

Table S2. Top 166 predicted regulatory RNAs by RSSVM.

Rank	GI	RSSVM	RNAz	QRNA	Terminator (T) Attenuator (A)	Gene Name	Gene Product	Knowledge of Regulation	Reference
1	24349136	1.000	1.000	Q(FP) ^a	T A	trpE	anthranilate synthase component I	RF00513 Trp_leader	Rfam
2	24345897	1.000	1.000	Q	T A	rsd	regulator of sigma D	Leader peptide, and transcription attenuator	(Vitreschak <i>et al.</i> 2004)
3	24346870	1.000	1.000	Q(FP)	T A	SO1202	conserved hypothetical protein	RF00005 tRNA	Rfam
4	24351250	1.000	0.998	Q(FP)	T A	SO4727	conserved hypothetical protein	RF00558 L20_leader	Rfam
5	24350784	1.000	0.998	Q	T -	ilvG	acetolactate synthase II, large subunit		
6	24347627	1.000	0.998		T A	ppiD	peptidyl-prolyl cis-trans isomerase D	RF00506 Thr_leader	Rfam
7	24349634	1.000	0.997	Q	T A	thrA	aspartokinase/threonine dehydrogenase, threonine-sensitive	RF00506 Thr_leader	Rfam
8	24347975	1.000	0.997	Q(FP)	T A	hisG	ATP phosphoribosyltransferase	RF00514 His_leader	Rfam
9	24349200	1.000	0.996	Q	T A	SO3069	conserved hypothetical protein		
10	24349922	1.000	0.992	Q	T A	SO3649	GTP-binding protein, GTP1/Obg family		
11	24347698	1.000	0.988	Q	T A	rmf	ribosome modulation factor		
12	24351271	1.000	0.916		T A	SO4742	transcriptional regulator, DeoR family		
13	24346855	1.000	0.643		T A	greA	transcription elongation factor GreA		
14	24348820	1.000	0.634		T A	SO2744	helicase		
15	24348163	1.000	0.542		T A	SO2223	peptidase, putative		
16	24347418	1.000	0.523			rpsB	ribosomal protein S2	RF00127 t44 RNA	Rfam
17	24346570	1.000	0.507		T A	ldhA	D-lactate dehydrogenase	Possible post-transcriptional effect	(Jiang <i>et al.</i> 2001)
18	24346427	1.000	0.409		T A	SO0858	sodium:alanine symporter family protein		

Table S2. Top 166 predicted regulatory RNAs by RSSVM (continued 1).

Rank	GI	RSSVM	RNAz	QRNA	Terminator (T) Attenuator (A)	Gene Name	Gene Product	Knowledge of Regulation	Reference
19	24346216	1.000	0.319		T A	SO0695	glutathione-regulated potassium-efflux system protein KefC, putative		
20	24348228	1.000	0.272		T A	ndk	nucleoside diphosphate kinase		
21	24349359	1.000	0.223			SO3191	chain length determinant protein		
22	24348648	1.000	0.150			SO2602	conserved hypothetical protein		
23	24348431	1.000	0.105		T -	aspS	aspartyl-tRNA synthetase	tRNA synthetase leader	
24	24350063	1.000	0.996	Q		SO3769	conserved hypothetical protein		
25	24348233	1.000	0.904			ilvI	acetolactate synthase III, large subunit	Leader peptide, and transcription attenuator	(Vitreschak <i>et al.</i> 2004)
26	24349427	1.000	0.862			flgB	flagellar basal-body rod protein FlgB	Putative GEMM element	(Weinberg <i>et al.</i> 2007)
27	24348700	1.000	0.241			aroH	phospho-2-dehydro-3-deoxyheptonate aldolase, trp-sensitive	Possible transcription termination	(Zurawski <i>et al.</i> 1981)
28	24346058	1.000	0.037		T A	plsC	1-acyl-sn-glycerol-3-phosphate acyltransferase	Leader peptide, and transcription attenuator	(Vitreschak <i>et al.</i> 2004)
29	24345795	1.000	0.850	Q	T -	SO0354	sodium/calcium exchanger		
30	24345909	1.000	0.999			purH	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase		
31	24347794	1.000	1.000	Q	T A	sucA	2-oxoglutarate dehydrogenase, E1 component		
32	24349814	1.000	0.570		T -	gshA	glutamate--cysteine ligase		
33	24349842	1.000	0.974	Q		SO3582	methyl-accepting chemotaxis protein		
34	24346699	1.000	1.000	Q		SO1071	conserved hypothetical protein	RF00080 yybP-ykoY	Rfam
35	24350656	1.000	0.998	Q	T A	leuA	2-isopropylmalate synthase	Leader peptide, and transcription attenuator	(Vitreschak <i>et al.</i> 2004)

Table S2. Top 166 predicted regulatory RNAs by RSSVM (continued 2).

Rank	GI	RSSVM	RNAz	QRNA	Terminator (T) Attenuator (A)	Gene Name	Gene Product	Knowledge of Regulation	Reference
36	24348336	1.000	0.235			ccoN	cytochrome c oxidase, cbb3-type, subunit I		
37	24347061	1.000	0.990	Q	T A	lepB	signal peptidase I		
38	24349573	1.000	0.455			SO3364	conserved hypothetical protein		
39	24347085	1.000	0.997	Q	T A	pheA	chorismate mutase/prephenate dehydratase	RF00513 Trp_leader	Rfam
40	24349420	1.000	0.868	Q		flgF	flagellar basal-body rod protein FlgF		
41	24345882	1.000	0.094			pdhR	pyruvate dehydrogenase complex repressor	PdhR-box in <i>E. coli</i>	(Ogasawara <i>et al.</i> 2007)
42	24350809	1.000	0.454			SO4366	conserved hypothetical protein		
43	24349259	1.000	0.914	Q	T A	tgt	queuine tRNA-ribosyltransferase		
44	24348337	1.000	0.939			SO2365	conserved hypothetical protein		
45	24349640	1.000	0.750		T A	SO3418	hypothetical protein		
46	24347081	1.000	0.095		T A	hcp	prismane protein		
47	24350912	1.000	0.995			moaA	molybdenum cofactor biosynthesis protein A		
48	24345525	1.000	0.407			ribB	3,4-dihydroxy-2-butanone 4-phosphate synthase		
49	24345845	1.000	0.864			SO0394	conserved hypothetical protein		
50	24348221	1.000	0.940		T -	rimK-2	ribosomal protein S6 modification protein		
51	24345862	1.000	0.997	Q		rho	transcription termination factor Rho		
52	24348056	1.000	0.893		T -	adhE	aldehyde-alcohol dehydrogenase	Stem-loop for occupying RBS in <i>E. coli</i>	(Membrillo-Hernandez and Lin 1999)
53	24351269	1.000	0.018		T A	SO4740	conserved hypothetical protein		
54	24348439	1.000	0.390		- A	SO2438	transcriptional regulator, LysR family		

Table S2. Top 166 predicted regulatory RNAs by RSSVM (continued 3).

Rank	GI	RSSVM	RNAz	QRNA	Terminator (T) Attenuator (A)	Gene Name	Gene Product	Knowledge of Regulation	Reference
55	24346560	1.000	0.196			ahpC	alkyl hydroperoxide reductase, C subunit		
56	24349996	1.000	0.459		T -	SO3711	conserved hypothetical protein		
57	24345468	1.000	0.476			hutI	imidazolonepropionase		
58	24349731	1.000	0.571			mexE	RND multidrug efflux membrane fusion protein MexE		
59	24349583	1.000	0.361			SO3371	conserved hypothetical protein		
60	24349939	1.000	0.397			fadD-2	long-chain-fatty-acid--CoA ligase		
61	24347619	1.000	0.947		T -	tig	trigger factor		
62	24345537	1.000	0.465			SO0150	lipoprotein, putative		
63	24347612	1.000	0.012	Q	T A	glnS	glutaminyl-tRNA synthetase	tRNA synthetase leader	(Cheung <i>et al.</i> 1985)
64	24346616	1.000	1.000	Q		SO1007	conserved hypothetical protein	RF00168 Lysine	Rfam
65	24347626	0.999	1.000	Q		SO1797	DNA-binding protein, HU family		
66	24347658	0.999	0.988	Q		SO1824	conserved hypothetical protein		
67	24349607	0.999	0.997	Q		SO3392	oxidoreductase, FMN-binding		
68	24348243	0.999	0.424			SO2286	sulfate permease family protein		
69	24350411	0.999	0.435			SO4048	cytochrome c family protein		
70	24349974	0.999	0.530			SO3694	conserved hypothetical protein		
71	24350483	0.999	0.918		T A	mshC	MSHA pilin protein MshC		
72	24350423	0.999	0.997			metJ	met repressor		
73	24348868	0.999	0.240	Q	T A	rne	ribonuclease E	RF00370 sroD RNA	Rfam
74	24348465	0.999	0.641	Q	T A	SO2458	transporter, putative		
75	24347241	0.999	0.419			SO1489	hypothetical protein		
76	24346750	0.999	0.000		- A	bfr2	bacterioferritin subunit 2		
77	24345794	0.999	0.535		T -	SO0353	TPR domain protein		
78	24345538	0.999	0.526		T A	SO0151	conserved hypothetical protein		
79	24346342	0.999	0.417			SO0793	hypothetical protein		
80	24347038	0.999	0.810	Q		SO1331	MutT/nudix family protein		
81	24348153	0.999	0.669			SO2216	sensory box protein		

Table S2. Top 166 predicted regulatory RNAs by RSSVM (continued 4).

Rank	GI	RSSVM	RNAz	QRNA	Terminator (T) Attenuator (A)	Gene Name	Gene Product	Knowledge of Regulation	Reference
82	24348420	0.999	0.094			SO2427	TonB-dependent receptor, putative		
83	24347590	0.998	0.451		T A	SO1769	glutamate decarboxylase, putative	Possible post- transcriptional regulation in <i>S.</i> <i>oneidensis</i>	(Yang <i>et al.</i> 2008)
84	24348152	0.998	0.474		T A	SO2215	sun protein, putative		
85	24347329	0.998	0.288	Q	T A	SO1560	phosphate-binding protein		
86	24349540	0.998	0.435		T A	SO3337	conserved domain protein		
87	24349811	0.998	0.697		T -	SO3556	cyclic nucleotide phosphodiesterase, putative		
88	24345631	0.998	0.999	Q(FP)	T -	rpoB	DNA-directed RNA polymerase, beta subunit	Transcriptional attenuation	(Ishihama and Fukuda 1980; Steward and Linn 1992)
89	24350422	0.998	0.100	Q		metB	cystathionine gamma-synthase		
90	24349961	0.998	0.424	Q		SO3683	coniferyl aldehyde dehydrogenase	Ribosomal protein leader	Rfam
91	24345625	0.998	1.000			rplJ	ribosomal protein L10		
92	24350610	0.997	0.259			ubiE	ubiquinone/menaquinone biosynthesis methlytransferase UbiE		
93	24346037	0.997	0.678			SO0547	conserved hypothetical protein	RF00522 PreQ1	Rfam
94	24350762	0.997	0.317			SO4329	conserved hypothetical protein		
95	24347883	0.996	0.396			ushA	5'-nucleotidase		
96	24349570	0.996	0.418			SO3361	conserved hypothetical protein		
97	24348938	0.996	0.545			SO2846	conserved hypothetical protein		
98	24349291	0.996	0.345			SO3140	thymidine kinase		
99	24347300	0.995	0.103			SO1538	isocitrate dehydrogenase, NAD- dependent		
100	24348781	0.995	0.986		- A	SO2715	TonB-dependent receptor	RF00059 TPP	Rfam

Table S2. Top 166 predicted regulatory RNAs by RSSVM (continued 5).

Rank	GI	RSSVM	RNAz	QRNA	Terminator (T) Attenuator (A)	Gene Name	Gene Product	Knowledge of Regulation	Reference
101	24348214	0.994	0.964			SO2263	Rrf2 family protein		
102	24350917	0.994	0.439			SO4454	methyl-accepting chemotaxis protein		
103	24349041	0.994	0.982	Q		SO2935	oxidoreductase, short-chain dehydrogenase/reductase family		
104	24346274	0.994	0.256		T A	SO0740	melanin biosynthesis protein TyrA, putative		
105	24349015	0.994	0.274	Q	T -	pflB	formate acetyltransferase	Possible post-transcriptional regulation	(Beliaev <i>et al.</i> 2002)
106	24350214	0.994	0.688			SO3896	outer membrane porin, putative	Post-transcriptional regulation in <i>S. oneidensis</i>	(Maier and Myers 2004)
107	24351072	0.993	0.890	Q		rpoH	RNA polymerase sigma-32 factor		
108	24347836	0.993	0.064			SO1963	conserved hypothetical protein		
109	24345633	0.992	0.988	Q	T A	rpsL	ribosomal protein S12	Ribosomal protein leader	(Yao <i>et al.</i> 2007)
110	24349105	0.992	0.359			SO2990	prophage LambdaSo, transcriptional regulator, Cro/CI family		
111	24346963	0.992	0.599			SO1274	conserved hypothetical protein		
112	24349403	0.990	0.179		T -	fliE	flagellar hook-basal body complex protein FliE	Putative GEMM element	(Weinberg <i>et al.</i> 2007)
113	24345796	0.990	0.385			SO0355	AMP-binding protein		
114	24347791	0.990	0.618			sdhC	succinate dehydrogenase, cytochrome b556 subunit		
115	24346525	0.989	0.015			fba	fructose-bisphosphate aldolase, class II, Calvin cycle subtype		
116	24345418	0.989	0.545			secB	protein-export protein SecB		
117	24350326	0.989	0.765	Q(FP)		lysC	aspartokinase III, lysine-sensitive	RF00168 Lysine	Rfam

Table S2. Top 166 predicted regulatory RNAs by RSSVM (continued 6).

Rank	GI	RSSVM	RNAz	QRNA	Terminator (T) Attenuator (A)	Gene Name	Gene Product	Knowledge of Regulation	Reference
118	24349226	0.989	0.057	Q(FP)		SO3089	fatty oxidation complex, beta subunit		
119	24346986	0.989	0.320			folB	dihydroneopterin aldolase		
120	24348446	0.989	0.420			thiC	thiamin biosynthesis protein ThiC	RF00059 TPP	Rfam
121	24348979	0.988	0.704	Q	- A	SO2882	conserved hypothetical protein		
122	24347613	0.988	0.267			SO1787	conserved hypothetical protein		
123	24350786	0.988	0.277	Q		ilvC	ketol-acid reductoisomerase		
124	24345621	0.987	0.108		T -	secE	preprotein translocase, SecE subunit	RNaseIII sites in the leader sequence of SecE in <i>E. coli</i>	(Chow and Dennis 1994)
125	24347051	0.987	0.969			nadB	L-aspartate oxidase	RF00522 PreQ1	Rfam
126	24346706	0.987	0.353	Q	T A	SO1075	conserved hypothetical protein		
127	24349968	0.987	0.493			SO3687	curli production assembly/transport component CsgE, putative		
128	24349655	0.986	0.932	Q		recA	recA protein		
129	24348006	0.985	0.006			hoxK	quinone-reactive Ni/Fe hydrogenase, small subunit precursor		
130	24348892	0.985	0.366			SO2805	conserved hypothetical protein		
131	24345589	0.982	0.512		T A	SO0190	MutT/nudix family protein		
132	24351101	0.982	0.994		T -	SO4606	cytochrome c oxidase, subunit II		
133	24346318	0.982	0.690			SO0774	5-formyltetrahydrofolate cyclo-ligase family protein	RF00013 6S RNA	Rfam
134	24348931	0.981	0.432			SO2842	peptidase, M23/M37 family		
135	24350327	0.980	0.029	Q	- A	SO3987	conserved hypothetical protein		
136	24349297	0.980	0.850		- A	etfB	electron transfer flavoprotein, beta subunit		
137	24346527	0.980	0.378			nhaD	Na ⁺ /H ⁺ antiporter		

Table S2. Top 166 predicted regulatory RNAs by RSSVM (continued 7).

Rank	GI	RSSVM	RNAz	QRNA	Terminator (T) Attenuator (A)	Gene Name	Gene Product	Knowledge of Regulation	Reference
138	24348231	0.979	0.402			ibpA	16 kDa heat shock protein A		
139	24347681	0.978	0.423			SO1844	extracellular nuclease, putative		
140	24349463	0.978	0.966	Q		SO3278	conserved hypothetical protein		
141	24348630	0.977	0.006	Q		SO2591	conserved hypothetical protein		
142	24350000	0.977	0.410			SO3715	oxygen-insensitive NAD(P)H nitroreductase		
143	24350064	0.976	0.858	Q	T A	SO3770	conserved hypothetical protein TIGR00153		
144	24351130	0.975	0.277		- A	SO4628	sulfatase		
145	24346130	0.975	0.040			crp	catabolite gene activator		
146	24346384	0.972	0.342			SO0826	conserved hypothetical protein		
147	24347716	0.972	0.456		T -	speA	biosynthetic arginine decarboxylase	Possible post- transcriptional regulation in <i>S.</i> <i>oneidensis</i>	(Yang <i>et al.</i> 2008)
148	24348388	0.971	0.017			cmk	cytidylate kinase		
149	24347035	0.971	0.393			SO1328	transcriptional regulator, LysR family		
150	24350162	0.971	0.796		T A	sfcA	malate oxidoreductase		
151	24349576	0.971	0.367			SO3367	conserved hypothetical protein TIGR00091		
152	24345923	0.970	0.418			fkbp-1	peptidyl-prolyl cis-trans isomerase FkbP		
153	24351092	0.967	0.333		T A	SO4600	antigen, putative		
154	24345880	0.967	0.415		T A	ampD	AmpD protein		
155	24349361	0.965	0.450			SO3193	polysaccharide biosynthesis protein		
156	24350020	0.964	0.413		- A	SO3733	hypothetical protein		
157	24346579	0.964	0.136			SO0975	hypothetical protein		
158	24348690	0.961	0.426			SO2639	hypothetical protein		

Table S2. Top 166 predicted regulatory RNAs by RSSVM (continued 8).

Rank	GI	RSSVM	RNAz	QRNA	Terminator (T) Attenuator (A)	Gene Name	Gene Product	Knowledge of Regulation	Reference
159	24345372	0.960	0.440		T A	SO0019	conserved hypothetical protein		
160	24350679	0.959	0.376			folE	GTP cyclohydrolase I		
161	24347079	0.958	0.524			aroF	phospho-2-dehydro-3-deoxyheptonate aldolase, tyrsensitive		
162	24348818	0.957	0.191			SO2742	sensor histidine kinase/response regulator		
163	24349925	0.956	0.102			rplU	ribosomal protein L21		
164	24348689	0.954	0.897		T A	ldh	leucine dehydrogenase		
165	24346880	0.954	0.623		- A	SO1210	TPR domain protein		
166	24349795	0.953	0.409		- A	SO3545	OmpA family protein		

^a. “Q” represents QRNA predictions that fit the “RNA” model in at least two pairwise alignments. “FP” indicates that the shuffled sequences were also identified as “RNA” by QRNA.

References

- Beliaev AS, Thompson DK, Khare T, Lim H, Brandt CC et al. (2002) Gene and protein expression profiles of *Shewanella oneidensis* during anaerobic growth with different electron acceptors. *Omics* 6(1): 39-60.
- Cheung AY, Watson L, Soll D (1985) Two control systems modulate the level of glutaminyl-tRNA synthetase in *Escherichia coli*. *Journal of bacteriology* 161(1): 212-218.
- Chow J, Dennis PP (1994) Coupling between mRNA synthesis and mRNA stability in *Escherichia coli*. *Molecular microbiology* 11(5): 919-931.
- Ishihama A, Fukuda R (1980) Autogenous and post-transcriptional regulation of RNA polymerase synthesis. *Molecular and cellular biochemistry* 31(3): 177-196.
- Jiang GR, Nikolova S, Clark DP (2001) Regulation of the *ldhA* gene, encoding the fermentative lactate dehydrogenase of *Escherichia coli*. *Microbiology (Reading, England)* 147(Pt 9): 2437-2446.
- Maier TM, Myers CR (2004) The outer membrane protein Omp35 affects the reduction of Fe(III), nitrate, and fumarate by *Shewanella oneidensis* MR-1. *BMC microbiology* 4: 23.
- Membrillo-Hernandez J, Lin EC (1999) Regulation of expression of the *adhE* gene, encoding ethanol oxidoreductase in *Escherichia coli*: transcription from a downstream promoter and regulation by *fnr* and *RpoS*. *Journal of bacteriology* 181(24): 7571-7579.
- Ogasawara H, Ishida Y, Yamada K, Yamamoto K, Ishihama A (2007) PdhR (pyruvate dehydrogenase complex regulator) controls the respiratory electron transport system in *Escherichia coli*. *Journal of bacteriology* 189(15): 5534-5541.
- Steward KL, Linn T (1992) Transcription frequency modulates the efficiency of an attenuator preceding the *rpoBC* RNA polymerase genes of *Escherichia coli*: possible autogenous control. *Nucleic acids research* 20(18): 4773-4779.

- Vitreschak AG, Lyubetskaya EV, Shirshin MA, Gelfand MS, Lyubetsky VA (2004) Attenuation regulation of amino acid biosynthetic operons in proteobacteria: comparative genomics analysis. *FEMS microbiology letters* 234(2): 357-370.
- Weinberg Z, Barrick JE, Yao Z, Roth A, Kim JN et al. (2007) Identification of 22 candidate structured RNAs in bacteria using the CMfinder comparative genomics pipeline. *Nucleic Acids Res* 35(14): 4809-4819.
- Yang Y, Harris DP, Luo F, Wu L, Parsons AB et al. (2008) Characterization of the *Shewanella oneidensis* Fur gene: roles in iron and acid tolerance response. *BMC genomics* 9 Suppl 1: S11.
- Yao Z, Barrick J, Weinberg Z, Neph S, Breaker R et al. (2007) A computational pipeline for high-throughput discovery of cis-regulatory noncoding RNA in prokaryotes. *PLoS computational biology* 3(7): e126.
- Zurawski G, Gunsalus RP, Brown KD, Yanofsky C (1981) Structure and regulation of aroH, the structural gene for the tryptophan-repressible 3-deoxy-D-arabino-heptulosonic acid-7-phosphate synthetase of *Escherichia coli*. *Journal of molecular biology* 145(1): 47-73.