

**Table S1.** Up-regulated genes in *Escherichia coli* O157:H7 adapted to sublethal level of thymol (1/2T), carvacrol (1/2C) or trans-cinnamaldehyde (1/2TC), compared to non-adapted cells ( $P_{adj} \leq 0.05$ , fold change  $\geq 5.0$ ). “-” indicates no detection of differentially expressed gene at the set criteria.

Gene ID	fold change <sup>a</sup>			Gene Product Description
	1/2T	1/2C	1/2TC	
<b>Cell Envelope</b>				
ECs1884	492.1	416.9	-	phage shock protein, PspD
ECs1883	528.5	434.0	-	PspC family transcriptional regulator
pspB	615.4	465.0	-	phage shock protein, PspB
ECs1881	763.2	634.3	-	phage shock protein, PspA
pspG	1459.2	1452.2	-	phage shock protein, PspG
cpxP	566.9	374.6	-	cell envelope toxicity response protein, CpxP
ECs2690	10.8	7.6	-	transcriptional regulator, RcsA
ECs2515	5.3	5.9	-	outer membrane protein
lpxC	11.0	9.1	-	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase
ECs2011	15.6	9.3	-	phosphatidate cytidyltransferase
ECs2348	-	6.2	-	membrane bound lysozyme inhibitor
<b>Heat Resistance</b>				
ECs1050	8.4	9.8	-	heat shock protein, HspQ
ECs4310	8.5	6.0	-	RNA polymerase factor sigma-32

ECs4626	22.2	25.2	-	heat shock chaperone, IbpB
ECs4627	12.0	13.8	-	heat shock protein, IbpA
ECs0165	13.8	8.5	-	serine endoprotease, degrade damaged proteins
ECs2539	15.4	7.5	-	heat shock protein, HtpX
<b>Acid Resistance</b>				
ECs5113	14.4	-		lysine decarboxylase 1, CadA
cadB	16.1	-		lysine/cadaverine antiporter, CadB
ECs2303	37.4	42.6		acid-shock protein, resistance against moderate acid
<b>Oxidative Stress Resistance</b>				
grxA	9.3	-	8.8	glutaredoxin, GrxA
ECs4834	10.5	-	-	superoxide dismutase, SodA
ECs5045	10.4	9.0	-	redox-sensitive transcriptional activator, SoxR
ECs5044	17.1	17.1	-	DNA-binding transcriptional regulator, SoxS
ECs2487	17.6	9.7	-	methionine sulfoxide reductase B
ECs3448	22.9	7.2	8.9	thioredoxin 2, TrxC
ECs3271	28.9	8.5	10.1	manganese transport protein, MntH
ECs0931	6.0	6.2	-	nitroreductase A
<b>Antibiotic Resistance</b>				
ECs2138	5.4	5.5	-	family transcriptional regulator, MarA
ECs2137	6.3	6.8	-	family transcriptional regulator, MarR
ECs0517	5.6	10.0	-	family transcriptional regulator, AcrR

ECs3332	5.3	-	-	multidrug efflux system, AcrD
ECs2882	21.9	-	-	multidrug efflux pump system protein, MdtA
ECs2883	15.3	-	-	multidrug efflux pump system protein, MdtB
ECs2884	15.4	-	-	multidrug efflux pump system protein, MdtC
ECs2885	8.4	-	-	multidrug efflux pump system protein, MdtE
ECs2305	21.7	6.4	-	multidrug efflux pump system protein, MdtI
ECs2306	8.6	-	-	multidrug efflux pump system protein, MdtJ
ECs0502	-	9.2	-	multidrug transporter membrane ATP-binding components, MdlA
ECs3121	5.2	-	-	antibiotic resistance protein, YwoG
ECs0427	5.3	6.0	-	peptide antibiotic transporter, SbmA
ECs5243	11.3	15.0	-	transposase, OrfA
orfB	5.1	-	-	transposase, OrfB
<b>Virulence</b>				
ECs5440	5.7	-	-	small toxic polypeptide
ECs3771	8.0	12.4	8.7	oxidoreductase, hemolysin III
ECs5277	5.5	-	-	protein FimF
ECs2107	-	6.1	-	adhesin
bssS	14.5	8.5	-	biofilm formation regulatory protein, BssS
tnaA	32.9	5.0	-	tryptophanase, TnaA
ECs4430	-	-	10.5	fimbrial chaperone protein, LpfB
ECs4431	-	-	18.5	fimbrial major protein, LpfA

**Metal Ion Homeostasis (iron, zinc, copper)**

ECs0635	9.8	-	-	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase
entF	7.9	5.5	-	enterobactin synthase subunit F, EntF
ECs0630	8.8	-	-	enterobactin exporter, EntS
ECs0634	11.3	5.8	-	2,3-dihydro-2,3-dihydroxybenzoate synthetase, EntB
entE	17.7	9.0	-	2,3-dihydroxybenzoate-AMP ligase, EntE
ECs0632	23.8	10.3	7.9	isochorismate synthase, EntC
ECs0627	5.6	5.3	5.3	iron-enterobactin transporter ATP-binding protein
ECs0628	8.8	-	5.8	iron-enterobactin transporter permease
ECs0629	12.6	10.1	9.4	iron-enterobactin transporter membrane protein
ECs0631	11.1	7.3	6.8	iron-enterobactin transporter periplasmic binding protein
ECs1360	5.8	-	-	bifunctional enterobactin receptor/adhesin, Iha
ECs0624	17.8	14.3	6.0	enterobactin/ferric enterobactin esterase, Fes
ECs4380	5.0	-	-	heme utilization/transport protein, ChuA
ECs4382	16.0	9.7	7.3	hemin binding protein, ShuT
hemH	9.4	-	7.4	ferrochelataase, HemH
ECs3917	5.8	-	-	ferrichrome iron receptor
ECs0154	7.2	6.9	8.3	ferrichrome outer membrane transporter
ECs1480	7.3	-	-	outer membrane receptor for Fe <sup>3+</sup> uptake, FhuE
ECs5327	10.1	10.3	5.0	ferrioxamine B reductase, FhuF
ECs3890	11.2	8.2	5.2	biopolymer transport protein, ExbB

ECs3889	5.7	-	-	biopolymer transport protein, ExbD
feoA	6.3	13.5	5.1	ferrous iron transport protein A, FeoA
feoB	5.3	7.7	-	ferrous iron transport protein B, FeoB
ECs3916	5.3	6.2	-	iron-siderophore iron ABC transporter ATP-binding protein
ECs2055	5.2	-	-	outer membrane receptor for iron transport
ECs5531	8.8	10.3	-	bacterioferritin-associated ferredoxin, bfd
znuA	-	-	-	high-affinity zinc transporter periplasmic protein, ZnuA
znuB	6.0	9.6	-	high-affinity zinc transporter membrane protein, ZnuB
znuC	17.1	23.9	-	high-affinity zinc transporter ATPase, ZnuC
copA	9.9	-	-	copper exporting ATPase, CopA

### **Quorum Sensing**

ECs2122	5.2	-	-	AI-2 transport system, LsrD
tqsA	13.7	16.9	-	AI-2 transport system, TqsA

### **Amino Acid Metabolism**

ECs4686	14.6	13.6	-	asparagine synthetase
ECs1874	6.0	-	-	glutamine synthetase
ECs4646	20.5	-	-	tryptophan transporter, TnaB
ECs3656	5.7	-	-	serine transporter, SdaC
ECs3194	5.0	-	-	lysine/arginine/ornithine transporter, ArgT
ECs0694	5.0	5.9	-	glutamate/aspartate transporter subunit, YbeJ
puuD	9.2	7.0	-	$\gamma$ -glutamyl- $\gamma$ -aminobutyrate hydrolase

putA	5.2	-	-	proline dehydrogenase
ECs2523	13.0	8.2	-	L-serine dehydratase 1
ECs3657	6.5	-	-	L-serine dehydratase
ECs0116	-	5.5	-	aromatic amino acid transporter, AroP

### **Fatty Acid Metabolism**

fadA	5.9	-	-	3-ketoacyl-CoA thiolase
fadB	13.2	5.7	-	multifunctional fatty acid oxidation complex $\alpha$ subunit
fadE	13.0	5.6	-	acyl-CoA dehydrogenase
fadI	8.4	8.6	-	3-ketoacyl-CoA thiolase

### **Carbohydrate Metabolism**

ECs3042	9.7	-	-	galactose-binding transport protein, MglB
ECs3041	12.5	-	-	galactose/methyl galactoside transporter ATP-binding protein, MglA
ECs3040	14.0	-	-	$\beta$ -methyl galactoside transporter inner membrane protein, MglC
ECs3043	-	5.2	-	mglBAC operon transcriptional regulator, GalS
ECs0512	-	9.3	-	maltose O-acetyltransferase
ECs4450	5.9	-	-	xylose transporter ATP-binding protein, XylG
ECs2369	12.1	16.6	-	putative arabinose efflux transporter, YdhC
ECs3571	5.6	8.2	-	cellobiose-specific PTS system, IIB
ECs4824	6.4	6.7	-	fructose-specific PTS system, FrvX
ECs4825	-	7.9	-	fructose-specific PTS system, IIB-like component
ECs3266	5.6	8.4	-	fructose-specific PTS system, II-like component

ECs2867	9.1	-	-	polysaccharide export protein, wza
ECs0309	6.0	12.3	-	transcriptional regulator, maltose system
ECs2328	6.0	9.6	-	transcriptional repressor MalI, maltose-glucose transport
ECs3976	6.6	5.7	-	transcriptional repressor ExuR, hexuronate utilization
ECs1862	15.1	-	-	transcription regulator, UidR
ECs4098	-	6.6	-	N-acetylneuraminase lyase
ECs5319	5.9	6.9	-	phosphoglycerol transferase I, MdoB
mdoC	-	5.6	-	glucans biosynthesis protein, MdoC
ECs5216	-	-	5.6	trehalose-6-phosphate hydrolase

#### **Nucleotide Metabolism**

purT	9.3	-	-	glycinamide ribonucleotide transformylase (GAR transformylase)
nrdF	12.1	-	-	ribonucleotide-diphosphate reductase $\beta$ subunit
nrdI	26.3	19.9	-	ribonucleotide reductase stimulatory protein
nrdH	17.6	18.0	-	glutaredoxin-like protein, NrdH
ECs3757	-	5.1	-	putative MFS transporter, purine transporter
ECs3538	12.3	6.2	-	ribonucleotide-diphosphate reductase $\alpha$ subunit

#### **Energy Metabolism**

ECs3565	5.2	6.7	-	anaerobic nitric oxide reductase transcriptional regulator, NorR
ECs3566	14.2	27.1	-	flavorubredoxin, FIRd
nirD	14.6	9.7	-	nitrite reductase small subunit, NirD
sdhA	11.8	-	-	succinate dehydrogenase flavoprotein subunit, SdhA

sdhB	10.8	-	-	succinate dehydrogenase iron-sulfur subunit, SdhB
sdhC	8.0	-	-	succinate dehydrogenase cytochrome b556 large membrane subunit, SdhC
sdhD	9.9	-	-	succinate dehydrogenase cytochrome b556 small membrane subunit, sdhD
sucA	5.8	-	-	2-oxoglutarate dehydrogenase subunit E1, SucA
sucC	5.2	-	-	succinyl-CoA synthetase $\beta$ subunit, SucC
ECs0752	5.4	-	-	dihydrolipoamide succinyltransferase
fumC	23.6	12.6	-	fumarate hydratase
ECs5051	5.6	-	-	acetyl-CoA synthetase
ECs4818	5.5	-	-	formate dehydrogenase-O $\gamma$ subunit
ECs4933	8.3	-	-	isocitrate lyase
ECs4820	11.7	7.4	-	formate dehydrogenase-O major subunit, FdoG
ECs4819	13.0	8.0	-	formate dehydrogenase-O iron-sulfur subunit, FdoH
ECs3445	10.2	12.4	-	autonomous glycyl radical cofactor, GrcA
ECs4216	8.9	7.6	-	nitrite reductase (NAD(P)H) subunit, NirB
ECs3127	12.9	8.7	7.5	anaerobic glycerol-3-phosphate dehydrogenase subunit B, GlpB
glpC	9.5	5.7	6.9	sn-glycerol-3-phosphate dehydrogenase subunit C, GlpC
glpD	15.5	5.0	9.1	glycerol-3-phosphate dehydrogenase, GlpD
ECs1885	34.0	33.3	-	thiosulfate:cyanide sulfurtransferase
ECs3090	5.0	-	-	cytochrome c biogenesis protein, CcmA
prpB	5.5	8.1	-	2-methylisocitrate lyase
ECs0654	5.6	-	-	citrate lyase $\alpha$ subunit, CitF



ECs4891	5.8	-	-	soluble pyridine nucleotide transhydrogenase
ECs3963	14.5	6.5	-	NADPH dehydrogenase
pdhR	6.5	5.9	-	transcriptional regulator PdhR

### **Regulatory Functions**

ECs3173	5.4	-	-	transcriptional regulator, lrhA
ECs2737	5.9	-	-	transcriptional regulator, PerC
ECs2886	7.8	-	-	two-component regulatory system, BaeS
ECs4598	9.7	12.9	-	DNA-binding protein, putative transcriptional regulator
ECs0501	16.8	28.1	-	Lrp-like transcriptional regulator, YbaO
ECs0513	-	10.9	-	hemolysin expression-modulating protein

### **Others/Unclassified**

cpsG	5.0	-	-	phosphomannomutase, CpsG
ECs2865	5.7	-	-	tyrosine kinase, Wze
ytfG	5.1	-	-	oxidoreductase, YtfG
ECs3932	8.6	20.0	-	oxidoreductase
ECs4383	5.1	-	-	coproporphyrinogen III oxidase
ECs1773	5.1	-	-	putative prophage maintenance protein
mokW	5.8	-	-	putative prophage maintenance protein, MokW
zraP	7.5	9.2	-	zinc resistance protein
ECs0917	15.0	19.0	-	dehydrogenase, YliI
ECs4240	-	6.0	-	dehydrogenase, YrfF

ECs2056	21.3	7.9	-	receptor
ECs4357	-	6.0	-	HicA-like protein, HicA-HicB TA system
ECs4356	-	5.1	-	HicB-like protein, HicA-HicB TA system
ECs4007	6.8	7.9	-	antitoxin PrlF of YhaV-PrIF TA system
ECs0552	7.7	8.1	-	protease
ECs3264	-	5.4	-	exoaminopeptidase
ECs3265	-	5.9	-	aminopeptidase
ECs1856	-	6.1	-	lipoprotein OsmB
ECs3842	14.1	16.6	-	uncharacterized transporter, yqgA
ECs3970	70.6	108.8	-	uncharacterized transporter, ygjT
ECs4432	25.2	-	20.2	uncharacterized resistance protein, yhjX
ECs3031	-	5.0	-	transporter
ECs5300	-	5.2	-	transporter, YjiO
ECs3285	-	5.2	-	sulfate transport protein CysZ
ECs0729	40.5	19.4	-	protein RhsC
ECs4114	-	6.7	-	p-hydroxybenzoic acid efflux subunit, AaeA
ECs1145	-	-	5.0	cold shock protein, CspG
<b>Unknown/Hypothetical</b>				
ECs4381	5.1	-	-	hypothetical protein
ECs2025	5.2	-	-	hypothetical protein
ECs0869	5.3	6.1	-	hypothetical protein

ECs5413	5.3	-	-	hypothetical protein
ECs2292	5.5	-	-	hypothetical protein
ECs5010	5.6	-	-	hypothetical protein
ECs0621	5.6	-	-	hypothetical protein
ECs0511	5.6	-	-	hypothetical protein
ECs5011	5.8	-	-	hypothetical protein
argD_1	5.8	5.3	-	unknown
ECs2144	5.8	-	-	hypothetical protein
ECs2010	5.9	6.6	-	hypothetical protein
ECs2434	5.9	6.3	-	hypothetical protein
ECs0636	6.0	-	-	hypothetical protein
ECs0551	6.0	6.0	-	hypothetical protein
ECs1431	6.1	8.5	-	unknown
ECs1525	6.4	-	-	hypothetical protein
ECs0069	6.5	5.3	-	hypothetical protein
ECs3528	6.5	7.5	-	hypothetical protein
ECs5400	6.7	7.2	-	hypothetical protein
ECs1266	6.8	6.3	-	hypothetical protein
ECs5584	6.9	11.6	-	hypothetical protein
ECs4220	6.9	7.8	-	hypothetical protein
ECs5381	7.0	9.5	-	hypothetical protein

ECs5195	7.4	5.3	-	hypothetical protein
ECs1091	8.0	-	-	unknown
ECs3328	8.1	13.0	-	hypothetical protein
ECs0497	8.1	8.8	-	hypothetical protein
ECs2556	8.8	6.6	-	hypothetical protein
ECs0930	8.9	8.8	-	hypothetical protein
ECs4086	9.1	10.9	-	hypothetical protein
ECs0121	9.3	12.6	-	hypothetical protein
rrsG	9.8	-	-	unknown
ECs0898	10.0	8.7	-	hypothetical protein
ECs5009	10.3	-	-	hypothetical protein
ECs2486	10.3	6.1	-	hypothetical protein
ECs1054	10.4	11.0	-	hypothetical protein
ECs1655	10.7	-	-	hypothetical protein
ssrS	11.1	13.6	-	unknown
ECs2040	11.1	9.1	-	hypothetical protein
ECs1491	12.6	7.2	-	hypothetical protein
ECs0914	12.8	10.4	-	hypothetical protein
ECs0646	13.4	13.3	-	hypothetical protein
ECs0923	14.0	19.2	-	hypothetical protein
ECs3669	15.0	7.8	-	hypothetical protein

ECs0429	15.0	29.9	-	hypothetical protein
ECs4597	15.9	15.7	-	hypothetical protein
csrB	16.6	8.8	-	unknown
rnpB	17.5	10.5	-	unknown
ECs3120	18.3	15.4	-	hypothetical protein
ECs1258	19.7	21.1	-	hypothetical protein
ECs0514	22.2	36.0	-	hypothetical protein
ECs1488	23.5	29.7	-	hypothetical protein
ssrA	26.1	14.5	-	unknown
rrlG	27.8	19.2	-	unknown
ECs3270	30.2	67.2	-	hypothetical protein
ECs2412	33.5	13.2	15.6	hypothetical protein
ECs0880	34.7	38.9	-	hypothetical protein
ECs1490	37.7	33.4	-	hypothetical protein
ECs4140	45.7	26.7	-	hypothetical protein
ECs5189	47.2	48.4	-	hypothetical protein
ECs3073	49.3	39.5	-	hypothetical protein
ECs4111	62.5	67.7	22.2	hypothetical protein
ECs0005	181.5	6.9	-	hypothetical protein
ECs0728	285.1	172.8	-	hypothetical protein
ECs2449	781.4	20.5	-	hypothetical protein

ECs2049	-	5.0	-	hypothetical protein
ECs3964	-	5.1	-	hypothetical protein
ECs5415	-	5.3	-	hypothetical protein
ECs4252	-	5.3	-	hypothetical protein
ECs4023	-	5.4	-	hypothetical protein
ECs2181	-	5.5	-	hypothetical protein
ECs4008	-	5.7	-	hypothetical protein
ECs3179	-	5.9	-	hypothetical protein
ECs3811	-	5.9	-	hypothetical protein
ECs2042	-	6.0	-	hypothetical protein
ECs5399	-	6.2	-	hypothetical protein
ECs4308	-	6.3	-	hypothetical protein
ECs0465	-	6.4	-	hypothetical protein
rpmE2_1	-	6.4	-	unknown
ECs2020	-	6.5	-	hypothetical protein
ECs2767	-	6.7	-	hypothetical protein
ECs2502	-	6.8	-	hypothetical protein
ECs3022	-	6.9	-	hypothetical protein
ECs2711	-	7.1	-	hypothetical protein
ECs0713	-	8.6	-	hypothetical protein
rpmJ_1	-	10.1	-	unknown

ECs4115	-	10.7	-	hypothetical protein
ECs2265	-	12.2	-	hypothetical protein
ECs4336	-	-	5.9	hypothetical protein

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<sup>a</sup>The values of gene expression fold change are averages of three independent biological replicates.

**Table S2.** Down-regulated genes in *Escherichia coli* O157:H7 adapted to sublethal level of thymol (1/2T) or carvacrol (1/2C), compared to non-adapted cells ( $P_{adj} \leq 0.05$ , fold change  $\geq 5.0$ ). “-” indicates no detection of differentially expressed gene at the set criteria.

Gene ID	fold change <sup>a</sup>		Gene Product Description
	1/2T	1/2C	
<b>Acid Resistance</b>			
ECs5097	-12.6	-15.5	arginine:agmatin antiporter
ECs5098	-11.7	-10.9	AraC family transcriptional regulator, AdiY
ECs5099	-21.1	-21.3	biodegradative arginine decarboxylase, AdiA
ECs4388	-14.6	-16.9	Mg <sup>2+</sup> transport ATPase, involved in cell density-dependent acid resistance
hdeB	-11.7	-8.9	acid-resistance protein
<b>Motility (flagella)</b>			
ECs4405	-22.8	-14.1	EAL domain-containing protein
ECs2601	-	-28.5	transcriptional activator, FlhC
ECs2602	-5.6	-16.7	transcriptional activator, FlhD
ECs1449	-5.5	-	anti-sigma-28 factor, FlgM
ECs1448	-20.6	-	flagella synthesis protein, FlgN
flgK	-5.0	-5.5	flagellar hook-associated protein, FlgK
fliA	-16.8	-12.2	flagellar biosynthesis sigma factor, FliA
fliD	-35.3	-18.5	flagellar capping protein, FliD
fliS	-23.3	-13.6	flagellar protein, FliS
ECs2665	-25.1	-8.2	flagellar biosynthesis protein, FliT



ECs2660	-5.6	-	flagella biosynthesis protein, FliZ
ECs2662	-29.2	-33.6	flagellin
motB	-26.7	-24.6	flagellar motor protein, MotB
ECs2600	-25.9	-16.7	flagellar motor protein, MotA
<b>Motility (chemotaxis)</b>			
ECs2596	-18.1	-15.6	methyl-accepting chemotaxis protein II
ECs2598	-32.9	-23.3	chemotaxis protein, CheA
ECs2597	-16.4	-19.5	purine-binding chemotaxis protein, CheW
ECs2591	-13.5	-13.9	chemotaxis protein, CheZ
ECs2594	-10.9	-9.7	chemotaxis methyltransferase, CheR
ECs2592	-20.7	-18.1	chemotaxis regulatory protein, CheY
ECs2595	-22.2	-15.0	methyl-accepting protein IV
ECs2593	-19.3	-20.2	chemotaxis-specific methylesterase
<b>Virulence</b>			
ECs2974	-	-8.7	Shiga toxin I subunit A
ECs2973	-	-8.7	Shiga toxin I subunit B
ECs1205	-5.8	-5.0	Shiga toxin 2 subunit A
hlyE	-5.8	-	hemolysin E
ECs1663	-	-9.1	outer membrane protease
ECs4573	-	-23.2	T3SS protein, EscJ
ECs4574	-	-11.0	T3SS protein, SepD
ECs4575	-5.4	-	T3SS protein, EscC

ECs4576	-	-13.3	T3SS protein, CesD
ECs4583	-	-22.2	T3SS protein
ECs1213	-5.1	-	endolysin
ECs1690	-6.4	-	transposase

### **Antibiotic Resistance**

ECs3247	-	-9.1	multidrug resistance protein K, EmrK
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### **Amino Acid Metabolism**

metF	-14.3	-20.2	5,10-methylenetetrahydrofolate reductase
ECs4759	-9.9	-11.4	5-methyltetrahydropteroyltriglutamate/homocysteine S-methyltransferase
glyA	-	-8.0	serine hydroxymethyltransferase
ilvM	-7.3	-	acetolactate synthase 2 regulatory subunit
ECs3784	-6.2	-	D-3-phosphoglycerate dehydrogenase
ECs0991	-5.6	-8.1	3-phosphoshikimate 1-carboxyvinyltransferase
dapD	-5.1	-	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase
ECs1029	-	-6.9	dihydroorotate dehydrogenase 2
pyrE	-	-5.7	orotate phosphoribosyltransferase
cysJ	-	-6.1	sulfite reductase $\alpha$ subunit
ECs3604	-	-5.2	adenylyl-sulfate kinase
ECs0146	-5.0	-5.7	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase
ECs3818	-	-11.4	S-adenosylmethionine synthetase

### **Nucleotide Metabolism**

ECs0585	-	-11.1	5-(carboxyamino)imidazole ribonucleotide mutase
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ECs0584	-	-6.9	5-(carboxyamino)imidazole ribonucleotide synthase
ECs3338	-	-5.3	phosphoribosylaminoimidazole-succinocarboxamide synthase
ECs3606	-	-6.1	sulfate adenylyltransferase subunit 2
ECs4530	-	-20.0	xanthine transporter

### **Carbohydrate Metabolism**

eutD	-	-10.3	phosphotransacetylase
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### **Regulatory Functions**

ECs3709	-9.3	-	transcriptional regulator, YgeH
ECs1142	-7.5	-10.4	regulator, YmcC
ECs5271	-7.1	-16.7	tyrosine recombinase, fimA regulator
ECs4578	-5.9	-5.9	negative regulator GrlR
ECs2334	-19.9	-	oriC-binding nucleoid-associated protein, YdgT
ECs4936	-	-7.0	acetate operon repressor
ECs0324	-	-5.7	regulator, YkgK
ECs1417	-5.7	-	DNA-binding transcriptional regulator, CsgD
ECs1416	-	-24.8	curli assembly protein, CsgE
ECs0275	-	-10.0	Regulatory protein, Cro

### **Cell Processes**

minE	-5.5	-7.4	cell division topological specificity factor, MinE
ECs1146	-	-9.5	cold shock gene, Sfa
ECs2533	-	-5.7	cold shock-like protein CspC
ECs5313	-6.2	-5.8	carbon starvation protein, YjiY

acpS	-5.5	-	4'-phosphopantetheinyl transferase
ECs4500	-5.0	-5.2	lipid A-core:surface polymer ligase, WaaL
spr	-	-7.2	outer membrane lipoprotein
ECs3104	-	-7.6	outer membrane porin protein C
<b>Others/Unclassified</b>			
oppB	-8.7	-	oligopeptide transporter permease, OppB
potB	-	-5.7	spermidine/putrescine ABC transporter
ECs4324	-17.8	-	lipoprotein
ECs3140	-17.1	-12.5	aluminum-inducible protein, aiS
ECs0801	-14.2	-	excisionase
ECs2631	-13.6	-	derepression protein epsilon
ECs1591	-8.4	-	prohead protease
ECs1590	-8.3	-	major head protein
ECs0602	-6.9	-19.8	H repeat-containing protein
ECs0342	-6.3	-	pyridine nucleotide-disulfide oxidoreductase
ECs5058	-6.2	-	formate-dependent nitrite reductase complex subunit, NrfG
ECs1212	-5.7	-	holin
ECs2463	-5.6	-	thiosulfate sulfur transferase
ECs0146	-5.0	-5.7	2-amino-4-hydroxy-6-hydroxymethyl dihydropteridine pyrophosphokinase
ECs1750	-7.1	-	voltage-gated potassium channel, kch
ECs1558	-	-10.4	tail assembly protein
etp	-	-5.3	phosphotyrosine-protein phosphatase

ECs1560	-	-5.2	secreted effector protein
ECs2491	-	-5.2	scaffolding protein in the formation of a murein-synthesizing holoenzyme
ECs1084	-	-23.8	anti-termination protein
ECs4430	-	-17.2	fimbrial chaperone protein
ECs1639	-	-16.9	minor tail protein

**Unknown/Hypothetical**

ECs3279	-53.7	-38.9	hypothetical protein
ECs1691	-50.2	-25.5	hypothetical protein
ECs1581	-29.3	-11.5	hypothetical protein
ECs5092	-22.9	-14.0	hypothetical protein
ECs1364	-22.2	-31.9	hypothetical protein
ECs2714	-20.2	-22.0	hypothetical protein
ECs4363	-19.2	-12.5	hypothetical protein
ECs4642	-19.1	-	hypothetical protein
ECs1580	-18.6	-	hypothetical protein
ECs1626	-17.7	-	hypothetical protein
ECs2187	-17.7	-7.0	hypothetical protein
ECs1578	-16.4	-	hypothetical protein
ECs4566	-13.9	-10.2	hypothetical protein
ECs1627	-13.4	-10.4	hypothetical protein
ECs1222	-12.9	-7.4	hypothetical protein
ECs3705	-12.8	-	hypothetical protein

ECs4586	-11.5	-9.0	hypothetical protein
ECs0317	-11.3	-8.2	hypothetical protein
ECs1569	-11.2	-16.1	hypothetical protein
ECs1179	-10.6	-15.2	hypothetical protein
ECs0876	-9.9	-	hypothetical protein
ECs5091	-8.1	-5.2	hypothetical protein
ECs5380	-7.5	-12.6	hypothetical protein
ECs4577	-7.5	-6.5	hypothetical protein
ECs1173	-7.1	-	hypothetical protein
ECs0534	-6.9	-	hypothetical protein
ECs2531	-6.8	-	hypothetical protein
ECs4563	-6.8	-	hypothetical protein
ECs1788	-6.7	-	hypothetical protein
ECs1210	-6.7	-	hypothetical protein
ECs1141	-6.7	-13.8	hypothetical protein
ECs5297	-6.4	-	hypothetical protein
ECs5109	-6.1	-	hypothetical protein
ECs1225	-5.9	-	hypothetical protein
ECs4378	-5.9	-6.2	hypothetical protein
ECs2918	-5.9	-	hypothetical protein
ECs2970	-5.9	-5.5	hypothetical protein
ECs5304	-5.8	-	hypothetical protein

ECs2414	-5.8	-	hypothetical protein
ECs0604	-5.6	-5.1	hypothetical protein
ECs5335	-5.6	-	hypothetical protein
ECs0061	-5.5	-	hypothetical protein
ECs1223	-5.5	-	hypothetical protein
ECs3706	-5.4	-6.2	hypothetical protein
ECs1224	-5.4	-	hypothetical protein
ECs1763	-5.3	-	hypothetical protein
ECs5257	-5.3	-10.2	hypothetical protein
ECs3139	-5.1	-	hypothetical protein
ECs4562	-5.1	-	hypothetical protein
ECs1656	-5.0	-	hypothetical protein
ECs4362	-5.0	-	hypothetical protein
ECs4587	-	-25.6	hypothetical protein
ECs1733	-	-24.5	hypothetical protein
ECs4579	-	-18.7	hypothetical protein
ECs5256	-	-18.6	hypothetical protein
ECs4584	-	-16.1	hypothetical protein
ECs1140	-	-14.5	hypothetical protein
ECs4542	-	-10.6	hypothetical protein
ECs1567	-	-10.2	hypothetical protein
ECs5305	-	-9.3	hypothetical protein

ECs2627	-	-9.2	hypothetical protein
ECs1139	-	-9.1	hypothetical protein
ECs4588	-	-7.1	hypothetical protein
ECs5259	-	-6.4	hypothetical protein
ECs3608	-	-5.9	hypothetical protein
ECs1576	-	-5.9	hypothetical protein
ECs4585	-	-5.8	hypothetical protein
ECs2534	-	-5.8	hypothetical protein
ECs2430	-	-5.7	hypothetical protein
ECs5260	-	-5.2	hypothetical protein
ECs2626	-	-5.2	hypothetical protein
ECs0472	-	-5.1	hypothetical protein
ECs4653	-	-5.0	hypothetical protein

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<sup>a</sup>The values of gene expression fold change are averages of three independent biological replicates.