Supplementary Information: Bacterial microcompartment utilisation in the human commensal *Escherichia coli* Nissle 1917

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1 Extended materials and methods

Tables S1-S3 contain statistical analysis, **Table S4** contains *eut* operon protein sequence homology between EcN and EcBW. **Tables S5-S7** contain summaries of models used in Flux Balance Analysis.

Table S 1: **Test statistics corresponding to values from Fig 2F, where the carry capacity is estimated with the Gompertz function $\pm$ standard error, where each condition for each species if compared to EA + B$_{12}$**

Species	Condition	Estimated Carry Capacity	P-value
EcBW	No addition	0.119 ± 0.00100	0.54
	EA	0.123 ± 0.00184	0.66
	B$_{12}$	0.130 ± 0.00128	0.08
	EA + B$_{12}$	0.121 ± 0.00356	
EcN	No addition	0.140 ± 0.000980	0.0000055
	EA	0.126 ± 0.00199	0.0000053
	B$_{12}$	0.120 ± 0.00118	0.0000033
	EA + B$_{12}$	0.262 ± 0.00367	
Sent	No addition	0.0793 ± 0.000516	0.00000029
	EA	0.0811 ± 0.000413	0.00000029
	B$_{12}$	0.0795 ± 0.000526	0.00000029
	EA + B$_{12}$	0.341 ± 0.00384	

Table S 2: **Test statistics corresponding to values from Fig 3B-C, where the mean fold change of cultures supplemented with EA + B$_{12}$ are compared to those supplemented with glucose instead, $\pm$ SEM.**

Species	Gene	Mean Fold Change	p-value
EcN	EutS	30.051 $\pm$ 0.877	0.0000085
	EutB	25.748 $\pm$ 0.890	0.000011
	EutR	12.740 $\pm$ 0.879	0.000000073
EcBW	EutS	219.176 $\pm$ 0.803	0.00000011
	EutB	1.245 $\pm$ 0.812	0.75
	EutR	170.989 $\pm$ 0.822	0.0000015

Table S 3: **Test statistics corresponding to values from Fig 4E, where the mean NH_4^+ concentration $\pm$ SEM is compared within each species when grown in media supplemented with either EA + B$_{12}$ or glucose as a carbon source.**

Species	Condition	Mean [NH_4^+]	p-value
EcN	EA + B$_{12}$	0.0360 $\pm$ 0.000649	0.000088
	Glucose	0.0228 $\pm$ 0.000505	
Sent	EA + B$_{12}$	0.0222 $\pm$ 0.000841	0.5353
	Glucose	0.0216 $\pm$ 0.000278	

Table S 4: **Protein sequence homology of proteins comprising** *eut* **operon between EcN and BW25113**

Protein	No. amino acids	% identity between EcN and BW25113
eutS	111	100.00
eutP	159	97.48
eutQ	233	97.00
eutT	267	100.00
eutD	338	99.70
eutM	97	100.00
eutN	95	100.00
eutE	467	98.93
eutJ	278	98.56
eutG	395	98.73
eutH	408	99.02
eutA	467	98.07
eutB	453	99.78
eutC	295	99.66
eutL	219	97.26
eutK	166	98.80
eutR	350	98.86

Table S 5: **Summary of each model used in this study**

	iJO1366 BW25113 2011	**iHM1533** EcN 2022	**STM_v1.0** Sent 2011
Chromosome size of strain (Mb)	4.63	5.44	4.86
Number of reactions	2583	3143	2546
Number of metabolites	1805	2261	1802
Number of genes	1367	1533	1271
Compartments	cytosol; extracellular space; periplasm	cytosol; extracellular space; periplasm	cytosol; extracellular space; periplasm

Table S 6: **Inclusion of metabolites of the *eut* BMC metabolic pathway within each model.** Metabolite ID and names are given as standard GEM notation, and each model name is given alongside its species and year the model was created.

Metabolite Name	Metabolite ID	iJO1366 EcBW 2011	iJO1366_CC EcBW 2024	iHM1533 EcN 2022	iHM1533_CC EcN 2024	STM v1.0 Sent 2011
Acetaldehyde	acald_e	×	×	×	×	×
Acetaldehyde	acald_c	✓	✓	✓	✓	✓
Acetyl phosphate	actp_c	✓	✓	✓	✓	✓
Acetyl-CoA	accoa_c	✓	✓	✓	✓	✓
Ammonium	nh4_e	✓	✓	✓	✓	✓
Ammonium	nh4_p	✓	✓	✓	✓	✓
Ammonium	nh4_c	✓	✓	✓	✓	✓
Coenzyme A	coa_c	✓	✓	✓	✓	✓
Ethanol	etoh_e	✓	✓	✓	✓	✓
Ethanol	etoh_p	✓	✓	✓	✓	✓
Ethanol	etoh_c	✓	✓	✓	✓	✓
Ethanolamine	etha_e	✓	✓	✓	✓	✓
Ethanolamine	etha_p	✓	✓	✓	✓	✓
Ethanolamine	etha_c	✓	✓	✓	✓	✓
H+	h_e	✓	✓	✓	✓	✓
H+	h_p	✓	✓	✓	✓	✓
H+	h_c	✓	✓	✓	✓	✓
NAD	nad_c	✓	✓	✓	✓	✓
NADH	nadh_c	✓	✓	✓	✓	✓
Phosphate	pi_e	✓	✓	✓	✓	✓
Phosphate	pi_p	✓	✓	✓	✓	✓
Phosphate	pi_c	✓	✓	✓	✓	✓

Table S 7: **Inclusion of reactions of the *eut* BMC metabolic pathway within each model.** Reaction ID and names are given as standard GEM notation, and each model name is given alongside its species and year the model was created.

| Reaction ID	Reaction	iJO1366 EcBW 2011	iJO1366_CC EcBW 2024	iHM1533 EcN 2022	iHM1533_CC EcN 2024	STM v1.0 Sent 2011
Ex_acald_e	acald_e <=>	✓	✓	✓	✓	✓
ALCD2x	etoh_c + nad_c <=>acald_c + h_c + nadh_c	✓	✓	✓	✓	✓
EX_nh4_e	nh4_e <=>	✓	✓	✓	✓	✓
NH4tpp	nh4_p <=>nh4_c	✓	✓	✓	✓	✓
NH4tex	nh4_e <=>nh4_p	✓	✓	✓	✓	✓
Ex_etoh_e	etoh_e <=>	✓	✓	✓	✓	✓
ETOHtrpp	etoh_p <=>etoh_c	✓	✓	✓	✓	✓
ETOHtex	etoh_e <=>etoh_p	✓	✓	✓	✓	✓
ETHAAL	etha_c –>acald_c + nh4_c	✓	✓	✓	✓	✓
EX_etha_e	etha_e –>	✓	✓	✓	✓	✓
ETHAt2pp	etha_p + h_p –>etha_c + h_c	✓	✓	✓	✓	✓
ETHAtex	etha_e <=>etha_p	✓	×	×	✓	✓
Ex_h_e	h_e <=>	✓	✓	✓	✓	✓
Ex_pi_e	pi_e <=>	✓	✓	✓	✓	✓
PItex	pi_e <=>pi_p	✓	✓	✓	✓	✓
PTAr	accoa_c + pi_c <=>actp_c + coa_c	✓	✓	✓	✓	✓
Htex	h_e <=>h_p	✓	✓	✓	✓	✓

2 Extended results
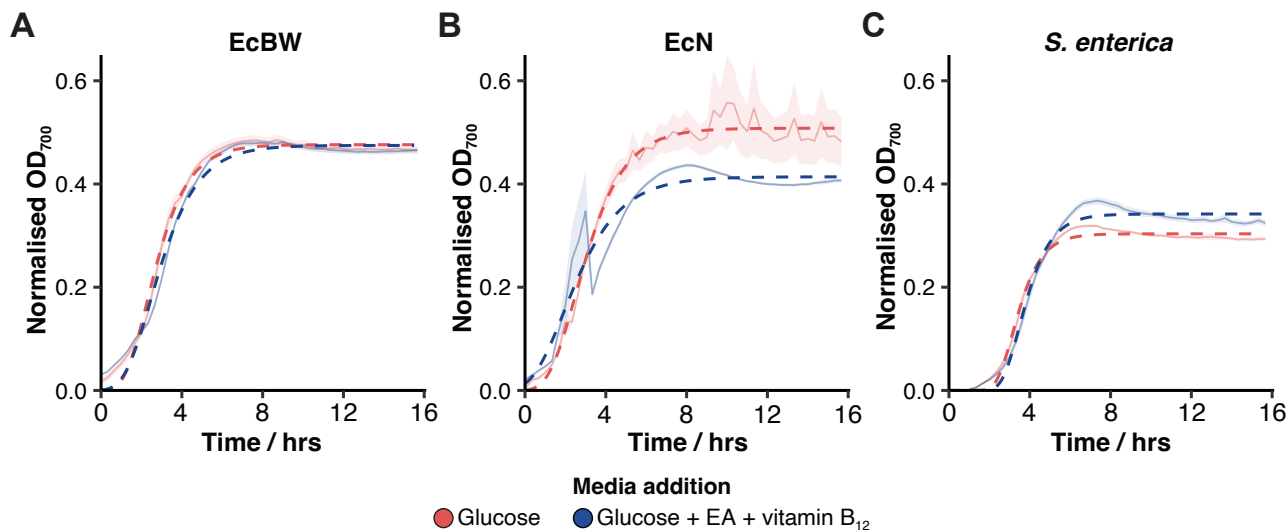
Figure S 1: **EA-dependent growth in *E. coli* Nissle 1917.** Growth curves of EcBW (**A**), EcN (**B**), and *S. enterica* (**C**) when grown in M9 supplemented with either glucose alone, or EA, vitamin B_{12} and glucose, in triplicate. The mean and standard error are shown with a solid line and a pale ribbon, respectively, and the data was fitted with the Gompertz function shown by the respective dashed lines.
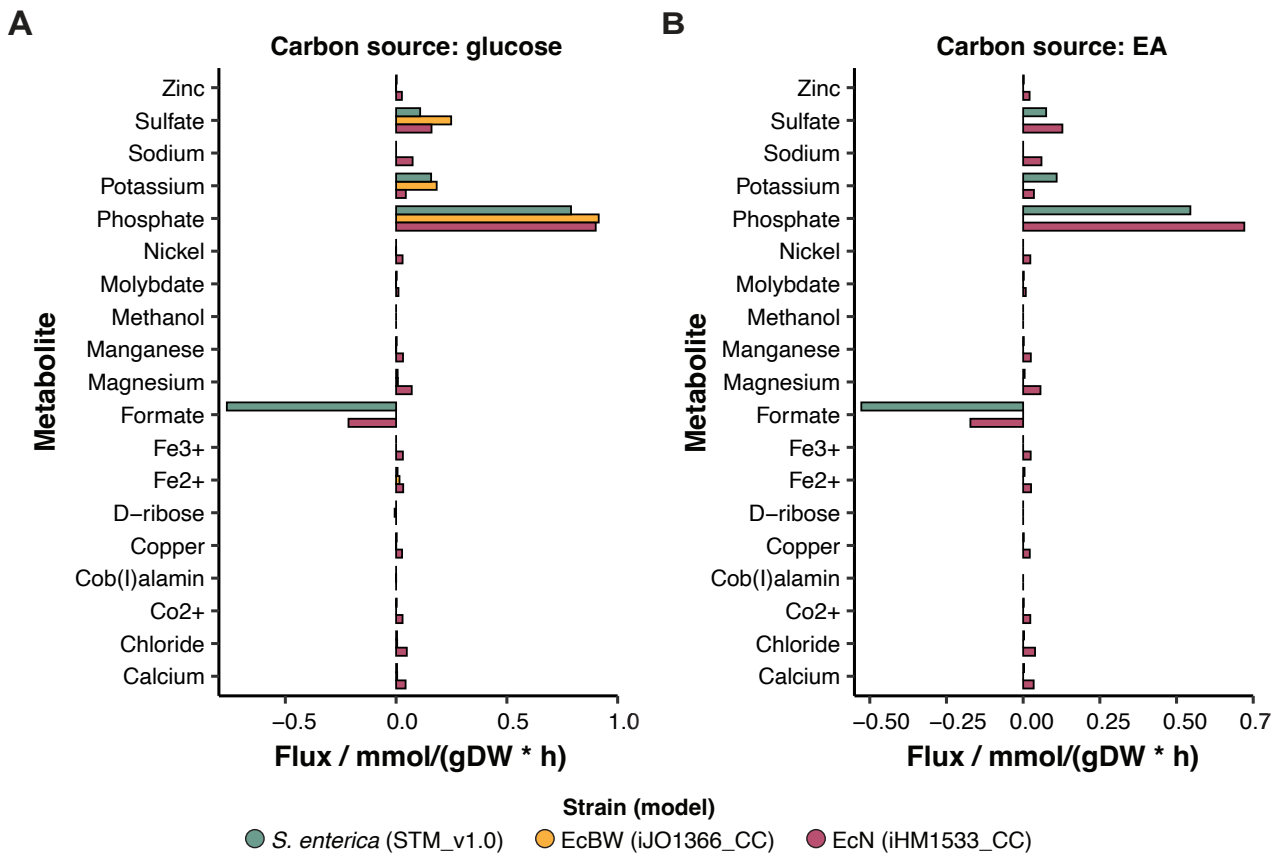
Figure S 2: **Metabolite flux prediction in *E. coli* Nissle 1917.** (**A & B**) Predicted flux from the FBA when the model is supplied with either EA or glucose as the sole carbon source, respectively .