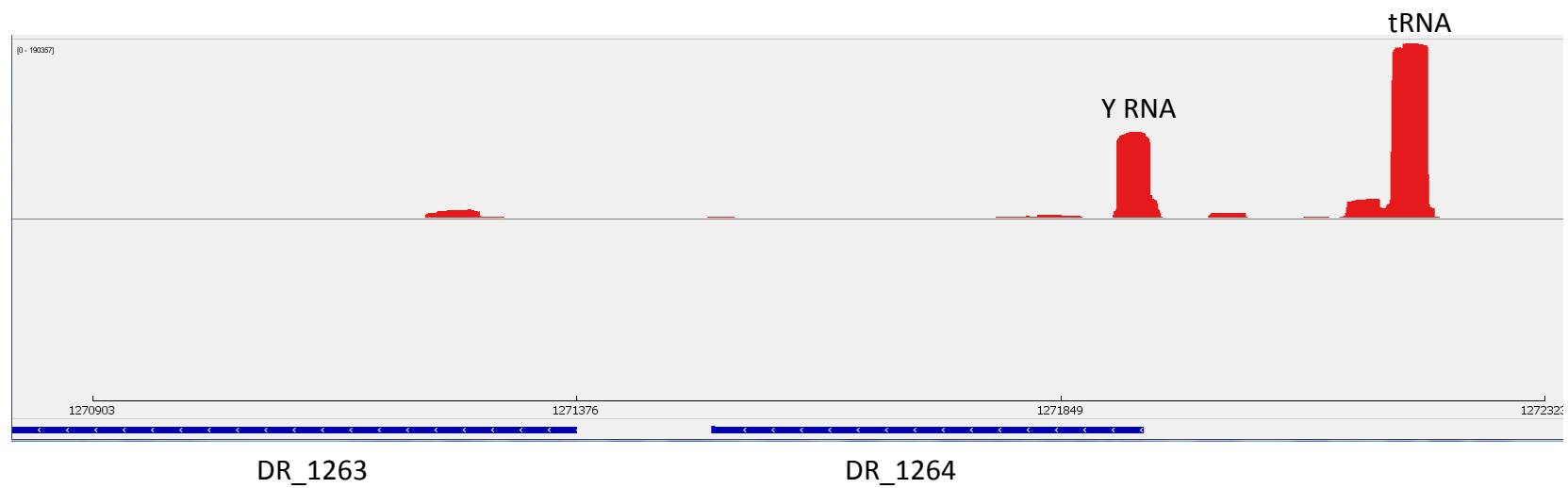
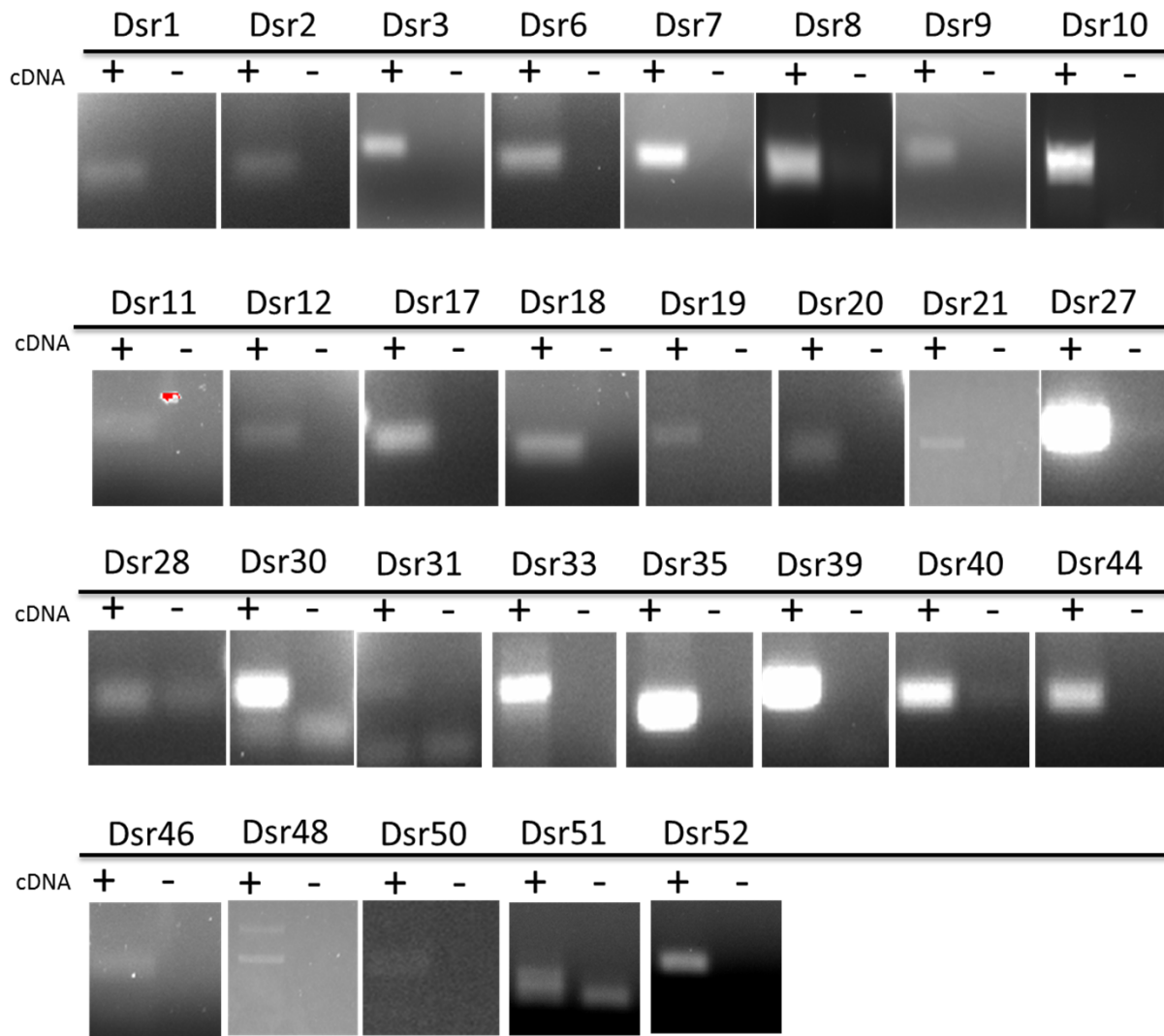


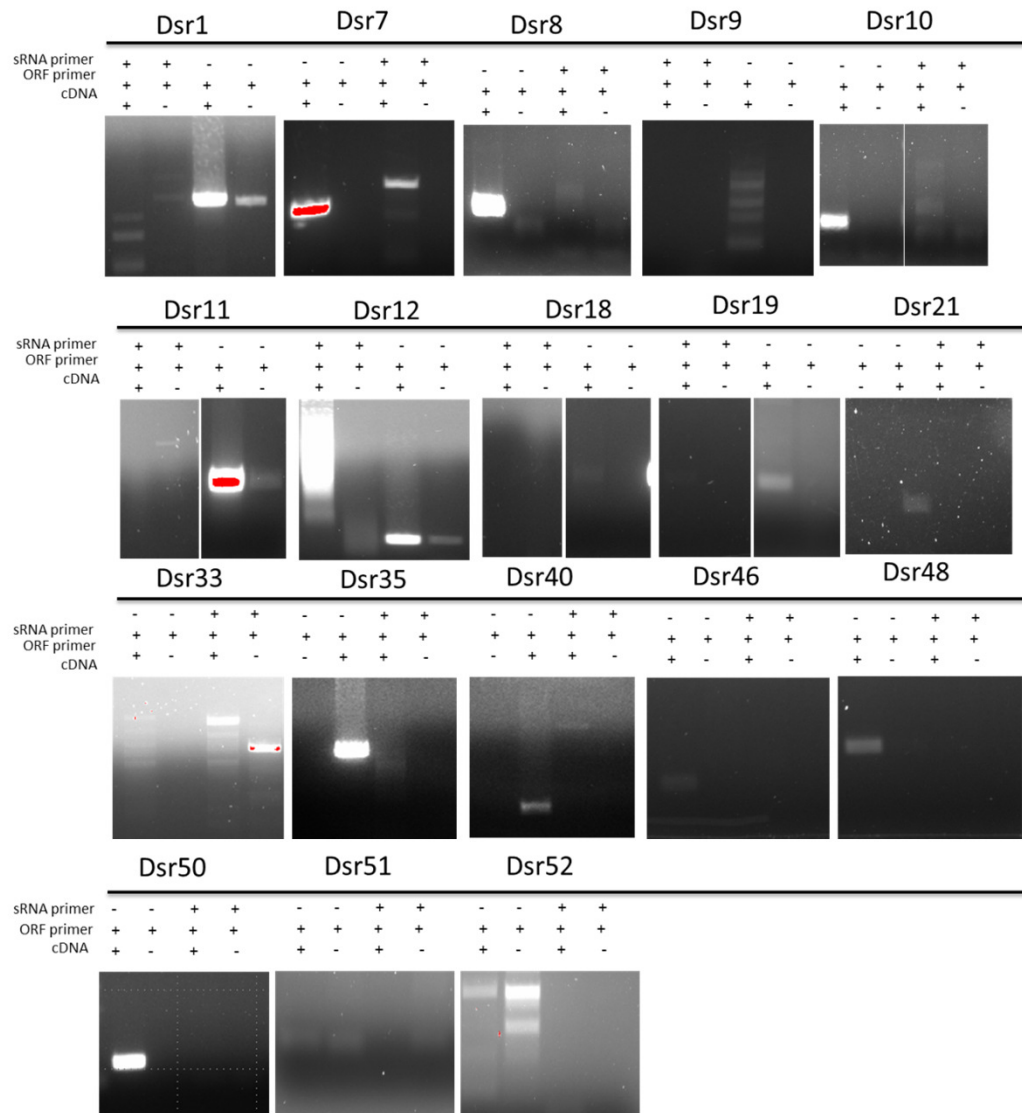
Supplementary Figure 1. Deep sequencing reads distribution.



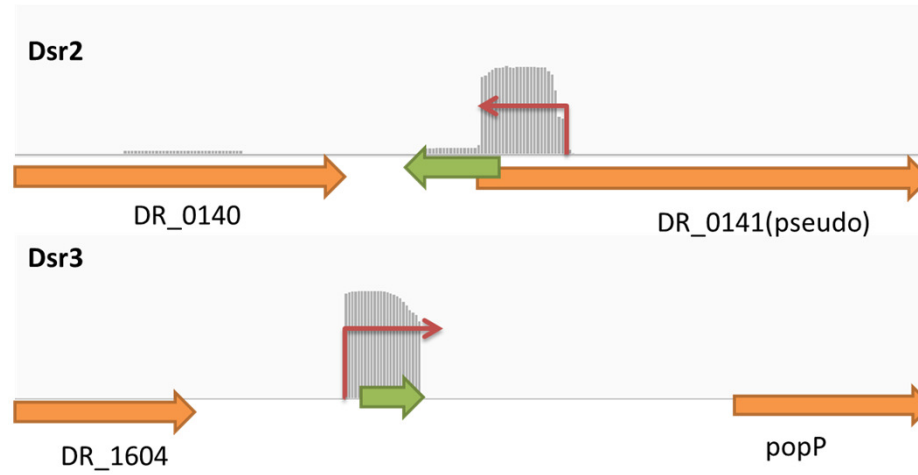
Supplementary Figure 2. Expression of the Y RNA was confirmed with the deep-seq data.



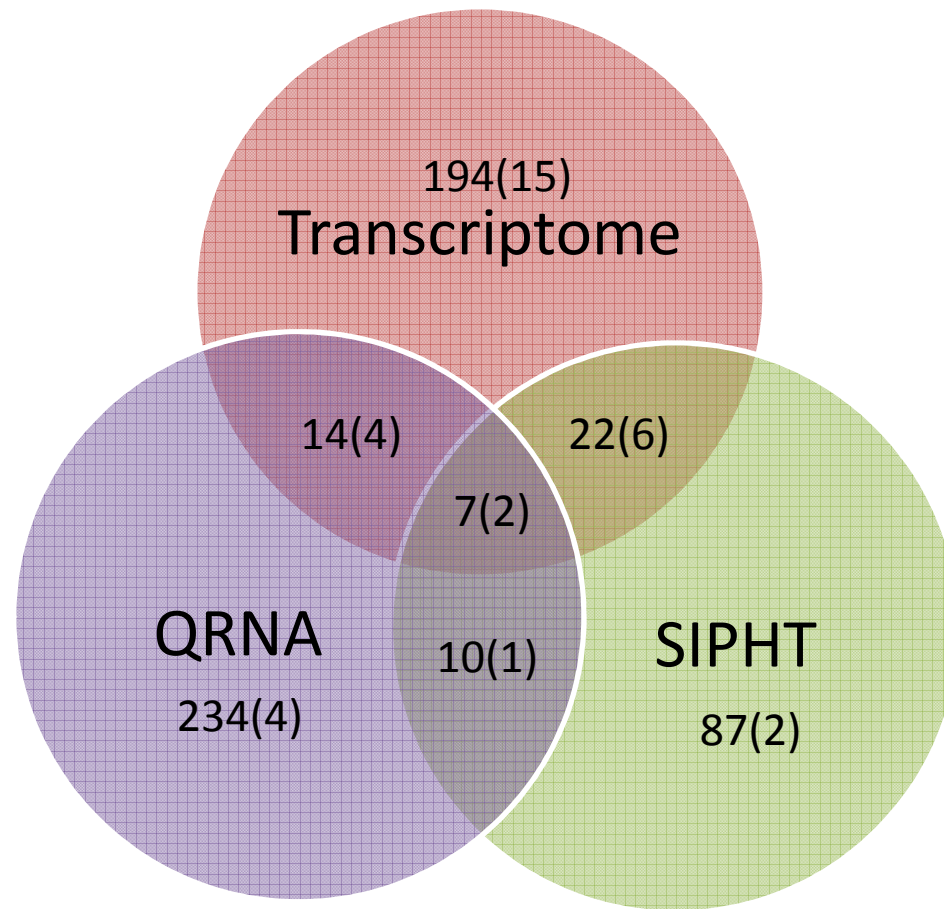
Supplementary Figure 3. RT-PCR for sRNAs identified in *D. radiodurans*.



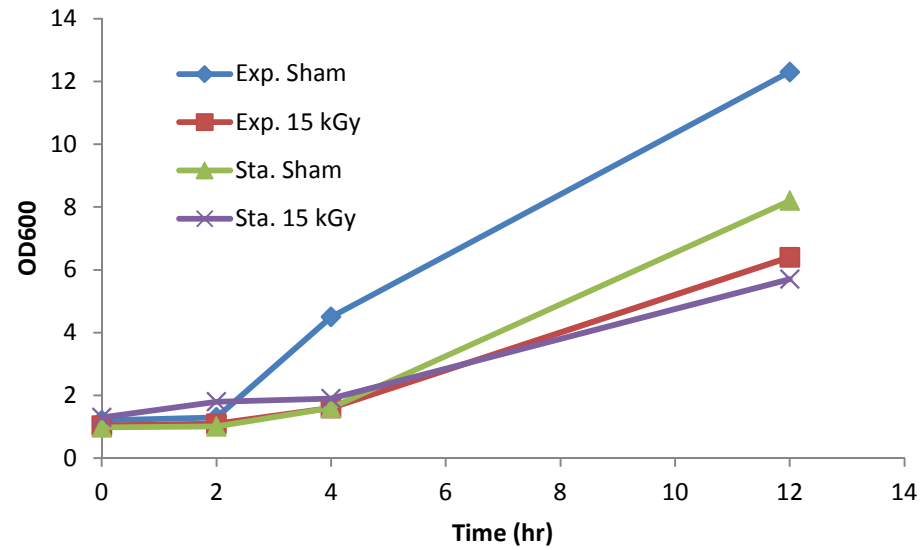
Supplementary Figure 4. RT-PCR for sRNA co-transcription verification.



Supplementary Figure 5. Selected examples of transcription starting sites identified by 5' Deep-RACE.

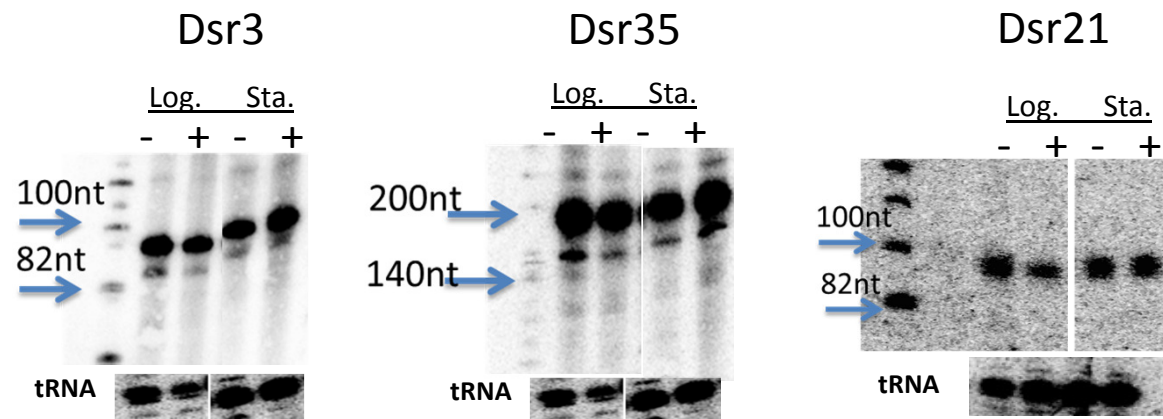


Supplementary Figure 6. Venn diagram of computational predicted sRNA candidates and deep-sequencing identified (transcriptome) sRNA candidates in *D. radiodurans*. The numbers indicate the sRNA candidates that were predicted using each method, with the numbers of sRNA confirmed by Northern blotting analysis in parentheses.

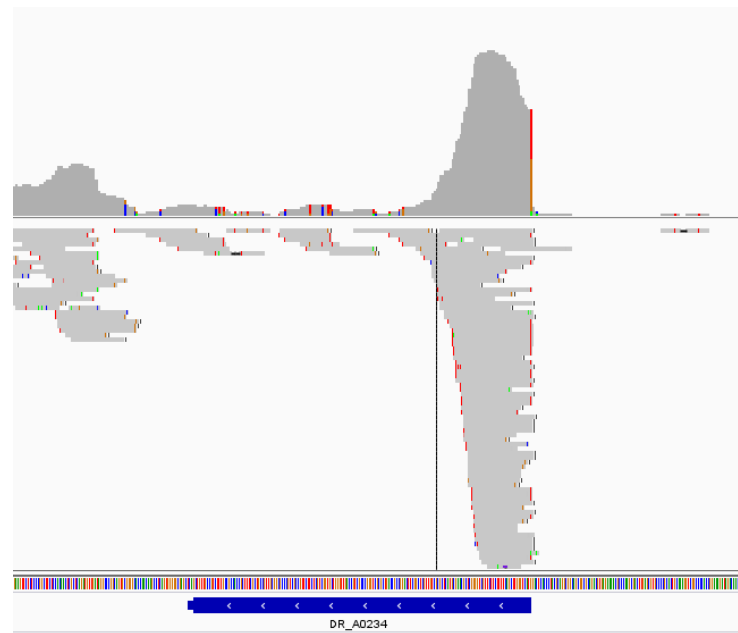


Survival rate (CFU)	15 kGy after 2hrs
exponential cells	8.13E-02
stationary cells	1.38E-02

Supplementary Figure 7. Cells survival rate after 15 kGy irradiation.



Supplementary Figure 8. Selected sRNAs of non-differential expression of. In each Northern blotting image. The left two lanes are RNA samples from exponential phase ($OD_{600} = 1$) cells, and the right two lanes are from stationary phase ($OD_{600} = 3$) cells. The first and third lanes are the control (sham irradiation) RNA samples, and the second and fourth lanes are the 15kGy irradiated RNA samples. The images of first two lanes and last two lanes are cut from the same gel in different parts. The band intensity change of each candidate is normalized to tRNA levels showed at the bottom of each blot.



Supplementary Figure 9. Expression of DR_A0234 is confirmed with the deep sequencing analysis.

Supplementary Table 1A. Predicted sRNAs by QRNA

family	genome	5'	3'	Size	adjacent genes
18286	gi 15805042 ref NC_001263.1	7806	7823	17	>DRA0007~DRA0008>
18065	gi 15805042 ref NC_001263.1	19144	19160	16	<DR0019~DR0020>
18080	gi 15805042 ref NC_001263.1	20644	20661	17	>DR0020~DR0021>
18188	gi 15805042 ref NC_001263.1	26109	26126	17	>DR0026~DR0027<
18258	gi 15805042 ref NC_001263.1	26631	26651	20	>DRA0024~DRA0025>
9394	gi 15805042 ref NC_001263.1	34724	34744	20	>DRA0031~DRA0032>
17953	gi 15805042 ref NC_001263.1	36102	36123	21	>DR0035~DR0036>
16060	gi 15805042 ref NC_001263.1	43484	43498	14	>DRA0038~DRA0039>
18203	gi 15805042 ref NC_001263.1	44569	44596	27	>DR0045~DR0046>
11124	gi 15805042 ref NC_001263.1	46095	46114	19	>DR0048~DR0049>
17506	gi 15805042 ref NC_001263.1	54681	54697	16	<DR0058~DR0059>
18285	gi 15805042 ref NC_001263.1	60562	60585	23	>tRNA-Met-3~DRA0056<
17631	gi 15805042 ref NC_001263.1	63260	63320	60	>DR0065~DR0066<
5792	gi 15805042 ref NC_001263.1	66724	66744	20	>DR0070~DR0071<
11733	gi 15805042 ref NC_001263.1	69330	69346	16	<DRA0063~DRA0064<
5592	gi 15805042 ref NC_001263.1	72625	72671	46	<DR0074~DR0075>
18232	gi 15805042 ref NC_001263.1	83035	83051	16	<DR0082~DR0083<
5798	gi 15805042 ref NC_001263.1	95529	95574	45	>DR0094~DR0095<
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16374	gi 15805042 ref NC_001263.1	183012	183043	31	<DR0182~DR0183<
18253	gi 15805042 ref NC_001263.1	188528	188550	22	>DRA0182~DRA0183<
2354	gi 15805042 ref NC_001263.1	188979	189051	72	1 >DR0184~DR0185>
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17694	gi 15805042 ref NC_001263.1	194167	194191	24	>DRA0186~DRA0188<

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18087	gi 15805042 ref NC_001263.1	213117	213133	16 <DR0211~DR0212<
18093	gi 15805042 ref NC_001263.1	216870	216951	81 <DR0215~DR0216<
5632	gi 15805042 ref NC_001263.1	222561	222585	24 >DR0221~DR0222<
18256	gi 15805042 ref NC_001263.1	223427	223446	19 >DRA0212~DRA0213>
18130	gi 15805042 ref NC_001263.1	236456	236479	23 >DR0238~DR0239>
18131	gi 15805042 ref NC_001263.1	237362	237382	20 >DR0239~DR0240<
16730	gi 15805042 ref NC_001263.1	248253	248304	51 >DR0251~DR0252>
17006	gi 15805042 ref NC_001263.1	250450	250470	20 <tRNA-Asp-3~DRrnaC23S>
16460	gi 15805042 ref NC_001263.1	250502	250524	22 <tRNA-Asp-3~DRrnaC23S>
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5758	gi 15805042 ref NC_001263.1	267627	267650	23 >DRA0254~DRA0255<
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18190	gi 15805042 ref NC_001263.1	299625	299643	18 <DR0297~DR0298<
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5769	gi 15805042 ref NC_001263.1	1302729	1302749	20	>DR1295~DR1296>
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18054	gi 15805042 ref NC_001263.1	1781858	1781874	16	<DR1753~DR1754>
18055	gi 15805042 ref NC_001263.1	1809520	1809539	19	>DR1779~DR1780>
18057	gi 15805042 ref NC_001263.1	1851909	1851929	20	<DR1825~DR1826<
18058	gi 15805042 ref NC_001263.1	1868548	1868564	16	>DR1841~DR1842<
17896	gi 15805042 ref NC_001263.1	1886390	1886409	19	>DR1863~DR1864<
18062	gi 15805042 ref NC_001263.1	1903478	1903493	15	<DR1882~DR1883>
5558	gi 15805042 ref NC_001263.1	1904237	1904266	29	>DR1883~DR1884<
18064	gi 15805042 ref NC_001263.1	1904435	1904459	24	7 >DR1883~DR1884<
18066	gi 15805042 ref NC_001263.1	1915413	1915435	22	>DR1895~DR1896>
17686	gi 15805042 ref NC_001263.1	1915793	1915817	24	>DR1896~DR1897<

3860	gi 15805042 ref NC_001263.1	1923582	1923602	20	>DR1904~DR1905<
5779	gi 15805042 ref NC_001263.1	1949116	1949138	22	<DR1927~DR1928<
17548	gi 15805042 ref NC_001263.1	1953251	1953268	17	<DR1931~DR1932>
17438	gi 15805042 ref NC_001263.1	1956907	1956923	16	>DR1936~DR1937<
17949	gi 15805042 ref NC_001263.1	1981107	1981128	21	>DR1960~DR1961>
18071	gi 15805042 ref NC_001263.1	1986461	1986477	16	<DR1964~DR1965<
18072	gi 15805042 ref NC_001263.1	1988926	1988942	16	>DR1967~DR1968<
18074	gi 15805042 ref NC_001263.1	2025948	2025964	16	<DR2005~DR2006<
18076	gi 15805042 ref NC_001263.1	2032119	2032138	19	>DR2013~DR2014<
18077	gi 15805042 ref NC_001263.1	2053999	2054017	18	<DR2038~DR2039<
18078	gi 15805042 ref NC_001263.1	2054106	2054122	16	<DR2038~DR2039<
18079	gi 15805042 ref NC_001263.1	2062073	2062093	20	<DR2049~DR2050<
18081	gi 15805042 ref NC_001263.1	2068854	2068871	17	>DR2053~DR2054<
18082	gi 15805042 ref NC_001263.1	2069297	2069336	39	<DR2054~DR2055>
16822	gi 15805042 ref NC_001263.1	2099749	2099793	44	<DR2087~DR2088<
18085	gi 15805042 ref NC_001263.1	2118294	2118310	16	>DR2108~tRNA-Leu-2<
17273	gi 15805042 ref NC_001263.1	2118674	2118693	19	<tRNA-Leu-2~DR2109>
18086	gi 15805042 ref NC_001263.1	2130322	2130346	24	>DR2126~DR2127>
4154	gi 15805042 ref NC_001263.1	2132603	2132619	16	>DR2129~DR2130<
17610	gi 15805042 ref NC_001263.1	2142254	2142269	15	<DR2139~DR2140>
5685	gi 15805042 ref NC_001263.1	2144289	2144313	24	>DR2141~DR2142<
18092	gi 15805042 ref NC_001263.1	2165755	2165775	20	<DR2168~DR2169<
18095	gi 15805042 ref NC_001263.1	2173666	2173684	18	>DR2175~DR2176>
17688	gi 15805042 ref NC_001263.1	2197606	2197630	24	>DR2198~DR2199>
17659	gi 15805042 ref NC_001263.1	2199501	2199543	42	>DR2199~DR2200<
18098	gi 15805042 ref NC_001263.1	2199718	2199746	28	>DR2199~DR2200<
5783	gi 15805042 ref NC_001263.1	2228282	2228300	18	>DR2232~DR2233<
5784	gi 15805042 ref NC_001263.1	2231180	2231212	32	>DR2235~DR2236<
18104	gi 15805042 ref NC_001263.1	2246235	2246393	158	<DRrrnaA23S~DR2253<
16382	gi 15805042 ref NC_001263.1	2246869	2246940	71	<DRrrnaA23S~DR2253<
18107	gi 15805042 ref NC_001263.1	2247075	2247143	68	<DRrrnaA23S~DR2253<
16375	gi 15805042 ref NC_001263.1	2248014	2248036	22	<DRrrnaA23S~DR2253<
17005	gi 15805042 ref NC_001263.1	2248068	2248088	20	<DRrrnaA23S~DR2253<
18120	gi 15805042 ref NC_001263.1	2259854	2259873	19	<DR2263~DR2264<

18122	gi 15805042 ref NC_001263.1	2271953	2272029	76	>DR2273~DR2274>
17952	gi 15805042 ref NC_001263.1	2314039	2314059	20	>DR2314~DR2315<
18126	gi 15805042 ref NC_001263.1	2315950	2315966	16	<DR2316~DR2317>
17549	gi 15805042 ref NC_001263.1	2321478	2321495	17	<DR2322~DR2323>
1746	gi 15805042 ref NC_001263.1	2329202	2329217	15	>DR2330~DR2331>
17913	gi 15805042 ref NC_001263.1	2334200	2334231	31	<DR2335~DR2336<
18128	gi 15805042 ref NC_001263.1	2351491	2351512	21	>DR2352~DR2353>
2364	gi 15805042 ref NC_001263.1	2364544	2364572	28	5 >DR2363a~DR2366<
17857	gi 15805042 ref NC_001263.1	2387119	2387178	59	<DR2385~DR2386<
18133	gi 15805042 ref NC_001263.1	2404281	2404329	48	>DR2402~DR2403<
18135	gi 15805042 ref NC_001263.1	2406823	2406854	31	<tRNA-Trp-1~DR2405>
18136	gi 15805042 ref NC_001263.1	2430227	2430242	15	>DR2427~DR2428<
18137	gi 15805042 ref NC_001263.1	2431585	2431602	17	<DR2428~DR2429>
18138	gi 15805042 ref NC_001263.1	2473197	2473212	15	<DR2476~DR2477>
17457	gi 15805042 ref NC_001263.1	2483042	2483058	16	>DR2485~DR2486>
17467	gi 15805042 ref NC_001263.1	2486621	2486673	52	>DR2488~DR2489>
17597	gi 15805042 ref NC_001263.1	2494184	2494200	16	<DR2495~DR2496>
18153	gi 15805042 ref NC_001263.1	2505703	2505718	15	<DR2505~DR2506<
18157	gi 15805042 ref NC_001263.1	2519074	2519091	17	<DR2516~DR2517>
18159	gi 15805042 ref NC_001263.1	2527078	2527094	16	<DR2524~DR2525<
18163	gi 15805042 ref NC_001263.1	2567674	2567689	15	<DR2565~DR2566>
17387	gi 15805042 ref NC_001263.1	2569003	2569026	23	>DR2566~DR2567>
1	gi 15805042 ref NC_001263.1	2579605	2579652	47	<DR2576~DR2577<
18166	gi 15805042 ref NC_001263.1	2585974	2586132	158	<DRrrnaB23S~DR2580<
16687	gi 15805042 ref NC_001263.1	2586608	2586679	71	<DRrrnaB23S~DR2580<
18173	gi 15805042 ref NC_001263.1	2586814	2586882	68	<DRrrnaB23S~DR2580<
18174	gi 15805042 ref NC_001263.1	2587082	2587127	45	<DRrrnaB23S~DR2580<
16461	gi 15805042 ref NC_001263.1	2587752	2587774	22	<DRrrnaB23S~DR2580<
17007	gi 15805042 ref NC_001263.1	2587806	2587826	20	<DRrrnaB23S~DR2580<

Supplementary Table 1b. Predicted sRNAs by SIPHT

Locus Name	UpGENE		Edirecti distUp					distDnG		DnGENEnum		BLASTExp		NumSearc
	umber	on	GENE	sRNAstart	end	dirsRNA	lensRNA	ENE	DnGENEdir.	ber	sRNAtype	BLASTscore	ect	hesPredic
Candidate_20_NC_001263	DR_0450	>>>	112	445674	445925 >>>		251	10 <<<	DR_0451	candidate	206	0.00022	1	
Candidate_3_NC_001263	DR_0693	>>>	166	709840	709988 >>>		148	33 >>>	DR_0694	candidate	293	1.50E-09	3	
Candidate_24_NC_001263	DR_0990	>>>	24	1007800	1007862 >>>		62	369 <<<	DR_0991	candidate	256	5.20E-07	1	
Candidate_25_NC_001263	DR_0990	>>>	321	1008097	1008156 >>>		59	75 <<<	DR_0991	candidate	231	1.10E-06	3	
Candidate_77_NC_001263	DR_1061	>>>	6	1072952	1073087 <<<		135	527 <<<	DR_1062	candidate	173	0.0026	1	
Candidate_31_NC_001263	DR_1149	>>>	186	1159362	1159424 >>>		62	198 >>>	DR_1150	candidate	335	8.10E-12	1	
Candidate_35_NC_001263	DR_1354	>>>	37	1361960	1362193 >>>		233	24 >>>	DR_1355	candidate	168	0.0039	1	
Candidate_84_NC_001263	DR_1354	>>>	37	1361960	1362035 >>>		75	182 >>>	DR_1355	candidate	168	0.0039	1	
Candidate_36_NC_001263	DR_1355	>>>	1	1363002	1363330 >>>		328	-6 >>>	DR_1356	candidate	646	1.20E-25	1	
Candidate_85_NC_001263	DR_1462	<<<	113	1475301	1475373 <<<		72	130 <<<	DR_1463	candidate	181	0.00063	1	
Candidate_87_NC_001263	DR_1515	>>>	44	1531402	1531584 >>>		182	16 >>>	DR_1516	candidate	172	0.00051	2	
Candidate_38_NC_001263	DR_1523	>>>	590	1539187	1539280 >>>		93	246 <<<	DR_1524	candidate	184	0.00086	2	
Candidate_40_NC_001263	DR_1695	>>>	150	1718480	1718674 >>>		194	80 >>>	DR_1696	candidate	251	5.50E-08	1	
Candidate_5_NC_001263	DR_1702	<<<	1	1725522	1725600 >>>		78	240 <<<	DR_1703	candidate	233	6.70E-07	1	
Candidate_41_NC_001263	DR_1714	>>>	20	1739125	1739360 >>>		235	71 >>>	DR_1715	candidate	265	1.40E-08	1	
Candidate_43_NC_001263	DR_1742	>>>	35	1771472	1771512 <<<		40	255 <<<	DR_1743	candidate	185	0.00014	4	
Candidate_47_NC_001263	DR_1883	>>>	44	1904230	1904265 <<<		35	246 <<<	DR_1884	candidate	200	2.80E-05	4	
Candidate_11_NC_001263	DR_1883	>>>	71	1904257	1904495 <<<		238	16 <<<	DR_1884	candidate	306	1.70E-10	2	
Candidate_48_NC_001263	DR_2058	>>>	5	2073196	2073481 >>>		285	5 >>>	DR_2059	candidate	175	0.00023	4	
Candidate_106_NC_001263	DR_2175	>>>	66	2173720	2173802 >>>		82	123 >>>	DR_2176	candidate	319	6.50E-11	3	
Candidate_56_NC_001263	DR_2199	>>>	132	2199589	2199774 >>>		185	16 <<<	DR_2200	candidate	236	4.70E-07	2	
Candidate_55_NC_001263	DR_2199	>>>	257	2199714	2199780 <<<		66	10 <<<	DR_2200	candidate	231	7.40E-07	2	
Candidate_8_NC_001263	DR_2235	>>>	-11	2231043	2231264 <<<		221	149 <<<	DR_2236	candidate	405	8.80E-15	1	
Candidate_110_NC_001263	DR_2546	<<<	105	2549548	2549736 >>>		188	-29 >>>	DR_2547	candidate	164	0.002	1	
Candidate_12_NC_001263	DR_0034	>>>	32	34728	34782 >>>		54	46 >>>	DR_0035	candidate	181	2.00E-09	3	
Candidate_115_NC_001263	DR_0034	>>>	32	34728	34765 >>>		37	63 >>>	DR_0035	candidate	181	2.00E-09	3	
Candidate_80_NC_001263	DR_0113	<<<	4	113000	113035 >>>		35	183 <<<	DR_0114	candidate	169	0.001	1	
Candidate_13_NC_001263	DR_0120	<<<	45	119390	119575 <<<		185	4 <<<	DR_0121	candidate	279	4.70E-09	1	
Candidate_14_NC_001263	DR_0122	>>>	154	121885	121976 >>>		91	-33 <<<	DR_0123	candidate	157	0.0038	1	
Candidate_15_NC_001263	DR_0144	<<<	119	143691	143793 >>>		102	-44 >>>	DR_0145	candidate	195	6.80E-05	2	
Candidate_16_NC_001263	DR_0153	>>>	2	154892	154979 >>>		87	-14 >>>	DR_0154	candidate	189	0.00019	2	
Candidate_89_NC_001263	DR_0157	>>>	-2	158961	159033 <<<		72	109 >>>	DR_0158	candidate	170	0.00055	3	
Candidate_17_NC_001263	DR_0166	>>>	13	169581	169644 >>>		63	233 >>>	DR_0167	candidate	154	0.0034	1	
Candidate_91_NC_001263	DR_0166	>>>	14	169582	169688 <<<		106	189 >>>	DR_0167	candidate	154	0.0034	1	
Candidate_18_NC_001263	DR_0198	<<<	18	202814	202884 <<<		70	23 <<<	DR_0199	candidate	170	0.0022	3	
Candidate_1_NC_001263	DR_0216	<<<	4	217429	217495 >>>		66	23 >>>	DR_0217	candidate	165	0.0018	1	
Candidate_19_NC_001263	DR_0404	>>>	91	407197	407315 >>>		118	3 <<<	DR_0405	candidate	149	0.0045	1	
Candidate_116_NC_001263	DR_0404	>>>	91	407197	407290 >>>		93	28 <<<	DR_0405	candidate	149	0.0045	1	
Candidate_117_NC_001263	DR_0432	>>>	27	431327	431480 >>>		153	62 >>>	DR_0433	candidate	176	0.00032	4	
Candidate_118_NC_001263	DR_0459	>>>	155	454792	454975 >>>		183	-61 <<<	DR_0460	candidate	251	1.40E-07	1	

Candidate_119_NC_001263	DR_0533 <<<	179	535940	536037 >>>	97	126 <<<	DR_0534	candidate	218	0.00017	1
Candidate_120_NC_001263	DR_0568 <<<	95	576822	576863 <<<	41	19 >>>	DR_t15	candidate	246	1.30E-07	2
Candidate_2_NC_001263	DR_0605 <<<	14	617656	617773 >>>	117	96 >>>	DR_0606	candidate	160	0.0013	3
Candidate_121_NC_001263	DR_0612 >>>	40	624795	624909 <<<	114	179 <<<	DR_0613	candidate	264	3.50E-08	1
Candidate_21_NC_001263	DR_0673 >>>	38	683747	683782 >>>	35	174 >>>	DR_0674	candidate	183	9.50E-05	1
Candidate_122_NC_001263	DR_0737 >>>	-65	751623	751863 <<<	240	8 >>>	DR_0738	candidate	184	0.00025	1
Candidate_22_NC_001263	DR_0774 >>>	26	791576	791770 >>>	194	42 >>>	DR_0775	candidate	150	0.0047	1
Candidate_123_NC_001263	DR_0774 >>>	26	791576	791745 >>>	169	67 >>>	DR_0775	candidate	150	0.0047	1
Candidate_124_NC_001263	DR_0868 <<<	-17	880670	880773 <<<	103	26 >>>	DR_0869	candidate	180	0.00021	4
RNaseP_bact_a_NC_001263	DR_0896 >>>	78	904611	905082 >>>	471	-19 <<<	DR_0897	RNaseP_bact_a	138	5.30E-56	2
RNaseP_bact_a_NC_001263	DR_0896 >>>	78	904611	905057 >>>	446	6 <<<	DR_0897	RNaseP_bact_a	138	5.30E-56	3
Candidate_23_NC_001263	DR_0960 >>>	249	974213	974296 >>>	83	39 <<<	DR_0961	candidate	155	0.0047	1
Candidate_26_NC_001263	DR_0996 >>>	1	1012254	1012379 >>>	125	-13 >>>	DR_0997	candidate	168	0.00052	1
Candidate_27_NC_001263	DR_1013 >>>	73	1026124	1026271 >>>	147	-16 <<<	DR_1014	candidate	199	1.80E-05	1
Candidate_74_NC_001263	DR_1013 >>>	73	1026124	1026240 >>>	116	15 <<<	DR_1014	candidate	199	1.80E-05	1
Candidate_75_NC_001263	DR_1033 >>>	6	1045625	1045804 >>>	179	64 <<<	DR_1034	candidate	262	2.20E-08	1
Candidate_28_NC_001263	DR_1052 >>>	37	1063849	1064008 <<<	159	206 <<<	DR_1053	candidate	219	7.00E-05	2
Candidate_76_NC_001263	DR_1055 <<<	16	1066642	1066789 <<<	147	36 <<<	DR_1056	candidate	374	3.60E-13	1
Candidate_29_NC_001263	DR_1092 >>>	15	1100573	1100662 >>>	89	480 >>>	DR_1093	candidate	220	0.00055	2
Candidate_79_NC_001263	DR_1110 <<<	19	1118433	1118558 <<<	125	102 <<<	DR_1111	candidate	182	0.00012	4
Candidate_30_NC_001263	DR_1110 <<<	183	1118597	1118646 <<<	49	14 <<<	DR_1111	candidate	168	0.00045	3
Candidate_81_NC_001263	DR_1190 >>>	33	1199663	1199803 <<<	140	51 >>>	DR_1191	candidate	205	8.70E-06	2
Candidate_32_NC_001263	DR_1197 >>>	-26	1205904	1205993 <<<	89	7 <<<	DR_1198	candidate	224	1.10E-06	3
Candidate_4_NC_001263	DR_1198 <<<	3	1207786	1207817 >>>	31	256 <<<	DR_1199	candidate	217	4.00E-06	1
Candidate_82_NC_001263	DR_1270 <<<	26	1278091	1278324 <<<	233	85 <<<	DR_1271	candidate	168	0.00055	2
Candidate_83_NC_001263	DR_1270 <<<	67	1278132	1278324 <<<	192	85 <<<	DR_1271	candidate	168	0.00055	2
Candidate_33_NC_001263	DR_1290 >>>	21	1297698	1297852 <<<	154	23 <<<	DR_1291	candidate	218	4.40E-06	2
Candidate_34_NC_001263	DR_1317 >>>	19	1323299	1323351 >>>	52	102 >>>	DR_1318	candidate	157	0.0026	1
Candidate_86_NC_001263	DR_1482 <<<	7	1496841	1496997 <<<	156	263 >>>	DR_1483	candidate	236	4.70E-07	2
Candidate_37_NC_001263	DR_1515 >>>	44	1531402	1531612 >>>	210	-12 >>>	DR_1516	candidate	172	0.00051	2
Candidate_39_NC_001263	DR_1523 >>>	590	1539187	1539449 >>>	262	77 <<<	DR_1524	candidate	184	0.00086	2
Candidate_88_NC_001263	DR_1560 <<<	-11	1579514	1579696 <<<	182	0 <<<	DR_1561	candidate	338	1.00E-11	1
Candidate_90_NC_001263	DR_1626 >>>	11	1649108	1649177 <<<	69	109 >>>	DR_1627	candidate	154	0.0034	1
Candidate_42_NC_001263	DR_1720 >>>	1	1747031	1747121 >>>	90	-26 <<<	DR_1721	candidate	176	0.00018	1
Candidate_92_NC_001263	DR_1730 >>>	70	1759017	1759072 <<<	55	37 >>>	DR_1731	candidate	191	7.20E-05	2
Candidate_44_NC_001263	DR_1742 >>>	111	1771548	1771767 <<<	219	0 <<<	DR_1743	candidate	180	0.00014	2
Candidate_45_NC_001263	DR_1777 >>>	32	1807701	1807771 >>>	70	98 >>>	DR_1778	candidate	311	1.80E-10	2
Candidate_46_NC_001263	DR_1777 >>>	32	1807701	1807867 >>>	166	2 >>>	DR_1778	candidate	311	1.80E-10	2
Candidate_93_NC_001263	DR_1777 >>>	32	1807701	1807840 >>>	139	29 >>>	DR_1778	candidate	311	1.80E-10	2
Candidate_94_NC_001263	DR_1791 <<<	33	1821083	1821164 <<<	81	81 <<<	DR_1792	candidate	170	0.00039	2
Candidate_95_NC_001263	DR_1795 <<<	79	1824449	1824513 >>>	64	61 >>>	DR_1796	candidate	154	0.0032	3
Candidate_96_NC_001263	DR_1816 <<<	120	1842183	1842299 >>>	116	44 >>>	DR_1817	candidate	196	2.20E-05	1
Candidate_97_NC_001263	DR_1853 <<<	85	1877109	1877223 <<<	114	36 <<<	DR_1854	candidate	216	4.30E-06	2
Candidate_98_NC_001263	DR_1913 >>>	1	1934839	1935030 >>>	191	240 >>>	DR_1914	candidate	171	0.0012	1
Candidate_99_NC_001263	DR_1939 <<<	852	1961392	1961460 >>>	68	852 >>>	DR_1940	candidate	241	5.80E-06	1

Candidate_100_NC_001263	DR_2007 <<<	57	2026748	2026868 >>>	120	17 >>>	DR_2008	candidate	302	8.30E-10	2
Candidate_10_NC_001263	DR_2044 <<<	126	2059614	2059652 <<<	38	41 <<<	DR_2045	candidate	221	3.60E-06	3
Candidate_102_NC_001263	DR_2049 <<<	33	2062018	2062186 >>>	168	9 <<<	DR_2050	candidate	260	4.80E-08	2
Candidate_101_NC_001263	DR_2049 <<<	87	2062072	2062136 <<<	64	59 <<<	DR_2050	candidate	273	1.40E-08	2
Candidate_49_NC_001263	DR_2097 >>>	18	2108858	2108920 <<<	62	0 <<<	DR_2098	candidate	152	0.0039	4
Candidate_50_NC_001263	DR_2116 >>>	30	2123286	2123333 >>>	47	89 >>>	DR_2117	candidate	169	0.00079	1
Candidate_103_NC_001263	DR_2141 >>>	11	2144195	2144326 <<<	131	35 <<<	DR_2142	candidate	249	1.80E-07	2
Candidate_51_NC_001263	DR_2141 >>>	97	2144281	2144326 <<<	45	35 <<<	DR_2142	candidate	249	1.80E-07	2
Candidate_52_NC_001263	DR_2146 >>>	11	2148782	2148909 <<<	127	171 <<<	DR_2147	candidate	157	0.0025	1
Candidate_53_NC_001263	DR_2164 >>>	12	2161984	2162125 <<<	141	78 <<<	DR_2165	candidate	214	3.30E-06	1
Candidate_104_NC_001263	DR_2166 >>>	43	2163698	2163817 >>>	119	58 >>>	DR_2167	candidate	199	3.10E-05	2
Candidate_105_NC_001263	DR_2173 <<<	64	2170091	2170203 >>>	112	-46 >>>	DR_2174	candidate	186	6.60E-05	3
Candidate_54_NC_001263	DR_2193 >>>	234	2190302	2190434 >>>	132	-61 >>>	DR_2194	candidate	181	0.0004	2
Candidate_9_NC_001263	DR_2209 <<<	293	2208594	2208695 <<<	101	90 >>>	DR_2210	candidate	190	0.00018	4
SRP_bact_NC_001263	DR_2235 >>>	79	2231133	2231275 >>>	142	138 <<<	DR_2236	SRP_bact	426	1.80E-15	4
SRP_bact_NC_001263	DR_2235 >>>	79	2231133	2231319 >>>	186	94 <<<	DR_2236	SRP_bact	426	1.80E-15	4
SRP_bact_NC_001263	DR_2235 >>>	79	2231133	2231257 >>>	124	156 <<<	DR_2236	SRP_bact	426	1.80E-15	4
SRP_bact_NC_001263	DR_2235 >>>	79	2231133	2231296 >>>	163	117 <<<	DR_2236	SRP_bact	426	1.80E-15	4
Candidate_107_NC_001263	DR_2240 <<<	172	2234792	2234857 <<<	65	7 >>>	DR_2241	candidate	161	0.0014	1
Candidate_57_NC_001263	DR_r06 <<<	60	2287080	2287112 >>>	32	228 <<<	DR_2288	candidate	317	8.30E-11	5
Candidate_108_NC_001263	DR_2305 >>>	9	2304081	2304156 <<<	75	27 <<<	DR_2306	candidate	87	0.0032	3
Candidate_58_NC_001263	DR_2340 >>>	47	2338934	2339097 >>>	163	-30 <<<	DR_2341	candidate	242	2.90E-07	1
Candidate_109_NC_001263	DR_2340 >>>	47	2338934	2339071 >>>	137	-4 <<<	DR_2341	candidate	242	2.90E-07	1
Candidate_59_NC_001263	DR_2462 >>>	26	2458848	2458897 >>>	49	203 >>>	DR_2463	candidate	156	0.0029	1
Candidate_60_NC_001263	DR_2462 >>>	26	2458848	2458972 >>>	124	128 >>>	DR_2463	candidate	156	0.0029	1
Candidate_61_NC_001263	DR_2526 >>>	5	2530270	2530411 <<<	141	26 >>>	DR_t43	candidate	252	1.50E-07	2
Candidate_62_NC_001263	DR_2526 >>>	41	2530306	2530354 >>>	48	83 >>>	DR_t43	candidate	239	6.70E-07	1
Candidate_6_NC_001263	DR_r09 <<<	78	2588017	2588183 >>>	166	62 <<<	DR_2580	candidate	187	8.90E-05	4
Candidate_63_NC_001263	DR_2594 >>>	18	2601736	2601848 >>>	112	60 <<<	DR_2595	candidate	163	0.0047	1
Candidate_64_NC_001263	DR_2594 >>>	18	2601736	2601830 >>>	94	78 <<<	DR_2595	candidate	163	0.0047	1
Candidate_111_NC_001263	DR_2606 >>>	22	2615517	2615585 <<<	68	397 <<<	DR_2607	candidate	189	0.00044	3
Candidate_112_NC_001263	DR_2606 >>>	217	2615712	2615820 <<<	108	162 <<<	DR_2607	candidate	180	0.0005	3
Candidate_65_NC_001263	DR_2606 >>>	246	2615741	2615820 <<<	79	162 <<<	DR_2607	candidate	180	0.0005	3
Candidate_66_NC_001263	DR_2606 >>>	372	2615867	2615942 <<<	75	40 <<<	DR_2607	candidate	319	7.40E-11	3
Candidate_67_NC_001263	DR_2610 <<<	55	2619300	2619403 <<<	103	131 <<<	DR_2611	candidate	179	0.00024	1
Candidate_68_NC_001263	DR_2618 >>>	41	2627873	2627916 >>>	43	90 >>>	DR_2619	candidate	166	0.00093	1
Candidate_69_NC_001263	DR_2624 >>>	4	2635244	2635325 >>>	81	-15 <<<	DR_2625	candidate	198	4.60E-05	4
Candidate_70_NC_001263	DR_2626 >>>	16	2638268	2638340 <<<	72	341 <<<	DR_2627	candidate	188	0.0019	4
Candidate_71_NC_001263	DR_2626 >>>	85	2638337	2638383 <<<	46	298 <<<	DR_2627	candidate	181	0.00031	1
Candidate_113_NC_001263	DR_2626 >>>	249	2638501	2638574 <<<	73	107 <<<	DR_2627	candidate	228	8.00E-07	2
Candidate_73_NC_001263	DR_2633 >>>	63	2644147	2644282 >>>	135	-19 >>>	DR_2634	candidate	277	1.40E-08	2
Candidate_114_NC_001263	DR_2633 >>>	63	2644147	2644257 >>>	110	6 >>>	DR_2634	candidate	277	1.40E-08	2

Supplementary Table 2. Probes for Northern blotting analysis

	Reverse	Forward	Secondary probe
Dsr1	TTT CCT TCA GAG TAT TAC TCC A	T GGA GTA ATA CTC TGA AGG AAA	CAA ACG GTG CCC CTT TTC CTT CAG AGT A
Dsr2	CTC CTG GGA GTG TGA AAT CAA CA	TG TTG ATT TCA CAC TCC CAG GAG	TGT GAA ATC AAC AGA ATC CGC TGC CCA
Dsr3	CCC AAA GAC AAG AGA CGG AAA TT	AAT TTC CGT CTC TTG TCT TTG GG	CCT GTC GAT GAA TTT CCG TCT CTT GTC TTT
Dsr4	CCC CTT CCA GAC TTC TTT TCG T	A CGA AAA GAA GTC TGG AAG GGG	
Dsr5	CCG CCG AGC TTT GAG ACC CCC T	A GGG GGT CTC AAA GCT CGG CGG	TGA AGT TCT TCT TCT AAG CTC CGC CGA GCT TT
Dsr6	TGG CAA CAG GCG TCC CAG ACA	GCC TGA TCA TCT GTC TGG GAC	AGC CTG ATC ATC TGT CTG GGA CGC CTG TT
Dsr7	CTG CGC CAG CTA AAG ACA CCG A	TCG GTG TCT TTA GCT GGC GCA G	GGC CCT TCA GCG TCG GTG TCT TTA GCT
Dsr8	GCG AAG TAA GAT TTT CAC TGA CAA G	CTT GTC AGT GAA AAT CTT ACT TCG C	
Dsr9	GTG ATT CAC GTT CCG GCA AAG AA	TT CTT TGC CGG AAC GTG AAT CAC	GCC ATG TAT ACT TGT GAT TCA CGT TCC GGC
Dsr10	CAA AAA TCC CCT CCC ACG ACG GGG AGG G	CAA AAC CCC CTC CCC GTC GTG GGA GGG GAT TTT TG	
Dsr11	GAA CAG CCG TTG CCT GAT CCG ACT	AGT CGG ATC AGG CAA CGG CTG TTC	CCT GAT CCG ACT GAC GAC TGA GGA GTG ACA AC
Dsr12	CAT GAA CCA GTA CGA TCT CAA	TTG AGA TCG TAC TGG TTC ATG	CGC TGA TGT TCG GGT TCA GGA TCA GGT T
Dsr13	ACT CCA CGA GTA TCA GGG CAA	GCA CTT CCT TGC CCT GAT ACT C	
Dsr14	CCG AAG TTC AGG ACA TTG AAG TGA	CCT CAC TTC AAT GTC CTG AAC	
Dsr15	GCA GTC AGC ATC AGT GTC TTT	CCT AAG ATG TGA CTC GCT ATG AA	
Dsr16	CGC ATG GCC TCT TTT CCT GCC	GGC AGG AAA AGA GGC CAT GCG	
Dsr17	CAT CAC AAG GTC GGG CCA TCA	TGA TGG CCC GAC CTT GTG ATG	AAT CTT GAT GGC CCG ACC TTG TGA TGA TTG C
Dsr18	ATT CAG TCT TTG TCA AGG CTA TGC	GCA TAG CCT TGA CAA AGA CTG AAT	CGC GAG TTG CTT CTG TGC TGT CCG CCG AAT
Dsr19	TTA TCC ACA GTG AAA CGT AGA CCT	AGG TCT ACG TTT CAC TGT GGA TAA	AAC GCT GAA CAG TCA TGC TTG AAA ATC CGC TT
Dsr20	GCG GGG AAA CTC CTG GTC GCG	CGC GAC CAG GAG TTT CCC CGC	TCC TGG TCG CGC CTG ACC TGC TTT TTC GGC A
Dsr21	CTG TGT TCA CGC TTC GGG CC	GGC CCG AAG CGT GAA CAC AG	AGT GCC CGG CCC GAA GCG TGA ACA CAG T
Dsr22	CGG GAA TGT TCG CAA AGT CTT CGT C	GAC GAA GAC TTT GCG AAC ATT CCC G	
Dsr23	CTC AGA AAC CTC GGG TTC AGT	TGC CGA CAC TGA ACC CGA GGT	
Dsr24	CCTGACCTTTAGTGTCTCGCGCTTGGTAGGG	TAC CAA GCG CGA GAC ACT AAA GGT C	
Dsr25	GGT GTA GAC TTC AGG CAC CCA AAC ATC TCT	AGA GAT GTT TGG GTG CCT GAA GTC TAC A	
Dsr26	GGATACGAACTGCCCGCTAGTGACAGTGATCGT	ACGATCACTGTCACTAGGCGGGCAGTTCGTATCC	
Dsr27	CTT GAG GCT TCT ATG ATC AAT TTC ATC GTC AGA CGA	TCG TCT GAC GAT GAA ATT GAT CAT AGA AGC CTC AAG	TGA GCT ACA CCT TCT TCC GCA GCA ACC T
Dsr28	GAC CTT TAG ACC CTC TTC CCT TAG AAC TT	AAG TTC TAA GGG AAG AGG GTC TAA AGG TC	CCT TTA GAC CCT CTT CCC TTA GAA CTT TTC C
Dsr29	GTACAAGTTAGCGTGTGAGGCTCAGATTTTCCACC	GGTGGAAAATCTGAGCCTCACACGCTAACTTGAC	
Dsr30	AGA AAA CAG TTC TCG AAT GGT CAG TGG CGC AAG CTG CT	GGA CGA GGG CTG TCA GGT GCA CAC	TCC GAA CAC GCT GGT CCT AAG CCA TGC ACT
Dsr31	AAC AGT TCT CGA ATG GTC AGT GGC GCA A	GGT TGA CGC TGA CCG GGA CAT AAA	AAA GGC CAG CAG CTT GCG CCA CTG ACC ATT
Dsr32	ATG AGG GCA GTC GAG ATG TAT TCC ATT GGG GT	CCC AAT GGA ATA CAT CTC GAC TGC CCT CAT	
Dsr33	TTT ATC CAG AGT CGG CGC AGG GAC C	GGT CCC TGC GCC GAC TCT GGA TAA A	TGC ACG TGC CAG GGC CGA ACA CCA ACT CT
Dsr34	CGA CCC TCA ACC ACG GCC TGA CCA GCA T	ATG CTG GTC AGG CCG TGG TTG AGG GTC G	
Dsr35	GGT TGT TCT TGT TGA TTT CGG TCA TC	GA TGA CCG AAA TCA ACA AGA ACA ACC	AGG CGT GCA GAT CTG GAT CAA CAA TTG GAC T
Dsr36	TAA GAC CTG CTT AGA AGC TT	CTT CTA AGC AGG TCT TAG CG	
Dsr37	GCC GCG ATT CCA GAG TTC GGA AGA T	GCC CAT CTT CCG AAC TCT GGA ATC G	
Dsr38	CTG AGC GCA ATG CCT GAA CGT GT	ACA CGT TCA GGC ATT GCG CTC AG	
Dsr39	TTG GTG GTG AGG TCG AGG TCA GAC GAA TAC A	T GTA TTC GTC TGA CCT CGA CCT CAC CAC CAA	TCA TGA GCT TCC CAT GAG GTC ATG GCC T
Dsr40	AAG TGT GGC AAC CTA ATC GGC TTA CC	GGT AAG CCG ATT AGG TTG CCA CAC TT	AAG CCG ATT AGG TTG CCA CAC TTG AGG CAT G
Dsr41	CAC CTC ACA CAA GCG AGA CGA CGA CAT GAA	TTC ATG TCG TCG TCT CGC TTG TGT GAG GTG	
Dsr42	CGCCTCGGACTCGAACCAGAACCC	GGGTTCTCGGTTTCGAGTCCGAGGCG	

Dsr43	GCGAGTGAGAACAGAATTTGATGTGTTG	TGG GTT GAG GGT TTC GCT GGA GGT	
Dsr44	CAC AGC TTT CGC CTG AAT GCC CGT CAC TC	CGT TTG CTG GTC ACC GGG GAA CTT CTC C	TAC ACT CTC AGA ACT TGA CTC TCA GGA CTT GCC AT
Dsr45	CAA TCC ACT CTG ACA GGC CCC TGA CAG	CTG TCA GGG GCC TGT CAG AGT GGA TTG	
Dsr46	AAA GGA GTT ACG CAC GCT CTG GCC GTC CA	TGG ACG GCC AGA GCG TGC GTA ACT CCT TT	ATC ACG TCA AAG GAG TTA CGC ACG CTC TGG CCG T
Dsr47	CGC TCT GAG TCA AAG ACT CCG GCA GGC AGA A	TTC TGC CTG CCG GAG TCT TTG ACT CAG AGC G	
Dsr48	TGA ATC TGG CGA GCT TCC AGT AAC CGA CAG GCC A	TGG CCT GTC GGT TAC TGG AAG CTC GCC AGA TTC A	TCT CTG TTT TTG GCC TGT CGG TTA CTG GAA GCT
Dsr49	GGG TCT TTC TAT GGG CTA CAG CTC AG	CTG AGC TGT AGC CCA TAG AAA GAC CC	
Dsr50	CACAGTCGGCTACGTCGCCATGAAGGC	GCCTTCATGGCGACGTAGCCGACTGTG	
Dsr51	GCA GCC ACT CCA GAA ATT CAC TCA GAC CTT TCA	TGA AAG GTC TGA GTG AAT TTC TGG AGT GGC TGC	
Dsr52	CTT GTT GAG AAA GTT CTC AAA GAG CCG TTG GTC	GAC CAA CGG CTC TTT GAG AAC TTT CTC AAC AAG	
Dsr53	CGA ATA CTG CAC CTG AAC TTG TTC ACC ACA GAG GAG GTC	GAC CTC CTC TGT GGT GAA CAA GTT CAG GTG CAG TAT TCG	
Dsr54	GCGAGTCTGACCGGAGACTGTCC	GGACAGTCTCCGGTCAGACTCGC	
Gsr1	TGT TCT TGC TGG TGG GCT TCG TGG CGG TGA	TCA CCG CCA CGA AGC CCA CCA GCA AGA ACA	
Gsr2	CCA TGA AGG GCC TGC GCG AGT TGA TTG ATT G	CAA TCA ATC AAC TCG CGC AGG CCC TTC ATG G	
Gsr3	TCG CCC TGC CCC ACT TGA CCA AGC GCA GAT T	AAT CTG CGC TTG GTC AAG TGG GGC AGG GCG A	
Gsr4	AA AAA AGC CCC AGC CGG AGC CAG GGC	GCC CTG GCT CCG GCT GGG GCT TTT TT	
Gsr5	G CGG CGA CCA GCC GAA TCA CGT CGA AGG AAT TGC GAA	TTC GCA ATT CCT TCG ACG TGA TTC GGC TGG TCG CCG C	
Gsr6	A GCG GAG GGC CAG TGT TGG CGC CTC	GAG GCG CCA ACA CTG GCC CTC CGC T	
Gsr7	AAG CAG CGG CAC CCG GAA ATC ATC C	GGA TGA TTT CCG GGT GCC GCT GCT T	
Gsr8	CTC CTG CCC AAC CCA TCA TGG TTG GCC ATA G	CTATGGCCAACCATGATGGGTTGGGCAGGAG	
Gsr9	AGT TAT CCA CAG TGA AAC GCG TGC CTG TGG ATA ACT	AGTTATCCACAGGCACGCGTTTCACTGTGGATAACT	
Gsr10	TAG TGT CTC GTG CTT GGT AGG GCC GAG GCG A	TCGCCTCGGCCCTACCAAGCACGAGACACTA	

Supplementary Table 3 RT-PCR Primers

Dsr1_Left GTAGGCAGTGTCCACCCTTG
Dsr1_Right GTTTGGTGCCCTTCTTTTT
Dsr1_Gene_left ACGCCGACTACGTCAAGAAC
Dsr1_Gene_Right CGTCGTGCGGAAGTAGAACT
Dsr2_Left GCAGCGGATTCTGTTGATTT
Dsr2_Right GGGTAACTGTTTGC GGTTCTC
Dsr3_Left TATCAACGCGACAGGAAAAA
Dsr3_Right GACGGAAATTCATCGACAGG
Dsr5_Left GCTCGGCGGAGCTTAGAA
Dsr5_Right CCGGCCTGAAGTTCTTCTTC
Dsr6_Left CCTCAAGCGACCATCCTG
Dsr6_Right GTGCAAGACCCGACAGTG
Dsr11_Left CTGACAAAACAGTGGCTTCC
Dsr11_Right TGATCCGACTGACGACTGAG
Dsr11_Gene_left GGCTACCTCGCCTACAAGG
Dsr11_Gene_right GTCGCCTTGA ACTTCTGGAG
Dsr12_Left ATGTTTCGGTTTCAGGATCAG
Dsr12_Right GCACCGACAGCAACTATG
Dsr12_Gene_left GGCCTTCTTGGTCTTCCACT
Dsr12_Gene_Right ATCCTGAACCCGAACATCAG
Dsr17_Left CTCCAGACGAAAGCCTCATC
Dsr17_Right CCATCAAGATTCACCGCTCT
Dsr18_Left GGCTTTTTTCGTTTTGGGTTT
Dsr18_Right GACGTCAGGCCGATTATTCA
Dsr18_Gene_left CGAGCACCTCGAACAAGAG
Dsr18_Gene_Right GATCGGAAGCTCGATTTTGA
Dsr19_Left TTTGAAGCGGATTTTCAAGC
Dsr19_Right AAAACGCTGAACAGTCATGC
Dsr19_Gene_left TTTTCATGGGGCAGTCACTC
Dsr19_Gene_right GGCCTGTGGATTCTTGAGG
Dsr20_Left ACCTTCCCTGCCGAAAAAG
Dsr20_Right GCGGGGAAACTCCTGGTC
Dsr27_Left CATCTGCTGTTGGTCCCTTT
Dsr27_Right GGCGTGAGCTACACCTTCTT
Dsr28_Left TGATGCTCCTTCGGAAAAGT
Dsr28_Right CCTTTAGACCCTCTTCCCTTAGA
Dsr28_Gene_left TCGGCTTCGTCTAGAACTT
Dsr28_Gene_Right GTGCAGAAGAAGCTCGATCC
Dsr30_Left CTGGTCCTAAGCCATGCACT
Dsr30_Right GACCGTATGACTCCCAGACC
Dsr31_Left GCCACTGACCATTTCGAGAAC
Dsr31_Right CATAAGCCCCCAGAAAACAG
Dsr33_Left CTGCGCCGACTCTGGATA
Dsr33_Right ACGTGCAGGGTCACCTTTAT
Dsr33_Gene_left GTCAGGTAGAGGCCGAACAC
Dsr33_Gene_right ACGATTCTGGAGTGGTACGC
Dsr35_Left CGAACCGTTTTCGTCTGAAT
Dsr35_Right GCGTGCTTCAGTGTTTTGTC
Dsr35_Gene_left TGAGGAGACGGATGACATTG
Dsr35_Gene_right ATTGGGGAAAGTCGATGATG
Dsr39_Left TGACCTCATGGGAAGCTCAT
Dsr39_Right GTCAGGACGTGCAGGAAGAT
Dsr40_Left CAAAATGCTCAGCAATGGAA
Dsr40_Right TGGCAACCTAATCGGCTTAC

Dsr40_Gene_left ATCGCGTGTCTCTCTGCTTT
Dsr40_Gene_Right GCTTGAAGCGACCCTCTCT
Dsr44_Left TGGCAAGTCCTGAGAGTCAA
Dsr44_Right TGGAGTAGTTTCGGTGCTGTT
Dsr46_Left CAGAGCGTGCCTAACTCCTT
Dsr46_Right AGCCGGATCACGTCAAAG
Dsr46_Gene_left GAGATCAACACCGTGGAGGT
Dsr46_Gene_Right CGGTCTTTTCGAGGTCGTC
Dsr48_Left CGCCTCTGCTCTCTCTGTTT
Dsr48_Right ATCTGGCGAGCTTCCAGTAA
Dsr48_Gene_left ATTCAGCGCCACGTTGTAG
Dsr48_Gene_right CCCGAGAGTGTCAAGGTGTT
Dsr18_gene_left_new CGAGCACCTCGAACAAGAG
Dsr18_gene_right_new GATCGGAAGCTCGATTTTGA
Dsr19_gene_left_new CCGGGTATTATCCCGTCTTG
Dsr19_gene_right_new AGCGTTTTACGGCGTCTATG
Dsr46_Gene_left_new TTACAAGCGTGACCTGATCG
Dsr46_Gene_right_new CGGTCTTTTCGAGGTCGTC
Dsr48_Gene_left_new GTCGGTGGCCTGAAAGTAGA
Dsr48_Gene_right_new GCGCCTACTTGATTTCCGTA
Dsr8_new AGGCCAGGGCTTGTCAGT
Dsr13_new GGGAGCCGCAGATGTTTCATTT
Dsr10_new GGG GTT TTG ACG TTC AGC
Dsr37_new AAA TGA ACA TCT GCG GCT CCC
Dsr50_new AGA TCA CCC TCA ACT TGA CCC
Dsr51_new GGG AAG GAT TGT CAG AAA AG
Dsr52_new GAC CAA CGG CTC TTT GAG A
Dsr8_left GTAGCGCTTCGAGACTTCGT
Dsr8_right TTCTGGAACGTGGTGAAGT
Dsr8_gene_left GCGTCTTCGAACTTCTGCTT
Dsr8_gene_right CGTCGAACAACTCATTACAGC
Dsr10_left1 TGC AGG GTC ACC TTT ATC CA
Dsr10_left2 ATAAAGGAAGGCGGGTCTT
Dsr10_right TGGACGAAAAGAAGTCTGGAA
Dsr10_dgene_left GGTCGTCCAGATTGACGTG
Dsr10_dgene_right GACCTGACGCTGCTTATCGT
Dsr10_ugene_left GTAATGCACGCCGAGGTAAT
Dsr10_ugene_right GAGCCAGGATTTTCCTTTCC
Dsr3_left_new, GCCTCTTTCTGTGATGAA
Dsr3_left_new, CTGCCCAAAGACAAGAGACG
Dsr5_left_new, CGGCGGAGCTTAGAAGAAG
Dsr5_right_new, GCC GAG GTT AAA GCC CTT
Dsr7_left_new, CTATAGGGACGGATGCCAAA
Dsr7_right_new, TAAAGACACCGACGCTGAAG
Dsr9_left_new, TTG GAC AGG GGT TCT TTG C
Dsr9_right_new, GATTCACGTTCCGGCAAA
Dsr21_left_new, ACAGGGGACTCGCCTTC
Dsr21_right_new, TTG TCG ATG CGC CCA CAG T
Dsr48_left_new, AAT GCT GGC GCC TCT GCT
Dsr48_right_new, AGCTTCCAGTAACCGACAGG

Dsr13_left, GGAATGACCCCCGGTGGGTGTG
Dsr13_right, TTT ATC GGG ACA AAT GAA CAT CT
Dsr13_dgene_left1, GGTCGCTGTTCTTTTCGTTT

Dsr13_dgene_left2, ATGCCACCGAAGATGTTGAT
Dsr13_dgene_right1, ATTGCGCTGGATACCAAGTT
Dsr13_dgene_right2, CTACGAAGCGCGTGAAGTC
Dsr37_left, GGTATCCCGCCCATCTTC
Dsr37_right, GCCGCGATTCCAGAGTTC
Dsr37_Dgene_left1, CGGCACCACTGAACTCATT
Dsr37_Dgene_right1, GCCACGAGGTCATTTTCAG
Dsr37_Dgene_left2, ATCGAACCGCAGGAGAAGTA
Dsr37_Dgene_right2, CACTCCTCGTCCACCCACT
Dsr37_Ugene_left1, ACCTGACCTTCGACCTGATG
Dsr37_Ugene_right1, ACAAACTCGCCCTTCTTGAC
Dsr37_Ugene_left2, CGAGCTGCACCTGAGTATCC
Dsr37_Ugene_right2, TGGGTCATGCTCAGAAACTG
Dsr50_left1, GTGATCTCGGCGTCTTTCTC
Dsr50_left2, GTGATCTCGGCGTCTTTCTC
Dsr50_right1, TCA AGT TGA GGG TGA TCT C
Dsr50_right2, GCATGATCAAGTACCGTAAGCA
Dsr50_Dgene_left1, GGAAGTTGACGTTACGTTG
Dsr50_Dgene_left2, CCACGTTGATCCAGTGACTC
Dsr50_Dgene_right1, GACGACCTGACCCTTCAGAG
Dsr50_Dgene_right2, CCACGTTGATCCAGTGACTC
Dsr51_left1, TGCCTTCTTTTCTGACAATCC
Dsr51_left2, ACGCCGTTAATTGCCTTCTT
Dsr51_right1, AAGACTTCAGGGGTGGGAAG
Dsr51_right2, GGTGGGAAGGATTGTCAGAA
Dsr51_Ugene_left1, TGCTCGGTGTTTTGTACTCG
Dsr51_Ugene_left2, AGAAGACCAGCTCGCTCAAG
Dsr51_Ugene_right1, CCAGACTCAGGAAGGTCAGG
Dsr51_Ugene_left2, AAGATGGCACAGCTTTTTGG
Dsr52_left1, GACCAACGGCTCTTTGAGAA
Dsr52_left2, CAGGGCGACCAACGGCTCTTTGA
Dsr52_right1, GCCGCTCTTTGTTGAGAAA
Dsr52_right2, GAA GCC TCC CCA GGG AGC
Dsr52_Ugene_left1, AGGTCATGGCGTTCAAGAGT
Dsr52_Ugene_left2, ACCAGAACACCGGCAAGA
Dsr52_Ugene_right1, CGGGAGCATGAGTTTCATC
Dsr52_Ugene_right2, GAC GAA ATT CGC GGC AAG G

Supplementary Table 4. Probes for 5' RACE

5'RACE_C1	CAAGCAGAAGACGGCATACTGACTC CAG AAC TTT GGA AAC GAC GC
5'RACE_C2	CAAGCAGAAGACGGCATACTGAGTC TCC TGG GAG TGT GAA ATC AAC A
5'RACE_C3	CAAGCAGAAGACGGCATACTGACCG TCT CTT GTC TTT GGG CAG T
5'RACE_C4	CAAGCAGAAGACGGCATACTGAGTC CCC TTC CAG ACT TCT TTT CGT
5'RACE_C5	CAAGCAGAAGACGGCATACTGACCG AGC TTT GAG ACC CCC T
5'RACE_C6	CAAGCAGAAGACGGCATACTGACAG CCT GAT CAT CTG TCT GGG AC
5'RACE_C7	CAAGCAGAAGACGGCATACTGAGGT GTC TTT AGC TGG CGC A
5'RACE_C9	CAAGCAGAAGACGGCATACTGAGTG ATT CAC GTT CCG GCA AAG AA
5'RACE_C11	CAAGCAGAAGACGGCATACTGAAAC AGC CGT TGC CTG ATC C
5'RACE_C12	CAAGCAGAAGACGGCATACTGAGGA TCA GGT TGA GAT CGT ACT GGT T
5'RACE_C14	CAAGCAGAAGACGGCATACTGAGGG CCT CAC TTC AAT GTC CTG AA
5'RACE_C16	CAAGCAGAAGACGGCATACTGACGC ATG GCC TCT TTT CCT GC
5'RACE_C17	CAAGCAGAAGACGGCATACTGATGA TGG CCC GAC CTT GTG ATG
5'RACE_C18	CAAGCAGAAGACGGCATACTGAGGG GTA TTC AGT CTT TGT CAA GGC T
5'RACE_C19	CAAGCAGAAGACGGCATACTGACAC AGT GAA ACG TAG ACC TGT GGA
5'RACE_C20	CAAGCAGAAGACGGCATACTGAAAA CTC CTG GTC GCG CCT
5'RACE_C21	CAAGCAGAAGACGGCATACTGAGCC CGA AGC GTG AAC ACA
5'RACE_C26	CAAGCAGAAGACGGCATACTGAAAC TGC CCG CCT AGT GAC A
5'RACE_C27	CAAGCAGAAGACGGCATACTGATCA TCG TCA GAC GAC TGA TCC AGA T
5'RACE_C29	CAAGCAGAAGACGGCATACTGATAC AAG TTA GCG TGT GAG GCT CAG A
5'RACE_C35	CAAGCAGAAGACGGCATACTGACGG TTC GTG AAT AGG TTG TTC TTG T
5'RACE_C39	CAAGCAGAAGACGGCATACTGAGGT GGT GAG GTC GAG GTC A
5'RACE_C42	CAAGCAGAAGACGGCATACTGACCT CGG ACT CGA ACC GAG AA
5'RACE_C1B	CAAGCAGAAGACGGCATACTGGA GGT GCC CCT TTT CCT TCA GAG TAT T
5'RACE_C2A	CAAGCAGAAGACGGCATACTGGA AAA TCA ACA GAA TCC GCT GCC CA
5'RACE_C4B	CAAGCAGAAGACGGCATACTGGA GGT TCC AAC GGA CGG CTC A
5'RACE_C4A	CAAGCAGAAGACGGCATACTGGA GAA GGG GAC GCC CGT TTT
5'RACE_C9A	CAAGCAGAAGACGGCATACTGGA TCC AAC CCA TCC TGG TTG GC
5'RACE_C16B	CAAGCAGAAGACGGCATACTGGA GCC GTA TAA TAC CCG ATT CCG GAC
5'RACE_C19B	CAAGCAGAAGACGGCATACTGGA GAA CAG TCA TGC TTG AAA ATC CGC T
5'RACE_C20A	CAAGCAGAAGACGGCATACTGGA GGC AGG GAA GGT GAG GAA AGT
5'RACE_C26A	CAAGCAGAAGACGGCATACTGGA GAT CGT CCG GTC TGG GAG AA
5'RACE_C7M	CAAGCAGAAGACGGCATACTGGA CAG CTA AAG ACA CCG ACG CTG AA

5'RACE_C17M	CAAGCAGAAGACGGCATACGA CAA TCA TCA CAA GGT CGG GCC AT
5'RACE_C21M	CAAGCAGAAGACGGCATACGA CTG TGT TCA CGC TTC GGG C
5'RACE_C39B	CAAGCAGAAGACGGCATACGA GTT CGC GCA TGA GGG CTT T
5'RACE_Univ	AATGATACGGCGACCACCGCACTGCGTTTGCTGGCTTTGATG

Supplementary Table 5. Potential sRNAs identified with deep sequencing and computational prediction

Name	Left end Coordinate	Right end Coordinate	Upstream Gene	Direction	Downstream Gene	Direction
Dsr1	2062149	2062238	DR_2049	<<<	DR_2050	elongatifactor Tu <<<
Dsr2	139794	139847	DR_0140	>>>	DR_0141	pseudogene >>>
Dsr3	1628175	1628269	DR_1604	>>>	DR_1605	response regulator >>>
Dsr4	1363180	1363292	DR_1355	>>>	DR_1356	phosphatidylglycerophosphatase B-like protein ABC transporter ATP-binding protein >>>
Dsr5	1133930	1134008	DR_1124	>>>	DR_1125	SLH family protein hypothetical protein >>>
Dsr6	904902	905055	DR_0896	>>>	DR_0897	ribosomal large subunit hypothetical protein <<<
Dsr7	1678888	1678979	DR_1654	>>>	DR_1655	hypothetical protein substrate-binding protein >>>
Dsr8	1286346	1286483	DR_1279	>>>	DR_1280	Mn family superoxide dismutase hypothetical protein >>>
Dsr9	927150	927218	rpoB D	<<<	DR_0913	NA-directed RNA polymerase subunit hypothetical protein >>>
Dsr10	1193477	1193597	DR_1184	>>>	DR_1185	MutT/nudix family protein S-layer-like array-like protein <<<
Dsr11	2378503	2378628	DR_2376	>>>	DR_2377	TetR family transcriptional regulator hypothetical protein <<<
Dsr12	99958	100135	DR_0097	<<<	DR_0098	hypothetical protein 30S ribosomal protein S6 succinyl-CoA synthetase subunit beta >>>
Dsr13	1253227	1253295	DR_1246	<<<	DR_1247	proline dipeptidase aat leu cyl/phenylalanyl-tRNA--protein transferase >>>
Dsr14	1737610	1737683	DR_1712	<<<	aat leu	extracellular solute-binding protein serine/threonine protein kinase-like protein <<<
Dsr15	1795976	1796045	DR_1768	<<<	DR_1769	hypothetical protein N-acetylmuramoyl-L-alanine protein >>>
Dsr16	2570268	2570308	DR_2567	>>>	DR_2568	amidase-like protein amidase-like protein >>>
Dsr17	709900	709987	DR_0692	>>>	DR_0694	nitrogen regulatory protein P-II hypothetical protein >>>
Dsr18	2615746	2615826	DR_2606	>>>	DR_2607	primosomal protein n', putative protein D/E <<<
Dsr19	121873	121947	DR_0122	>>>	DR_0123	hypothetical protein isomerase <<<
Dsr20	904568	904621	DR_0896	>>>	DR_0897	ribosomal large subunit hypothetical protein <<<
Dsr21	2338982	2339068	DR_2340	>>>	DR_2341	recombinase A birA bifunctional protein <<<
Dsr22	354490	354549	DR_0353	<<<	DR_0354	ribonuclease exodeoxyribonuclease III <<<
Dsr23	355330	355425	DR_0353	<<<	DR_0354	ribonuclease exodeoxyribonuclease III <<<
Dsr24	175430	175497	DR_0173	<<<	DR_0174	peptide chain release factor 2 50S ribosomal protein L13 >>>
Dsr25	391550	391605	DR_0392	<<<	DR_0393	hypothetical protein elongatifactor G >>>
Dsr26	2119087	2119175	DR_2109	>>>	DR_2110	ribosomal protein S14 30S ribosomal protein S8 >>>
Dsr27	364745	364815	DR_0363	>>>	DR_0364	peptide ABC transporter periplasmic peptide-binding protein peptide ABC transporter permease >>>
Dsr28	714670	714735	DR_0698	>>>	DR_0700	v-type ATP synthase subunit C V-type ATP synthase subunit A >>>

Dsr29	989450	989575	DR_0971	electrtransfer flavoprotein subunit	<<<	DR_0972	hypothetical protein	>>>
Dsr30	1948885	1949103	DR_1927	transposase	<<<	DR_1928	glycerol kinase	<<<
Dsr31	1996601	1996689	DR_1974	ATP-dependent protease LA	>>>	DR_1975	leucyl/phenylalanyl-tRNA--protein transferase	<<<
Dsr32	863930	863995	DR_0852	hypothetical protein	>>>	DR_0853	gliding motility protein	<<<
Dsr33	1363038	1363086	DR_1355	phosphatidylglycerophosphatase B-like protein	>>>	DR_1356	ABC transporter ATP-binding protein	>>>
Dsr34	2086115	2086205	DR_2070	membrane lipoprotein	>>>	DR_2071	phosphoglucosamine mutase	<<<
Dsr35	2208220	2208508	DR_2209	SudD-like protein	<<<	DR_2210	hypothetical protein	>>>
Dsr36	1077622	1077690	DR_1066	hypothetical protein	<<<	DR_1067	hypothetical protein	<<<
Dsr37	1207864	1207917	DR_1198	GTP-binding elongatifactor family	<<<	DR_1199	protease I	<<<
Dsr38	136856	137056	DR_0138	hypothetical protein	>>>	DR_0139	GTP-binding protein HflX	>>>
Dsr39	1028950	1029203	DR_1016	trmE tRNA modificatiGTPase	>>>	DR_1017	rRNA methylase	>>>
Dsr40	1538050	1538245	DR_1522	pyrroline-5-carboxylate reductase	>>>	DR_1523	putative transposase	>>>
Dsr41	428347	428441	DR_0429	cytochrome-like protein	>>>	DR_0430	rtcB protein	>>>
Dsr42	214696	214774	DR_0213	hypothetical protein	<<<	DR_0214	hypothetical protein	>>>
Dsr43	1646233	1646390	DR_1624	RNA helicase	<<<	DR_1625	amidase	>>>
Dsr44	2598170	2598310	DR_2590	irABC transporter ATP-binding	>>>	DR_2591	hypothetical protein	<<<
Dsr45	218420	218572	DR_0217	thiosulfate sulfurtransferase deoxyguanosine	>>>	DR_0218	hypothetical protein	>>>
Dsr46	301054	301123	DR_0299	kinase/deoxyadenosine kinase	<<<	DR_0300	serine protease Do, putative	<<<
Dsr47	302481	302680	DR_0301	hypothetical protein	<<<	DR_0302	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)	>>>
Dsr48	454581	454688	DR_0459	hypothetical protein	>>>	DR_0460	acetyl-CoA synthase	<<<
Dsr49	918726	918800	DR_0900	cell wall protein, putative	>>>	DR_0911	DNA-directed RNA polymerase, beta subunit	<<<
Dsr50	1688729	1688850	DR_1662	L-threonine 3-dehydrogenase	<<<	DR_1663	hypothetical protein	>>>
Dsr51	1866869	1867060	DR_1838	GTP pyrophosphokinase	<<<	DR_1839	peptidyl-prolyl cis-trans isomerase, FKBP-type	>>>
Dsr52	2025845	2025918	DR_2005	50S ribosomal protein L35	<<<	DR_2006	hypothetical protein	<<<
Dsr53	2059450	2059620	DR_2044	50S ribosomal protein L10	<<<	DR_2045	50S ribosomal protein L1	<<<
Dsr54	2251638	2251754	DR_225	5 hypothetical protein	<<<	DR_2256	transketolase	>>>
Dsr55	5989	6207	DR_0005	hypothetical protein	forward	DR_0006	metal-dependent hydrolase	reverse
Dsr56	12749	12805	DR_0011	hypothetical protein	reverse	DR_0012	chromosome partitioning protein	reverse
Dsr57	13292	13339	DR_0011	hypothetical protein	reverse	DR_0012	chromosome partitioning protein	reverse
Dsr58	97386	97487	DR_0095	ABC transporter ATP-binding protein	reverse	DR_0096	ABC transporter ATP-binding protein	reverse
Dsr59	100775	101136	DR_0099	single-stranded DNA-binding protein	forward	ssb	single-stranded DNA-binding protein	forward

Dsr60	101394	101444 ssb	single-stranded DNA-binding protein	forward	rpsR	30S ribosomal protein S18	forward
Dsr61	103814	103865 DR_0104	hypothetical protein	forward	DR_0105	hypothetical protein	forward
Dsr62	119544	119592 DR_0120	smf protein	reverse	DR_0121	hypothetical protein	reverse
Dsr63	125342	125408 DR_0127	hypothetical protein	reverse	DR_0128	grpE protein	reverse
Dsr64	150550	150641 DR_0149	MutT/nudix family protein	reverse	DR_0150	hypothetical protein	reverse
Dsr65	202798	202851 recR	recombinatiprotein RecR	reverse	DR_0199	hypothetical protein	reverse
Dsr66	231037	231096 DR_0231	RNA methyltransferase	forward	DR_0232	hypothetical protein	forward
Dsr67	253605	253664 DR_0255	putative transposase deoxyguanosine	reverse	DR_r03	rRNA-5S ribosomal RNA	forward
Dsr68	301054	301123 DR_0299	kinase/deoxyadenosine kinase	reverse	DR_0300	serine protease Do, putative glucosamine-fructose-6-phosphate	reverse
Dsr69	302481	302531 DR_0301	hypothetical protein	reverse	DR_0302	aminotransferase	forward
Dsr70	308096	308175 DR_0306	30S ribosomal protein S7	forward	DR_0307	elongatifactor G	forward
Dsr71	330779	330905 DR_0334	lipase	reverse	DR_0335	ATP-dependent RNA helicase	forward
Dsr72	334219	334285 DR_0336	fatty-acid-CoA ligase	reverse	DR_0337	hypothetical protein	reverse
Dsr73	339425	339523 DR_t09	tRNA-Leu	reverse	rpsO	30S ribosomal protein S15 cytochrome complex iron-sulfur subunit	forward
Dsr74	339761	339820 rpsO	30S ribosomal protein S15 cytochrome c-type biogenesis heme	forward	DR_0342		reverse
Dsr75	346268	346327 DR_0348	exporter protein C	reverse	DR_0349	ATP-dependent protease LA	forward
Dsr76	348836	348902 DR_0349	ATP-dependent protease LA	forward	DR_0350	hypothetical protein	reverse
Dsr77	351490	351555 DR_0351	hypothetical protein	reverse	DR_0352	hypothetical protein	reverse
Dsr78	355607	355720 DR_0353	ribonuclease	reverse	DR_0354	exodeoxyribonuclease III	reverse
Dsr79	357700	357752 DR_0356	BioC methyltransferase	reverse	DR_0357	hypothetical protein peptide ABC transporter periplasmic peptide-bonding protein	reverse
Dsr80	362697	362744 ddl	D-alanyl-alanine synthetase A	reverse	DR_0363		forward
Dsr81	391149	391251 DR_0392	hypothetical protein	reverse	DR_0393	elongatifactor G alpha-dextran endo-1,6,-alpha glucosidase	forward
Dsr82	407179	407235 DR_0404	hypothetical protein	forward	DR_0405		reverse
Dsr83	412525	412604 DR_0408	response regulator	reverse	DR_0409	hypothetical protein	forward
Dsr84	421579	421633 DR_0420	ATP-dependent helicase	forward	DR_0421	hypothetical protein	reverse
Dsr85	454581	454688 DR_0459	hypothetical protein	forward	DR_0460	acetyl-CoA synthase	reverse
Dsr86	456821	456872 DR_0460	acetyl-CoA synthase	reverse	DR_0461	pantothenate kinase	forward
Dsr87	484405	484477 DR_0480	C32 tRNA thiolase	forward	DR_0481	hypothetical protein	reverse
Dsr88	520109	520164 DR_0513	integrase	reverse	DR_0514	hypothetical protein	reverse
Dsr89	534853	534907 DR_0532	hypothetical protein	reverse	DR_0533	hypothetical protein	reverse
Dsr90	547706	547774 DR_0540	hypothetical protein	reverse	DR_0541	hypothetical protein	reverse
Dsr91	551572	551627 DR_0546	hypothetical protein	reverse	DR_0547	hypothetical protein	forward

Dsr92	560475	560548 DR_0554	hypothetical protein	forward	DR_0555	glutamate-1-semialdehyde aminotransferase	forward
Dsr93	567642	567740 DR_0560	hypothetical protein	reverse	DR_0561	maltose ABC transporter	
Dsr94	574257	574479 DR_0566	hypothetical protein	forward	DR_0567	periplasmic maltose-binding protein	forward
Dsr95	611756	611822 DR_0599	aminoglycoside N3-acetyltransferase	reverse	DR_0600	threonine hydratase	reverse
Dsr96	611848	611911 DR_0599	aminoglycoside N3-acetyltransferase	reverse	DR_0600	hypothetical protein	reverse
Dsr97	619869	619939 groEL	chaperonin GroEL	forward	DR_0608	hypothetical protein	forward
Dsr98	624856	624939 DR_0612	arginine utilizatiprotein RocB	forward	DR_0613	hypothetical protein	reverse
Dsr99	646243	646302 DR_0630	cell divisiprotein FtsA	forward	DR_0631	cell divisiprotein FtsZ	forward
Dsr100	646337	646398 DR_0630	cell divisiprotein FtsA	forward	DR_0631	cell divisiprotein FtsZ	forward
Dsr101	647418	647514 DR_0631	cell divisiprotein FtsZ	forward	DR_0632	hypothetical protein	reverse
Dsr102	656829	656892 DR_0644	hypothetical protein	reverse	DR_0645	molybdopterin-guanine dinucleotide biosynthesis protein A	forward
Dsr103	691890	691977 DR_0684	carbamoyl phosphate synthase small subunit	forward	DR_0685	hypothetical protein	forward
Dsr104	691997	692091 DR_0684	carbamoyl phosphate synthase small subunit	forward	DR_0685	hypothetical protein	forward
Dsr105	707709	707783 DR_0691	hypothetical protein	forward	DR_0692	nitrogen regulatory protein P-II	forward
Dsr106	802843	802961 DR_0788	branched-chain amino acid ABC transporter periplasmic amino acid-	reverse	DR_0789	O-acetylserine (thiol)-lyase	forward
Dsr107	814090	814241 DR_0799	glucose-fructose oxidoreductase	forward	DR_0800	hypothetical protein	reverse
Dsr108	847984	848091 DR_0835	hypothetical protein	forward	DR_0836	hypothetical protein	forward
Dsr109	876585	876655 DR_0864	hypothetical protein	forward	DR_0865	ferric uptake regulatiprotein	forward
Dsr110	918726	918787 DR_0910	cell wall protein	forward	DR_0911	DNA-directed RNA polymerase subunit beta'	reverse
Dsr111	923490	923546 DR_0911	DNA-directed RNA polymerase subunit beta'	reverse	rpoB	DNA-directed RNA polymerase subunit beta	reverse
Dsr112	928621	928709 DR_0914	hypothetical protein	forward	DR_0915	hypothetical protein	reverse
Dsr113	928780	928834 DR_0914	hypothetical protein	forward	DR_0915	hypothetical protein	reverse
Dsr114	959461	959617 DR_0944	thioredoxin	forward	DR_0945	hypothetical protein	reverse
Dsr115	968017	968091 DR_0955	hypothetical protein	forward	DR_0956	hypothetical protein	reverse
Dsr116	972589	972698 DR_0959	peptide ABC transporter permease electrtransfer flavoprotein subunit beta	reverse	DR_0960	hypothetical protein	forward
Dsr117	989604	989658 DR_0971	beta	reverse	DR_0972	hypothetical protein	forward
Dsr118	1066578	1066733 aspC	aspartyl-tRNA synthetase	reverse	DR_1056	hypothetical protein	reverse
Dsr119	1073491	1073550 DR_1061	NADPH quinone oxidoreductase	forward	DR_1062	FemA-like protein	reverse
Dsr120	1102258	1102356 DR_1093	tryptophanyl-tRNA synthetase II	forward	DR_1094	hypothetical protein	reverse

Dsr121	1130754	1130824	DR_1122	prephenate dehydrogenase UDP-N-acetylglucosamine 1- carboxyvinyltransferase	forward	DR_1123	UDP-N-acetylglucosamine 1- carboxyvinyltransferase	reverse
Dsr122	1132136	1132227	DR_1123	carboxyvinyltransferase	reverse	DR_1124	SLH family protein	forward
Dsr123	1193472	1193540	DR_1184	MutT/nudix family protein	forward	DR_1185	S-layer-like array-like protein	reverse
Dsr124	1212826	1212880	DR_1201	hypothetical protein	forward	DR_1202	hypothetical protein	reverse
Dsr125	1225291	1225369	DR_1217	IcIR family transcriptional regulator	forward	DR_1218	hypothetical protein	reverse
Dsr126	1232746	1232890	DR_1225	mannosyltransferase	reverse	DR_1226	hypothetical protein	forward
Dsr127	1245848	1245918	DR_1237	hypothetical protein ribonucleoprotein Ro/SS-A-like protein	reverse	DR_1238	homocitrate synthase	reverse
Dsr128	1270383	1270490	DR_1262	hypothetical protein	reverse	DR_1263	hypothetical protein	reverse
Dsr129	1271380	1271490	DR_1263	hypothetical protein	reverse	DR_1264	hypothetical protein	reverse
Dsr130	1275113	1275174	DR_1266	prolyl-tRNA synthetase	forward	DR_1267	hypothetical protein	forward
Dsr131	1290889	1290949	DR_1283	phosphoenolpyruvate carboxylase	forward	DR_1284	hypothetical protein	forward
Dsr132	1295996	1296062	DR_1289	DNA helicase RecQ	reverse	DR_1290	extracellular solute-binding protein	forward
Dsr133	1301289	1301344	DR_1293	hypothetical protein	forward	rpsP	30S ribosomal protein S16	reverse
Dsr134	1301564	1301706	rpsP	30S ribosomal protein S16	reverse	DR_1295	PecM-like protein	forward
Dsr135	1302774	1302835	DR_1295	PecM-like protein	forward	DR_1296	transposase	forward
Dsr136	1304720	1304779	DR_1297	hypothetical protein	forward	DR_1298	hypothetical protein	forward
Dsr137	1362011	1362081	uvrC	excinuclease ABC subunit C	forward	DR_1355	phosphatidylglycerophosphatase B- like protein	forward
Dsr138	1394841	1394948	DR_1388	hypothetical protein	forward	DR_1389	competence protein ComF	forward
Dsr139	1442709	1442805	DR_1439	hypothetical protein	reverse	DR_1440	cation-transporting ATPase	reverse
Dsr140	1442861	1442933	DR_1439	hypothetical protein	reverse	DR_1440	cation-transporting ATPase ribose-phosphate	reverse
Dsr141	1458080	1458130	DR_1455	hypothetical protein	reverse	DR_1456	pyrophosphokinase ribose-phosphate	forward
Dsr142	1458163	1458230	DR_1455	hypothetical protein	reverse	DR_1456	pyrophosphokinase	forward
Dsr143	1475283	1475385	DR_1462	hypothetical protein	reverse	DR_1463	hypothetical protein	reverse
Dsr144	1476946	1476997	DR_1465	hypothetical protein	forward	DR_1466	hypothetical protein	forward
Dsr145	1497161	1497239	DR_1482	2-isopropylmalate synthase	reverse	DR_1483	hypothetical protein	forward
Dsr146	1529094	1529145	rpsB	30S ribosomal protein S2	reverse	DR_1514	2-phosphoglycerate kinase	forward
Dsr147	1531387	1531517	DR_1515	hypothetical protein	forward	DR_1516	acetolactate synthase large subunit	forward
Dsr148	1556222	1556292	DR_1538	osmotically inducible protein C	forward	DR_1539	hypothetical protein	reverse
Dsr149	1569537	1569618	DR_1551	carboxyl-terminal protease	forward	DR_1552	hypothetical protein	reverse
Dsr150	1589905	1589979	DR_1570	peptide ABC transporter permease	reverse	DR_1571	peptide ABC transporter periplasmic peptide-bonding protein	reverse

			peptide ABC transporter periplasmic					
Dsr151	1591756	1591833 DR_1571	peptide-bonding protein	reverse	DR_1572	helicase-related protein	forward	
Dsr152	1601187	1601257 DR_1579	hypothetical protein	forward	DR_1580	hypothetical protein	forward	
Dsr153	1641033	1641090 DR_1619	hypothetical protein	reverse	DR_1620	ketoacyl reductase	reverse	
Dsr154	1665468	1665520 malQ	4-alpha-glucanotransferase	forward	DR_1638	hypothetical protein	forward	
Dsr155	1688729	1688801 tdh	L-threonine 3-dehydrogenase	reverse	DR_1663	hypothetical protein	forward	
						glucose-1-phosphate		
Dsr156	1710710	1710787 DR_1688	hypothetical protein	reverse	DR_1689	adenyltransferase	reverse	
Dsr157	1713889	1713963 DR_1691	heat shock protein-like protein	forward	DR_1692	long-chain fatty-acid-CoA ligase	forward	
Dsr158	1721846	1721898 DR_1698	tRNA-dihydrouridine synthase A	forward	DR_1699	hypothetical protein	reverse	
Dsr159	1732423	1732482 DR_1707	DNA-directed DNA polymerase	reverse	DR_1708	hypothetical protein	reverse	
Dsr160	1751585	1751640 DR_1724	hypothetical protein	reverse	DR_1725	WD repeat-containing protein	reverse	
Dsr161	1781881	1781936 DR_1753	septum site-determining protein	reverse	DR_1754	hypothetical protein	forward	
Dsr162	1793690	1793741 DR_1765	hypothetical protein	reverse	DR_1766	anthranilate synthase component II	forward	
Dsr163	1814538	1814592 DR_1785	3-isopropylmalate dehydrogenase	forward	DR_1786	hypothetical protein	forward	
Dsr164	1831400	1831487 DR_1804	hypothetical protein	forward	DR_1805	hypothetical protein	reverse	
						phospho-2-dehydro-3-		
Dsr165	1842183	1842349 DR_1816	hypothetical protein	reverse	DR_1817	deoxyheptonate aldolase	forward	
						FKBP-type peptidyl-prolyl cis-trans		
Dsr166	1866869	1867060 DR_1838	GTP pyrophosphokinase	reverse	DR_1839	isomerase	forward	
Dsr167	1886932	1887065 DR_1864	hypothetical protein	reverse	DR_1865	cell divisiprotein MraZ	forward	
Dsr168	1917798	1917946 DR_1898	recombinatifactor protein RarA	forward	DR_1899	hypothetical protein	reverse	
						GntR family transcriptional		
Dsr169	1923514	1923621 DR_1904	hypothetical protein	forward	DR_1905	regulator	reverse	
Dsr170	2002417	2002532 DR_1979	hypothetical protein	forward	DR_1980	hypothetical protein	forward	
Dsr171	2016362	2016447 DR_1993	hypothetical protein	forward	DR_1994	hypothetical protein	reverse	
Dsr172	2025845	2025918 rpml	50S ribosomal protein L35	reverse	DR_2006	hypothetical protein	reverse	
Dsr173	2031052	2031111 DR_2012	hypothetical protein	reverse	glpX	fructose 1,6-bisphosphatase II	forward	
Dsr174	2059486	2059554 rplJ	50S ribosomal protein L10	reverse	rplA	50S ribosomal protein L1	reverse	
Dsr175	2073391	2073457 DR_2058	hypothetical protein	forward	DR_2059	glycyl-tRNA synthetase	forward	
Dsr176	2081138	2081197 DR_2065	prepilin peptidase, type IV	forward	DR_2066	hypothetical protein	reverse	
Dsr177	2144282	2144344 DR_2141	hypothetical protein	forward	DR_2142	hypothetical protein	reverse	
Dsr178	2170106	2170198 DR_2173	hypothetical protein	reverse	leuS	leucyl-tRNA synthetase	forward	
						ribosomal protein S6		
Dsr179	2190322	2190394 DR_2193	hypothetical protein	forward	DR_2194	modificatiprotein	forward	
						tellurium resistance protein TerB		
Dsr180	2217634	2217694 DR_2219	hypothetical protein	forward	DR_2220	(terB) putative	forward	

Dsr181	2231154	2231258	DR_2235	hypothetical protein	forward	DR_2236	hypothetical protein	reverse
Dsr182	2251638	2251754	DR_2255	hypothetical protein	reverse	DR_2256	transketolase	forward
Dsr183	2272037	2272118	DR_2273	DNA topology modulatiprotein FlaR-like protein	forward	DR_2274	hypothetical protein	forward
Dsr184	2329057	2329171	DR_2330	ferredoxin	forward	DR_2331	hypothetical protein	forward
Dsr185	2364702	2364802	DR_2363a	hypothetical protein	forward	rpmF	50S ribosomal protein L32	reverse
Dsr186	2367919	2367969	DR_2368	hypothetical protein	forward	DR_2369	hypothetical protein	reverse
Dsr187	2376431	2376525	DR_2374	ribonucleoside-diphosphate reductase-like protein	forward	DR_2375	transcriptielongatifactor	forward
Dsr188	2399466	2399536	DR_2395	Na ⁺ /H ⁺ antiporter	reverse	DR_2396	TetR family transcriptional regulator	forward
Dsr189	2420961	2421072	DR_2417m	hypothetical protein	reverse	DR_2418	DNA-binding response regulator	forward
Dsr190	2428535	2428609	DR_2424	putative transposase	reverse	DR_2425	hypothetical protein	reverse
Dsr191	2441816	2441897	DR_2440	nifR3 protein	reverse	DR_2441	hypothetical protein	forward
Dsr192	2460066	2460155	DR_2463	transport protein	forward	DR_2464	FKBP-type peptidyl-prolyl cis-trans isomerase	forward
Dsr193	2511570	2511640	DR_2508	hexagonally packed intermediate-layer surface protein	reverse	DR_2509	hypothetical protein	reverse
Dsr194	2526760	2526836	fimA	adhesin B	reverse	rpmB	50S ribosomal protein L28	reverse
Dsr195	2533724	2533831	DR_2530	hypothetical protein	forward	DR_2531	thiosulfate sulfurtransferase	forward
Dsr196	2549580	2549658	DR_2546	hypothetical protein	reverse	DR_2547	glutamyl-tRNA reductase	forward
Dsr197	2583287	2583340	DR_2577	S-layer protein	reverse	tgt	queuine tRNA-ribosyltransferase	reverse
Dsr198	2590640	2590724	DR_2582	hypothetical protein	reverse	DR_2583	malate dehydrogenase	forward
Dsr199	2615530	2615685	DR_2606	primosomal protein n', putative	forward	DR_2607	molybdenum cofactor biosynthesis protein D/E	reverse

QRNA predicitions selected for Northern blottign analysis

Name	Left end Coordinat e	Right end Coordinat e	size	Upstream Gene	Direction	Downstre am Gene	Direction
Qpr1	904780	904815		35 >DR0896	forward	DR0897<	reverse
Qpr2	153714	153731		17 <DR0152	reverse	DR0153>	forward
Qpr3	747854	747870		16 <DR0731	reverse	DR0732>	forward
Qpr4	1956907	1956923		16 >DR1936	forward	DR1937<	reverse
Qpr5	213117	213133		16 <DR0211	reverse	DR0212<	reverse
Qpr6	2231180	2231212		32 >DR2235	forward	DR2236<	reverse
Qpr7	2364544	2364572		28 >DR2363a	forward	DR2366<	reverse
Qpr8	1904237	1904266		29 >DR1883	forward	DR1884<	reverse
Qpr9	1073181	1073198		17 >DR1061	forward	DR1062<	reverse
Qpr10	2248014	2248036		<DRrrnaA 22 23S	reverse	DR2253< DRrrnaC2	reverse
Qpr11	250502	250524		<tRNA- 22 Asp-3	reverse	3S>	forward
Qpr12	153639	153670		31 <DR0152	reverse	DR0153>	forward
Qpr13	2248068	2248088		<DRrrnaA 20 23S	reverse	DR2253< DRrrnaC2	reverse
Qpr14	250450	250470		<tRNA- 20 Asp-3	reverse	3S>	forward
Qpr15	2486621	2486673		52 >DR2488	forward	DR2489>	forward
Qpr16	54681	54697		16 <DR0058	reverse	DR0059>	forward
Qpr17	2199501	2199543		42 >DR2199	forward	DR2200<	reverse
Qpr18	1008098	1008122		24 >DR0990	forward	DR0991<	reverse
Qpr19	1771480	1771504		24 >DR1742	forward	DR1743<	reverse
Qpr20	1361988	1362017		29 >DR1354	forward	DR1355>	forward
Qpr21	1771701	1771725		24 >DR1742	forward	DR1743<	reverse
Qpr22	1904435	1904459		24 >DR1883	forward	DR1884<	reverse
Qpr23	2173666	2173684		18 >DR2175	forward	DR2176>	forward
Qpr24	2199718	2199746		28 >DR2199	forward	DR2200<	reverse

Qpr25	2431585	2431602	17 <DR2428	reverse	DR2429>	forward
			<tRNA-		DRrrnaC2	
Qpr26	251149	251194	45 Asp-3	reverse	3S>	forward
Qpr27	2519074	2519091	17 <DR2516	reverse	DR2517>	forward
			<tRNA-		DRrrnaC2	
Qpr28	252144	252302	158 Asp-3	reverse	3S>	forward
Qpr29	331017	331034	17 <DR0334	reverse	DR0335>	forward
Qpr30	355149	355168	19 <DR0353	reverse	DR0354<	reverse
Qpr31	502175	502199	24 >DR0500	forward	DR0501<	reverse
Qpr32	578578	578595	17 >DR0569	forward	DR0570>	forward
Qpr33	732103	732123	20 <icsA	reverse	DR0714<	reverse
Qpr34	750899	750915	16 >DR0736	forward	DR0737>	forward
Qpr35	904620	904669	49 >DR0896	forward	DR0897<	reverse

SIPHT predicitions selected for Northern blottign analysis

Name	UpGENumber	sRNAstart	end	dirsRNA	lensRNA	UpGENEname	UpGENEdir.	DnGENEdir.	DnGENEnumber	DnGENEname
Spr1	DR_1462	1475301	1475373	<<<	72	hypothetical_protein	<<<	<<<	DR_1463	hypothetical_protein (dimethylallyl)adenosine_tRNA_methylt
Spr2	DR_1149	1159362	1159424	>>>	62	Na+/H+_antiporter	>>>	>>>	DR_1150	hiotransferas
Spr3	DR_0990	1008097	1008156	>>>	59	acetoin_utilization_protein lactoylglutathione_lyase-	>>>	<<<	DR_0991	class_V_aminotransferase
Spr4	DR_1695	1718480	1718674	>>>	194	like_protein	>>>	>>>	DR_1696	DNA_mismatch_repair_protein_MutL
Spr5	DR_0450	445674	445925	>>>	251	hypothetical_protein	>>>	<<<	DR_0451	glutamine_synthase
Spr6	DR_0693	709840	709988	>>>	148	ammonium_transporter	>>>	>>>	DR_0694	hypothetical_protein
Spr7	DR_0990	1007800	1007862	>>>	62	acetoin_utilization_protein NADPH_quinone_oxidoreductas	>>>	<<<	DR_0991	class_V_aminotransferase
Spr8	DR_1061	1072952	1073087	<<<	135	e	>>>	<<<	DR_1062	FemA-like_protein phosphatidylglycerophosphatase_B-
Spr9	DR_1354	1361960	1362193	>>>	233	excinuclease_ABC_subunit_C	>>>	>>>	DR_1355	like_protein phosphatidylglycerophosphatase_B-
Spr10	DR_1354	1361960	1362035	>>>	75	excinuclease_ABC_subunit_C phosphatidylglycerophosphatas	>>>	>>>	DR_1355	like_protein
Spr11	DR_1355	1363002	1363330	>>>	328	e_B-like_protein	>>>	>>>	DR_1356	ABC_transporter_ATP-binding_protein
Spr12	DR_1515	1531402	1531584	>>>	182	hypothetical_protein	>>>	>>>	DR_1516	acetolactate_synthase_large_subunit
Spr13	DR_1523	1539187	1539280	>>>	93	putative_transposase kanamycin_resistance_protein-	>>>	<<<	DR_1524	cephalosporin_acylase inositol_monophosphatase_family_prot
Spr14	DR_1702	1725522	1725600	>>>	78	like_protein	<<<	<<<	DR_1703	ein
Spr15	DR_1714	1739125	1739360	>>>	235	hypothetical_protein	>>>	>>>	DR_1715	hypothetical_protein
Spr16	DR_1742	1771472	1771512	<<<	40	glucose-6-phosphate_isomerase	>>>	<<<	DR_1743	fosmidomycin_resistance_protein
Spr17	DR_1883	1904230	1904265	<<<	35	hypothetical_protein	>>>	<<<	DR_1884	transcriptional_regulator
Spr18	DR_1883	1904257	1904495	<<<	238	hypothetical_protein	>>>	<<<	DR_1884	transcriptional_regulator
Spr19	DR_2058	2073196	2073481	>>>	285	hypothetical_protein	>>>	>>>	DR_2059	glycyl-tRNA_synthetase
Spr20	DR_2175	2173720	2173802	>>>	82	hypothetical_protein	>>>	>>>	DR_2176	hypothetical_protein
Spr21	DR_2199	2199589	2199774	>>>	185	ATP- dependent_DNA_helicase_RecG- like_protein	>>>	<<<	DR_2200	orotidine_5%60- phosphate_decarboxylase
Spr22	DR_2199	2199714	2199780	<<<	66	ATP- dependent_DNA_helicase_RecG- like_protein	>>>	<<<	DR_2200	orotidine_5%60- phosphate_decarboxylase
Spr23	DR_2235	2231043	2231264	<<<	221	hypothetical_protein	>>>	<<<	DR_2236	hypothetical_protein
Spr24	DR_2546	2549548	2549736	>>>	188	hypothetical_protein	<<<	>>>	DR_2547	glutamyl-tRNA_reductase

Supplementary Table 6. sRNAs predicted by Rfam

Name	Left end Coordinate	Right end Coordinate	Size	Rfam Prediction	Upstream Gene	Direction	Downstre am Gene	Direction
gi 15805042 ref NC_001263.1	150539	150734	195	Tbox	DR_0149 MutT/nudix family protein	<<<	DR_0150 hypothetical protein	<<<
gi 15805042 ref NC_001263.1	2073216	2073494	278	T-Box	DR_2058 hypothetical protein	>>>	DR_2059 glycyl-tRNA synthetase	>>>
gi 15805042 ref NC_001263.1	863318	863553	235	tmRNA	DR_0851 4-hydroxybenzoate octaprenyltransferase	<<<	DR_00852 hypothetical protein	>>>

Supplementary Table 7. Target RNA prediction

Gene	Target protein	Binding ene	Binding sRNA
DR_0095	ABC transporter ATP-binding protein	-12.51	Dsr10
DR_0095	ABC transporter ATP-binding protein	-14.02	Dsr13
ruvA	Holliday junction DNA helicase RuvA	-10.88	Dsr13
DR_2574	transcriptional regulator	-10.15	Dsr14rc
DR_0601	DNA primase	-10.11	Dsr14rc
DR_0335	ATP-dependent RNA helicase	-13.03	Dsr25
DR_1696	DNA mismatch repair protein MutL	-15.63	Dsr26
DR_1477	DNA repair protein	-16.08	Dsr26
recA	recombinase A	-11.5	Dsr26
DR_0601	DNA primase	-12.05	Dsr32rc
DR_1648	ABC transporter ATP-binding protein	-19.16	Dsr37
DR_1105	DNA repair protein RadA	-10.57	Dsr37rc
DR_0406	ABC transporter ATP-binding protein	-10.49	Dsr8
DR_1581	ABC transporter ATP-binding protein	-11.78	Dsr8
DR_0881	cation transport system protein	-15.25	Dsr8
DR_1105	DNA repair protein RadA	-11.27	Dsr8rc
DR_1581	ABC transporter ATP-binding protein	-10	NB-Dsr1
DR_1572	helicase-related protein	-10.62	NB-Dsr1
DR_0074	TetR family transcriptional regulator	-11.4	NB-Dsr1
DR_0475	ABC transporter ATP-binding protein	-11.99	NB-Dsr11
DR_0997	CRP/FNR family transcriptional regulator	-12.48	NB-Dsr12
DR_0416	ppGpp-regulated growth inhibitor suppressor (-12.57	NB-Dsr12
DR_2145	ABC transporter ATP-binding protein	-10.01	NB-Dsr17
DR_0601	DNA primase	-12.32	NB-Dsr17
DR_2418	DNA-binding response regulator	-13.72	NB-Dsr17
ruvA	Holliday junction DNA helicase RuvA	-12.32	NB-Dsr17
DR_0743	response regulator	-10.57	NB-Dsr18
recA	recombinase A	-13.29	NB-Dsr2
DR_0144	transposase	-28.76	NB-Dsr2
DR_0065	ATP-dependent helicase	-11.89	NB-Dsr3
DR_2519	MerR family transcriptional regulator	-11.29	NB-Dsr3
DR_1927	transposase	-20.9	NB-Dsr30
DR_0440	Holliday junction resolvase	-10.06	NB-Dsr31
DR_1379		-15.29	NB-Dsr33
DR_1581	ABC transporter ATP-binding protein	-18.17	NB-Dsr44
DR_1126	single-stranded-DNA-specific exonuclease	-10.69	NB-Dsr44
DR_1379	TetR family transcriptional regulator	-10.79	NB-Dsr44