

Table S1. List of primers

Name	Sequence
Primers for qRT-PCR	
prpB_F	GCGCCATGATCACAAAATC
prpB_R	GAAATCGATGATTAAAGCCGGTG
prpC_F	CATTGCGAATTTGAAGAAGTGG
prpC_R	GTTTGTCTGGCAATATCCCGCG
prpD_F	AAATGTGCTGTTCAAATCTCC
prpD_R	TAATCTGCCGCCGTTAAGC
prpE_F	GATGTATGGCTATAACGTGCAG
prpE_R	GAGATACTCTCTTCAATCTCGC
prpR_F	CGGCTTCTTCTGCCAGATC
prpR_R	GATGTGTTACAGGCACTGGC
acs_F	CATGTGGTGGTACTGAAGCGTAC
acs_R	CTTCAAACATCAGCGTGGTCGC
cobB_F	AGAAATTCAGCCTAACGCCG
cobB_R	ATCCATGCCGAGTGGCATTTC
pta_F	CGGTTGATGAACAGGGTCGT
pta_R	CTTCGTTGATGATGGTCGCAT
gyrA_F (<i>reference gene</i>)	TGGTGACGTAATCGGTAAATACCA
gyrA_R (<i>reference gene</i>)	GTTATCAACGAAATCGACCGTC
Primers for PCR and Sanger sequencing	
acs_check_F	TTGTGGGTTACGATGGCATCG
acs_check_R	CTACATTTAACGCTTATGCCAC
cobB_check_F	AACAGAGGTTGCTATGCTGTC
cobB_check_R	TGATAAGCGTAGTGCATCAGG
prpE_check_F	GTAAGGCGTAAGTTCAACAGG
prpE_check_R	GCATCCGACAATAACCTACTC
prpR_check_F	GGATAAAGCGTTCGCGCTGC
prpR_check_R	GCGTTTCAGTTAACGTTTCAGGC
prpC_check_F	CCGGAACGCCAGAAAGTGC
prpC_check_R	GAAATCGATGATTAAAGCCGGTG

Table S2 Cq values for qRT-PCR efficiency test

Cq_rep1	Cq_rep2	Mean_Cq	SD	Dilution	Log2Dilution	Efficiency(%)
<i>acs</i>						
22.71	22.67	22.69	0.03	1	0	97.88
23.95	23.74	23.84	0.15	2	-1	
25.03	24.81	24.92	0.15	4	-2	
25.96	26.02	25.99	0.04	8	-3	
26.77	26.79	26.78	0.02	16	-4	
<i>cobB</i>						
22.45	22.47	22.46	0.01	1	0	101.16
23.47	23.43	23.45	0.03	2	-1	
24.78	24.63	24.70	0.11	4	-2	
25.29	25.51	25.40	0.15	8	-3	
26.50	26.30	26.40	0.14	16	-4	
<i>pta</i>						
21.95	21.98	21.97	0.02	1	0	97.56
22.82	22.98	22.90	0.11	2	-1	
23.66	24.00	23.83	0.24	4	-2	
25.04	25.35	25.19	0.22	8	-3	
25.95	26.06	26.00	0.08	16	-4	
<i>prpB</i>						
22.29	22.31	22.30	0.01	1	0	100.32
23.60	23.26	23.43	0.24	2	-1	
24.84	24.27	24.55	0.40	4	-2	
25.37	25.34	25.35	0.02	8	-3	
26.18	26.46	26.32	0.19	16	-4	
<i>prpC</i>						
20.01	20.04	20.02	0.02	1	0	103.60
20.94	20.77	20.86	0.12	2	-1	
22.01	21.76	21.88	0.18	4	-2	
22.90	23.02	22.96	0.09	8	-3	
23.57	23.88	23.73	0.22	16	-4	
<i>prpD</i>						
19.88	19.91	19.89	0.02	1	0	98.03
21.18	20.79	20.98	0.27	2	-1	
22.02	21.73	21.88	0.21	4	-2	
22.98	22.81	22.90	0.12	8	-3	
24.05	24.12	24.09	0.04	16	-4	
<i>prpE</i>						
23.04	22.77	22.90	0.19	1	0	98.13
24.03	23.58	23.80	0.32	2	-1	
24.82	25.05	24.93	0.16	4	-2	
25.74	26.02	25.88	0.20	8	-3	
26.81	27.20	27.01	0.28	16	-4	

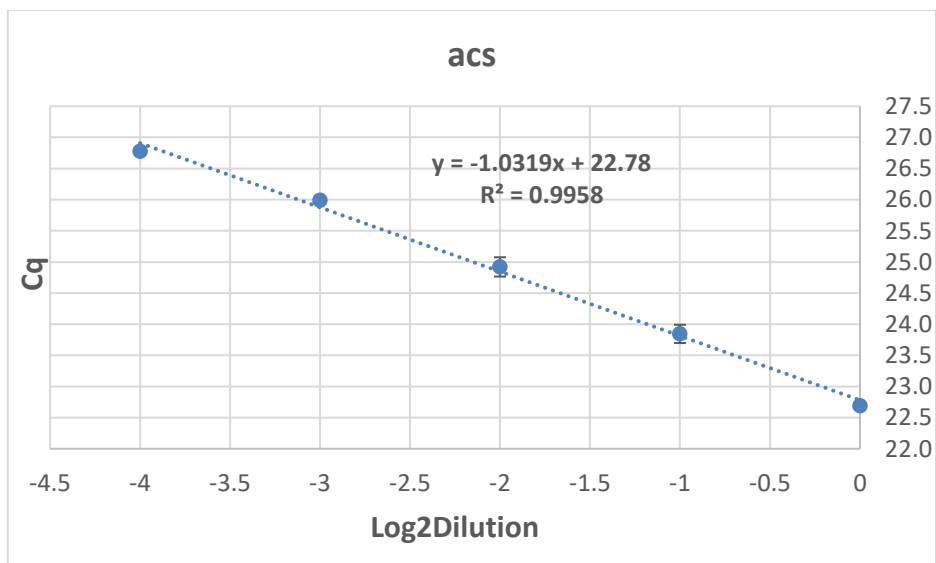
<i>prpR</i>						
22.32	22.29	22.30	0.02	1	0	104.37
23.21	23.05	23.13	0.11	2	-1	
23.91	24.16	24.03	0.17	4	-2	
25.14	25.21	25.18	0.05	8	-3	
25.99	25.99	25.99	0.01	16	-4	
<i>gyrA (reference gene)</i>						
20.96	20.88	20.92	0.03	1	0	96.76
22.18	21.74	21.96	0.16	2	-1	
22.99	22.73	22.86	0.09	4	-2	
24.16	23.85	24.01	0.11	8	-3	
25.23	25.06	25.14	0.06	16	-4	

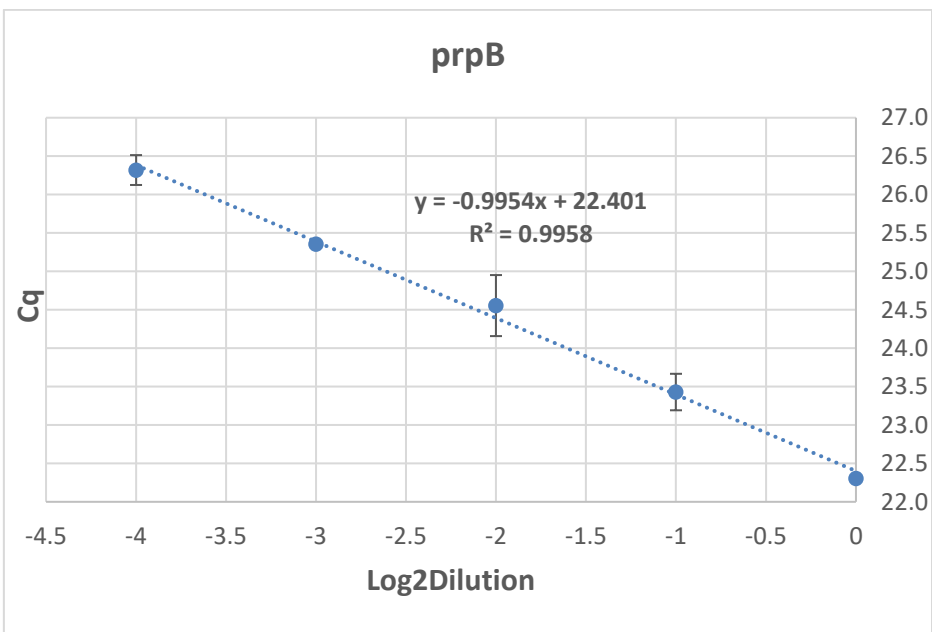
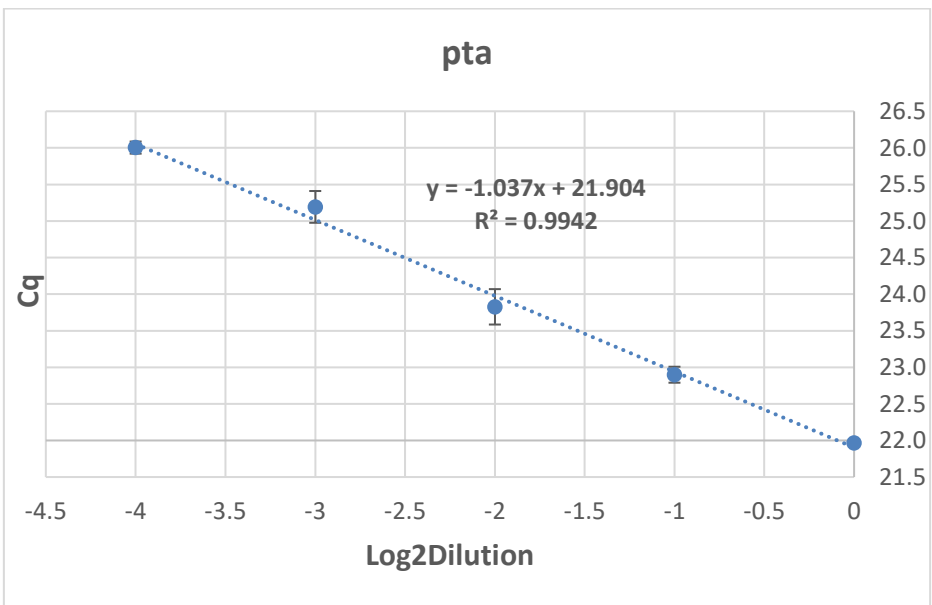
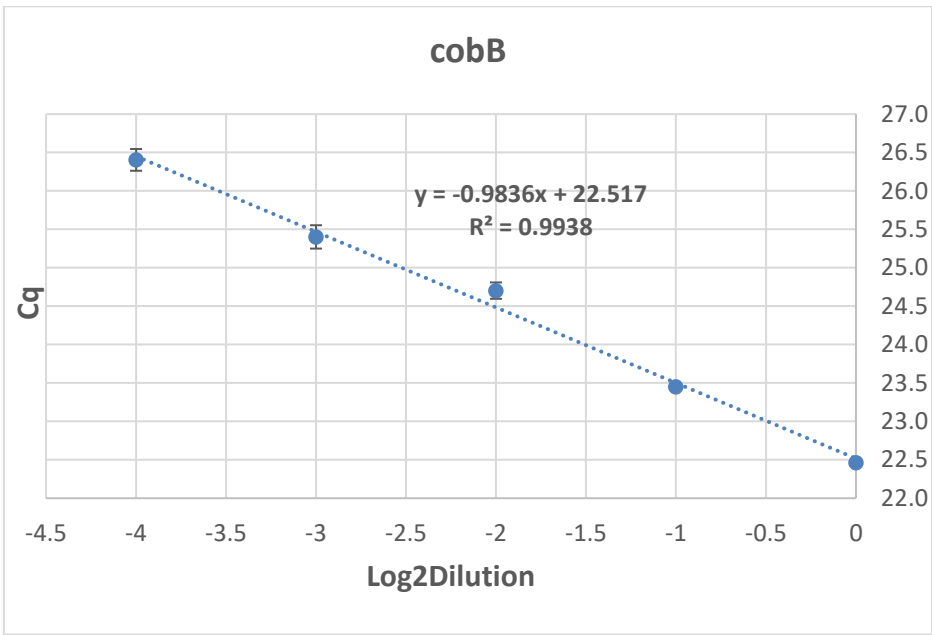
SD – standard deviation

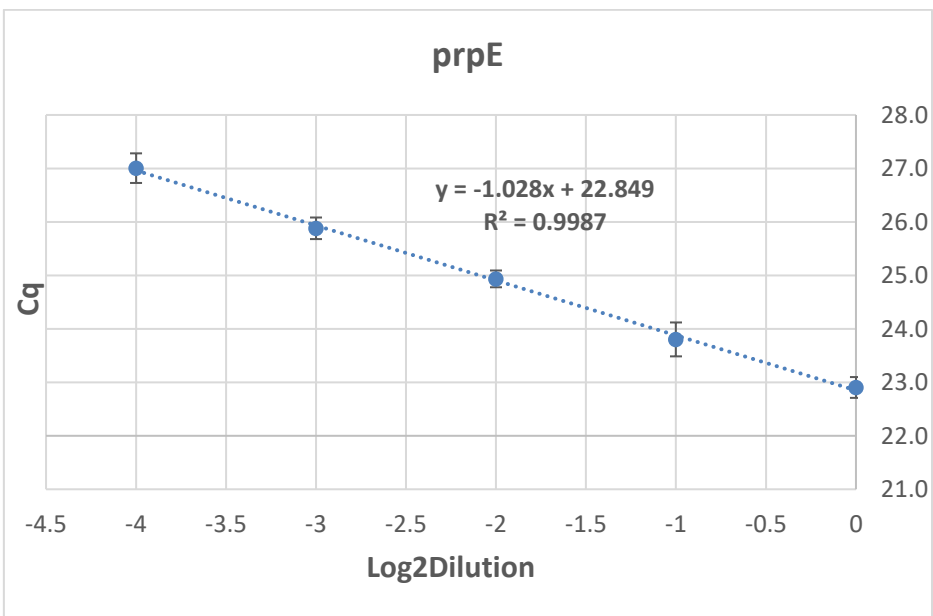
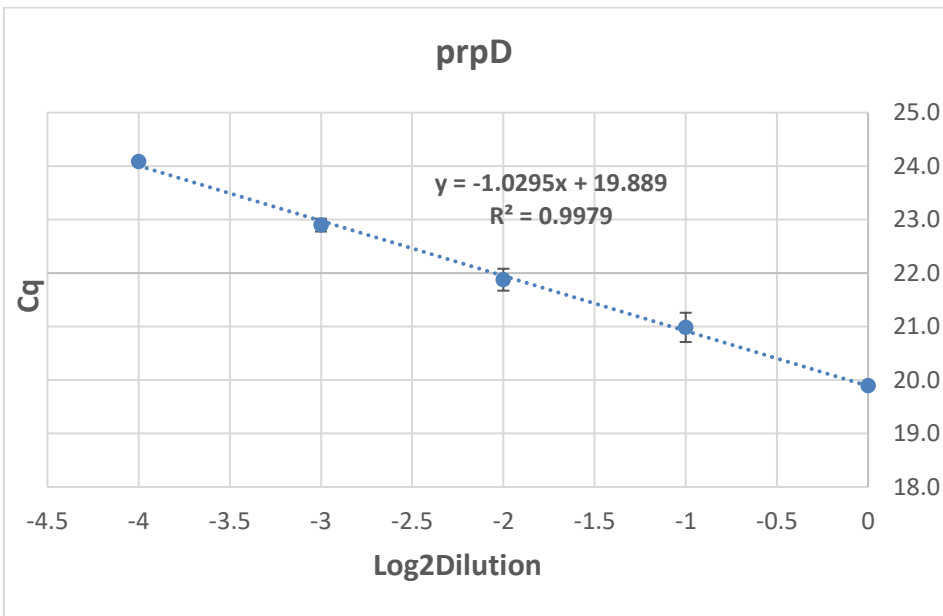
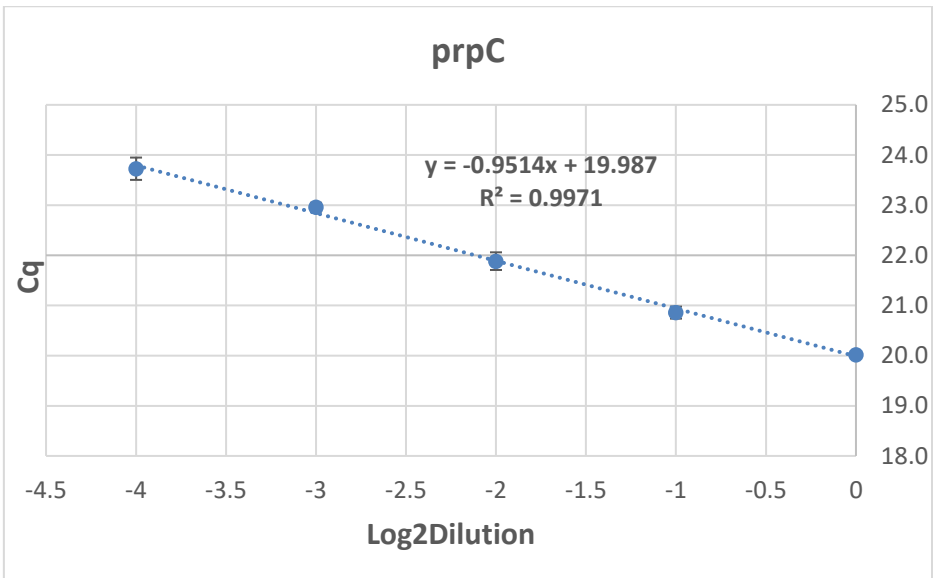
PCR primer efficiency was calculated as

$$\text{Efficiency (\%)} = (2^{-1/\text{slope value}} - 1) * 100$$

This data was used to plot standard curves and calculate qRT-PCR efficiency for each primer pairs







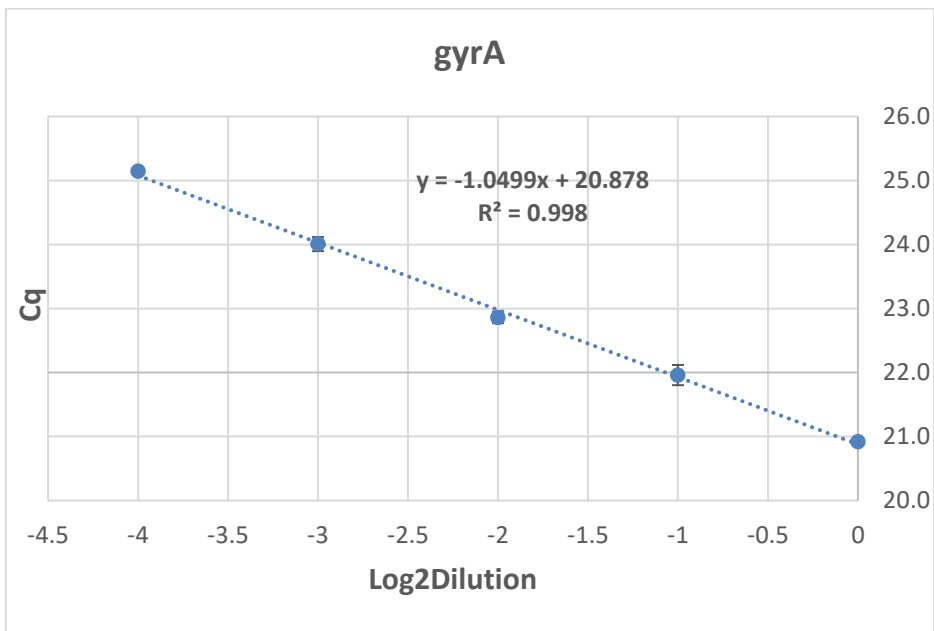
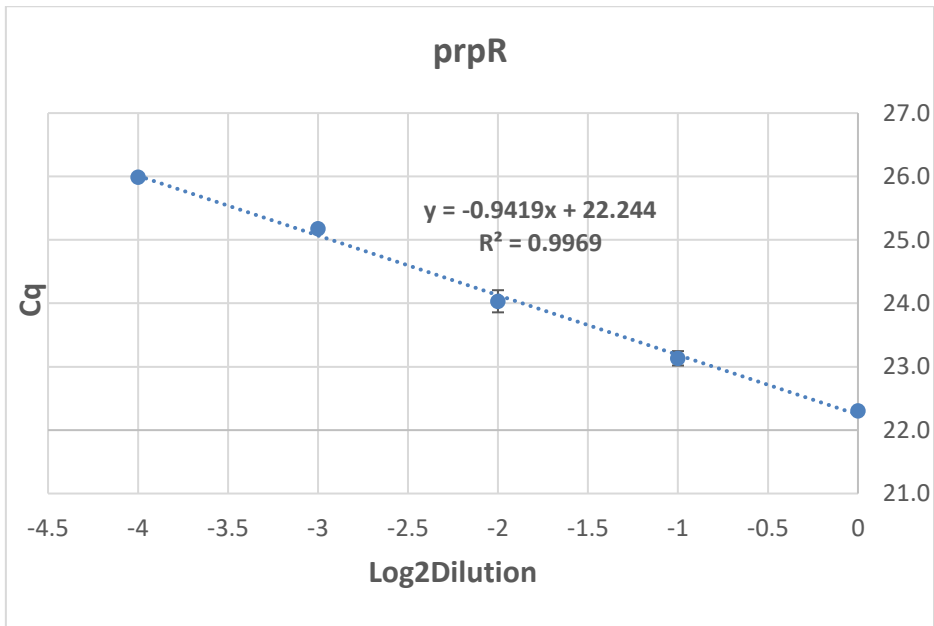


Figure S1 Standard curves for qRT-PCR efficiency

We used R package Growthcurver (Sprouffske K, Wagner A. Growthcurver: an R package for obtaining interpretable metrics from microbial growth curves. BMC Bioinformatics 17, 172 (2016).) for fitting growth curve data by the standard logistic equation common in ecology and evolution (Crow JF, Kimura M. An Introduction to Population Genetics Theory. Caldwell, NJ: Harper and Row, Publishers, Inc.; 1970), (Rockwood LL. Introduction to Population Ecology, 2nd ed. West Sussex: Wiley; 2015). (Figure S1).

The logistic equation gives the number of cells N_t at time t :

$$N_t = \frac{k}{1 + \left(\frac{k - n_0}{n_0}\right)e^{-rt}}$$

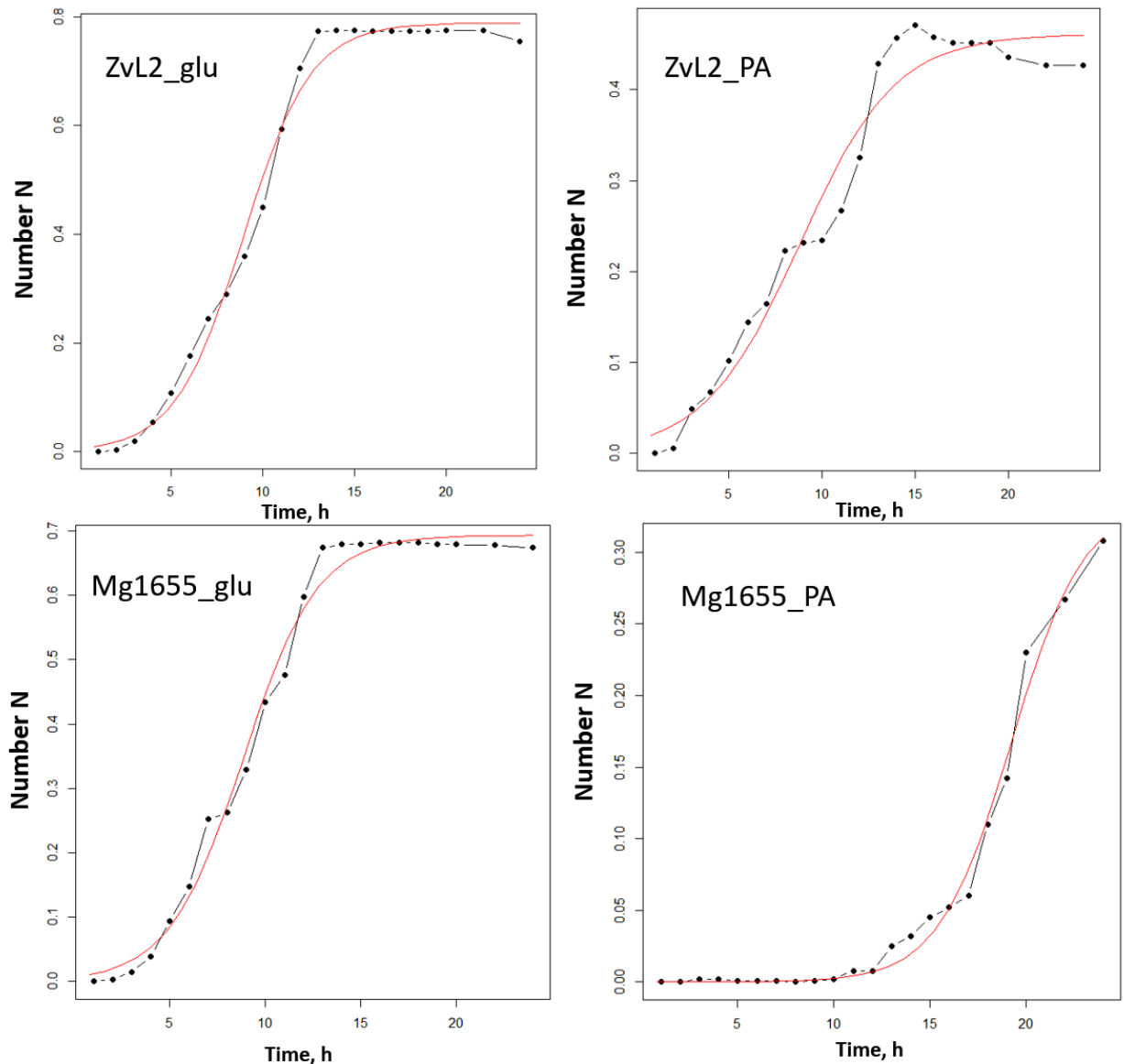


Figure S2. The plot of the raw growth curve data and the best fit logistic curve for ZvL2 isolate (ZvL2) and laboratory strain *E.coli* K12 MG1655 (Mg1655) cultivated on M9 minimal medium with the addition of glucose (Glu) or sodium propionate (PA).

We extracted the value of arguments for all fitting curves (Table S2)

Table S3. The value of arguments

Arguments	Samples			
	ZvL2 glu	ZvL2 PA	Mg1655 glu	Mg1655 PA
k	0.789	0.461	0.693	0.335
k_se	0.0117	0.0147	0.0103	0.0162
k_p	4.42E-24	7.54E-18	4.19E-24	1.85E-14
n0	0.00632	0.01470	0.00717	0.00001
n0_se	0.0021	0.00556	0.00218	1.03E-05
n0_p	0.00733	0.0163	0.00383	0.251
r	0.541	0.389	0.516	0.531
r_se	0.0383	0.0465	0.0354	0.0475
r_p	1.59E-11	8.62E-08	8.99E-12	8.48E-10
sigma	0.0308	0.0321	0.0265	0.0102
df	19	19	19	19
t_mid	8.9	8.79	8.83	19.2
t_gen	1.28	1.78	1.34	1.3
auc_l	11.9	6.98	10.5	1.65
auc_e	11.9	6.92	10.5	1.68
note				

Description of the arguments

- k The carrying capacity parameter
- k_se The standard error of the carrying capacity parameter
- k_p The p value of the carrying capacity parameter
- n0 The initial population size
- n0_se The standard error of the initial population size
- n0_p The p value of the initial population size
- r The growth rate
- r_se The standard error of the growth rate
- r_p The p value of the growthrate
- sigma Residual standard error from non-linear least squares fit of the model to the data
- df Degrees of freedom
- t_mid The time at the inflection point of the logistic curve (occurs at half of the carrying capacity)
- t_gen The maximum doubling time, obtained by evaluating the the unrestrained growth of the population with growth rate r
- auc_l The area under the curve of the fitted logistic equation from time 0 to time t
- auc_e The area under the curve of the measurements.
- note Feedback on common problems with fitting the logistic curve to the data

Table S4. Adjusted P-values for pairwise comparison of all groups in each experiment

Caco2. adherence						
	Mg1655 Glu	Mg1655 initial	Mg1655 PA	ZvL2 Glu	ZvL2 initial	ZvL2 PA
Mg1655 initial	1.59E-02	-	-	-	-	-
Mg1655 PA	6.15E-03	9.10E-04	-	-	-	-
ZvL2 Glu	2.65E-01	9.45E-01	5.03E-02	-	-	-
ZvL2 initial	1.56E-02	6.25E-02	6.15E-03	1.04E-01	-	-
ZvL2 PA	7.30E-04	9.10E-04	7.30E-04	2.04E-03	2.65E-02	-
ZvL2 PA-Glu	5.46E-01	6.15E-03	2.69E-03	2.02E-01	1.42E-02	7.30E-04

Caco2. invasion						
	Mg1655 Glu	Mg1655 initial	Mg1655 PA	ZvL2 Glu	ZvL2 initial	ZvL2 PA
Mg1655 initial	9.97E-03	-	-	-	-	-
Mg1655 PA	7.99E-02	6.60E-04	-	-	-	-
ZvL2 Glu	3.20E-04	4.30E-04	3.50E-04	-	-	-
ZvL2 initial	1.80E-04	1.80E-04	1.80E-04	3.50E-04	-	-
ZvL2 PA	3.50E-04	3.70E-04	3.50E-04	6.30E-04	3.15E-03	-
ZvL2 PA-Glu	2.31E-01	3.04E-01	3.27E-02	3.20E-04	1.80E-04	3.50E-04

Macrophages. 6h postinfection						
	Mg1655 Glu	Mg1655 initial	Mg1655 PA	ZvL2 Glu	ZvL2 initial	ZvL2 PA-Glu
Mg1655 initial	1.60E-05	-	-	-	-	-
Mg1655 PA	5.77E-01	3.80E-06	-	-	-	-
ZvL2 Glu	1.40E-12	6.51E-01	3.80E-09	-	-	-
ZvL2 initial	1.60E-09	2.10E-04	2.20E-11	1.10E-06	-	-
ZvL2 PA-Glu	1.37E-01	7.10E-05	2.38E-01	1.10E-04	1.60E-07	-
ZvL2 PA	7.10E-11	1.00E-06	1.40E-12	8.70E-09	8.80E-04	3.20E-09

Macrophages. 24h postinfection						
	Mg1655 Glu	Mg1655 initial	Mg1655 PA	ZvL2 Glu	ZvL2 initial	ZvL2 PA
Mg1655 initial	1.20E-06	-	-	-	-	-
Mg1655 PA	6.84E-01	7.60E-07	-	-	-	-
ZvL2 Glu	8.40E-08	7.08E-01	6.50E-08	-	-	-
ZvL2 initial	4.20E-07	8.20E-06	3.50E-07	1.00E-05	-	-
ZvL2 PA	3.40E-15	1.40E-12	2.00E-16	7.80E-14	2.90E-02	-
ZvL2 PA-Glu	5.79E-01	7.50E-07	7.37E-01	1.00E-07	1.70E-07	2.00E-16