

Table S2. List of sixty six known *E. coli* K12-MG1655 sRNA TUs that were identified by sRNAscanner.

<i>Start1^a</i>	<i>D1^b</i>	<i>D2^c</i>	<i>End3^d</i>	<i>Score1^e</i>	<i>Score2^f</i>	<i>Score3^g</i>	<i>CSS^h</i>	<i>Strandⁱ</i>	<i>Comment^j</i>
111	12	151	316	4.34949	2.91965	8.24484	15.514	p	<i>Thr_leader</i>
17035	18	49	17144	2.05755	5.37638	5.88234	13.3163	p	<i>sokC</i>
77321	16	218	77597	2.05755	4.59522	7.4388	14.0916	p	<i>sgrS</i>
83929	13	308	83567	3.32784	3.57357	8.94716	15.84857	c	<i>Leu_leader</i>
123005	16	50	122898	2.52555	2.52761	7.46332	12.51648	c	<i>tp2</i>
686023	13	69	685900	3.16148	2.35325	5.63453	11.14926	c	<i>sroC</i>
887288	16	44	887187	2.30619	2.41939	4.3023	9.02788	c	<i>rybB</i>
1143676	18	325	1144061	1.78929	1.96413	6.06757	9.82099	p	<i>rne5</i>
1145823	17	103	1145985	2.89322	2.41939	4.42801	9.74062	p	<i>sraB_PsrD</i>
1229971	14	44	1229872	2.15777	2.91965	4.70722	9.78464	c	<i>C0299</i>
1268516	12	48	1268618	3.22762	4.52908	7.36021	15.1169	p	<i>rdlA</i>
1269051	12	48	1269153	3.22762	4.52908	7.36021	15.1169	p	<i>rdlB</i>
1269586	12	48	1269688	3.22762	4.52908	7.36021	15.1169	p	<i>rdlC</i>
1286580	15	233	1286870	3.37605	3.37499	4.51164	11.2627	p	<i>rtt</i>
1321167	17	123	1320986	4.98548	1.57218	10.3006	16.85826	c	<i>Trp_leader</i>
1403698	12	240	1403992	3.22762	4.16136	4.46953	11.8585	p	<i>IS061_isrA</i>
1403838	17	105	1403675	1.93771	2.41939	6.46964	10.82674	c	<i>IS061</i>
1416309	16	240	1416607	2.59164	4.16136	7.85388	14.6069	p	<i>dicF</i>
1435036	18	163	1435259	2.67391	4.02883	8.77217	15.4749	p	<i>micC</i>
1489561	15	45	1489460	2.30619	6.03031	7.95298	16.28948	c	<i>rydC</i>
1647347	14	68	1647471	4.18314	1.57215	5.70936	11.4647	p	<i>dicF</i>
1762888	17	141	1762689	2.94218	2.59375	6.94529	12.48122	c	<i>rydB</i>
1768361	17	86	1768506	2.00385	4.35473	9.29241	15.651	p	<i>rprA</i>
1903414	17	217	1903690	3.16148	4.59522	5.77931	13.536	p	<i>yybP_YkoY</i>
1921041	18	264	1921365	2.35439	3.57357	6.39807	12.326	p	<i>sraC_ryeA</i>
1956288	13	40	1956194	2.20597	4.52908	5.25889	11.99394	c	<i>ryeF</i>
1986058	16	140	1985861	3.32784	5.37638	5.29614	14.00036	c	<i>IS092_isrB</i>
2023396	14	101	2023240	2.67391	3.94136	10.6813	17.29657	c	<i>dsrA</i>
2031614	17	95	2031768	3.96383	4.02883	7.47558	15.4682	p	<i>rseX</i>
2069307	17	174	2069540	3.91487	4.42087	8.43539	16.7711	p	<i>IS102_isrC</i>
2087914	12	204	2088172	2.79376	4.42087	5.82731	13.0419	p	<i>His_Leader</i>
2151167	15	158	2151382	2.20597	2.81143	5.82675	10.8441	p	<i>QUAD1a</i>
2151634	17	120	2151813	4.98548	2.91965	4.3799	12.285	p	<i>QUAD1b</i>
2165060	14	112	2165228	1.56998	2.41939	5.19922	9.18859	p	<i>ryeE</i>
2311116	16	179	2311353	3.32784	1.57215	6.17275	11.0727	p	<i>micF</i>
2651506	16	174	2651738	4.18314	4.52908	6.219	14.9312	p	<i>IS128</i>
2651640	16	40	2651738	2.35439	2.59375	6.219	11.1671	p	<i>ryfA</i>
2689131	14	133	2689320	2.42528	1.57213	4.72639	8.7238	p	<i>tke1</i>
2689441	13	216	2689171	2.52549	6.03031	5.13033	13.68613	c	<i>tke1_glmY</i>
2698120	14	314	2698490	1.71845	2.31673	5.02186	9.05704	p	<i>ryfB</i>
2698505	18	57	2698622	2.57375	2.41939	8.78396	13.7771	p	<i>ryfC</i>

2744415	17	136	2744221	2.42528	2.55192	7.47016	12.44736	c	<i>rpsP</i> 5'
2753699	14	306	2754061	1.78929	2.55192	8.43406	12.7753	p	<i>tmRNA</i>
2885267	15	268	2885592	1.93771	3.94138	4.91637	10.7955	p	<i>sokX</i>
2922580	17	348	2922174	2.57379	2.52761	5.43862	10.54002	c	<i>csrB</i>
2940683	17	186	2940928	3.10778	5.18301	9.27923	17.57	p	<i>gcvB</i>
2967539	13	197	2967288	2.89322	2.41939	4.62762	9.94023	c	<i>sraE_omrA_omrB</i>
2974292	18	114	2974119	3.96383	1.57212	8.70576	14.24171	c	<i>sraE_omrA_omrB</i>
3054837	17	201	3055097	4.98548	2.33186	4.83957	12.1569	p	<i>QUAD1c/rygC</i>
3119318	12	281	3119653	2.52553	5.18301	4.51171	12.2203	p	<i>C0719</i>
3182845	15	290	3182499	2.20597	1.57209	4.87838	8.65644	c	<i>sroG</i>
3192921	17	129	3192734	3.76171	3.57357	4.10227	11.43755	c	<i>QUAD1d_rygD</i>
3193204	16	250	3192897	3.96383	4.42087	5.40649	13.79119	c	<i>QUAD1e_rygE</i>
3236360	17	171	3236590	4.34949	2.91965	8.45355	15.7227	p	<i>yybP_ykoY_psrN</i>
3268402	13	151	3268197	2.20597	3.57357	5.00101	10.78055	c	<i>RNaseP_bact_a</i>
3309786	12	305	3309428	3.96383	4.16136	4.71052	12.83571	c	<i>S15</i>
3579074	18	76	3578939	1.61818	5.37638	10.1226	17.11716	c	<i>ryhB_SraI</i>
3662852	17	86	3662997	1.93771	4.59522	9.1865	15.7194	p	<i>gadY</i>
3698129	12	48	3698231	3.22762	4.52908	7.22135	14.9781	p	<i>rdlD</i>
3706755	17	101	3706596	3.76171	2.81143	6.20238	12.77552	c	<i>rttR</i>
3851074	17	169	3850847	3.54715	1.76547	6.46886	11.78148	c	<i>lstR-2</i>
3851226	16	322	3850847	2.15777	4.16136	6.46886	12.78799	c	<i>lstR-1</i>
3984402	12	210	3984666	2.20597	1.76546	7.35598	11.3274	p	<i>sraJ_glmZ</i>
4047915	15	63	4048035	1.78929	2.81143	5.71214	10.3129	p	<i>Spot_42</i>
4049024	16	225	4049307	2.52551	3.57357	5.66983	11.7689	p	<i>csrC</i>
4156454	18	100	4156295	2.89322	4.02883	6.48072	13.40277	c	<i>oxyS</i>

^a Start of the sRNAsScanner-predicted transcriptional unit (TU).

^b Length of the sequence-independent spacer between the identified [-35] and [-10] promoter boxes.

^c Predicted length of sRNA transcript-encoding region.

^d End coordinate of the predicted sRNA TU.

^e Sum of scores (SS) value for the identified orphan [-35] promoter box.

^f Sum of scores (SS) value for the identified orphan [-10] promoter box.

^g Sum of scores (SS) value for the identified orphan rho-independent terminator.

^h Cumulative sum of scores (CSS) value of the predicted sRNA TU.

ⁱ The coding strand of the predicted sRNA TU; p, positive; c, complementary.

^j Identity of the sRNAsScanner-predicted known *E. coli* K12-MG1655 sRNA TU as recorded in the Rfam [34] and/or sRNAMap [1] databases based on their location coordinates and orientation.