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Table S1. Primers used for PCR amplification and Sanger sequencing to verify the mutations of strains evolved of *Salmonella* Thyphimurium LT2. F: Forward; R: Reverse.

Gene	F primer (5' → 3')	R primer (5' → 3')
<i>flhA</i>	GGCAGGAACCCCATATCCTG	GCCGGTCTGATTGGTGAAGA
<i>fliH</i>	TGTGGACGATCGCAGTATCC	CATCAGCCGTGAGGCGATAA
<i>lon</i>	AGTACCTTGATTCGCCAGCC	TGGCCCAACGAGGTTTTACC
<i>nirC</i>	CAGCCAACAAAGAGGCAGTG	ATAAACGCCAGCAGACACCA
<i>wbaV</i>	GCCATAACATGCCATAGCCA	GCAGTGATGATGCTCTTGCG
<i>rob</i>	ATAAAATCCTGCACGCCGGT	AAGTGGCACCTGCAGAGAAT
<i>sseG</i>	TGTTAACGCGCCTGAGGAAT	ACGTTGTTCTGGCGTTACCT
<i>argR</i>	GCCGCCGTATGGATAAGGAT	GTCGTAACCGCCTACCAGTC
<i>yfhP</i>	TTCATCCTTCAGACGACCGC	GTCAATATCGCACGGAACG
<i>rrsH</i>	GCAACGCGAAGAACCTTACC	TTTGATTCTGTTCCGGGCG

Gene	Sense	Primer sequence
<i>lon</i>	F	CGAAGGCTACATCAAGCTGAACAAAAAATTCGCGCGGAAGTGCTGACGTTCTAATTTTTGTTGACACTCTATC
	R	CACGGCTTTGAACCGCGAGATACTCAAGGATGCGGTCTTTCACGCGCTCCATCAAAGGGAAAACTGTCCATATGC
<i>yfhP</i>	F	AAGTAACCGCGTCAATATCGCACGGAACGCTAAATACCTGACTAATTTACTCCTAATTTTTGTTGACACTCTATC
	R	GCAGGGACAAGTCTGACATTCCCGAGTAATTTGGTCAACTATTTACTTGAATCAAAGGGAAAACTGTCCATATGC
<i>wbaV</i>	F	ATATTTATGTGACAGAAAAGAGACCGGGTGTGATTAGTTGAGATTAGAATCCTAATTTTTGTTGACACTCTATC
	R	CGTTTTAAAGATATATTTTTACTGTAAAAATCATTAGCTAATTTTAAATAATCAAAGGGAAAACTGTCCATATGC
<i>nirC</i>	F	TAAGTGTGCGGCTAACGCTGCGCGCATCGCACGCCTGTCGGCGAATAATCTCCTAATTTTTGTTGACACTCTATC
	R	TTGCCAGACAAACCAGCCAGTTACACAGCGCGCCTTTGAAGAACAGTACCATCAAAGGGAAAACTGTCCATATGC
<i>rob</i>	F	GTTTATCGAAATCAGCAGTGGCGCTGCGTTTGACCGCGCGTCCAATTCTGTCCTAATTTTTGTTGACACTCTATC
	R	CGGGATGCGCCGACTGAACATAGCCATCGGCCTGCTCTTGCGGCAGTGCGATCAAAGGGAAAACTGTCCATATGC
<i>fliH</i>	F	TCTGGCGGAAACCGGCGAAATGGTGATTGGCAGCGGCGAGGATACCTATGATTCCGGGGATCCGTCGACC
	R	CGAGATCGTCGGGGGTCCAGACTTGCCACGGCAATTCATTAGACATAGGTTGTAGGCTGGAGCTGCTTCG
<i>flhA</i>	F	CCTTCCGGTGCCAGAAGCGCTGGATTTTATGAACGAGAAGAATACTGATGATTCCGGGGATCCGTCGACC
	R	CAGGGGAAAGAGCAACAACGCCAGCCATTTACGCATTATTTTCTCCAATTGTAGGCTGGAGCTGCTTCG

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Table S3. A (maximum OD595), μ_m (maximum specific growth rate; h⁻¹) and λ (lag time; h) values and error standard of the modified Gompertz model obtained from at least 3 independently growth curves of *Salmonella* Typhimurium LT2 wild type (SeWT) (A) and evolved strains: SeCarA (B), SeCarB (C), SeCarC (D) at different concentrations of carvacrol. The goodness of the fit is shown by R^2 and adjusted R^2 values and the root mean square error (RMSE).

A) SeWT									
Carvacrol ($\mu\text{L/L}$)	Values			Standard error			Godness of fit		
	A	μ_{max}	λ	A	μ_{max}	λ	R^2	$Adj R^2$	RMSE
0	0.718	0.159	3.185	0.020	0.035	0.509	0.938	0.932	0.069
	0.639	0.174	2.987	0.017	0.036	0.414	0.946	0.940	0.056
	0.645	0.211	3.238	0.019	0.057	0.452	0.918	0.910	0.069
	0.751	0.138	2.741	0.021	0.025	0.526	0.936	0.930	0.070
100	0.573	0.154	5.718	0.008	0.017	0.227	0.986	0.985	0.028
	0.525	0.166	5.339	0.015	0.021	0.211	0.989	0.987	0.024
	0.573	0.131	5.279	0.005	0.008	0.148	0.995	0.995	0.017
	0.587	0.158	5.836	0.006	0.013	0.161	0.993	0.993	0.020

B) SeCarA									
Carvacrol ($\mu\text{L/L}$)	Values			Standard error			Godness of fit		
	A	μ_{max}	λ	A	μ_{max}	λ	R^2	$Adj R^2$	RMSE
0	0.724	0.329	3.521	0.012	0.060	0.216	0.972	0.969	0.045
	0.782	0.179	2.938	0.020	0.037	0.473	0.942	0.936	0.071
	0.821	0.207	2.917	0.019	0.039	0.403	0.946	0.941	0.069
	0.829	0.137	2.410	0.023	0.023	0.537	0.938	0.932	0.074
100	0.569	0.390	4.559	0.005	0.052	0.096	0.991	0.990	0.020
	0.639	0.162	3.692	0.014	0.027	0.359	0.963	0.959	0.048
	0.503	0.347	4.853	0.005	0.037	0.086	0.993	0.992	0.018

C) SeCarB									
Carvacrol ($\mu\text{L/L}$)	Values			Standard error			Godness of fit		
	A	μ_{max}	λ	A	μ_{max}	λ	R^2	$Adj R^2$	RMSE
0	0.834	0.170	2.314	0.026	0.040	0.597	0.911	0.902	0.090
	0.760	0.199	2.630	0.023	0.047	0.491	0.924	0.915	0.078
	0.821	0.161	2.021	0.024	0.033	0.567	0.909	0.901	0.085
	0.624	0.296	3.052	0.009	0.031	0.121	0.995	0.994	0.019
100	0.616	0.293	3.738	0.013	0.070	0.276	0.951	0.946	0.051
	0.623	0.361	3.473	0.015	0.118	0.292	0.934	0.927	0.058
	0.643	0.414	3.567	0.008	0.076	0.143	0.978	0.975	0.034

D) SeCarC

Carvacrol ($\mu\text{L/L}$)	Values			Standard error			Godness of fit		
	A	μ_{max}	λ	A	μ_{max}	λ	R^2	$Adj R^2$	$RMSE$
0	0.841	0.201	2.817	0.015	0.027	0.309	0.970	0.967	0.052
	0.809	0.214	3.134	0.017	0.039	0.365	0.959	0.955	0.061
	0.811	0.172	2.887	0.015	0.022	0.329	0.970	0.967	0.051
100	0.612	0.232	3.861	0.014	0.052	0.324	0.956	0.951	0.051
	0.635	0.166	3.373	0.018	0.040	0.493	0.931	0.924	0.065
	0.645	0.194	4.360	0.014	0.037	0.347	0.961	0.957	0.051

E) SeCarD

Carvacrol ($\mu\text{L/L}$)	Values			Standard error			Godness of fit		
	A	μ_{max}	λ	A	μ_{max}	λ	R^2	$Adj R^2$	$RMSE$
0	0.791	0.370	3.210	0.022	0.132	0.419	0.902	0.893	0.089
	0.814	0.306	3.350	0.021	0.080	0.377	0.939	0.933	0.077
	0.830	0.155	2.317	0.027	0.031	0.567	0.925	0.917	0.083
100	0.647	0.275	4.300	0.009	0.041	0.190	0.985	0.984	0.032
	0.642	0.209	3.959	0.010	0.031	0.246	0.977	0.974	0.038
	0.703	0.153	2.995	0.016	0.025	0.413	0.953	0.949	0.056
	0.704	0.177	3.314	0.015	0.031	0.373	0.957	0.952	0.055

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79 **Table S4.** Genetic variations detected by whole genome sequencing (WGS) between SeWT and
80 the reference genome of *Salmonella* Typhimurium LT2 (NCBI accession: NC_003197.2). Single
81 nucleotide variation (SNV). insertion (Ins) and deletion (Del).

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Genome position	Genes	Locus tag	Mutation*	Change	Information
290.718	<i>rrsH</i>	STM0249	SNV: C1529A	No coding	RNA 16S ribosomal
364.623	<i>crl</i>	STM0319	Del: -T 104	Frame shift	Sigma factor-binding protein
416.555	<i>prpR</i>	STM0367	SNV: C1159T	Leu387Phe	Operon regulator
453.939	<i>brnQ</i>	STM0399	SNV: C681T	Silent mutation (Tyr227)	Branched-chain amino acid transport system carrier protein
509.118	<i>cypD</i>	STM0452	SNV: T450A	Asp150Glu	Peptidylprolyl isomerase
608.859	<i>fimH</i>	STM0547	SNV: G182C	Gly61Ala	Adhesin
1.205.933	Intergenic <i>wraB</i> - <i>yedF</i>	STM1119 STM1120	SNV: G → A	No coding	-
1.778.104	<i>ycjF</i>	STM1684	SNV: T821C	Leu274Pro	UPF0283 membrane protein
1.841.398	-	STM1747	SNV: G98A	Arg33Gln	Hypothetical protein
1.849.642	<i>hnr</i>	STM1753	SNV: T305G	Val102Gly	Regulator of RpoS
3.469.143	<i>dacB</i>	STM3300	SNV: C483T	Silent mutation (Ser161)	Transpeptidase
3.673.628	<i>malQ</i>	STM3513	SNV: T287G	Leu96Arg	4-Alpha-glucanotransferase
3.675.952	<i>malP</i>	STM3514	Del: -GCCGCCTG 358	Frame shift	Alpha-1.4 phosphorylase
3.819.815	-	STM3633	SNV: T562C	Silent mutation (Leu188)	LacI family transcriptional regulator
4.122.937	<i>gppA</i>	STM3913	SNV: G385T	Gly129Cys	Pyrophosphatase
4.122.950	<i>gppA</i> <i>rhlB</i>	STM3913 STM3914	Del: -1.179 pb	Knock-out (<i>gppA</i> , <i>rhlB</i>)	Pyrophosphatase ATP-dependent RNA helicase RhlB
4.291.432	<i>yiiQ</i>	STM4082	SNV: G323A	Stop-gain	Hypothetical protein
4.294.693	<i>glpK</i>	STM4086	SNV: G1171A	Asp391Asn	Glycerol kinase
4.697.694	<i>treB</i>	STM4454	Ins: + A 543	Frame shift	Pseudogene (trehalose metabolism)

83 *Position respect to the start of the coding region.