

TABLE S1. *E. coli* O157:H7 genes exhibiting >2-fold difference (p<0.01) in all clinical and spinach strains compared to environmental strains

Locus (Gene)	RM6069 Clinical	RM6655 Clinical	RM6658 Clinical	RM9998 Spinach	RM10002 Spinach	RM6067 Spinach	RM9992 Spinach	RM9997 Spinach	Function
Z4930 (<i>gadA</i>)	-159.74	-113.77	-158.48	-154.32	-192.31	-24.39	1.90	1.49	glutamate decarboxylase isozyme
Z4921 (<i>hdeB</i>)	-145.14	-90.91	-93.46	-64.94	-53.76	-22.57	1.60	1.69	hypothetical protein
Z4922 (<i>hdeA</i>)	-135.50	-113.64	-125.47	-68.97	-59.52	-24.81	1.02	1.27	hypothetical protein
Z3692 (<i>yfeT</i>)	-128.70	-114.68	-94.34	-64.10	-51.81	-23.20	1.17	1.16	hypothetical protein
Z4923 (<i>hdeD</i>)	-45.05	-23.81	-36.90	-51.02	-49.50	-9.26	1.04	-1.09	hypothetical protein
Z4925 (<i>yhiE</i>)	-29.41	-19.57	-36.90	-11.42	-11.15	-10.88	3.31	2.88	hypothetical protein
Z4376 (<i>ygiW</i>)	-23.26	-13.37	-16.00	-10.57	-12.48	-5.21	1.75	1.45	hypothetical protein
Z3526 (<i>elaB</i>)	-22.68	-18.35	-36.76	-25.51	-26.74	-4.65	1.11	-1.05	hypothetical protein
Z1034 (<i>dps</i>)	-21.69	-32.57	-16.29	-7.94	-7.46	-8.06	2.14	2.03	DNA protection during starvation conditions
Z4926 (<i>yhiU</i>)	-19.38	-9.80	-13.44	-10.22	-11.03	-6.13	1.98	2.24	hypothetical protein
Z5977 (<i>osmY</i>)	-18.76	-20.70	-26.88	-17.64	-21.01	-7.46	2.44	2.67	hyperosmotically inducible periplasmic protein
Z4920 (<i>yhiD</i>)	-18.48	-13.68	-12.66	-22.22	-30.86	-9.17	-2.12	-2.02	putative transport ATPase
Z2949 (<i>otsA</i>)	-15.53	-10.66	-16.81	-15.75	-15.38	-6.41	1.79	1.68	trehalose 6-phosphate synthase
Z3260 (Z3260)	-15.13	-12.06	-10.11	-6.17	-7.35	-6.37	3.17	3.16	fructose-bisphosphate aldolase
Z4454 (Z4454)	-14.27	-16.21	-16.13	-11.88	-14.68	-3.55	-1.19	-1.34	hypothetical protein
Z5644 (<i>yjbJ</i>)	-13.18	-19.34	-17.57	-18.02	-14.97	-4.72	-1.13	1.00	hypothetical protein
Z4452 (<i>yqiD</i>)	-12.71	-23.31	-16.72	-12.06	-14.79	-3.57	-1.15	-1.14	hypothetical protein
Z2950 (<i>otsB</i>)	-12.45	-9.62	-12.25	-20.88	-21.69	-7.09	1.67	1.54	trehalose 6-phosphatase

Z4453 (<i>yqjE</i>)	-12.21	-18.94	-15.04	-12.25	-14.41	-3.23	-1.02	1.06	hypothetical protein
Z2761 (<i>katE</i>)	-12.02	-7.81	-12.42	-11.63	-14.84	-4.72	2.85	2.80	catalase; hydroperoxidase HPII(III)
Z2858 (Z2858)	-11.93	-11.31	-9.17	-5.52	-5.62	-6.71	3.18	3.21	hypothetical protein
Z4927 (<i>yhiV</i>)	-11.71	-6.25	-7.41	-7.14	-11.27	-5.26	1.46	1.69	putative transport system permease protein
Z2883 (Z2883)	-11.42	-15.20	-16.05	-12.42	-11.66	-2.65	-1.04	1.24	hypothetical protein
Z2769 (<i>osmE</i>)	-11.03	-13.26	-12.59	-6.71	-7.87	-5.21	-1.07	-1.01	activator of <i>ntrL</i> gene
Z5008 (<i>aldB</i>)	-10.73	-7.63	-8.93	-8.40	-12.38	-3.29	1.73	1.67	aldehyde dehydrogenase B (lactaldehyde dehydrogenase)
Z4451 (<i>yqjC</i>)	-10.70	-15.80	-8.93	-4.29	-3.95	-3.36	2.27	2.53	hypothetical protein
Z3972 (<i>ygaM</i>)	-10.01	-12.69	-21.46	-21.51	-22.57	-5.21	-1.65	-1.67	hypothetical protein
Z0425 (<i>yahO</i>)	-9.71	-6.13	-15.29	-38.76	-20.79	-2.51	-1.93	-1.98	hypothetical protein
Z2228 (<i>osmC</i>)	-9.09	-7.30	-6.90	-4.35	-5.15	-4.67	1.14	1.32	osmotically inducible protein
Z2553 (<i>yciG</i>)	-9.01	-4.74	-3.13	-14.51	-9.01	-3.75	-1.18	1.11	hypothetical protein
Z4928 (<i>yhiW</i>)	-8.62	-5.03	-6.25	-5.05	-5.92	-7.19	1.76	2.42	transcriptional regulator, AraC family
Z1686 (<i>msyB</i>)	-8.47	-9.62	-8.06	-6.94	-7.25	-4.03	1.25	1.15	acidic protein suppresses mutants lacking function of protein export
Z0859 (<i>phrB</i>)	-8.40	-7.09	-8.70	-10.35	-10.14	-3.47	-1.26	-1.29	deoxyribodipyrimidine photo-lyase type I
Z4908 (<i>slp</i>)	-8.33	-4.29	-5.26	-4.59	-4.35	-5.05	4.71	5.38	outer membrane protein induced after carbon starvation
Z2217 (Z2217)	-8.20	-5.13	-5.75	-4.72	-4.61	-5.59	-1.71	-1.20	hypothetical protein
Z0858 (<i>ybgA</i>)	-8.06	-5.56	-7.94	-8.13	-8.77	-3.33	1.74	1.64	hypothetical protein
Z4986 (<i>yiaH</i>)	-8.06	-12.64	-12.84	-9.01	-8.55	-5.71	1.55	1.23	hypothetical protein
Z3045 (Z3045)	-8.00	-8.00	-11.68	-14.03	-11.48	-2.07	1.50	1.41	hypothetical protein
Z0923 (Z0923)	-7.75	-7.63	-6.80	-7.04	-6.45	-5.13	2.19	2.28	putative homeobox protein

Z1391 (<i>hyaC</i>)	-7.58	-5.46	-10.49	-13.99	-14.62	-7.19	-1.06	-1.20	probable Ni/Fe-hydrogenase 1 b-type cytochrome subunit
Z2219 (Z2219)	-7.52	-4.12	-6.54	-7.25	-9.17	-4.76	-1.53	-1.48	hypothetical protein
Z2837 (<i>yeaQ</i>)	-7.30	-10.04	-7.52	-7.87	-6.25	-1.95	-1.07	-1.01	hypothetical protein
Z0607 (<i>ybaT</i>)	-7.19	-6.41	-9.17	-13.51	-12.80	-5.26	-1.48	-1.32	putative amino acid/amine transport protein
Z3964 (<i>ygaU</i>)	-6.90	-6.58	-9.43	-8.77	-8.40	-3.75	-1.06	-1.34	hypothetical protein
Z4426 (<i>ygjG</i>)	-6.85	-3.48	-6.21	-5.88	-5.10	-4.26	2.96	2.38	diamine aminotransferase
Z4919 (Z4919)	-6.62	-2.83	-12.11	-6.99	-7.58	-3.95	-1.68	-1.81	putative ATP-binding protein of ABC transport system
Z1392 (<i>hyaD</i>)	-6.54	-6.45	-8.00	-14.49	-15.63	-7.58	-1.93	-1.97	Hydrogenase 1 maturation peptidase HyaD. Aspartic peptidase.
Z5709 (<i>phnB</i>)	-6.41	-5.24	-17.06	-9.26	-8.13	-2.89	2.03	1.73	hypothetical protein
Z1243 (<i>ycaC</i>)	-6.37	-5.46	-6.10	-10.81	-10.00	-2.11	1.90	1.66	hypothetical protein
Z1685 (<i>yceK</i>)	-6.21	-9.43	-5.75	-10.63	-12.20	-4.12	-2.00	-2.13	hypothetical protein
Z3252 (Z3252)	-6.17	-4.50	-8.20	-8.62	-7.46	-3.24	1.15	1.08	hypothetical protein
Z1394 (<i>hyaF</i>)	-6.13	-4.74	-6.13	-7.94	-8.85	-5.78	-1.25	-1.36	nickel incorporation into hydrogenase-1 proteins
Z0606 (<i>ybaS</i>)	-6.10	-5.65	-7.04	-11.57	-6.02	-6.85	1.40	1.24	L-glutaminase
Z0992 (<i>ybhB</i>)	-6.10	-5.32	-4.81	-3.37	-3.26	-4.88	2.30	2.01	phospholipid-binding protein, PBP family
Z1091 (<i>artM</i>)	-6.02	-4.02	-5.32	-4.29	-4.18	-2.40	-1.08	-1.08	L-arginine ABC transporter membrane protein
Z1504 (Z1504)	-6.02	-4.95	-4.17	-4.37	-4.59	-1.51	1.89	1.78	amino terminal fragment of WrbA
Z1393 (<i>hyaE</i>)	-5.88	-5.13	-5.65	-10.17	-9.62	-7.87	-1.43	-1.17	processing of HyaA and HyaB proteins
Z1422 (<i>yccJ</i>)	-5.81	-8.77	-4.31	-5.43	-5.52	-1.99	2.34	1.99	hypothetical protein
Z3721 (<i>tktB</i>)	-5.81	-5.13	-4.67	-3.04	-4.57	-2.58	1.50	1.52	transketolase
Z0400 (<i>betI</i>)	-5.78	-4.65	-4.83	-1.90	-2.70	-3.85	1.22	1.39	transcriptional regulator BetI

Z2230 (<i>rpsV</i>)	-5.71	-11.15	-3.64	-1.72	-1.33	-2.58	3.13	3.10	SSU ribosomal protein S22P
Z2232 (<i>adhP</i>)	-5.68	-5.43	-5.99	-5.85	-6.94	-3.44	1.13	1.08	alcohol dehydrogenase
Z3048 (Z3048)	-5.65	-6.90	-4.31	-3.97	-2.22	-3.57	-1.60	-1.51	hypothetical protein
Z4455 (<i>yqjF</i>)	-5.49	-4.18	-5.05	-4.72	-5.35	-1.90	-1.15	-1.06	hypothetical protein
Z1531 (Z1531)	-5.41	-4.95	-4.72	-2.21	-2.92	-4.81	1.91	1.83	hypothetical protein
Z1389 (<i>hyaA</i>)	-5.32	-3.92	-3.42	-5.85	-8.40	-4.48	1.20	1.24	hydrogenase-1 small subunit
Z3249 (Z3249)	-5.29	-4.78	-9.80	-6.85	-6.80	-1.63	2.07	1.94	hypothetical protein
Z1951 (<i>ycgB</i>)	-5.21	-3.80	-6.33	-6.99	-8.26	-1.93	1.74	2.08	putative sporulation protein
Z0480 (<i>psiF</i>)	-5.08	-3.37	-3.50	-4.18	-3.82	-2.80	1.27	1.11	induced by phosphate starvation
Z2710 (<i>ynhD</i>)	-5.05	-2.92	-3.58	-3.15	-4.18	-2.22	2.64	1.89	Iron-regulated ABC transporter ATPase subunit SufC
Z3720 (<i>talA</i>)	-5.05	-4.74	-4.29	-2.82	-4.29	-3.00	2.39	2.42	transaldolase
Z2824 (<i>yeaH</i>)	-4.98	-3.40	-3.50	-5.75	-5.08	-2.12	1.25	1.51	hypothetical protein
Z4456 (<i>yqjG</i>)	-4.90	-3.16	-4.78	-3.62	-4.12	-2.29	1.48	1.23	putative transferase
Z2661 (<i>sodC</i>)	-4.81	-4.67	-4.93	-3.94	-4.88	-2.74	2.05	2.08	superoxide dismutase precursor (Cu-Zn)
Z5876 (<i>yjgB</i>)	-4.81	-3.76	-5.62	-6.94	-7.69	-2.34	1.21	-1.09	putative oxidoreductase
Z4890 (<i>yhiM</i>)	-4.78	-3.86	-6.21	-7.52	-6.85	-4.88	1.76	1.28	hypothetical protein
Z3042 (<i>dsrB</i>)	-4.74	-6.90	-6.49	-10.54	-9.90	-2.79	-3.55	-4.10	hypothetical protein
Z3380 (<i>yehZ</i>)	-4.67	-3.17	-5.81	-6.94	-5.52	-2.17	2.44	3.10	putative transport system permease protein
Z2709 (<i>ynhC</i>)	-4.63	-3.10	-4.55	-5.26	-6.37	-2.32	1.44	1.16	Iron-regulated ABC transporter permease protein SufD
Z5729 (<i>yjdJ</i>)	-4.59	-5.52	-4.20	-4.22	-3.97	-1.80	1.13	1.16	hypothetical protein
Z4695 (Z4695)	-4.48	-11.11	-5.15	-5.29	-4.46	-3.19	-1.79	-1.17	putative iron storage homoprotein, bacterioferritin

Z4365 (<i>yqhE</i>)	-4.44	-3.64	-3.39	-3.06	-2.75	-2.82	1.82	1.70	putative enzyme
Z5245 (<i>asnA</i>)	-4.39	-12.66	-8.55	-8.13	-9.62	1.04	-2.09	-1.96	aspartate-ammonia ligase
Z0503 (<i>yajB</i>)	-4.33	-7.35	-4.61	-3.48	-2.93	-3.14	-1.09	-1.03	putative glycoprotein
Z2708 (Z2708)	-4.22	-2.61	-3.64	-3.52	-4.15	-2.22	1.52	1.40	cysteine desulfurase
Z3378 (<i>yehX</i>)	-4.08	-2.62	-4.48	-4.55	-6.02	-2.36	-1.64	-1.32	putative ATP-binding component of a transport system
Z4722 (<i>fic</i>)	-4.08	-4.22	-4.88	-4.35	-5.05	-2.63	-1.19	-1.41	induced in stationary phase, recognized by rpoS, affects cell division
Z1418 (<i>cbpA</i>)	-4.00	-3.60	-3.48	-2.84	-2.98	-2.87	2.39	2.05	curved DNA-binding protein; functions closely related to DnaJ
Z0539 (<i>bolA</i>)	-3.98	-5.85	-3.66	-2.77	-2.27	-2.96	1.13	1.08	transcriptional regulator, BolA protein family
Z2707 (<i>ynhA</i>)	-3.98	-3.38	-3.98	-4.46	-3.85	-1.66	1.24	-1.03	Cysteine desulfuration protein SufE
Z3722 (Z3722)	-3.95	-4.22	-3.82	-3.61	-3.19	-3.38	1.00	1.35	hypothetical protein
Z4958 (<i>dppD</i>)	-3.95	-2.84	-4.15	-2.59	-3.53	-2.19	-1.21	-1.17	putative ATP-binding component of dipeptide transport system
Z1092 (<i>artQ</i>)	-3.92	-3.70	-3.79	-3.37	-4.42	-2.21	-1.23	-1.18	L-arginine ABC transporter membrane protein
Z4418 (<i>rpsU</i>)	-3.92	-12.41	-4.29	-1.11	1.00	-1.84	-1.50	-1.16	SSU ribosomal protein S21P
Z0475 (Z0475)	-3.82	-2.77	-3.53	-3.37	-4.12	-3.17	1.06	1.14	hypothetical protein
Z1105 (<i>poxB</i>)	-3.69	-2.93	-3.11	-6.71	-6.10	-2.13	2.68	3.13	pyruvate dehydrogenase (cytochrome)
Z0027 (<i>rpsT</i>)	-3.68	-10.60	-3.86	1.61	1.73	-2.53	1.15	1.77	SSU ribosomal protein S20P
Z4981 (<i>cspA</i>)	-3.68	-20.66	-8.55	1.01	1.10	-6.37	-1.25	-1.22	cold-shock DNA-binding protein family
Z1036 (<i>ompX</i>)	-3.66	-11.11	-4.18	-1.90	-1.67	-4.44	-1.48	-1.05	outer membrane protein X
Z4151 (Z4151)	-3.64	-4.26	-4.00	-2.66	-3.48	-2.92	-1.31	-1.27	hypothetical protein
Z4628 (<i>yhdV</i>)	-3.51	-3.16	-2.99	-4.88	-4.76	-3.16	-2.20	-2.67	hypothetical protein
Z2523 (<i>osmB</i>)	-3.50	-10.58	-4.03	-1.59	-2.39	-4.48	1.66	2.42	osmotically inducible lipoprotein

Z0399 (<i>betB</i>)	-3.48	-2.82	-2.78	-1.94	-2.04	-2.97	1.54	1.26	betaine aldehyde dehydrogenase
Z5728 (<i>yjdI</i>)	-3.48	-3.26	-3.33	-3.86	-3.12	-1.92	1.14	1.03	hypothetical protein
Z2270 (<i>yncB</i>)	-3.45	-2.80	-4.00	-6.02	-4.76	-2.75	1.03	-1.13	putative oxidoreductase
Z5601 (<i>aceA</i>)	-3.42	-11.07	-4.55	-4.55	-6.80	-2.76	1.37	1.01	isocitrate lyase
Z3017 (<i>amyA</i>)	-3.40	-3.36	-4.39	-3.14	-3.58	-1.97	2.02	2.18	cytoplasmic alpha-amylase
Z2775 (<i>spy</i>)	-3.38	-2.94	-5.18	-1.51	-1.52	-2.96	2.25	2.31	periplasmic protein related to spheroblast formation
Z1397 (<i>appA</i>)	-3.28	-2.23	-2.82	-2.88	-3.06	-3.62	1.14	1.18	phosphoanhydride phosphorylase; pH 2.5 acid phosphatase; periplasmic
Z4935 (<i>yhjD</i>)	-3.27	-2.44	-3.30	-4.35	-5.13	-2.18	1.03	1.11	hypothetical protein
Z0486 (<i>aroM</i>)	-3.21	-2.43	-4.29	-3.22	-3.27	-2.33	1.06	-1.07	protein of aro operon, regulated by aroR
Z1396 (<i>appB</i>)	-3.11	-2.92	-2.53	-2.60	-3.39	-3.30	-1.19	-1.18	probable third cytochrome oxidase, subunit II
Z1417 (<i>yccD</i>)	-3.11	-3.05	-2.35	-4.46	-3.98	-2.44	1.04	-1.04	hypothetical protein
Z1009 (<i>ybhP</i>)	-3.10	-2.69	-3.13	-3.61	-4.02	-2.38	-1.13	-1.01	hypothetical protein
Z2704 (<i>pykF</i>)	-3.07	-4.72	-3.76	-2.30	-2.06	-2.45	1.84	1.88	pyruvate kinase (EC 2.7.1.40)
Z1094 (<i>artP</i>)	-3.06	-3.00	-2.75	-1.68	-1.51	-2.19	2.33	2.29	L-arginine ABC transporter ATP-binding protein
Z3804 (<i>csiE</i>)	-3.06	-2.51	-2.60	-1.77	-1.86	-2.09	2.88	2.66	transcriptional antiterminator, BglG family
Z4931 (<i>yhjA</i>)	-3.04	-2.99	-4.46	-8.93	-8.85	-4.07	-1.89	-2.02	putative cytochrome C peroxidase
Z0720 (<i>ybdK</i>)	-2.97	-2.29	-4.15	-3.79	-4.35	-1.94	1.52	1.31	hypothetical protein
Z1993 (<i>chaC</i>)	-2.94	-3.11	-4.22	-4.08	-4.76	-1.18	1.35	1.20	cation transport regulator
Z2186 (Z2186)	-2.93	-2.46	-3.23	-4.33	-4.02	-3.08	1.23	-1.01	trans-aconitate 2-methyltransferase
Z3772 (<i>guaB</i>)	-2.90	-9.17	-5.99	-3.13	-2.64	-2.46	-2.24	-2.10	inosine-5'-monophosphate dehydrogenase
Z4547 (<i>rpmA</i>)	-2.89	-12.76	-6.13	-1.97	-1.79	-2.13	-2.52	-2.04	LSU ribosomal protein L27P

Z2162 (<i>ydeI</i>)	-2.88	-5.49	-3.30	-3.77	-3.38	-2.69	-1.03	-1.01	hypothetical protein
Z3385 (<i>yohD</i>)	-2.85	-2.44	-3.03	-3.69	-3.55	-1.90	-1.22	-1.56	hypothetical protein
Z0752 (<i>ybdR</i>)	-2.84	-2.14	-2.54	-3.05	-2.92	-3.10	1.00	1.01	putative oxidoreductase
Z4094 (<i>eno</i>)	-2.84	-5.43	-3.04	-1.06	-1.28	-1.36	2.08	2.24	enolase (EC 4.2.1.11)
Z2711 (<i>ynhE</i>)	-2.82	-2.42	-4.02	-5.00	-5.35	-1.74	2.04	1.55	Iron-regulated ABC transporter membrane component SufB
Z2554 (<i>yciF</i>)	-2.80	-2.25	-2.67	-3.22	-4.03	-2.33	2.56	2.59	putative structural proteins
Z3998 (<i>csrA</i>)	-2.80	-6.41	-2.43	-1.93	-2.20	-1.82	-1.42	-1.23	carbon storage regulator
Z4359 (<i>exbB</i>)	-2.78	-6.71	-5.03	-2.52	-2.83	-2.78	-1.01	-1.40	uptake of enterochelin; tonB-dependent uptake of B colicins
Z5694 (Z5694)	-2.77	-2.97	-3.02	-6.02	-7.14	-2.60	-3.31	-2.89	hypothetical protein
Z2899 (<i>yebF</i>)	-2.76	-6.02	-4.61	-4.18	-4.41	-1.47	-1.62	-1.42	hypothetical protein
Z4961 (<i>dppA</i>)	-2.76	-2.74	-3.33	-1.34	-1.56	-1.75	3.60	3.60	dipeptide transport protein
Z0565 (<i>ybaY</i>)	-2.75	-3.04	-3.02	-2.49	-2.59	-2.44	1.19	1.09	glycoprotein/polysaccharide metabolism
Z3771 (<i>guaA</i>)	-2.73	-6.62	-2.81	-1.25	-1.07	-2.33	1.04	1.07	GMP synthase (glutamine-hydrolyzing)
Z4126 (Z4126)	-2.71	-5.81	-4.13	-4.83	-4.24	-2.16	1.01	1.40	hypothetical protein
Z5968 (<i>fhuF</i>)	-2.68	-3.27	-3.32	-1.41	-1.49	-2.97	1.21	1.18	hypothetical protein
Z4957 (<i>dppF</i>)	-2.66	-2.90	-3.69	-2.48	-2.89	-1.81	-1.23	-1.31	putative ATP-binding component of dipeptide transport system
Z2330 (<i>hslJ</i>)	-2.65	-3.44	-2.62	-1.54	-1.51	-2.44	1.42	1.75	heat shock protein hslJ
Z4458 (<i>yhaI</i>)	-2.64	-2.29	-2.65	-2.94	-3.61	-1.66	-1.35	-1.69	putative cytochrome
Z0093 (<i>ftsL</i>)	-2.61	-3.77	-2.56	-1.67	-1.27	-1.28	1.24	1.26	cell division protein; ingrowth of wall at septum
Z4661 (<i>mscL</i>)	-2.60	-3.77	-2.53	-1.82	-1.20	-1.23	1.56	1.53	large-conductance mechanosensitive channel
Z4607 (<i>mreD</i>)	-2.60	-3.98	-3.38	-2.87	-3.22	-1.90	-2.44	-1.80	rod shape-determining protein

Z2885 (<i>pphA</i>)	-2.59	-2.61	-2.95	-3.46	-3.06	-1.43	-1.47	-1.71	protein phosphatase 1 modulates phosphoproteins, signals protein misfolding
Z4995 (<i>bax</i>)	-2.59	-3.64	-2.28	1.00	-1.02	-1.31	1.91	2.79	putative ATP-binding protein
Z0401 (<i>betT</i>)	-2.58	-2.93	-4.22	-2.56	-3.22	-3.40	-1.78	-1.78	high-affinity choline transport
Z4057 (<i>ygbE</i>)	-2.54	-3.66	-2.76	-2.70	-3.15	-2.23	-1.80	-1.49	putative cytochrome oxidase subunit
Z3796 (Z3796)	-2.53	-6.06	-2.53	1.37	1.30	-2.04	1.25	1.59	hypothetical protein
Z3798 (Z3798)	-2.51	-6.06	-2.82	1.27	1.28	-2.49	1.41	1.14	transcriptional regulator, BadM/Rrf2 family
Z3795 (<i>iscA</i>)	-2.47	-6.06	-2.69	-1.14	-1.18	-1.84	-1.09	-1.04	iron-sulfur cluster assembly protein
Z0588 (<i>ybaB</i>)	-2.46	-6.67	-3.00	-1.48	-1.11	-1.74	-1.19	1.07	hypothetical protein
Z0780 (<i>mrdB</i>)	-2.46	-2.82	-2.92	-1.73	-1.96	-1.89	-1.66	-1.63	cell elongation-specific peptidoglycan biosynthesis regulator RodA
Z4549 (<i>rplU</i>)	-2.45	-11.29	-3.65	-1.04	-1.16	-1.81	-1.81	-1.04	LSU ribosomal protein L21P
Z1395 (<i>appC</i>)	-2.44	-2.46	-2.19	-1.70	-3.17	-2.80	1.20	1.47	probable third cytochrome oxidase, subunit I
Z0195 (<i>rnhB</i>)	-2.43	-3.66	-3.14	-2.15	-2.04	-1.44	-2.00	-1.64	RNase HII
Z0589 (<i>recR</i>)	-2.43	-4.35	-2.59	-1.90	-1.76	-1.40	-1.35	-1.26	DNA replication and repair protein RecR
Z0783 (<i>ybeB</i>)	-2.42	-4.65	-3.45	-1.19	-1.33	-1.50	1.11	1.38	hypothetical protein
Z2739 (<i>btuE</i>)	-2.40	-3.14	-2.60	-2.32	-2.10	-2.07	1.12	1.20	vitamin B12 transport
Z1923 (Z1923)	-2.39	-4.93	-6.33	-18.73	-8.70	-2.30	1.34	1.05	unknown protein encoded by prophage CP-933X
Z5013 (<i>yibF</i>)	-2.39	-2.54	-2.68	-2.16	-2.53	-2.02	-1.09	-1.11	putative S-transferase
Z0790 (<i>ybeL</i>)	-2.39	-3.77	-2.40	-3.47	-2.80	-2.39	-1.70	-1.48	putative alpha helical protein
Z5453 (<i>sodA</i>)	-2.38	-4.76	-4.12	-2.54	-2.58	-3.18	-1.02	-1.14	superoxide dismutase, manganese
Z5756 (<i>blc</i>)	-2.34	-2.87	-2.23	-4.78	-6.06	-1.96	-1.26	-1.37	outer membrane lipoprotein (lipocalin)
Z1740 (<i>ptsG</i>)	-2.34	-2.30	-2.22	-1.64	-1.98	-1.37	1.67	1.95	PTS system D-glucose-specific IIC component / IIB component

Z2268 (Z2268)	-2.33	-2.86	-2.73	-1.62	-1.82	-2.39	1.06	1.21	putative outer membrane receptor for iron transport
Z3682 (<i>ptsI</i>)	-2.30	-5.43	-2.05	-1.16	-1.08	-2.03	1.35	1.85	phosphoenolpyruvate--protein phosphotransferase
Z0777 (<i>dacA</i>)	-2.30	-3.70	-2.28	1.26	1.17	-2.13	1.93	2.51	penicillin-binding protein 6. Serine peptidase.
Z0787 (<i>holA</i>)	-2.29	-2.80	-2.27	1.04	-1.08	-1.54	-1.29	-1.03	DNA polymerase III, delta subunit
Z3797 (<i>yfhO</i>)	-2.28	-6.49	-2.72	1.34	1.41	-2.10	1.58	1.65	cysteine desulfurase IscS
Z3657 (Z3657)	-2.27	-3.34	-3.29	-2.58	-2.61	-3.00	-1.30	-1.07	hypothetical protein
Z5478 (<i>hslU</i>)	-2.23	-6.13	-3.68	-1.79	-1.35	-1.43	1.24	1.56	ATP-dependent protease ATP-binding subunit
Z5464 (<i>tpiA</i>)	-2.23	-4.17	-2.92	-1.33	-1.36	-1.88	1.70	1.73	triosephosphate isomerase
Z2244 (<i>narZ</i>)	-2.22	-2.04	-2.98	-5.49	-3.56	-2.99	-1.56	-1.52	respiratory nitrate reductase alpha subunit apoprotein
Z5194 (<i>rpmH</i>)	-2.21	-6.45	-2.65	1.33	1.10	-1.12	-1.17	1.36	LSU ribosomal protein L34P
Z0821 (<i>asnB</i>)	-2.19	-3.36	-2.16	-1.29	-1.56	-1.01	2.08	2.58	asparagine synthase (glutamine-hydrolysing)
Z3413 (<i>lysP</i>)	-2.19	-2.48	-2.72	-1.98	-1.75	-1.19	1.17	1.30	lysine-specific permease
Z1922 (Z1922)	-2.18	-2.34	-2.82	-6.17	-9.01	-2.87	2.73	2.84	unknown protein encoded by prophage CP-933X
Z1749 (<i>ycfJ</i>)	-2.17	-2.52	-3.19	-2.29	-2.77	-1.49	-1.30	-1.18	hypothetical protein
Z3275 (Z3275)	-2.17	-2.13	-2.12	-1.34	-1.27	-2.23	1.34	1.49	hypothetical protein
Z0932 (Z0932)	-2.16	-3.94	-3.52	-1.89	-1.85	-1.81	1.77	2.00	hypothetical protein
Z5195 (<i>mpA</i>)	-2.14	-5.88	-2.74	1.12	1.19	-1.22	-1.14	1.29	ribonuclease P protein component
Z2741 (<i>himA</i>)	-2.12	-4.59	-2.00	-1.13	-1.32	-1.80	1.27	1.35	integration host factor alpha subunit
Z3377 (<i>yehW</i>)	-2.11	-2.16	-2.97	-3.88	-3.89	-1.60	-2.00	-2.14	putative transport system permease protein uptake of enterochelin; tonB-dependent uptake of B colicins
Z4358 (<i>exbD</i>)	-2.10	-4.81	-3.72	-1.67	-1.23	-2.12	-1.25	-1.04	uptake of B colicins
Z0925 (<i>gpmA</i>)	-2.08	-5.95	-2.23	-1.17	-1.13	-2.05	1.09	1.58	phosphoglycerate mutase

Z2269 (Z2269)	-2.04	-2.27	-2.30	-4.57	-3.92	-2.29	-1.34	-1.28	transcriptional regulator, GntR family
Z4154 (<i>aas</i>)	-2.04	-5.52	-5.68	-4.52	-5.43	-2.33	-3.94	-3.89	2-acyl-glycerophospho-ethanolamine acyltransferase
Z2030 (<i>tonB</i>)	-2.02	-4.24	-2.72	-1.85	-1.79	-1.83	-1.32	-1.36	energy transducer; uptake of iron, cyanocobalimin; sensitivity to colicins
Z3691 (<i>ucpA</i>)	6.34	3.26	10.49	9.61	9.67	3.04	1.29	2.11	short chain dehydrogenase
Z0740 (<i>cstA</i>)	6.02	2.88	7.53	4.83	3.10	3.28	1.35	1.64	carbon starvation protein
Z4208 (<i>ygeV</i>)	5.86	5.37	11.04	10.70	10.63	1.78	2.02	2.53	putative transcriptional regulator
Z4217 (Z4217)	5.85	8.19	15.66	11.59	10.76	1.15	-1.21	-1.83	selenate reductase, Fe-S subunit (IMGterm)
Z4214 (Z4214)	4.61	6.04	7.68	3.67	3.58	2.01	-1.33	-1.80	predicted molybdenum cofactor sulfurylase (IMGterm)
Z4207 (Z4207)	4.52	5.23	6.22	4.35	3.66	1.28	1.14	-1.32	putative dehydrogenase
Z1190 (Z1190)	4.38	4.65	5.65	4.23	4.42	2.14	1.01	1.18	putative glucosyltransferase
Z4216 (<i>ygfJ</i>)	4.25	5.34	7.54	4.35	4.37	1.93	-1.15	-1.08	hypothetical protein
Z4302 (<i>ansB</i>)	4.11	2.57	7.11	5.03	4.93	2.13	-1.11	-1.03	asparaginase (EC 3.5.1.1) (IMGterm)
Z2565 (Z2565)	4.10	2.16	5.02	7.35	9.08	1.91	2.35	2.81	putative chaperone protein
Z0038 (<i>carB</i>)	4.05	3.20	5.79	11.54	7.07	-1.01	-1.31	-1.43	carbamoyl-phosphate synthase large subunit (IMGterm)
Z4351 (Z4351)	3.99	2.37	5.39	6.19	6.32	4.70	1.34	1.82	putative hydrogenase subunit
Z4468 (<i>tdcC</i>)	3.69	2.82	5.27	4.17	5.15	3.00	1.40	1.85	anaerobically inducible L-threonine, L-serine permease
Z1629m (Z1629m)	3.65	3.54	4.50	3.27	3.35	1.86	-1.10	-1.08	glycosyl transferase
Z0078 (Z0078)	3.64	3.45	3.63	2.67	2.56	2.71	1.75	1.46	hypothetical protein
Z0742 (<i>ybdH</i>)	3.63	3.52	4.26	2.78	2.32	2.30	1.40	1.19	putative oxidoreductase
Z5670 (<i>nrfB</i>)	3.59	2.90	4.02	4.34	5.21	2.93	1.44	1.68	respiratory nitrite reductase specific menaquinol--cytochrome-c reductase complex subunit NrfB precursor (IMGterm)
Z0040 (Z0040)	3.57	4.48	6.49	6.42	6.61	2.02	1.12	1.04	transcriptional regulator of cai operon

Z2946 (<i>flhD</i>)	3.39	2.24	4.99	17.49	20.22	1.91	1.69	1.99	transcriptional activator FlhD
Z5504m (<i>frwC</i>)	3.37	4.14	6.20	8.22	5.18	3.38	2.06	2.44	PTS system IIC component (IMGterm)
Z4218 (Z4218)	3.31	3.34	5.05	5.34	4.17	1.21	-3.85	-6.25	proteoglycan
Z2956 (<i>yecI</i>)	3.28	3.51	5.49	5.63	5.40	2.31	1.76	1.52	ferritin-like protein
Z1399 (<i>yccY</i>)	3.19	3.63	4.98	12.04	11.54	2.03	3.76	3.43	putative phosphatase
L7049 (<i>hlyB</i>)	2.98	4.06	3.69	5.46	7.17	2.33	2.64	2.23	hemolysin transport protein
L7031 (L7031)	2.97	2.45	2.60	2.67	2.56	1.46	1.16	1.02	StcE -like peptidase. Metallo peptidase. MEROPS family M66 (IMGterm)
Z4885 (<i>yhiH</i>)	2.94	4.48	5.56	5.86	5.59	2.10	1.54	1.11	putative ATP-binding component of a transport system, fragment 1
Z1931 (Z1931)	2.86	3.30	7.32	9.04	9.73	1.95	1.94	2.66	outer membrane protein 3b (a), protease VII
Z4215 (Z4215)	2.85	3.68	5.58	4.47	3.79	1.61	1.87	2.23	hypothetical protein
Z4470 (<i>tdcA</i>)	2.79	2.74	3.94	1.51	1.94	1.97	-1.73	-1.41	transcriptional activator of <i>tdc</i> operon
Z5910 (<i>fimB</i>)	2.70	2.47	3.74	3.51	3.94	1.35	1.10	-1.04	recombinase involved in phase variation; regulator for <i>fimA</i>
Z3401 (Z3401)	2.50	4.08	5.43	4.42	5.10	1.94	2.01	1.23	putative oxidoreductase
Z5957 (<i>yjjM</i>)	2.49	2.92	2.87	1.84	1.97	1.28	1.16	-1.01	transcriptional regulator, GntR family (IMGterm)
Z3402 (<i>yeiA</i>)	2.48	2.84	4.27	2.57	2.57	2.16	1.26	1.17	dihydroorotate oxidase B, catalytic subunit (EC 1.3.3.1) (IMGterm)
Z2844 (<i>yeaV</i>)	2.44	3.00	3.13	9.63	7.59	2.56	2.86	3.60	putative transport protein
Z2696 (Z2696)	2.39	2.36	2.57	-1.40	-1.64	1.71	-1.51	-1.87	hypothetical protein
Z5953 (<i>yjiY</i>)	2.26	2.44	2.97	2.86	2.33	1.80	1.01	1.09	putative carbon starvation protein
Z1401 (<i>ymcA</i>)	2.21	2.51	2.85	4.31	4.21	1.92	1.18	1.21	hypothetical protein
Z2585 (<i>bioD</i>)	2.10	2.28	2.61	2.03	1.85	2.12	1.49	1.62	dethiobiotin synthase (EC 6.3.3.3) (IMGterm)
Z4036 (<i>hypB</i>)	2.08	2.04	2.73	3.51	4.21	2.30	1.75	2.33	guanine-nucleotide binding protein, functions as nickel donor for large subunit of hydrogenase 3

Z2036 (<i>intO</i>)	2.07	2.25	2.28	1.41	1.64	1.87	1.61	1.15	putative integrase for prophage CP-933O
Z1172 (<i>terA</i>)	2.02	2.39	2.60	3.46	2.49	1.81	3.08	2.78	putative phage inhibition, colicin resistance and tellurite resistance protein
