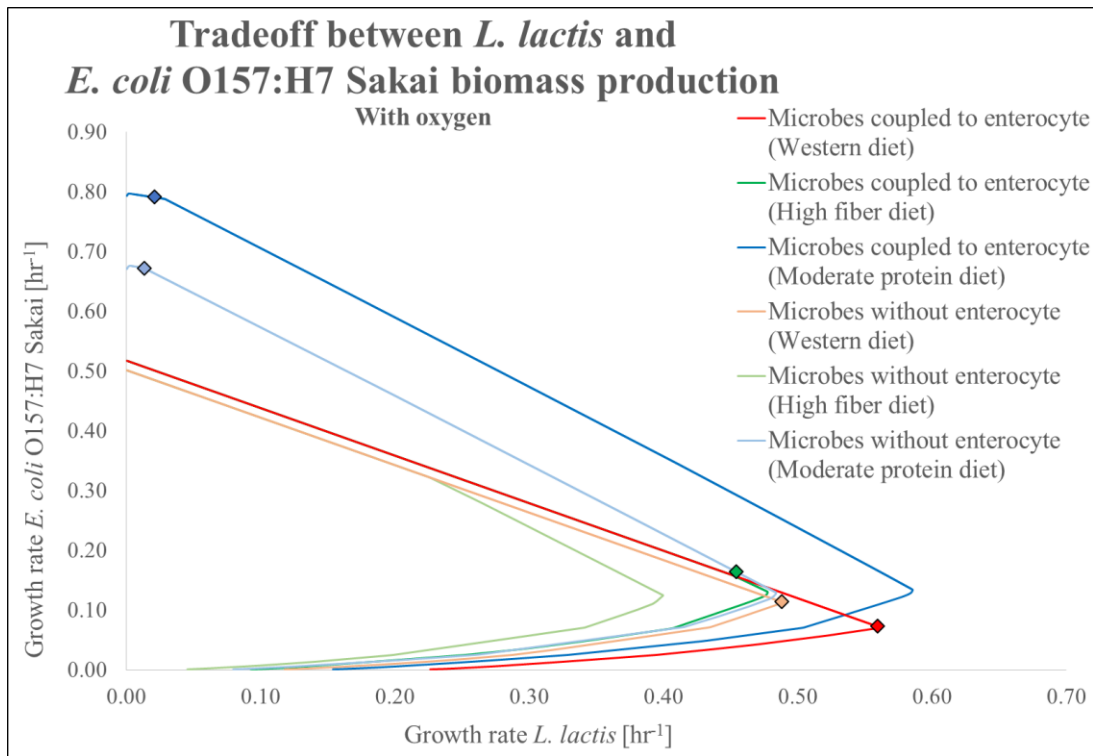


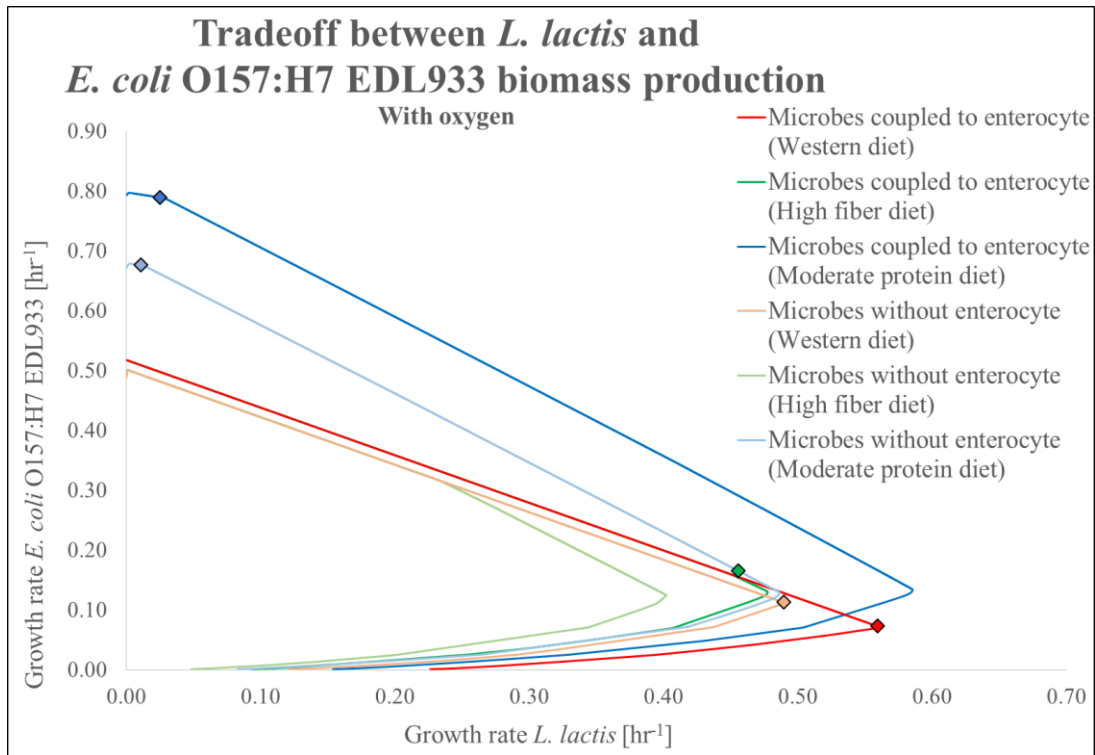
Figure S1.76



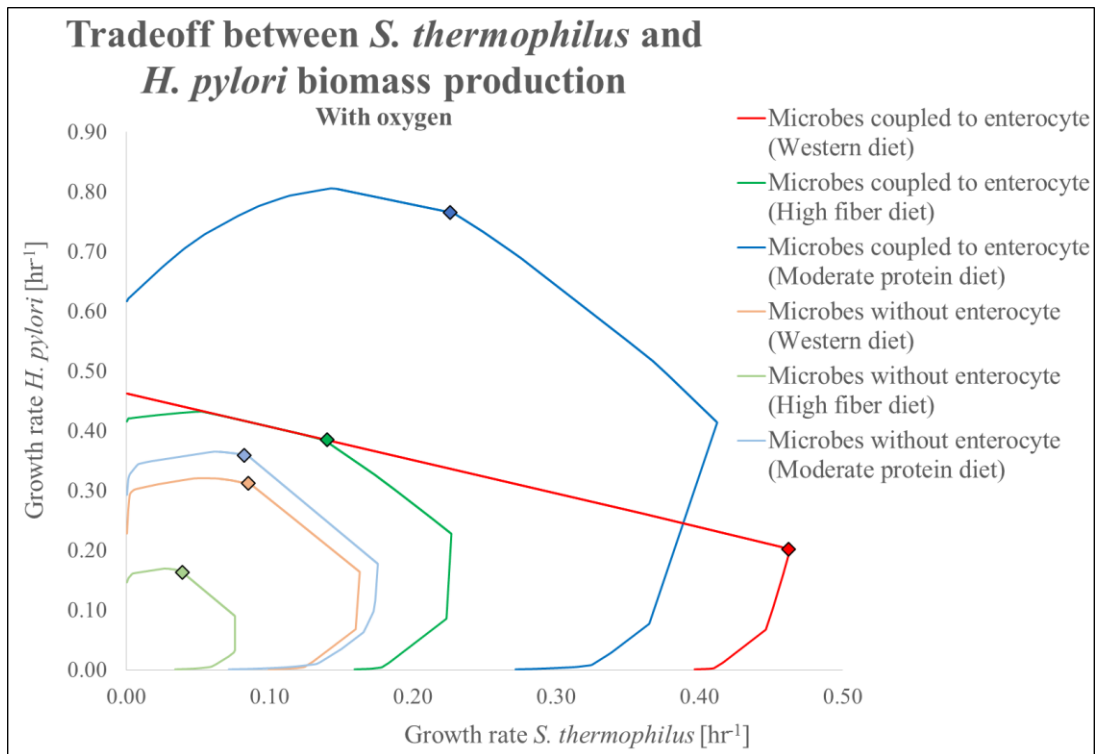
**Figure S1.77**



**Figure S1.78**



**Figure S1.79**



**Figure S1.80**

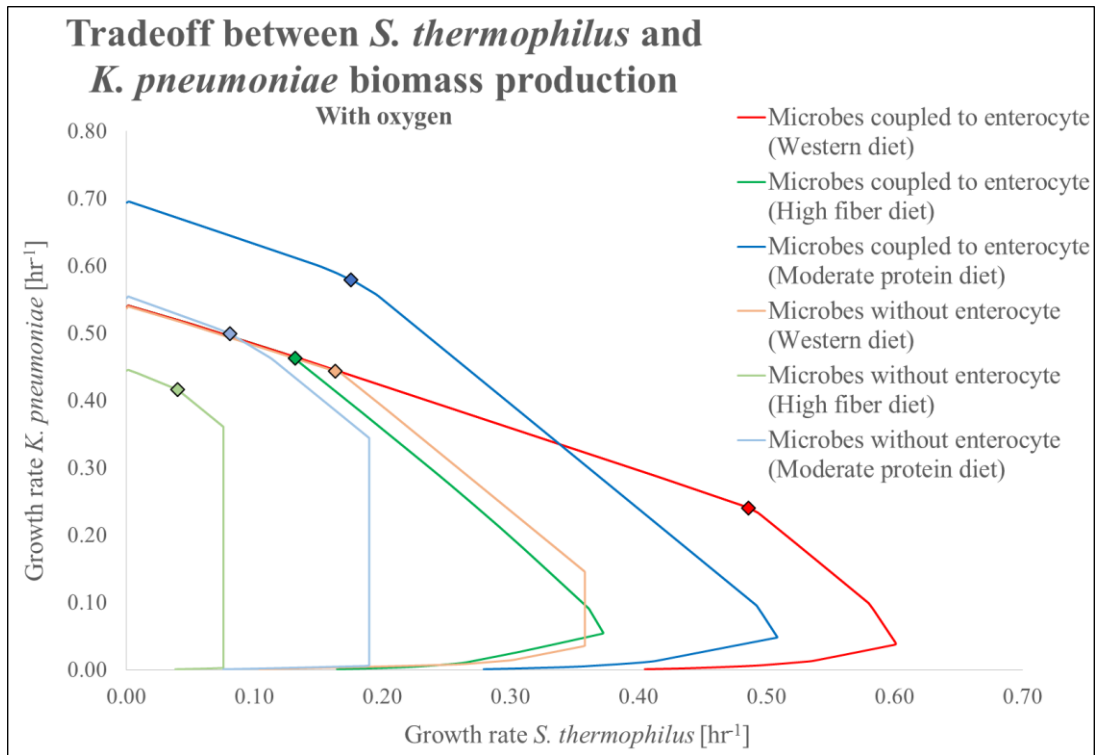


Figure S1.81

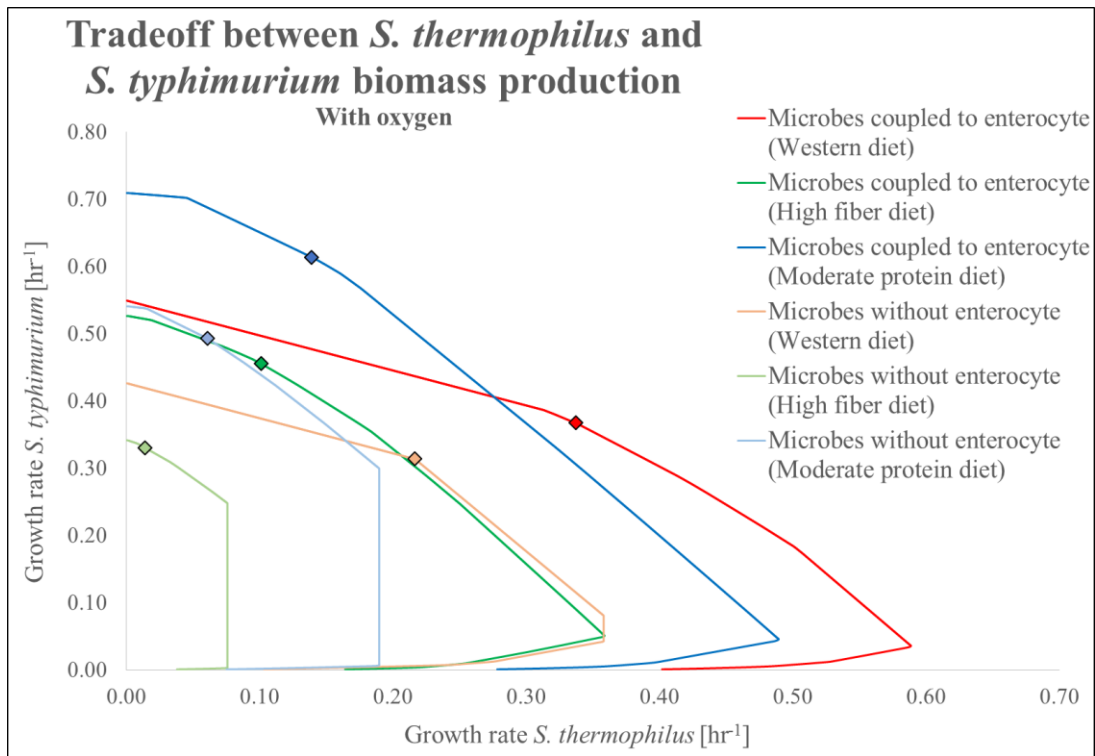


Figure S1.82

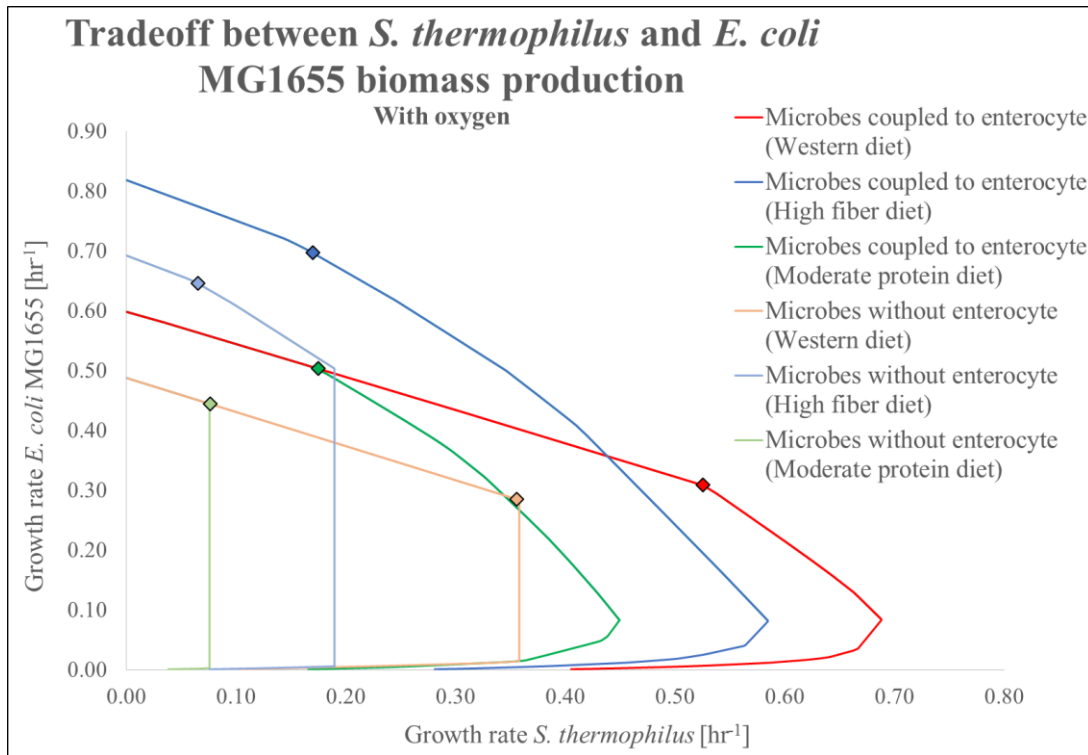


Figure S1.83

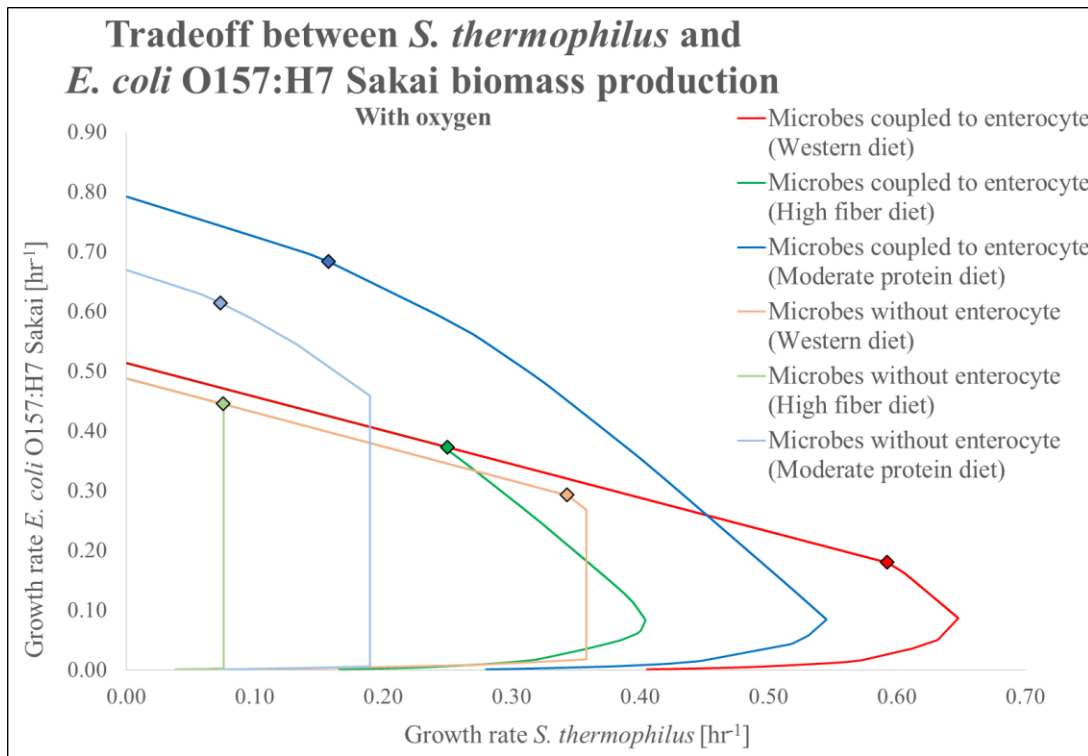


Figure S1.84



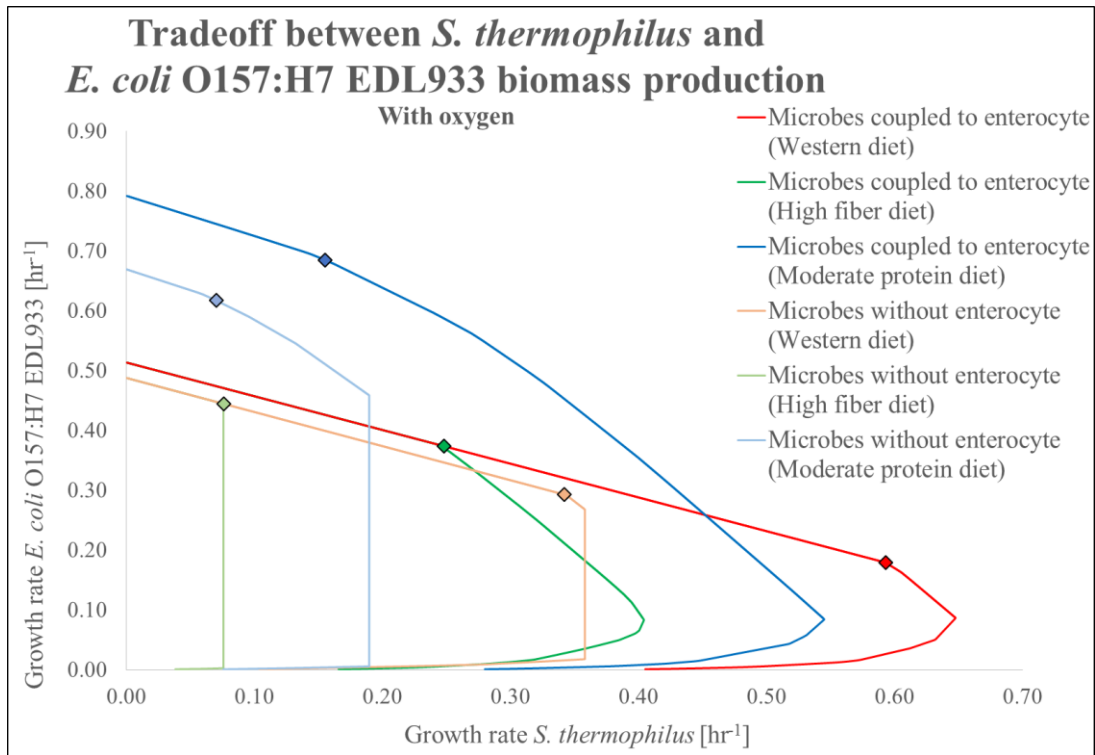


Figure S1.85

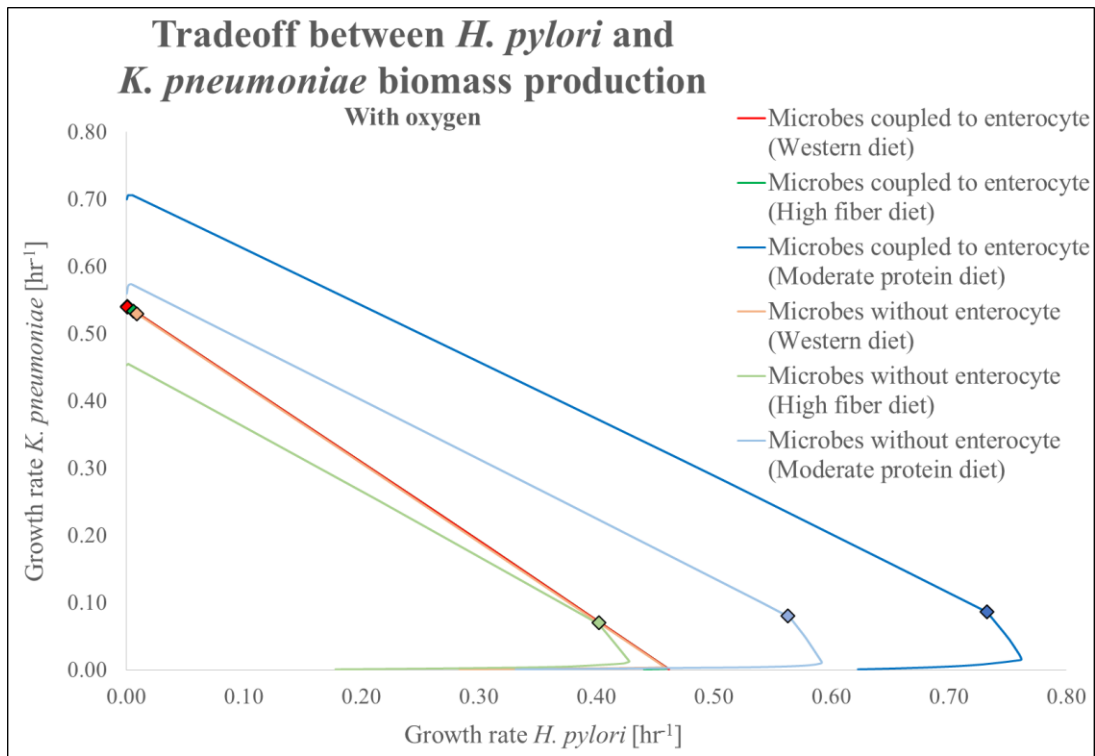


Figure S1.86

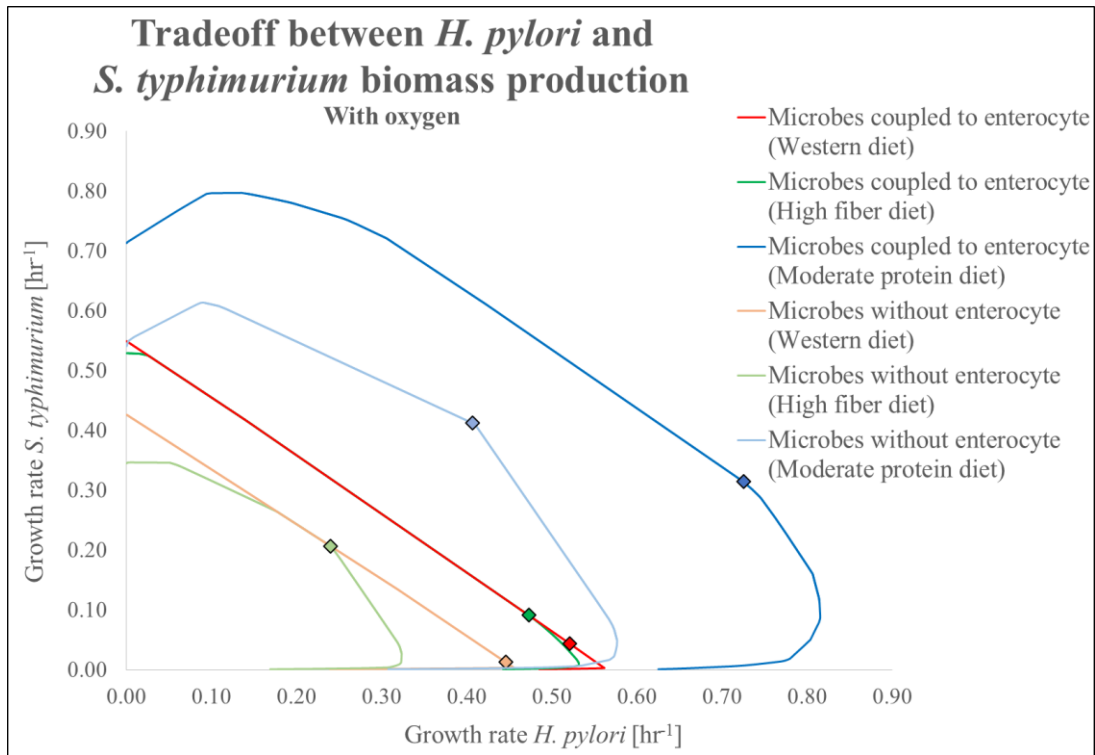


Figure S1.87

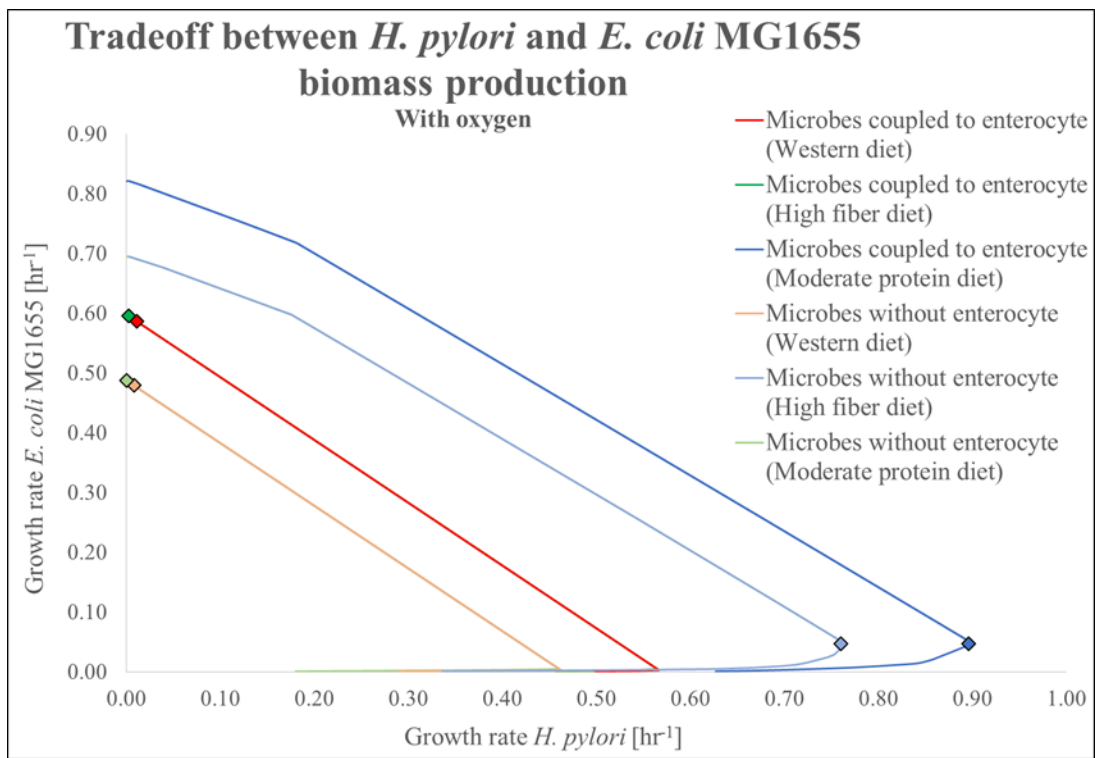
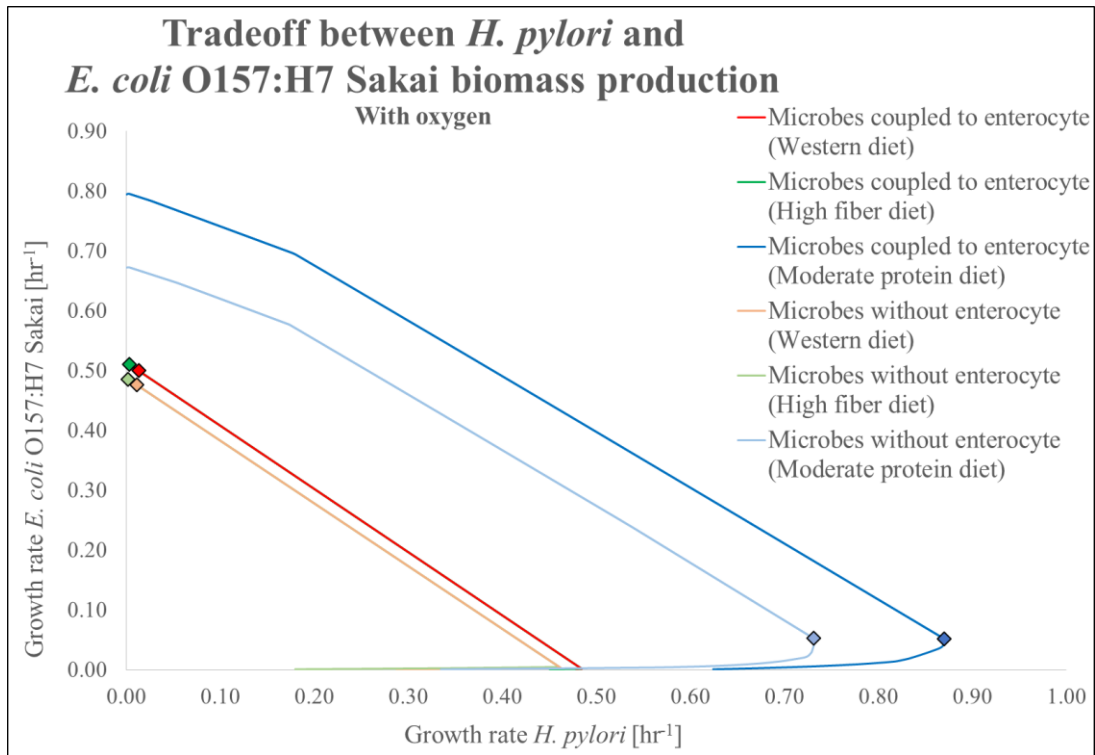
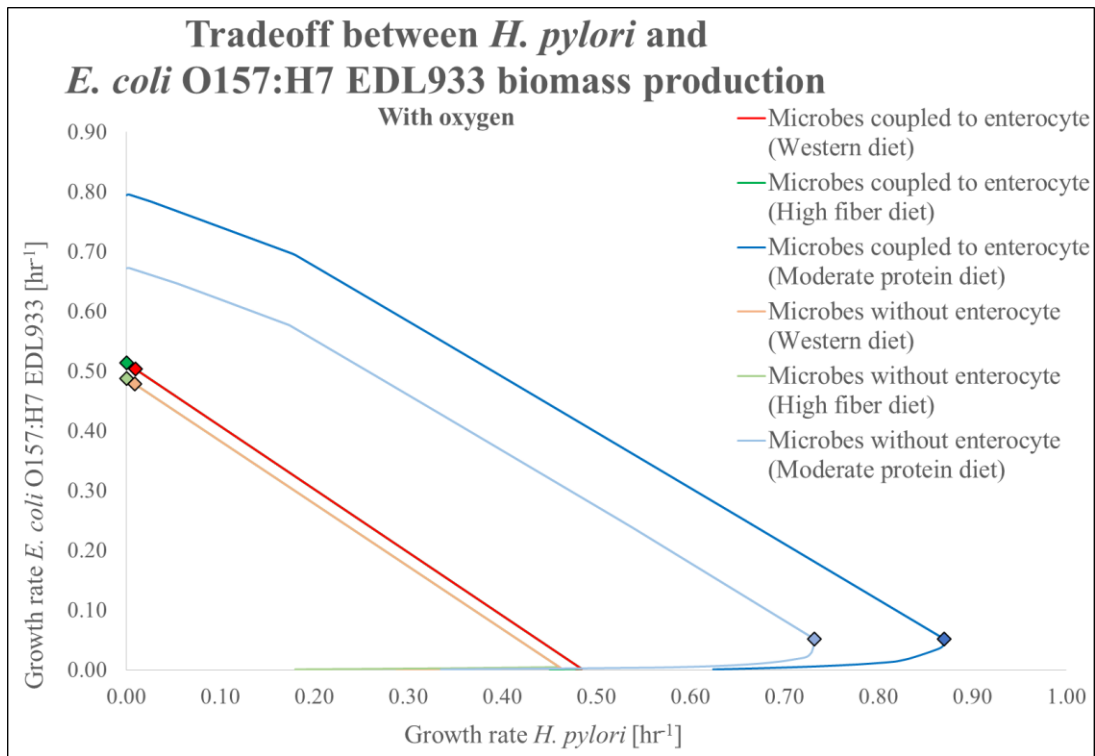


Figure S1.88



**Figure S1.89**



**Figure S1.90**

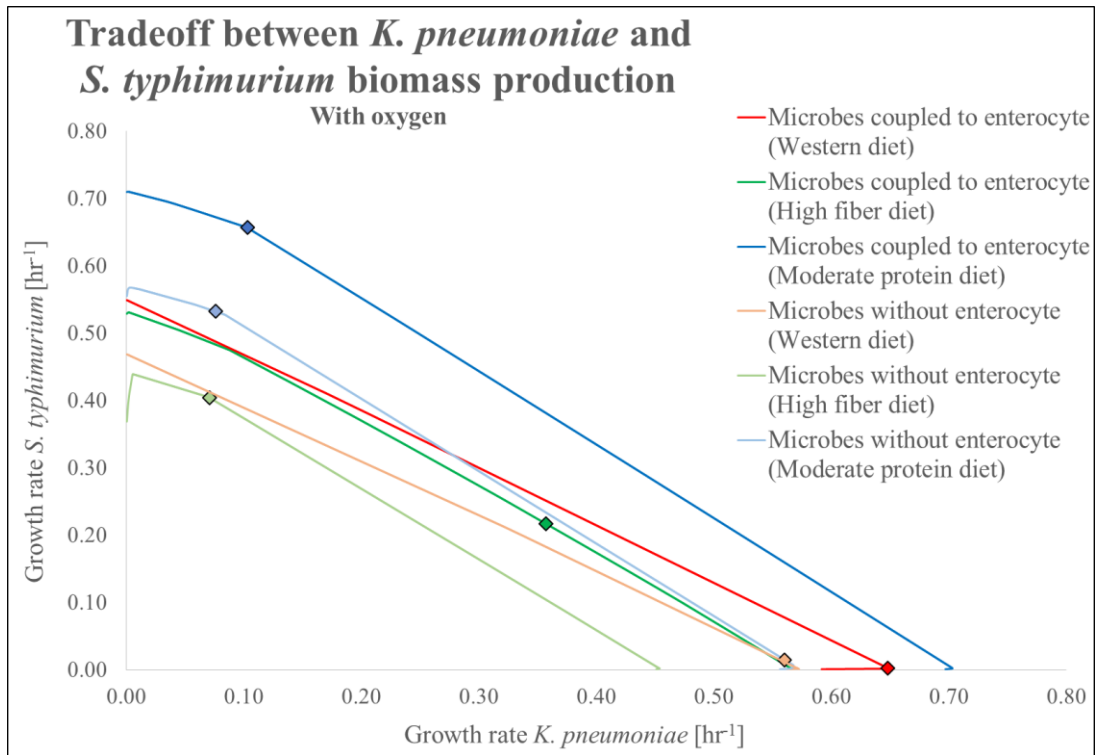


Figure S1.91

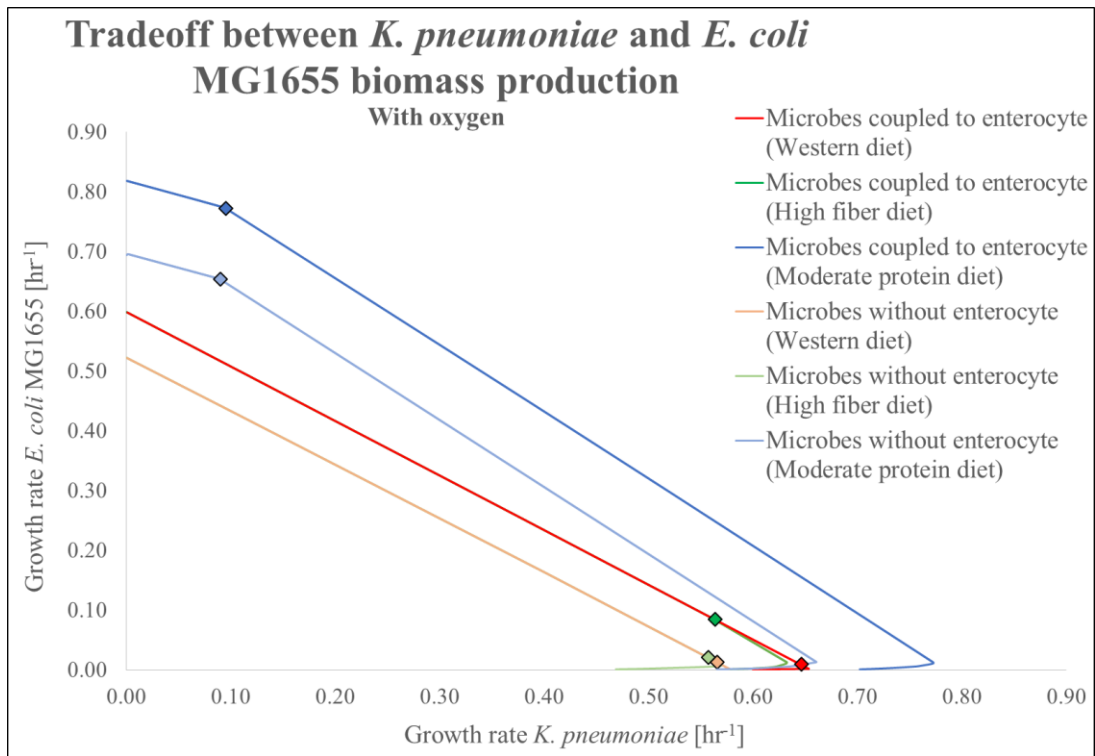
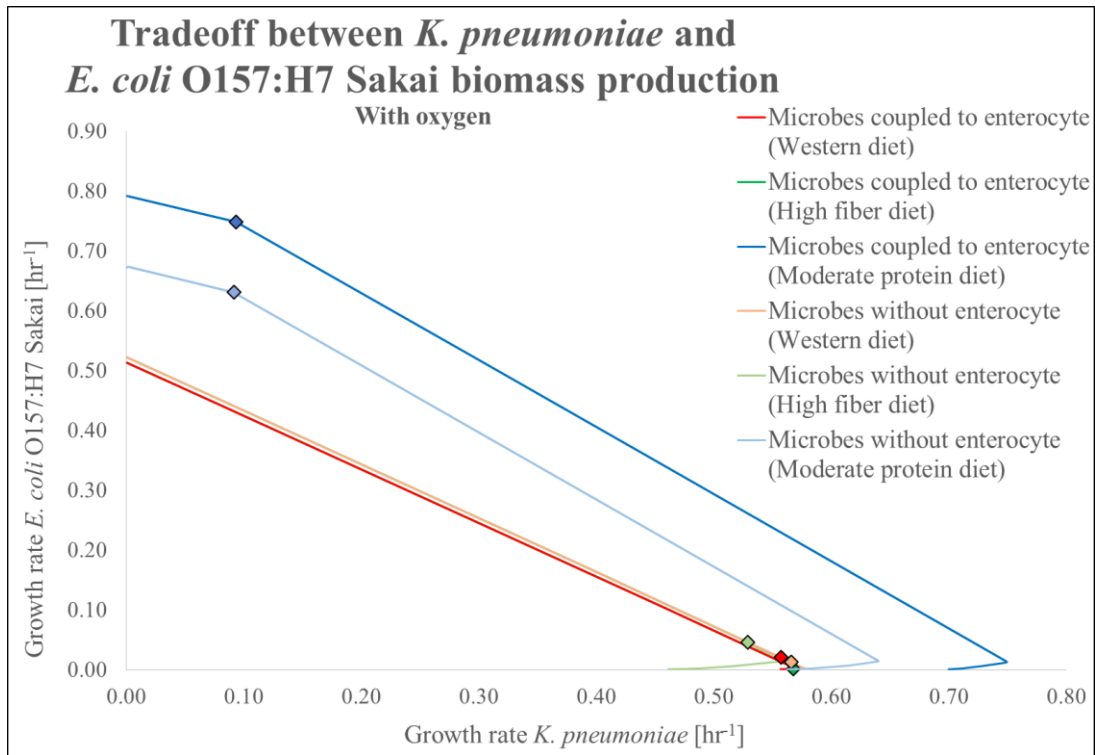
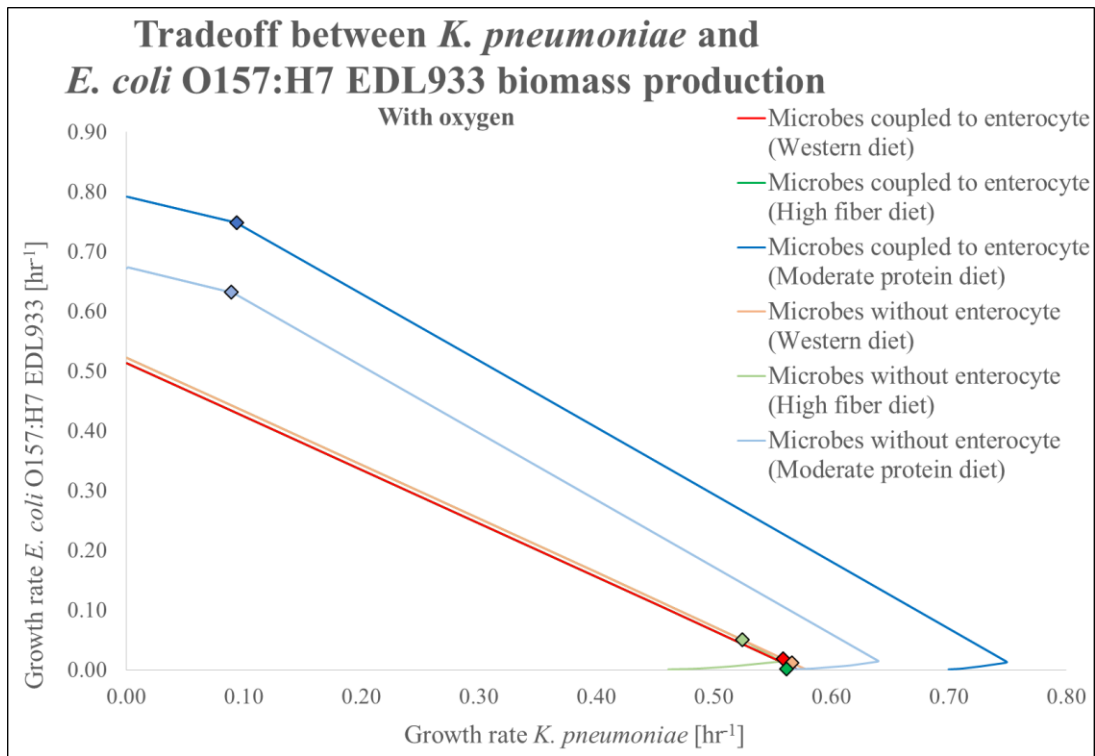


Figure S1.92



**Figure S1.93**



**Figure S1.94**

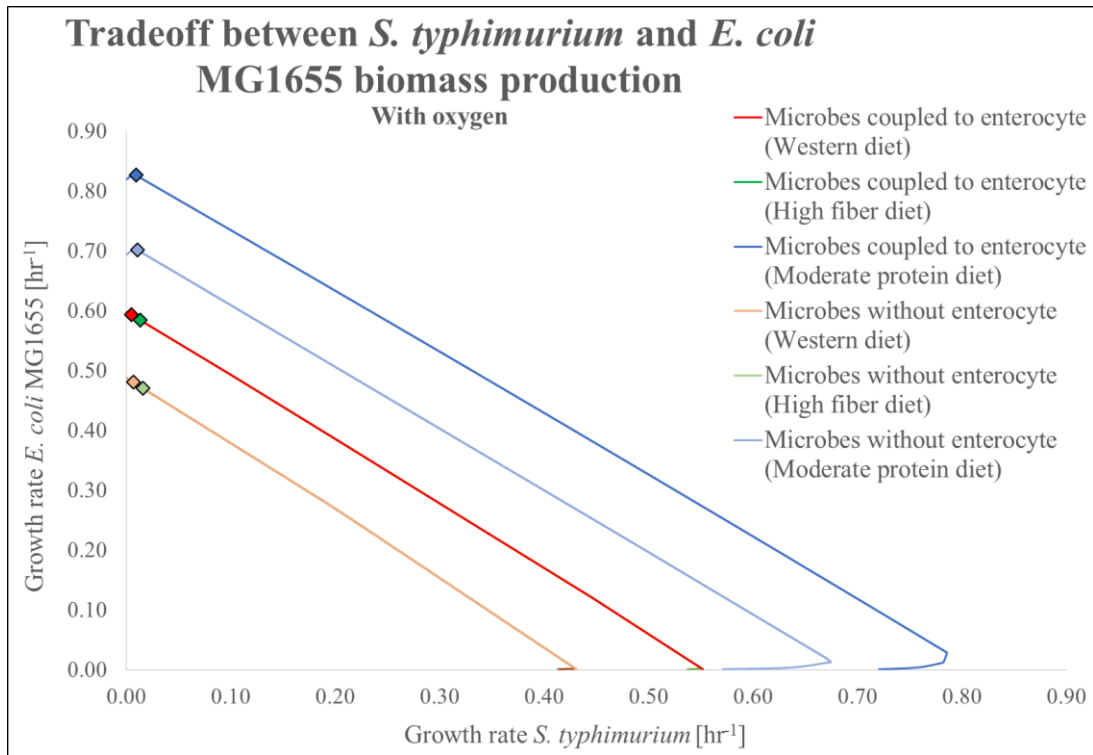


Figure S1.95

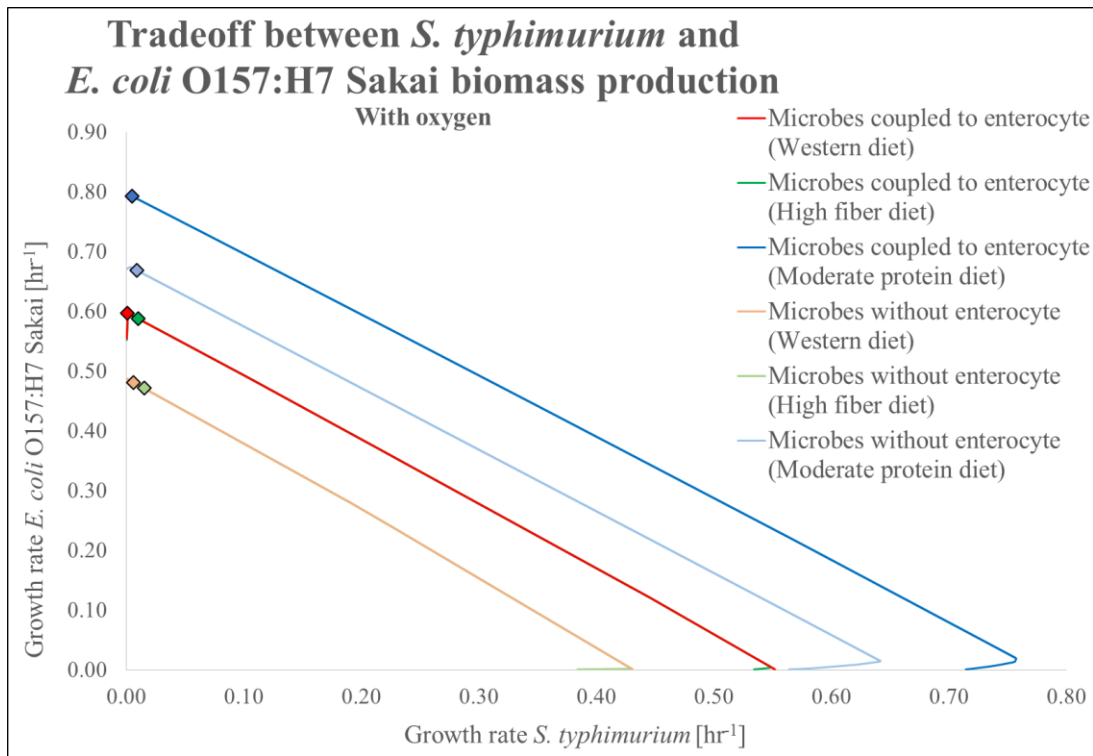
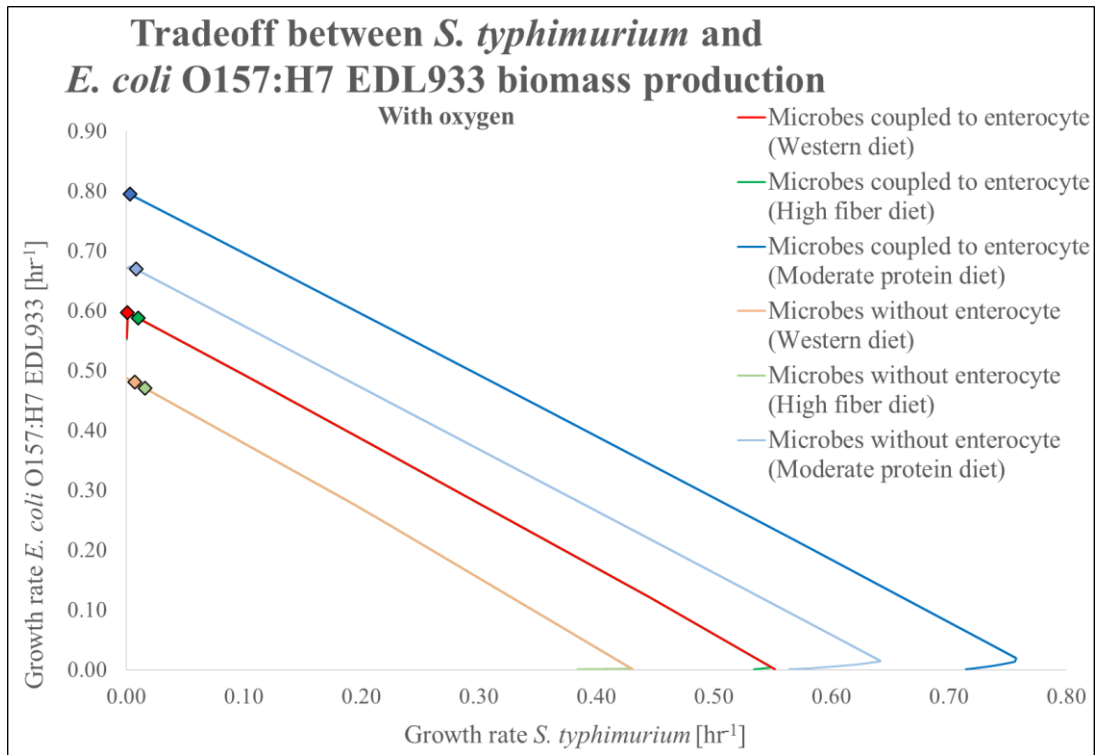
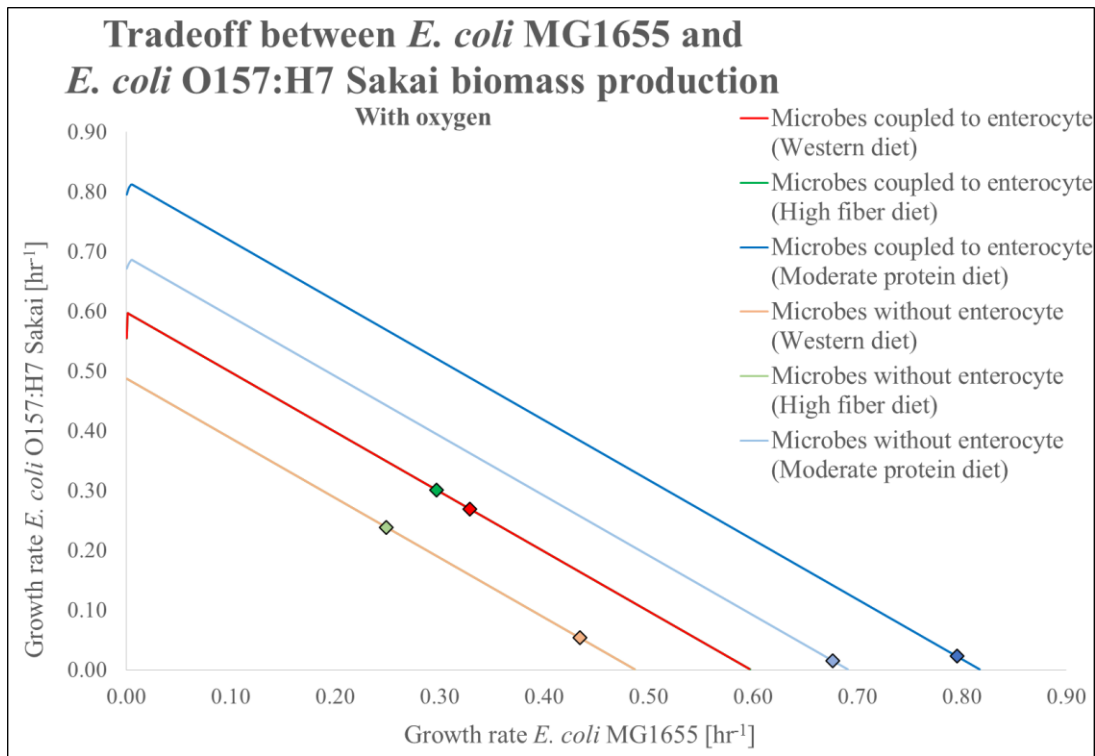


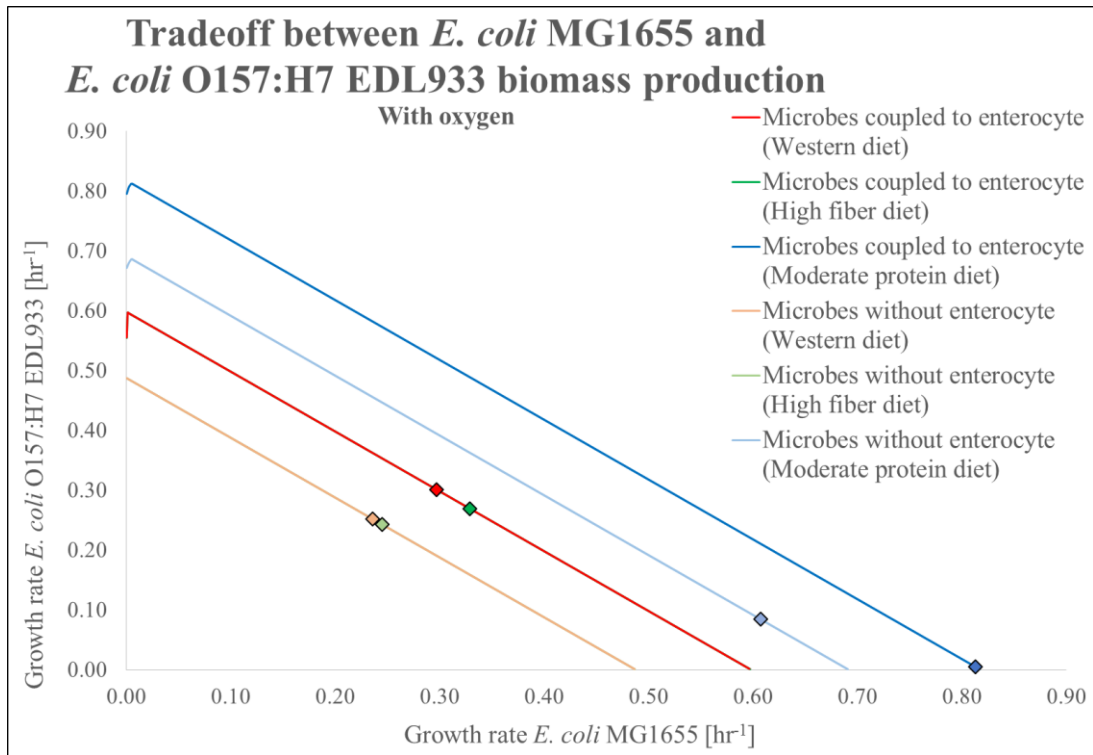
Figure S1.96



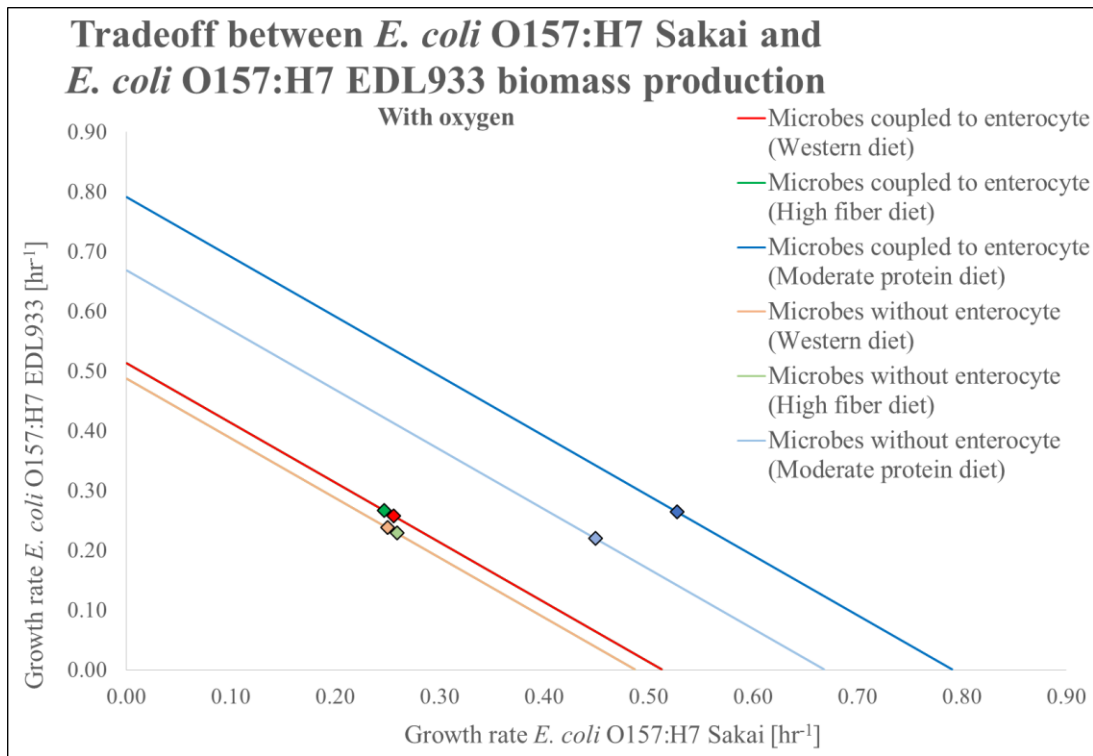
**Figure S1.97**



**Figure S1.98**

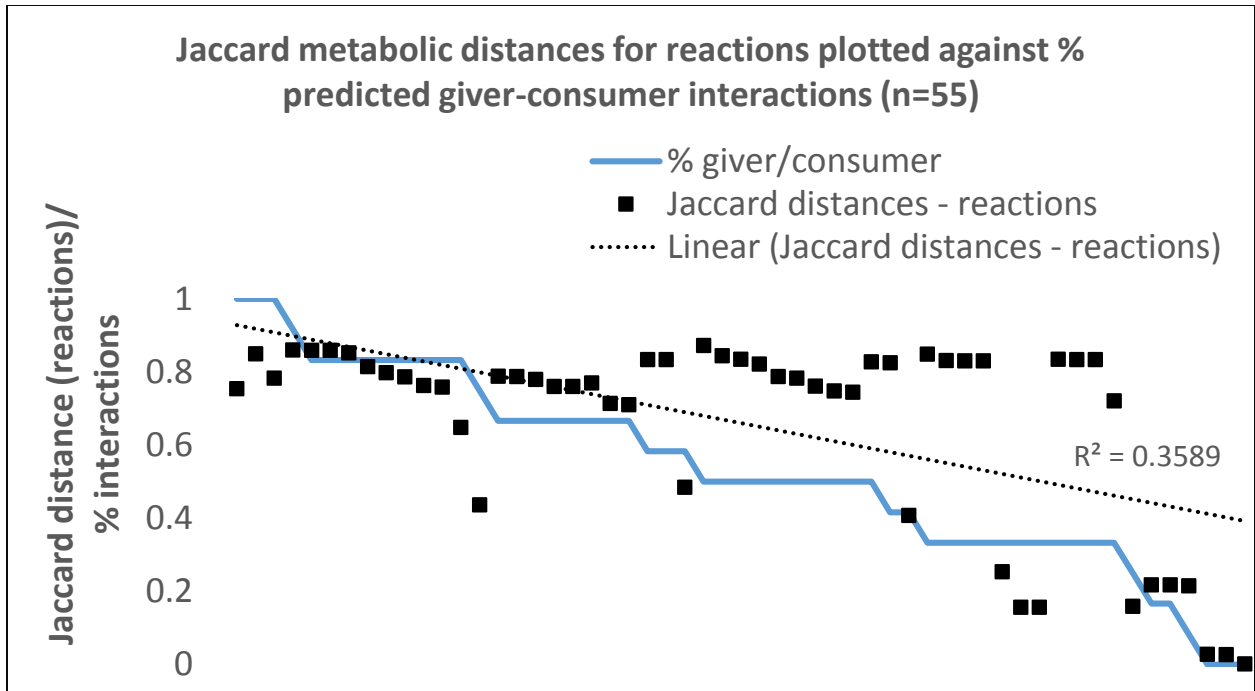


**Figure S1.99**

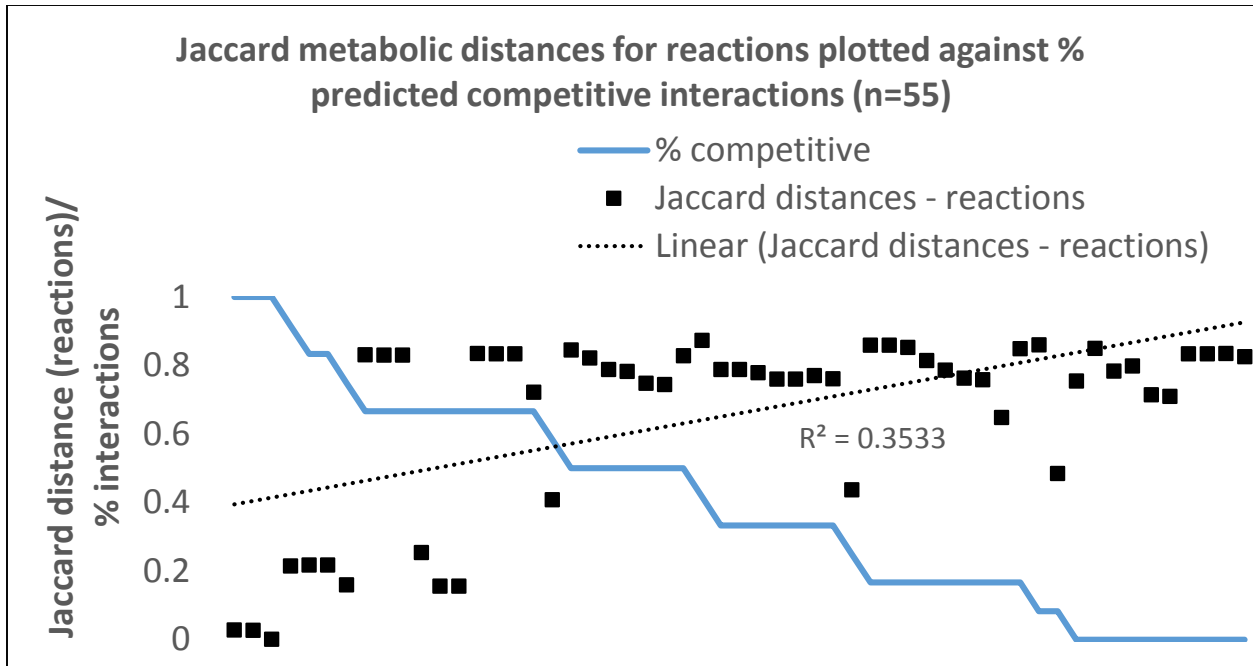


**Figure S1.100**

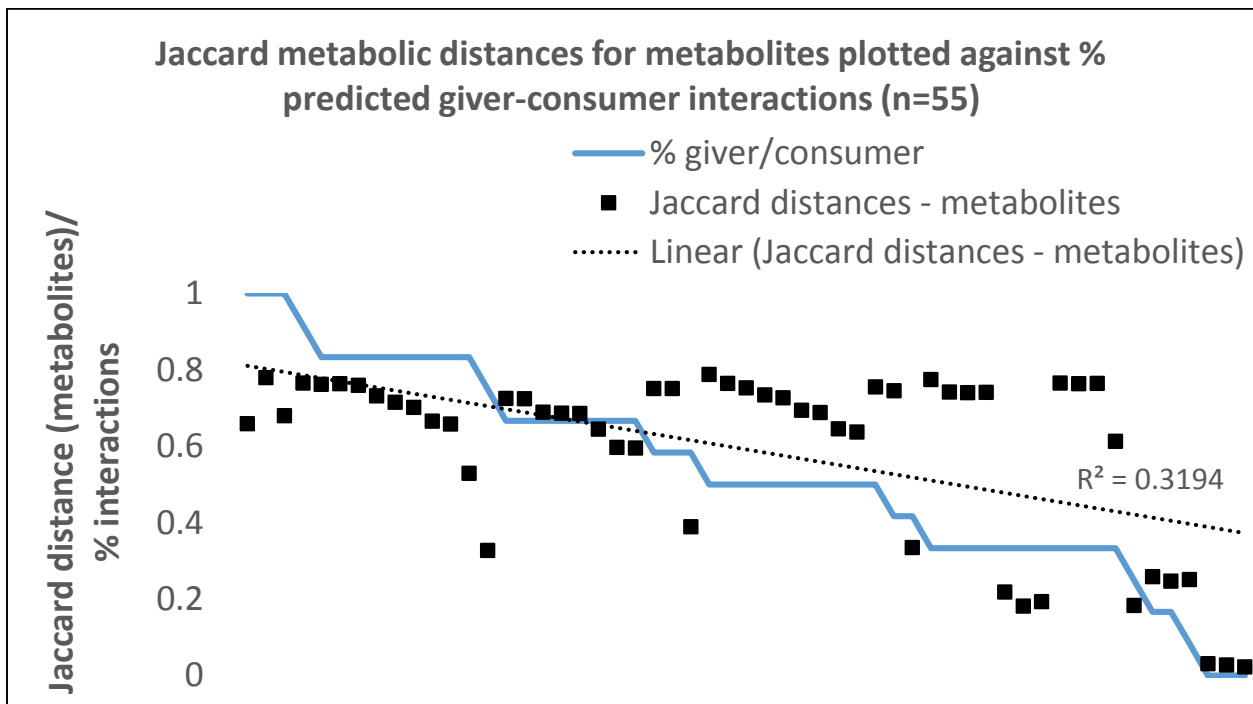




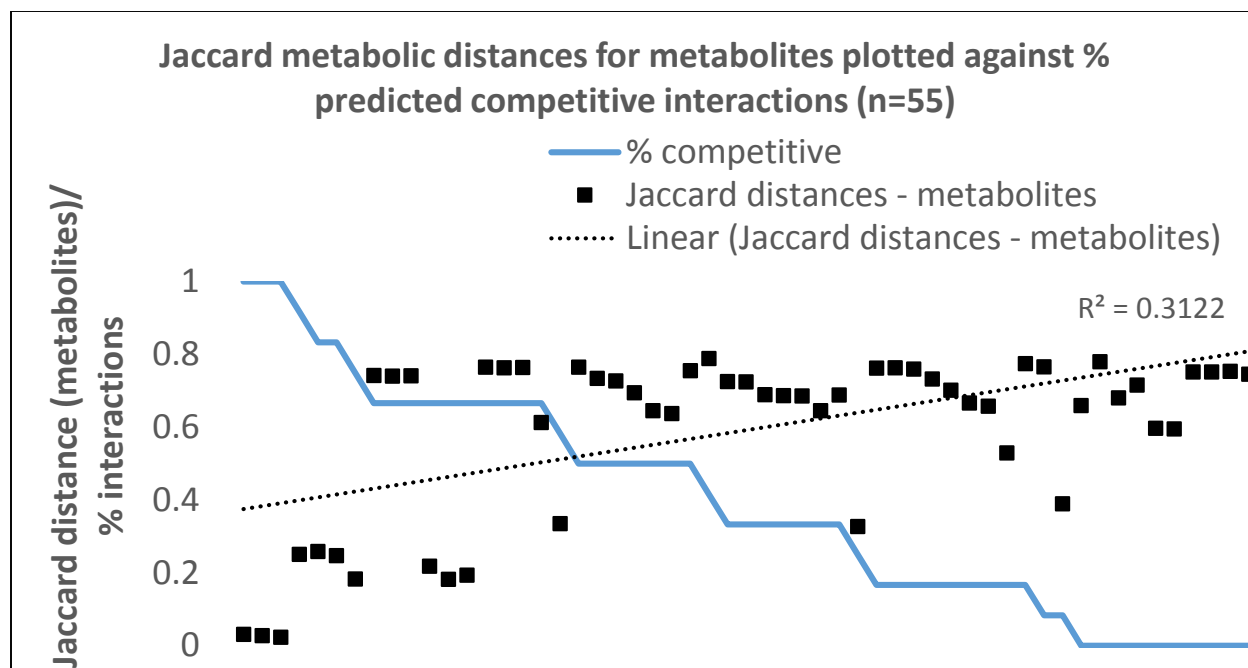
**Figure S2a):** Jaccard metabolic distances for each pair (reactions) plotted against percentage of giver/ consumer interactions for each pair, and display of R-squared value for the correlation between Jaccard distance and giver/ consumer interactions.



**Figure S2b):** Jaccard metabolic distances for each pair (reactions) plotted against percentage of competitive interactions for each pair, and display of R-squared value for the correlation between Jaccard distance and competitive interactions.



**Figure S2c):** Jaccard metabolic distances for each pair (metabolites) plotted against percentage of giver/ consumer interactions for each pair, and display of R-squared value for the correlation between Jaccard distance and giver/ consumer interactions.

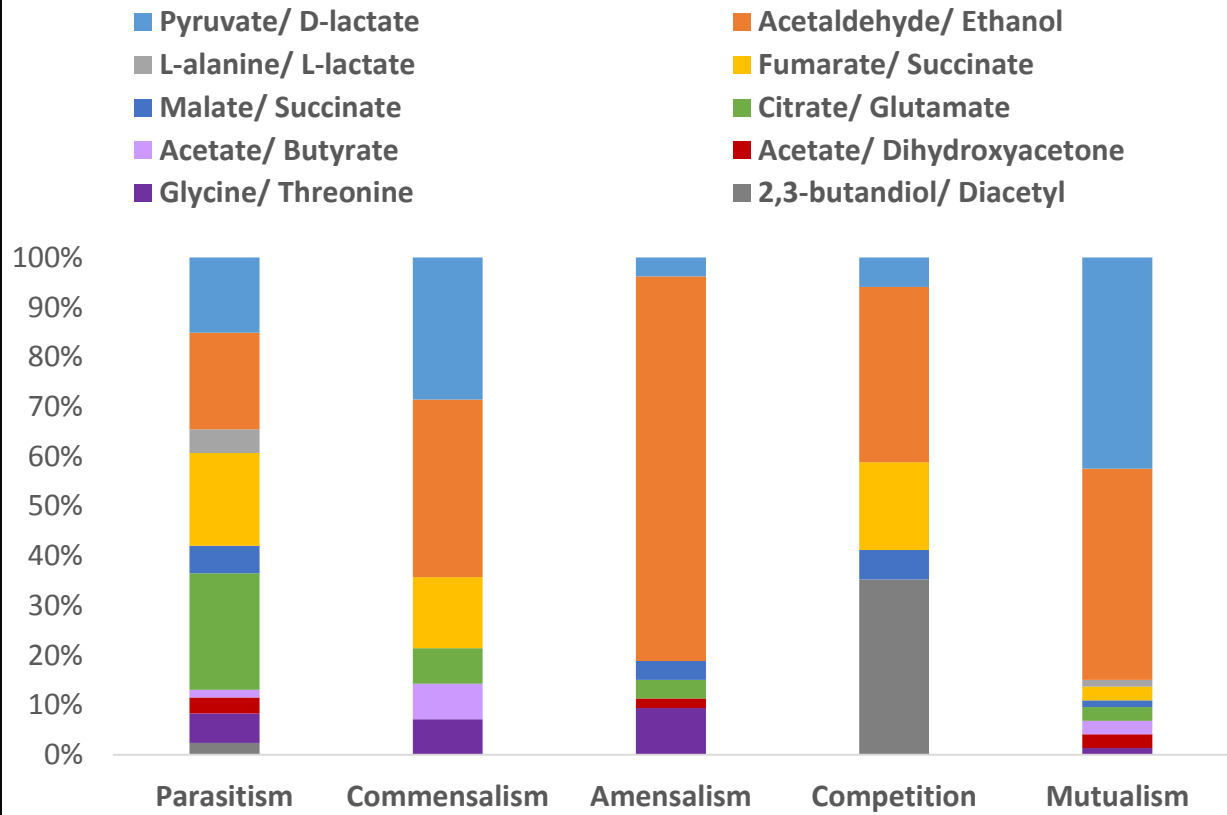


**Figure S2d):** Jaccard metabolic distances for each pair (metabolites) plotted against percentage of competitive interactions for each pair, and display of R-squared value for the correlation between Jaccard distance and competitive interactions.

# exchange strategies		- oxygen						+ oxygen						Total # of scenarios			
		- sIEC			+ sIEC			- sIEC			+ sIEC						
0	1	2	3	WD	HFD	PD	WD	HFD	PD	WD	HFD	PD	WD	HFD	PD		
M1	M2																
<i>B. thetaotaomicron</i>	<i>F. prausnitzii</i>															12	
	<i>L. plantarum</i>															12	
	<i>L. lactis</i>															12	
	<i>S. thermophilus</i>															12	
	<i>H. pylori</i>															6	
	<i>K. pneumoniae</i>															12	
	<i>S. typhimurium</i>															12	
	<i>E. coli</i> MG1655															12	
	<i>E. coli</i> Sakai															12	
	<i>E. coli</i> EDL933															12	
<i>F. prausnitzii</i>	<i>L. plantarum</i>															12	
	<i>L. lactis</i>															12	
	<i>S. thermophilus</i>															12	
	<i>H. pylori</i>															6	
	<i>K. pneumoniae</i>															12	
	<i>S. typhimurium</i>															12	
	<i>E. coli</i> MG1655															12	
	<i>E. coli</i> Sakai															12	
	<i>E. coli</i> EDL933															12	
	<i>L. plantarum</i>	<i>L. lactis</i>															12
<i>S. thermophilus</i>																12	
<i>H. pylori</i>																6	
<i>K. pneumoniae</i>																12	
<i>S. typhimurium</i>																12	
<i>E. coli</i> MG1655																12	
<i>E. coli</i> Sakai																12	
<i>E. coli</i> EDL933																12	
<i>L. lactis</i>		<i>S. thermophilus</i>															12
		<i>H. pylori</i>															6
	<i>K. pneumoniae</i>															12	
	<i>S. typhimurium</i>															12	
	<i>E. coli</i> MG1655															12	
	<i>E. coli</i> Sakai															12	
	<i>E. coli</i> EDL933															12	
	<i>S. thermophilus</i>	<i>H. pylori</i>															6
		<i>K. pneumoniae</i>															12
		<i>S. typhimurium</i>															12
<i>E. coli</i> MG1655																12	
<i>E. coli</i> Sakai																12	
<i>E. coli</i> EDL933																12	
<i>H. pylori</i>	<i>K. pneumoniae</i>															6	
	<i>S. typhimurium</i>															6	
	<i>E. coli</i> MG1655															6	
	<i>E. coli</i> Sakai															6	
	<i>E. coli</i> EDL933															6	
<i>K. pneu</i>	<i>S. typhimurium</i>															12	
	<i>E. coli</i> MG1655															12	
	<i>E. coli</i> Sakai															12	
	<i>E. coli</i> EDL933															12	
<i>S. typh</i>	<i>E. coli</i> MG1655															12	
	<i>E. coli</i> Sakai															12	
	<i>E. coli</i> EDL933															12	
EC MG1655	<i>E. coli</i> Sakai															12	
	<i>E. coli</i> EDL933															12	
EC Sakai	<i>E. coli</i> EDL933															12	
# interactions/ scenario		37	38	36	23	23	44	40	37	39	22	25	47				

**Figure S3:** Number of metabolic exchange strategies (defined in Table S6) displayed per pair in the 12 scenarios. WD = Western diet, HFD = high fiber diet, PD = protein diet, sIEc = small intestinal enterocyte.

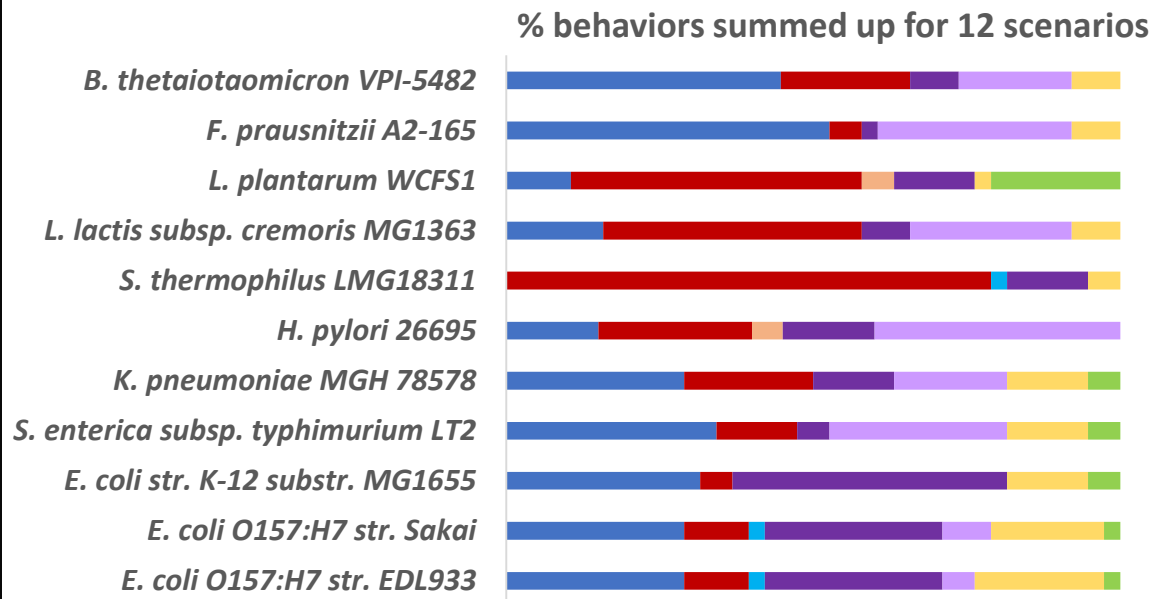
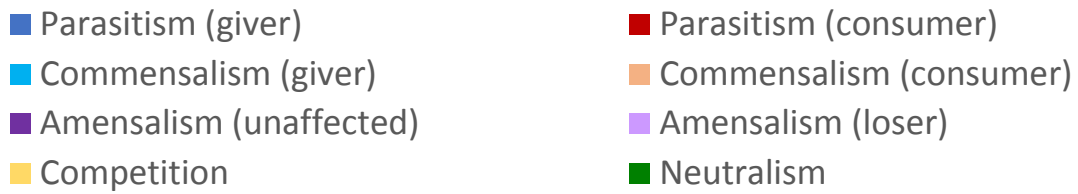
## Percentages of utilized exchange strategies shown per interaction type



	<b>Total exchange strategies #</b>	<b>Pairs #</b>	<b>Exchanges/pair</b>
<b>Parasitism</b>	252	299	0.84
<b>Commensalism</b>	14	21	0.67
<b>Neutralism</b>	0	1	0.00
<b>Amensalism</b>	53	175	0.30
<b>Competition</b>	17	67	0.25
<b>Mutualism</b>	73	37	1.97

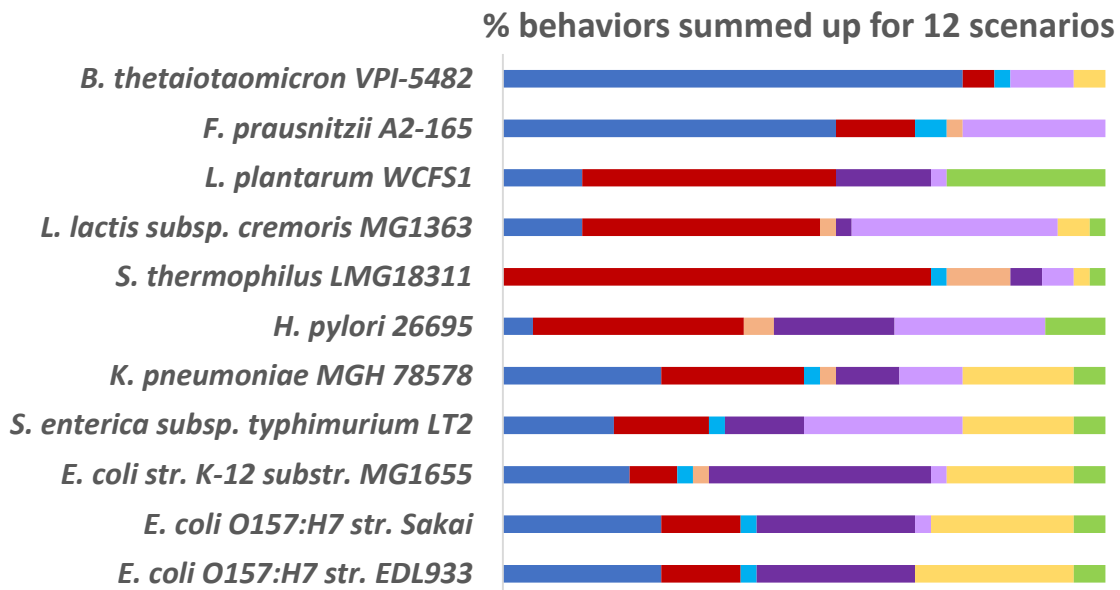
**Figure S4:** Number of metabolite exchange strategies (defined in Table S6) computed per interaction type and pair, and percentage of exchange strategies computed for each interaction type.

## Microbes classified by interactions Western diet (4 scenarios total)



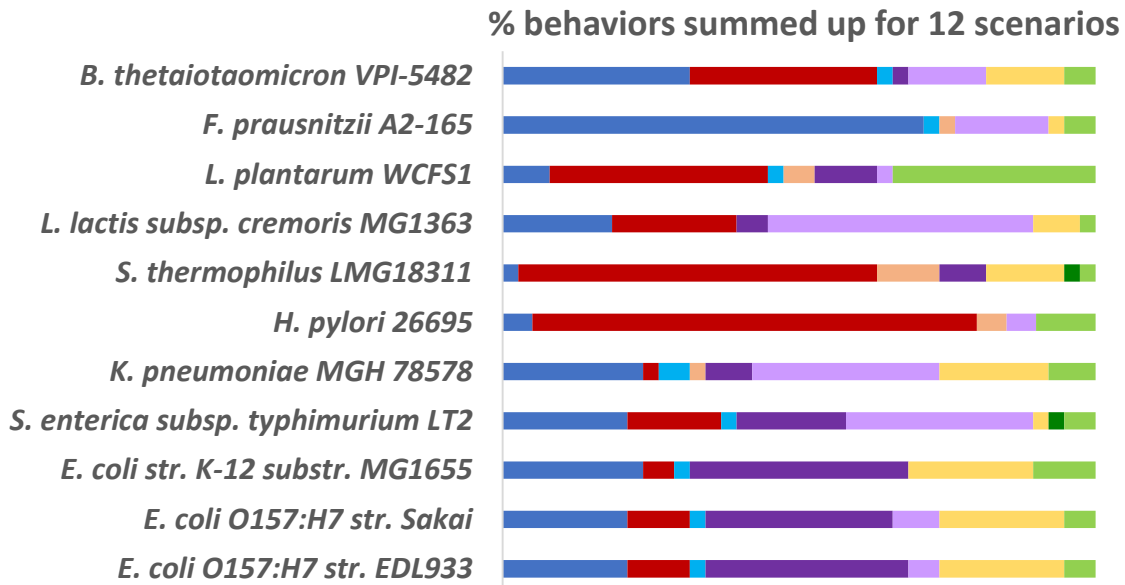
**Figure S5a:** Microbes classified by % interactions participated in on Western diet. The plot sums up 40 interactions per microbe in four scenarios (Figure 2c), with the exception of *H. pylori* for which only 20 interactions were calculated as no growth was predicted without oxygen. In total, 400 interactions were predicted on Western diet (200 pairs).

## Microbes classified by interactions High fiber diet (4 scenarios total)



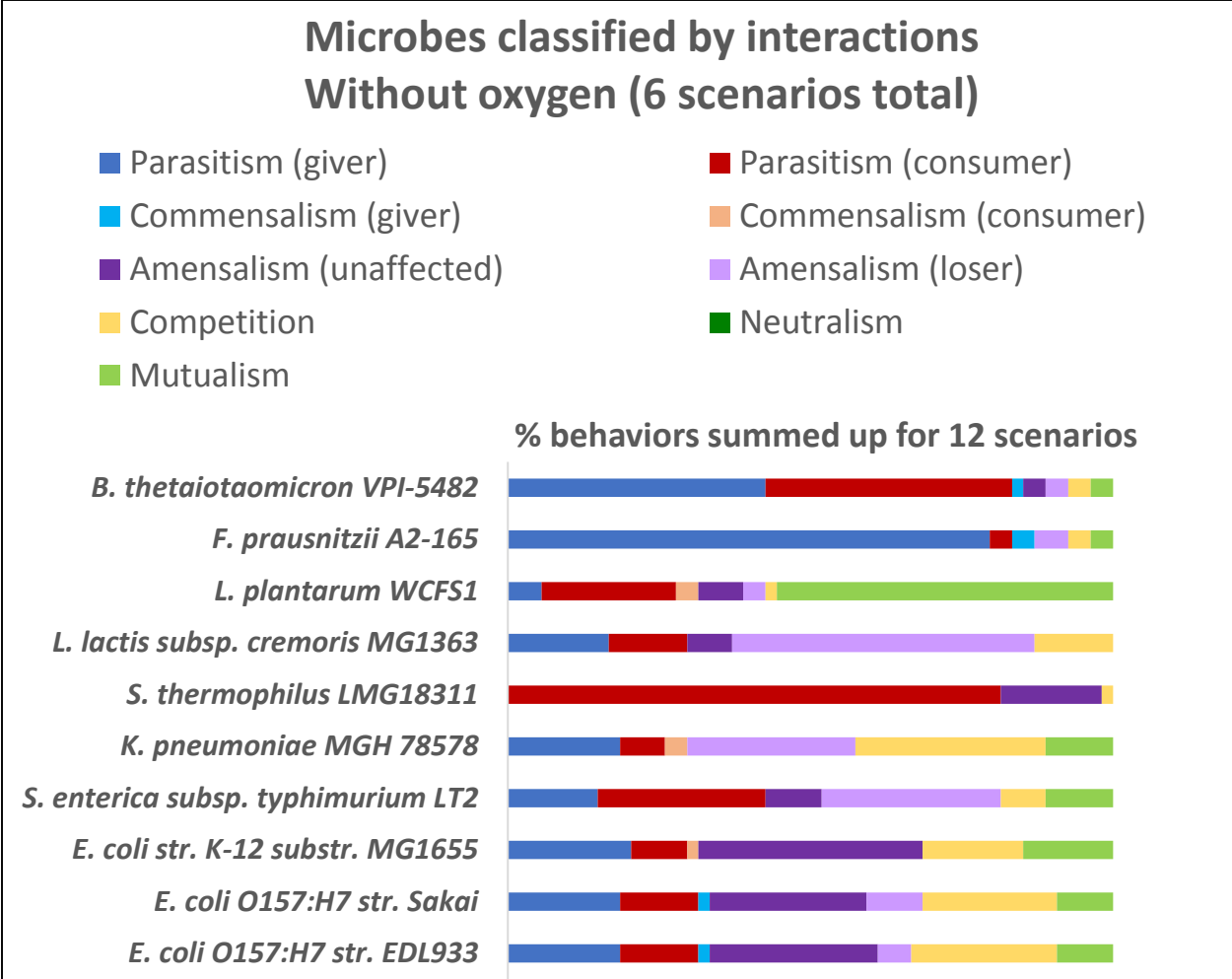
**Figure S5b:** Microbes classified by % interactions participated in on High fiber diet. The plot sums up 40 interactions per microbe in four scenarios (Figure 2c), with the exception of *H. pylori* for which only 20 interactions were calculated as no growth was predicted without oxygen. In total, 400 interactions were predicted on High fiber diet (200 pairs).

## Microbes classified by interactions Protein diet (4 scenarios total)



**Figure S5c:** Microbes classified by % interactions participated in on Protein diet. The plot sums up 40 interactions per microbe in four scenarios (Figure 2c), with the exception of *H. pylori* for which only 20 interactions were calculated as no growth was predicted without oxygen. In total, 400 interactions were predicted on Protein diet (200 pairs).



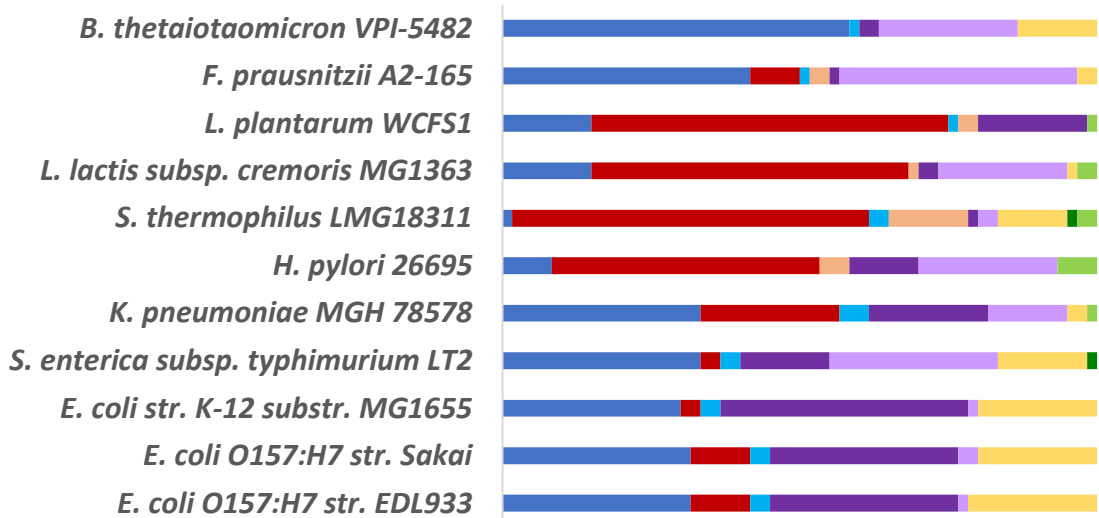


**Figure S6a:** Microbes classified by % interactions participated in on scenarios without oxygen (six in total, Figure 2c). The plot sums up 54 interactions per microbe. In total, 540 interactions were predicted on scenarios without oxygen (270 pairs).

## Microbes classified by interactions With oxygen (6 scenarios total)



% behaviors summed up for 12 scenarios

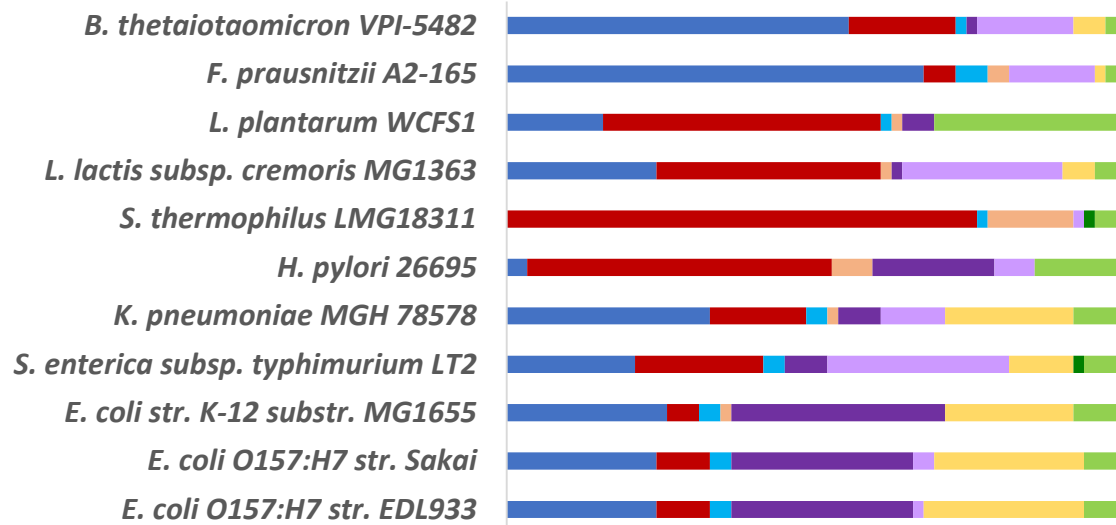


**Figure S6b:** Microbes classified by % interactions participated in on scenarios with oxygen (six in total, Figure 2c). The plot sums up 60 interactions per microbe. In total, 660 interactions were predicted on scenarios without oxygen (330 pairs).

## Microbes classified by interactions Without enterocyte (6 scenarios total)

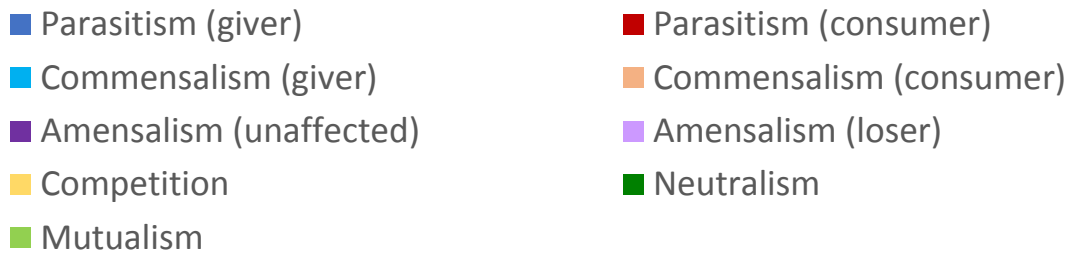


% behaviors summed up for 12 scenarios

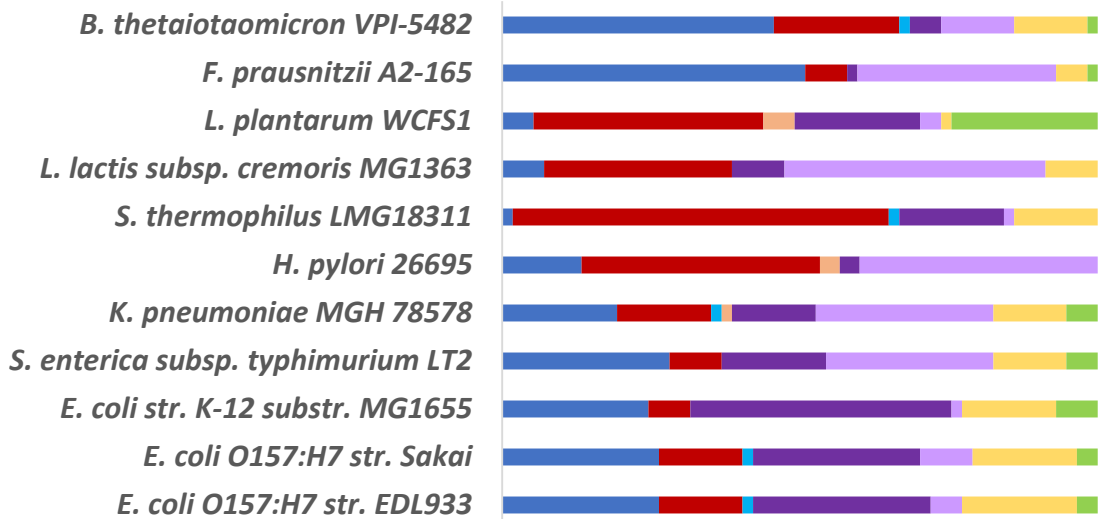


**Figure S7a:** Microbes classified by % interactions participated in on scenarios without enterocyte. The plot sums up 60 interactions per microbe in six scenarios (Figure 2c), with the exception of *H. pylori* for which only 30 interactions were calculated as no growth was predicted without oxygen. In total, 600 interactions were predicted on scenarios without enterocyte (300 pairs).

## Microbes classified by interactions With enterocyte (6 scenarios total)



% behaviors summed up for 12 scenarios



**Figure S7b:** Microbes classified by % interactions participated in on scenarios with enterocyte. The plot sums up 60 interactions per microbe in six scenarios (Figure 2c), with the exception of *H. pylori* for which only 30 interactions were calculated as no growth was predicted without oxygen. In total, 600 interactions were predicted on scenarios with enterocyte (300 pairs).

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