Name	**Dir**	**Location**	**5' sum**	**Sliding window ratio**	**5' Ratio**	**Promoter**	**Terminator**	**Type**
Spy_sRNA_205+	+	205	537	0.964093357	1	YES	NO	upstream
Spy_sRNA_3452+	+	3452	42	1	1	YES	NO	upstream
Spy_sRNA_22517+	+	22517	28	0.56	0.666666667	NO	NO	upstream
Spy_sRNA_22595+	+	22595	871	0.927582535	0.899793388	NO	NO	upstream
Spy_sRNA_22607+	+	22607	16448	0.994377607	0.940853449	NO	NO	downstream
Spy_sRNA_22679+	+	22679	1577	0.888450704	0.732466326	NO	NO	upstream
Spy_sRNA_22687+	+	22687	3485	0.941891892	0.623100304	NO	NO	downstream
Spy_sRNA_22868+	+	22868	8827	0.986697966	0.808629535	NO	NO	downstream
Spy_sRNA_22942+	+	22942	4230	0.860981071	0.711761736	NO	NO	downstream
Spy_sRNA_28438+	+	28438	70	0.945945946	0.945945946	NO	NO	downstream
Spy_sRNA_28785+	+	28785	89	0.946808511	0.956989247	NO	NO	upstream
Spy_sRNA_28976+	+	28976	264	0.956521739	0.96	NO	YES	upstream
Spy_sRNA_28985+	+	28985	2307	0.981702128	0.878857143	NO	YES	downstream
Spy_sRNA_30516+	+	30516	103	0.962616822	0.980952381	YES	NO	upstream
Spy_sRNA_33952+	+	33952	105	0.972222222	0.92920354	YES	NO	upstream
Spy_sRNA_63584+	+	63584	140	0.979020979	0.972222222	YES	YES	IGR
Spy_sRNA_73055+	+	73055	12	0.8	0.571428571	NO	NO	downstream
Spy_sRNA_73113+	+	73113	56	0.98245614	0.717948718	NO	NO	IGR
Spy_sRNA_75867+	+	75867	451	0.941544885	0.937629938	YES	NO	IGR
Spy_sRNA_78598+	+	78598	157	0.97515528	0.897142857	NO	NO	IGR
Spy_sRNA_84729+	+	84729	167	0.994047619	0.954285714	NO	NO	upstream
Spy_sRNA_85005+	+	85005	283	0.933993399	0.904153355	NO	NO	upstream
Spy_sRNA_85105+	+	85105	241	0.983673469	0.665745856	NO	NO	upstream
Spy_sRNA_85111+	+	85111	3021	0.937325473	0.917958067	NO	NO	downstream
Spy_sRNA_85192+	+	85192	317	0.951951952	0.946268657	NO	NO	upstream
Spy_sRNA_85346+	+	85346	170	0.977011494	0.923913043	NO	YES	upstream
Spy_sRNA_85365+	+	85365	336	0.884210526	0.585365854	NO	YES	downstream
Spy_sRNA_90946-	-	90946	26	0.896551724	0.928571429	YES	NO	upstream
Spy_sRNA_93359+	+	93359	712	0.994413408	0.99719888	YES	YES	downstream
Spy_sRNA_109928-	-	109928	17	0.85	0.944444444	YES	NO	upstream
Spy_sRNA_110234-	-	110234	10	1	1	YES	NO	IGR
Spy_sRNA_111629+	+	111629	93	0.989361702	0.939393939	NO	YES	IGR
Spy_sRNA_116594-	-	116594	19	0.863636364	1	YES	NO	IGR
Spy_sRNA_116781+	+	116781	270	0.97826087	0.974729242	NO	NO	IGR
Spy_sRNA_132392+	+	132392	20	0.833333333	0.833333333	NO	NO	upstream
Spy_sRNA_145677+	+	145677	63	0.538461538	1	YES	NO	IGR
Spy_sRNA_148619+	+	148619	15	1	1	YES	NO	IGR
Spy_sRNA_155629+	+	155629	46	1	1	YES	YES	IGR
Spy_sRNA_157098+	+	157098	19	0.678571429	1	YES	NO	upstream
Spy_sRNA_183525-	-	183525	70	0.945945946	0.909090909	NO	YES	downstream
Spy_sRNA_184532+	+	184532	6498	0.979942693	0.980978261	YES	NO	IGR
Spy_sRNA_185785+	+	185785	87	0.97752809	0.896907216	NO	YES	downstream
Spy_sRNA_190336+	+	190336	313	0.907246377	0.931547619	YES	NO	IGR
Spy_sRNA_190345+	+	190345	1368	0.93891558	0.767246214	NO	NO	IGR
Spy_sRNA_192528-	-	192528	10	1	1	NO	NO	Antisense
Spy_sRNA_199636-	-	199636	18	0.529411765	0.529411765	YES	NO	upstream
Spy_sRNA_199875+	+	199875	32	1	1	NO	NO	upstream
Spy_sRNA_204807+	+	204807	31	1	1	YES	YES	upstream
Spy_sRNA_207513+	+	207513	37	1	1	YES	NO	upstream
Spy_sRNA_208331+	+	208331	86	0.966292135	0.934782609	YES	NO	IGR
Spy_sRNA_213738+	+	213738	586	0.981574539	0.98487395	YES	YES	IGR
Spy_sRNA_214164+	+	214164	60	1	0.983606557	YES	NO	upstream
Spy_sRNA_216511+	+	216511	75	0.789473684	0.914634146	YES	NO	IGR
Spy_sRNA_224567-	-	224567	120	0.967741935	0.902255639	YES	NO	upstream
Spy_sRNA_224570-	-	224570	11	0.846153846	1	YES	NO	upstream
Spy_sRNA_232198+	+	232198	49	0.590361446	0.765625	YES	NO	upstream
Spy_sRNA_235753+	+	235753	591	0.985	0.942583732	YES	NO	IGR
Spy_sRNA_237128+	+	237128	73	0.948051948	0.829545455	YES	NO	upstream

Spy_sRNA_239475+	+	239475	1075	0.994449584	0.997217069	YES	NO	IGR
Spy_sRNA_243404-	-	243404	11	0.785714286	0.916666667	YES	NO	upstream
Spy_sRNA_246499+	+	246499	20	0.571428571	0.606060606	YES	NO	upstream
Spy_sRNA_248497+	+	248497	21	1	1	YES	NO	downstream
Spy_sRNA_255200-	-	255200	18	1	1	YES	NO	IGR
Spy_sRNA_256844+	+	256844	117	1	1	YES	NO	IGR
Spy_sRNA_279320+	+	279320	30	1	0.833333333	YES	NO	upstream
Spy_sRNA_280485+	+	280485	10	1	1	YES	NO	upstream
Spy_sRNA_289278+	+	289278	89	1	1	YES	NO	upstream
Spy_sRNA_294211+	+	294211	79	0.951807229	0.951807229	YES	NO	upstream
Spy_sRNA_298224+	+	298224	14	0.583333333	0.518518519	NO	YES	IGR
Spy_sRNA_301694+	+	301694	19	0.904761905	0.904761905	YES	NO	upstream
Spy_sRNA_304314+	+	304314	130	0.896551724	0.872483221	YES	NO	upstream
Spy_sRNA_307010-	-	307010	20	0.769230769	0.588235294	NO	NO	IGR
Spy_sRNA_308033-	-	308033	17	1	1	YES	NO	upstream
Spy_sRNA_308381-	-	308381	15	1	1	YES	NO	upstream
Spy_sRNA_312070+	+	312070	10	0.909090909	1	YES	NO	upstream
Spy_sRNA_318401+	+	318401	131	0.873333333	0.992424242	YES	NO	downstream
Spy_sRNA_318404+	+	318404	641	0.971212121	0.809343434	YES	NO	IGR
Spy_sRNA_319190+	+	319190	88	0.988764045	1	YES	YES	IGR
Spy_sRNA_319330+	+	319330	72	0.642857143	0.595041322	NO	YES	IGR
Spy_sRNA_323924+	+	323924	13	1	1	YES	NO	upstream
Spy_sRNA_324852+	+	324852	20	0.714285714	1	YES	NO	upstream
Spy_sRNA_332124+	+	332124	25	1	1	YES	NO	upstream
Spy_sRNA_334719+	+	334719	177	0.977900552	0.786666667	YES	NO	downstream
Spy_sRNA_335396+	+	335396	1553	0.987285442	0.735670298	NO	YES	downstream
Spy_sRNA_335649+	+	335649	47	1	1	NO	NO	IGR
Spy_sRNA_336387+	+	336387	23	1	1	YES	NO	upstream
Spy_sRNA_340904-	-	340904	31	0.96875	1	YES	YES	upstream
Spy_sRNA_342470-	-	342470	10	1	1	YES	NO	upstream
Spy_sRNA_349331+	+	349331	131	1	1	YES	NO	IGR
Spy_sRNA_350644+	+	350644	22	1	0.785714286	YES	NO	IGR
Spy_sRNA_360152-	-	360152	11	1	0.846153846	YES	NO	upstream
Spy_sRNA_363023-	-	363023	27	1	1	YES	NO	upstream
Spy_sRNA_367128+	+	367128	12	1	1	YES	YES	upstream
Spy_sRNA_371426+	+	371426	35	0.972222222	1	YES	NO	IGR
Spy_sRNA_374062+	+	374062	15	1	0.882352941	NO	YES	downstream
Spy_sRNA_374194-	-	374194	21	0.954545455	0.7	NO	NO	downstream
Spy_sRNA_379816+	+	379816	71	0.934210526	1	YES	NO	upstream
Spy_sRNA_382162+	+	382162	110	0.674846626	1	YES	NO	upstream
Spy_sRNA_383044+	+	383044	29	0.725	0.878787879	YES	NO	upstream
Spy_sRNA_384678-	-	384678	10	1	1	NO	NO	Antisense
Spy_sRNA_388211+	+	388211	34	0.739130435	0.772727273	YES	NO	IGR
Spy_sRNA_392987+	+	392987	128	0.882758621	0.96969697	YES	YES	Antisense
Spy_sRNA_402107+	+	402107	28	1	0.903225806	YES	YES	IGR
Spy_sRNA_403520+	+	403520	92	1	0.978723404	YES	NO	upstream
Spy_sRNA_409843-	-	409843	11	1	1	YES	NO	upstream
Spy_sRNA_413307-	-	413307	19	1	1	YES	NO	upstream
Spy_sRNA_413428+	+	413428	308	0.990353698	0.993548387	YES	NO	upstream
Spy_sRNA_416968+	+	416968	682	0.995620438	0.995620438	YES	YES	downstream
Spy_sRNA_450289+	+	450289	17	1	1	YES	NO	IGR
Spy_sRNA_455336+	+	455336	10	1	0.909090909	NO	YES	IGR
Spy_sRNA_468277-	-	468277	18	1	1	YES	NO	Antisense
Spy_sRNA_471090+	+	471090	29	0.763157895	0.707317073	YES	NO	upstream
Spy_sRNA_474768-	-	474768	73	0.890243902	0.924050633	YES	NO	upstream
Spy_sRNA_474941+	+	474941	25	0.862068966	0.862068966	YES	NO	upstream
Spy_sRNA_477376+	+	477376	13	0.541666667	0.8125	YES	NO	IGR
Spy_sRNA_477597-	-	477597	12	1	0.8	NO	YES	Antisense
Spy_sRNA_477704+	+	477704	25	0.694444444	0.892857143	NO	NO	downstream

Spy_sRNA_479555-	-	479555	38	0.95	0.974358974	YES	NO	upstream
Spy_sRNA_479679+	+	479679	26	0.962962963	0.962962963	YES	NO	upstream
Spy_sRNA_480655+	+	480655	42	0.933333333	0.512195122	NO	NO	downstream
Spy_sRNA_480696-	-	480696	15	0.833333333	0.535714286	NO	NO	downstream
Spy_sRNA_482204-	-	482204	11	1	0.647058824	YES	NO	upstream
Spy_sRNA_482963-	-	482963	65	1	1	YES	YES	IGR
Spy_sRNA_483933-	-	483933	10	1	1	YES	NO	upstream
Spy_sRNA_487471-	-	487471	11	1	1	YES	NO	upstream
Spy_sRNA_490543+	+	490543	26	0.866666667	0.928571429	YES	NO	upstream
Spy_sRNA_492136+	+	492136	946	0.932938856	0.997890295	YES	NO	IGR
Spy_sRNA_493609+	+	493609	26	0.764705882	1	YES	NO	upstream
Spy_sRNA_499566+	+	499566	28	0.651162791	0.666666667	YES	NO	upstream
Spy_sRNA_500055+	+	500055	62	0.939393939	0.939393939	YES	YES	IGR
Spy_sRNA_516068+	+	516068	302	0.949685535	0.875362319	YES	NO	downstream
Spy_sRNA_519904+	+	519904	64	1	1	NO	NO	IGR
Spy_sRNA_529558+	+	529558	24	1	1	YES	YES	IGR
Spy_sRNA_531081+	+	531081	22	0.916666667	0.956521739	YES	YES	IGR
Spy_sRNA_531128+	+	531128	55	0.982142857	0.555555556	NO	NO	IGR
Spy_sRNA_531147-	-	531147	25	0.714285714	0.806451613	YES	NO	downstream
Spy_sRNA_532788-	-	532788	64	1	1	YES	YES	IGR
Spy_sRNA_544833+	+	544833	20	1	1	YES	NO	IGR
Spy_sRNA_573707+	+	573707	14	1	1	YES	NO	upstream
Spy_sRNA_576081-	-	576081	238	0.991666667	1	YES	NO	upstream
Spy_sRNA_577456+	+	577456	21	1	1	YES	NO	upstream
Spy_sRNA_578076+	+	578076	11	0.846153846	0.916666667	YES	NO	upstream
Spy_sRNA_579683+	+	579683	259	0.973684211	0.973684211	YES	NO	downstream
Spy_sRNA_580337+	+	580337	32	1	0.96969697	YES	YES	upstream
Spy_sRNA_580354+	+	580354	181	0.952631579	0.815315315	NO	YES	IGR
Spy_sRNA_583888+	+	583888	15	1	0.9375	YES	NO	IGR
Spy_sRNA_586507+	+	586507	38	1	1	YES	NO	upstream
Spy_sRNA_598538+	+	598538	22	1	1	YES	NO	IGR
Spy_sRNA_598591+	+	598591	41	1	0.976190476	NO	NO	IGR
Spy_sRNA_614604+	+	614604	36	0.923076923	0.947368421	YES	NO	upstream
Spy_sRNA_614841+	+	614841	30	0.909090909	0.517241379	NO	NO	upstream
Spy_sRNA_621599+	+	621599	11	1	0.916666667	NO	NO	upstream
Spy_sRNA_623726+	+	623726	33	1	1	YES	YES	IGR
Spy_sRNA_639369+	+	639369	757	0.994743758	0.994743758	YES	NO	upstream
Spy_sRNA_640102-	-	640102	139	1	1	YES	NO	upstream
Spy_sRNA_640195+	+	640195	27	0.75	1	YES	NO	upstream
Spy_sRNA_644794+	+	644794	26	1	1	YES	NO	upstream
Spy_sRNA_658201+	+	658201	313	0.993650794	0.993650794	YES	NO	upstream
Spy_sRNA_661400+	+	661400	1010	0.992141454	0.989226249	YES	YES	downstream
Spy_sRNA_668479+	+	668479	72	0.98630137	0.96	YES	NO	upstream
Spy_sRNA_672321-	-	672321	18	1	1	YES	NO	IGR
Spy_sRNA_676268+	+	676268	178	1	0.994413408	YES	NO	IGR
Spy_sRNA_680207+	+	680207	79	0.580882353	0.637096774	YES	YES	IGR
Spy_sRNA_687854+	+	687854	17	1	1	YES	NO	upstream
Spy_sRNA_693150+	+	693150	160	1	0.909090909	YES	NO	IGR
Spy_sRNA_694150+	+	694150	21	1	1	YES	NO	IGR
Spy_sRNA_699921+	+	699921	273	0.992727273	0.978494624	YES	NO	IGR
Spy_sRNA_704619+	+	704619	36	0.6	0.818181818	YES	NO	IGR
Spy_sRNA_709052+	+	709052	37	1	0.948717949	NO	NO	upstream
Spy_sRNA_712512+	+	712512	17	1	1	YES	NO	downstream
Spy_sRNA_712646+	+	712646	11	0.523809524	0.523809524	YES	NO	upstream
Spy_sRNA_723539+	+	723539	151	0.961783439	0.993421053	YES	NO	upstream
Spy_sRNA_728180+	+	728180	17	0.85	0.944444444	NO	NO	Antisense
Spy_sRNA_730063-	-	730063	43	0.955555556	0.934782609	YES	NO	upstream
Spy_sRNA_733950+	+	733950	51	0.980769231	0.980769231	NO	NO	upstream
Spy_sRNA_737211+	+	737211	12	1	1	YES	NO	upstream

Spy_sRNA_737945+	+	737945	54	0.830769231	0.84375	NO	YES	downstream
Spy_sRNA_743787+	+	743787	50	1	1	YES	NO	upstream
Spy_sRNA_744487+	+	744487	12	0.923076923	1	YES	YES	IGR
Spy_sRNA_746178+	+	746178	405	0.948477752	0.849056604	YES	NO	upstream
Spy_sRNA_752328+	+	752328	42	1	0.976744186	YES	NO	upstream
Spy_sRNA_758046+	+	758046	14	0.56	0.875	YES	NO	upstream
Spy_sRNA_758340+	+	758340	11	1	0.55	YES	NO	upstream
Spy_sRNA_758343+	+	758343	78	0.987341772	0.795918367	YES	NO	upstream
Spy_sRNA_758432+	+	758432	41	1	0.976190476	NO	NO	downstream
Spy_sRNA_758483+	+	758483	48	0.979591837	0.539325843	NO	YES	IGR
Spy_sRNA_759981+	+	759981	51	0.980769231	0.980769231	YES	NO	upstream
Spy_sRNA_759999+	+	759999	83	0.965116279	0.62406015	NO	NO	IGR
Spy_sRNA_760746-	-	760746	541	0.916949153	0.937608319	YES	NO	upstream
Spy_sRNA_760908+	+	760908	28	0.965517241	0.965517241	NO	NO	upstream
Spy_sRNA_764140-	-	764140	27	1	1	YES	NO	IGR
Spy_sRNA_773110+	+	773110	21	1	1	YES	NO	upstream
Spy_sRNA_775776+	+	775776	13	0.866666667	0.866666667	YES	NO	upstream
Spy_sRNA_779816+	+	779816	123	0.611940299	0.9609375	YES	YES	IGR
Spy_sRNA_779831-	-	779831	13	1	0.65	NO	NO	upstream
Spy_sRNA_779886-	-	779886	26	0.962962963	0.962962963	YES	NO	IGR
Spy_sRNA_780010-	-	780010	198	0.994974874	0.99	YES	YES	downstream
Spy_sRNA_781630-	-	781630	34	0.693877551	0.693877551	YES	NO	upstream
Spy_sRNA_783335-	-	783335	30	0.9375	0.9375	YES	YES	upstream
Spy_sRNA_792465-	-	792465	20	1	1	YES	YES	IGR
Spy_sRNA_800113+	+	800113	48	0.979591837	1	YES	NO	upstream
Spy_sRNA_800319+	+	800319	19	0.863636364	0.633333333	NO	YES	downstream
Spy_sRNA_800369-	-	800369	206	0.958139535	0.953703704	YES	YES	IGR
Spy_sRNA_821179+	+	821179	13	0.65	0.764705882	NO	NO	upstream
Spy_sRNA_825891-	-	825891	18	0.947368421	1	YES	NO	upstream
Spy_sRNA_825970+	+	825970	11	0.5	0.523809524	YES	YES	IGR
Spy_sRNA_834540+	+	834540	12	0.923076923	1	YES	YES	upstream
Spy_sRNA_846830-	-	846830	13	1	1	YES	NO	upstream
Spy_sRNA_848756+	+	848756	14	1	0.933333333	NO	NO	upstream
Spy_sRNA_854464-	-	854464	184	0.989247312	0.924623116	YES	YES	IGR
Spy_sRNA_854545-	-	854545	19	0.558823529	0.95	YES	YES	IGR
Spy_sRNA_860730+	+	860730	105	1	1	YES	NO	downstream
Spy_sRNA_860871+	+	860871	238	0.987551867	0.944444444	NO	NO	IGR
Spy_sRNA_860937+	+	860937	24	1	0.75	NO	NO	IGR
Spy_sRNA_861003+	+	861003	25	0.961538462	0.625	NO	NO	IGR
Spy_sRNA_861045+	+	861045	14	0.933333333	0.736842105	NO	NO	IGR
Spy_sRNA_861069+	+	861069	253	0.996062992	0.92	NO	NO	IGR
Spy_sRNA_861135+	+	861135	282	0.992957746	0.992957746	NO	NO	IGR
Spy_sRNA_861201+	+	861201	209	0.995238095	0.981220657	NO	NO	IGR
Spy_sRNA_878614+	+	878614	155	0.981012658	0.956790123	YES	NO	upstream
Spy_sRNA_882398+	+	882398	72	0.9	0.911392405	YES	YES	IGR
Spy_sRNA_883534+	+	883534	60	0.952380952	0.779220779	NO	YES	downstream
Spy_sRNA_896408-	-	896408	11	1	1	YES	NO	upstream
Spy_sRNA_896698+	+	896698	130	0.992366412	0.992366412	YES	NO	upstream
Spy_sRNA_896885-	-	896885	10	0.909090909	0.909090909	NO	NO	Antisense
Spy_sRNA_921480+	+	921480	133	1	1	YES	NO	IGR
Spy_sRNA_924338-	-	924338	28	0.965517241	1	NO	NO	Antisense
Spy_sRNA_930739+	+	930739	12	1	1	YES	NO	IGR
Spy_sRNA_930742+	+	930742	12	1	0.5	YES	NO	IGR
Spy_sRNA_934144+	+	934144	10	0.555555556	1	YES	NO	upstream
Spy_sRNA_944235+	+	944235	37	0.973684211	1	YES	NO	upstream
Spy_sRNA_946822-	-	946822	197	1	1	YES	NO	upstream
Spy_sRNA_946941+	+	946941	1351	0.858322745	0.859414758	YES	NO	upstream
Spy_sRNA_950946+	+	950946	13	0.764705882	0.764705882	YES	YES	IGR
Spy_sRNA_953896-	-	953896	36	1	1	YES	NO	upstream

Spy_sRNA_956690+	+	956690	22	0.846153846	0.956521739	YES	NO	upstream
Spy_sRNA_979619+	+	979619	66	0.970588235	1	NO	NO	Antisense
Spy_sRNA_987427+	+	987427	89	0.659259259	1	YES	NO	upstream
Spy_sRNA_992257-	-	992257	24	0.96	0.96	YES	YES	upstream
Spy_sRNA_995868-	-	995868	24	1	0.923076923	YES	NO	upstream
Spy_sRNA_996147-	-	996147	321	0.990740741	0.99380805	YES	YES	downstream
Spy_sRNA_1016434-	-	1016434	44	0.977777778	1	YES	NO	upstream
Spy_sRNA_1017640+	+	1017640	339	0.971346705	0.979768786	YES	NO	upstream
Spy_sRNA_1023066-	-	1023066	14	1	0.583333333	YES	YES	downstream
Spy_sRNA_1032107+	+	1032107	34	0.918918919	0.918918919	NO	NO	Antisense
Spy_sRNA_1039491-	-	1039491	10	0.833333333	0.833333333	YES	NO	upstream
Spy_sRNA_1046169-	-	1046169	678	0.99122807	0.99122807	YES	NO	upstream
Spy_sRNA_1046345+	+	1046345	168	1	1	YES	NO	IGR
Spy_sRNA_1051808+	+	1051808	18	1	1	NO	NO	Antisense
Spy_sRNA_1052999-	-	1052999	14	0.636363636	0.736842105	YES	NO	upstream
Spy_sRNA_1053443-	-	1053443	94	0.979166667	0.979166667	YES	NO	upstream
Spy_sRNA_1055518-	-	1055518	54	0.981818182	0.981818182	YES	NO	IGR
Spy_sRNA_1056178-	-	1056178	15	0.714285714	0.75	YES	NO	upstream
Spy_sRNA_1058985-	-	1058985	60	1	1	YES	NO	upstream
Spy_sRNA_1062296+	+	1062296	443	0.969365427	1	NO	NO	upstream
Spy_sRNA_1063616-	-	1063616	154	1	1	NO	NO	Antisense
Spy_sRNA_1065004+	+	1065004	54	0.981818182	0.981818182	YES	NO	upstream
Spy_sRNA_1065030+	+	1065030	378	0.984375	0.857142857	NO	NO	IGR
Spy_sRNA_1071698+	+	1071698	18	1	1	YES	NO	upstream
Spy_sRNA_1093241-	-	1093241	13	1	1	YES	NO	upstream
Spy_sRNA_1093376+	+	1093376	1908	0.975959079	0.987066736	YES	NO	upstream
Spy_sRNA_1106573-	-	1106573	13	0.928571429	0.928571429	YES	YES	IGR
Spy_sRNA_1109453-	-	1109453	10	1	0.666666667	NO	YES	IGR
Spy_sRNA_1110925-	-	1110925	60	0.952380952	1	YES	YES	IGR
Spy_sRNA_1116927-	-	1116927	12	1	1	YES	NO	upstream
Spy_sRNA_1122674-	-	1122674	21	0.954545455	0.954545455	YES	YES	upstream
Spy_sRNA_1125188-	-	1125188	34	1	1	YES	NO	upstream
Spy_sRNA_1126903-	-	1126903	34	1	1	YES	NO	IGR
Spy_sRNA_1137587-	-	1137587	42	0.954545455	0.857142857	YES	NO	upstream
Spy_sRNA_1139116-	-	1139116	278	1	1	YES	NO	upstream
Spy_sRNA_1141334-	-	1141334	20	1	0.909090909	YES	NO	IGR
Spy_sRNA_1153040-	-	1153040	44	1	1	YES	NO	downstream
Spy_sRNA_1154171-	-	1154171	15	0.882352941	0.833333333	YES	NO	upstream
Spy_sRNA_1156231-	-	1156231	10	1	1	YES	NO	IGR
Spy_sRNA_1165579-	-	1165579	4209	0.995977283	0.995741661	YES	NO	upstream
Spy_sRNA_1178332-	-	1178332	19	0.791666667	0.863636364	YES	NO	upstream
Spy_sRNA_1181051-	-	1181051	11	1	1	YES	NO	upstream
Spy_sRNA_1185490-	-	1185490	87	0.988636364	0.988636364	YES	NO	upstream
Spy_sRNA_1186876-	-	1186876	14	1	0.875	YES	NO	downstream
Spy_sRNA_1188825-	-	1188825	32	0.96969697	0.96969697	YES	NO	upstream
Spy_sRNA_1189708+	+	1189708	16	0.941176471	1	YES	YES	upstream
Spy_sRNA_1212757+	+	1212757	31	0.96875	0.96875	YES	YES	IGR
Spy_sRNA_1221370-	-	1221370	18	0.620689655	0.642857143	YES	YES	IGR
Spy_sRNA_1222613-	-	1222613	76	0.938271605	0.737864078	NO	NO	downstream
Spy_sRNA_1222954-	-	1222954	156	0.981132075	0.987341772	YES	NO	upstream
Spy_sRNA_1226446-	-	1226446	20	0.571428571	0.869565217	NO	NO	upstream
Spy_sRNA_1232004-	-	1232004	14	1	1	YES	NO	upstream
Spy_sRNA_1232985-	-	1232985	15	1	1	YES	NO	upstream
Spy_sRNA_1238404-	-	1238404	67	0.917808219	0.985294118	YES	NO	upstream
Spy_sRNA_1238613+	+	1238613	12	0.923076923	0.923076923	NO	NO	IGR
Spy_sRNA_1251166-	-	1251166	30	0.967741935	0.967741935	YES	YES	IGR
Spy_sRNA_1254928-	-	1254928	68	0.894736842	0.985507246	YES	NO	upstream
Spy_sRNA_1257527-	-	1257527	11	1	1	YES	NO	upstream
Spy_sRNA_1260092-	-	1260092	197	0.933649289	0.938095238	YES	NO	IGR

Spy_sRNA_1267683-	-	1267683	21	1	1	YES	NO	IGR
Spy_sRNA_1275654-	-	1275654	24	1	1	YES	NO	upstream
Spy_sRNA_1275740+	+	1275740	85	1	1	YES	NO	upstream
Spy_sRNA_1280820-	-	1280820	448	0.584856397	0.589473684	YES	YES	downstream
Spy_sRNA_1290161+	+	1290161	13	1	1	NO	YES	Antisense
Spy_sRNA_1295825-	-	1295825	62	0.96875	0.984126984	YES	YES	downstream
Spy_sRNA_1296703+	+	1296703	176	0.972375691	1	YES	YES	upstream
Spy_sRNA_1296706+	+	1296706	1759	0.995472552	0.906701031	YES	YES	IGR
Spy_sRNA_1301352-	-	1301352	28	0.933333333	0.875	YES	NO	upstream
Spy_sRNA_1325671+	+	1325671	64	1	0.955223881	NO	NO	Antisense
Spy_sRNA_1328813+	+	1328813	26	1	1	YES	NO	upstream
Spy_sRNA_1330456-	-	1330456	248	0.980237154	0.984126984	NO	YES	downstream
Spy_sRNA_1330659-	-	1330659	128	0.992248062	0.955223881	NO	NO	upstream
Spy_sRNA_1337660-	-	1337660	173	0.723849372	0.726890756	YES	NO	upstream
Spy_sRNA_1340437+	+	1340437	28	0.736842105	0.756756757	NO	NO	upstream
Spy_sRNA_1341945+	+	1341945	28	0.666666667	0.651162791	NO	NO	Antisense
Spy_sRNA_1343232-	-	1343232	10	1	0.909090909	YES	NO	upstream
Spy_sRNA_1355857-	-	1355857	37	0.973684211	0.973684211	YES	NO	upstream
Spy_sRNA_1365555-	-	1365555	267	0.613793103	0.878289474	NO	NO	downstream
Spy_sRNA_1365939-	-	1365939	38	0.974358974	0.775510204	YES	NO	IGR
Spy_sRNA_1366822-	-	1366822	11	1	0.733333333	NO	NO	Antisense
Spy_sRNA_1371249-	-	1371249	14	1	1	NO	NO	IGR
Spy_sRNA_1375200-	-	1375200	20	0.64516129	0.952380952	YES	NO	upstream
Spy_sRNA_1379849-	-	1379849	17	0.80952381	0.62962963	NO	NO	downstream
Spy_sRNA_1381968+	+	1381968	23	1	1	NO	YES	Antisense
Spy_sRNA_1389821-	-	1389821	23	0.958333333	1	YES	NO	upstream
Spy_sRNA_1392001-	-	1392001	17	1	1	NO	NO	upstream
Spy_sRNA_1400292-	-	1400292	36	0.9	0.734693878	NO	YES	downstream
Spy_sRNA_1404921-	-	1404921	121	0.96031746	0.930769231	YES	YES	downstream
Spy_sRNA_1405544-	-	1405544	14	1	1	YES	NO	upstream
Spy_sRNA_1409517-	-	1409517	22	0.956521739	0.956521739	YES	YES	upstream
Spy_sRNA_1411615+	+	1411615	75	1	0.986842105	YES	NO	IGR
Spy_sRNA_1424640-	-	1424640	14	1	1	NO	YES	IGR
Spy_sRNA_1430184-	-	1430184	147	0.769633508	0.720588235	YES	YES	IGR
Spy_sRNA_1430359-	-	1430359	31	1	0.756097561	YES	YES	upstream
Spy_sRNA_1431858-	-	1431858	46	0.541176471	0.696969697	YES	NO	upstream
Spy_sRNA_1433682+	+	1433682	13	0.866666667	0.866666667	YES	YES	upstream
Spy_sRNA_1439780+	+	1439780	74	0.986666667	0.986666667	YES	NO	IGR
Spy_sRNA_1442795+	+	1442795	18	0.947368421	1	YES	NO	upstream
Spy_sRNA_1443306+	+	1443306	1315	0.993202417	0.998481397	YES	NO	IGR
Spy_sRNA_1443406+	+	1443406	195	0.890410959	0.663265306	NO	NO	IGR
Spy_sRNA_1453419-	-	1453419	113	0.830882353	0.88976378	YES	YES	downstream
Spy_sRNA_1455775-	-	1455775	57	0.75	1	YES	NO	IGR
Spy_sRNA_1461003-	-	1461003	35	0.972222222	0.972222222	NO	NO	IGR
Spy_sRNA_1467463-	-	1467463	32	1	1	YES	NO	IGR
Spy_sRNA_1471286-	-	1471286	72	0.947368421	0.96	YES	NO	upstream
Spy_sRNA_1471625-	-	1471625	15	0.6	0.833333333	NO	YES	Antisense
Spy_sRNA_1473492-	-	1473492	17	1	1	YES	NO	upstream
Spy_sRNA_1476508-	-	1476508	11	1	1	YES	NO	upstream
Spy_sRNA_1494888-	-	1494888	28	1	0.965517241	YES	NO	upstream
Spy_sRNA_1499056-	-	1499056	30	0.666666667	1	YES	NO	upstream
Spy_sRNA_1516735+	+	1516735	37	1	1	YES	NO	IGR
Spy_sRNA_1519971-	-	1519971	77	0.6875	1	YES	NO	IGR
Spy_sRNA_1520537+	+	1520537	12	1	1	YES	NO	upstream
Spy_sRNA_1522747-	-	1522747	32	1	1	YES	NO	upstream
Spy_sRNA_1526660-	-	1526660	12	1	1	YES	NO	upstream
Spy_sRNA_1530865+	+	1530865	16	1	0.941176471	YES	NO	upstream
Spy_sRNA_1532594-	-	1532594	10	0.909090909	0.909090909	YES	NO	upstream
Spy_sRNA_1532746+	+	1532746	54	1	1	YES	NO	upstream

Spy_sRNA_1537282+	+	1537282	337	0.994100295	0.99704142	YES	YES	upstream
Spy_sRNA_1541142+	+	1541142	31	1	1	YES	NO	Antisense
Spy_sRNA_1545203+	+	1545203	18	0.947368421	1	YES	NO	upstream
Spy_sRNA_1551952+	+	1551952	13	0.684210526	0.684210526	NO	NO	IGR
Spy_sRNA_1555636-	-	1555636	24	0.96	0.923076923	YES	NO	upstream
Spy_sRNA_1555761+	+	1555761	69	1	1	YES	NO	IGR
Spy_sRNA_1559809-	-	1559809	265	0.967153285	0.977859779	YES	NO	upstream
Spy_sRNA_1561898-	-	1561898	96	1	1	YES	NO	upstream
Spy_sRNA_1562939-	-	1562939	136	0.99270073	0.985507246	YES	NO	upstream
Spy_sRNA_1564097-	-	1564097	13	0.866666667	0.928571429	NO	NO	IGR
Spy_sRNA_1566328-	-	1566328	69	0.896103896	1	YES	NO	upstream
Spy_sRNA_1566698-	-	1566698	6351	0.880982106	0.979336931	YES	NO	IGR
Spy_sRNA_1567948-	-	1567948	22	1	1	YES	NO	upstream
Spy_sRNA_1568211-	-	1568211	245	0.960784314	0.949612403	YES	YES	upstream
Spy_sRNA_1571806-	-	1571806	467	0.987315011	1	YES	NO	upstream
Spy_sRNA_1573589+	+	1573589	10	1	0.909090909	YES	NO	upstream
Spy_sRNA_1584529+	+	1584529	14	1	1	NO	NO	Antisense
Spy_sRNA_1605887+	+	1605887	14	1	1	YES	NO	upstream
Spy_sRNA_1610157-	-	1610157	68	0.985507246	0.985507246	NO	NO	IGR
Spy_sRNA_1612019-	-	1612019	18	0.75	0.666666667	YES	NO	upstream
Spy_sRNA_1614211-	-	1614211	39	1	0.928571429	NO	NO	upstream
Spy_sRNA_1620465-	-	1620465	301	0.986885246	0.99339934	YES	NO	IGR
Spy_sRNA_1626497+	+	1626497	30	1	1	YES	NO	upstream
Spy_sRNA_1632799-	-	1632799	26	0.8125	0.8125	YES	NO	upstream
Spy_sRNA_1638003-	-	1638003	29	1	1	YES	NO	upstream
Spy_sRNA_1638588-	-	1638588	35	0.673076923	0.660377358	YES	NO	upstream
Spy_sRNA_1646906-	-	1646906	39	0.764705882	0.795918367	YES	NO	upstream
Spy_sRNA_1651365-	-	1651365	11	0.55	0.916666667	YES	NO	upstream
Spy_sRNA_1652986+	+	1652986	14	1	0.823529412	YES	NO	upstream
Spy_sRNA_1663522+	+	1663522	1270	0.997643362	1	YES	NO	IGR
Spy_sRNA_1663725+	+	1663725	226	0.99122807	0.64756447	NO	NO	IGR
Spy_sRNA_1666770-	-	1666770	12	1	1	NO	NO	Antisense
Spy_sRNA_1680620-	-	1680620	37	0.902439024	0.606557377	NO	YES	IGR
Spy_sRNA_1680670-	-	1680670	22	1	1	YES	YES	IGR
Spy_sRNA_1683632-	-	1683632	11	1	1	YES	NO	upstream
Spy_sRNA_1685305-	-	1685305	57	0.966101695	0.93442623	YES	NO	IGR
Spy_sRNA_1696212-	-	1696212	31	1	1	NO	NO	upstream
Spy_sRNA_1696383+	+	1696383	13	1	1	YES	NO	IGR
Spy_sRNA_1696464-	-	1696464	248	0.876325088	0.888888889	NO	NO	IGR
Spy_sRNA_1696905-	-	1696905	33	0.868421053	0.785714286	NO	YES	downstream
Spy_sRNA_1697906-	-	1697906	32	1	1	NO	NO	upstream
Spy_sRNA_1702727-	-	1702727	102	0.990291262	0.990291262	YES	NO	upstream
Spy_sRNA_1713593-	-	1713593	87	0.97752809	0.956043956	YES	NO	downstream
Spy_sRNA_1716417-	-	1716417	15	0.555555556	0.517241379	YES	NO	upstream
Spy_sRNA_1719908+	+	1719908	49	1	1	YES	NO	upstream
Spy_sRNA_1721621-	-	1721621	61	1	1	NO	YES	IGR
Spy_sRNA_1727750-	-	1727750	16	1	1	YES	NO	IGR
Spy_sRNA_1728167-	-	1728167	48	0.979591837	0.979591837	YES	NO	IGR
Spy_sRNA_1728672-	-	1728672	56	1	0.933333333	YES	YES	upstream
Spy_sRNA_1729044+	+	1729044	35	1	1	YES	NO	upstream
Spy_sRNA_1746346+	+	1746346	42	0.954545455	1	YES	NO	IGR
Spy_sRNA_1750524-	-	1750524	39	1	1	YES	NO	IGR
Spy_sRNA_1755445-	-	1755445	2101	0.99197356	0.992911153	YES	YES	IGR
Spy_sRNA_1762559-	-	1762559	25	0.961538462	1	YES	NO	upstream
Spy_sRNA_1764396-	-	1764396	29	1	0.966666667	YES	NO	IGR
Spy_sRNA_1765647-	-	1765647	29	0.878787879	1	YES	NO	upstream
Spy_sRNA_1766154-	-	1766154	13	1	1	YES	NO	upstream
Spy_sRNA_1767633-	-	1767633	18	0.9	1	YES	NO	downstream
Spy_sRNA_1775122-	-	1775122	15	1	0.9375	YES	YES	IGR

Spy_sRNA_1778807-	-	1778807	182	0.892156863	0.896551724	YES	NO	IGR
Spy_sRNA_1786666+	+	1786666	148	0.826815642	0.826815642	YES	YES	IGR
Spy_sRNA_1790614+	+	1790614	637	0.871409029	0.9953125	YES	NO	upstream
Spy_sRNA_1797333-	-	1797333	27	0.964285714	0.931034483	YES	NO	IGR
Spy_sRNA_1799042+	+	1799042	306	0.996742671	0.971428571	YES	NO	IGR
Spy_sRNA_1811977-	-	1811977	61	0.910447761	0.924242424	YES	NO	IGR
Spy_sRNA_1820593-	-	1820593	447	0.995545657	0.986754967	YES	YES	IGR
Spy_sRNA_1822599+	+	1822599	24	1	1	YES	NO	upstream
Spy_sRNA_1829634-	-	1829634	47	1	1	YES	NO	upstream
Spy_sRNA_1840712-	-	1840712	41	1	0.976190476	NO	NO	IGR
Spy_sRNA_1842269-	-	1842269	36	0.818181818	0.818181818	YES	NO	IGR
Spy_sRNA_1848235-	-	1848235	121	0.991803279	0.870503597	NO	YES	upstream
Spy_sRNA_1848336-	-	1848336	157	0.73364486	0.726851852	YES	YES	upstream
Spy_sRNA_1849261+	+	1849261	1263	0.967816092	0.975289575	YES	YES	Antisense
Spy_sRNA_1849426+	+	1849426	203	0.975961538	0.980676329	YES	YES	upstream
Spy_sRNA_1850309+	+	1850309	21	0.583333333	0.875	YES	NO	upstream

Table S1. Novel putative regulatory RNAs identified by bioinformatics analysis of the sRNA sequencing data

For each identified putative sRNA, the identifier, direction and 5’ coordinates are indicated. The 5' sum corresponds to the number of reads with a 5’ end at this position. The sliding window ratio corresponds to the ratio of 5’ ends of reads that start at that position including all 5’ ends of reads in a window of 11 nt. The 5' ratio corresponds to the ratio 5’ end_sum with all reads at that position. A predicted promoter element is defined when located at most 10 nt upstream of the location. A predicted Rho-independent terminator is defined when located at most 300 nt downstream of the location. The filtering parameter used here are Fend > 10, Fendratio > 0.5 and 5' end_local > 0.5. We also removed rRNAs, tRNAs and all sRNAs located in CDSs from the list of putative sRNAs shown here. The location of sRNAs (see column “Type”) is indicated as follows: upstream, within the 5’ UTR of a gene; downstream, within the 3’ UTR of a gene; IGR, intergenic region; CDS: coding sequence; antisense, antisense to a coding sequence. sRNAs that were also found in the visual inspection of the genome using the Integrative Genomics Viewer (IGV) software are highlighted in grey.

Name	Coordinates		Size	Predicted function	Strand		Predicted localization	Upstream		Downstream		Coverage	21	14, 15	16	19	20	18	This study	bioinf.	NB
Spy_sRNA22942	22942	22959	18	no	1	→ → →	**3' UTR**	SPy_t10	tRNA-Pro	SPy_r03	16S ribosomal RNA	6636							1	YES	
Spy_sRNA73113	73113	73156	44	no	1	→ → →	**3' UTR**	SPy_0071	rpmD: 50S ribosomal protein L30	SPy_0072	rplO: 50S ribosomal protein L15	92							1	YES	
Spy_sRNA75867	75867	75890	24	no	1	→ → →	**5' UTR**	SPy_0074	adk: adenylate kinase	SPy_0075	infA: translation initiation factor IF-1	523	SPync002							YES	
Spy_sRNA78598	78598	78644	47	no	1	→ → →	**3' UTR**	SPy_0080a	rplQ: 50S ribosomal protein L17	SPy_r03	16S ribosomal RNA	347			x					YES	
Spy_sRNA93359	93359	93453	95	**Lacto-rpoB**	1	→ → →	**5' UTR**	SPy_0097	pbp1b: penicillin-binding protein 1B	SPy_0098	rpoB: DNA-directed RNA polymerase subunit beta	779	SPync003		x		sRNAscan7 (NB)			YES	+
Spy_sRNA111629	111629	111647	19	no	1	→ → ←	**IGR**	SPy_0117	hypothetical protein	SPy_0121	deoxyguanosine kinase/deoxyadenosine kinase	99							1	YES	-
Spy_sRNA112285	112264	112285	22	no	-1	→ ← ←	**3' UTR**	SPy_0117	hypothetical protein	SPy_0121	deoxyguanosine kinase/deoxyadenosine kinase	38							1	NO	-
Spy_sRNA116781	116781	117055	275	no	1	← → →	**IGR**	SPy_0124	rofA: regulatory protein	SPy_0127	signal peptidase I	1269	SPync004		x					YES	
Spy_sRNA145677	145677	145722	46	no	1	→ → →	**5' UTR**	SPy_0159	hypothetical protein	SPy_0160	purA: adenylosuccinate synthetase	120		2006						YES	-
Spy_sRNA155629	155629	155707	79	no	1	← → →	**5' UTR**	SPy_0171	hypothetical protein	SPy_0172	metB: cystathionine beta-lyase	55							1	YES	
Spy_sRNA174217	174217	174356	140	no	1	→ → →	**5' UTR**	SPy_0185	polA: DNA polymerase I	SPy_0186	hypothetical protein	83	SPync010							NO	
Spy_sRNA185785	185785	185834	50	no	1	→ → →	**3' UTR**	SPy_0203	tgt: queuine tRNA-ribosyltransferase	SPy_0205	hypothetical protein	100							1	YES	
Spy_sRNA190336	190336	190414	79	**SRP**	1	← → →	**IGR**	SPy_0210	peptidoglycan endo-beta-N-acetylglucosaminidase	SPy_0212	speG: exotoxin G precursor	7008		2006	x	RNA190950 (NB)	sRNASpy490186c			YES	+
Spy_sRNA195261	195121	195261	141	**csRNA**	-1	← ← →	**IGR**	SPy_0216	RivR : regulatory protein	SPy_0217	transposase	13	SPync013			SR195750 (NB)				NO	+
Spy_sRNA196710	196710	196794	85	no	1	→ → →	**5' UTR**	SPy_0219	hypothetical protein	SPy_0223	hypothetical protein	9							1	NO	
Spy_sRNA208331	208331	208413	83	no	1	→ → →	**5' UTR**	SPy_0238	hypothetical protein	SPy_0239	gtlX: glutamyl tRNA synthetase	147							1	YES	
Spy_sRNA213738	213738	213968	231	**FasX**	1	→ → →	**IGR**	SPy_0245	fasA: putative response regulator	SPy_0246	rnpA: ribonuclease P	1083	SPync015		x	SR14350 (NB)	490206/MOSES2 (NB)	SSRC4		YES	
Spy_sRNA224567	224538	224567	30	no	-1	← ← →	**5' UTR**	SPy_0259	hypothetical protein	SPy_0260	hypothetical protein	139			x					YES	
Spy_sRNA235753	235753	235934	182	no	1	→ → →	**5' UTR**	SPy_0269	prgA: surface exclusion protein	SPy_0271	rpsL: 30 ribosomal protein S12	893	SPync016				sRNASpy490229			YES	
Spy_sRNA239475	239475	239520	46	no	1	→ → →	**5' UTR**	SPy_0273	fusA: elongation factor G	SPy_0274	plr: glyceraldehyde 3 phosphate dehydrogenase	1171	SPync017							YES	
Spy_sRNA254010	253951	254010	60	no	-1	→ ← ←	**IGR**	SPy_0290	hypothetical protein	SPy_0292	dacA: D-ala-D-ala carboxylpeptidase	106							1	NO	-
Spy_sRNA255200	255117	255200	84	no	-1	→ ← ←	**IGR**	SPy_0290	hypothetical protein	SPy_0292	dacA: D-ala-D-ala carboxylpeptidase	21	SPync020							YES	
Spy_sRNA291637	291637	291800	164	no	1	→ → →	**IGR**	SPy_0334	hypothetical protein	SPy_0337	CsrS: sensory transduction histidine kinase	108	SPync022							NO	-
Spy_sRNA294211	294211	294244	34	no	1	→ → →	**5' UTR**	SPy_0337	csrS: sensory transduction histidine kinase	SPy_0338	nrdR: transcriptional regulator NrdR	136							1	YES	
Spy_sRNA307010	306980	307010	31	no	-1	→ ← ←	**3' UTR**	SPy_0349	greA: transcription elongation factor GreA	SPy_0351	oxaA-like protein	46		2006			mopsRNA1			YES	
Spy_sRNA318404	318404	318505	102	**23S-methyl**	1	→ → →	**5' UTR**	SPy_0370	hypothetical protein	SPy_0371	23S rRNA methyl transferase	1094	SPync024		x		sRNASpy490305			YES	+
Spy_sRNA319190	319190	319386	197	**FMN**	1	→ → →	**5' UTR**	SPy_0371	23S rRNA methyltransferase	SPy_0373	riboflavin transporter	731	SPync025	2006/2008		RNA319780	sRNASpy490306			YES	
Spy_sRNA320648	320648	320691	44	no	1	→ → →	**3' UTR**	SPy_0374	hypothetical protein	SPy_0376	hypothetical protein	84	SPync026							NO	
Spy_sRNA327370	327370	327397	28	no	1		**as to CDS**	SPy_0383	ferrichrome ABC transporter permease			7							1	NO	
Spy_sRNA334719	334719	334786	68	no	1	→ → →	**5' UTR or 3' UTR**	SPy_0393	hypothetical protein	SPy_0395	clpP: ATP dependent clp protease proteolytic subunit	261	SPync027							YES	
Spy_sRNA335396	335396	335441	46	no	1	→ → →	**3' UTR**	SPy_0395	clpP: ATP dependent clp protease proteolytic subunit	SPy_0397	hypothetical protein	2148							1	YES	-
Spy_sRNA335649	335649	335693	45	no	1	→ → →	**IGR**	SPy_0395	clpP: ATP dependent clp protease proteolytic subunit	SPy_0397	hypothetical protein	48							1	YES	-
Spy_sRNA340985	340985	341067	83	no	1	← → →	**IGR**	SPy_0408	hypothetical protein	SPy_0410	arsenate reductase	7	SPync028							NO	
Spy_sRNA349331	349331	349430	100	no	1	→ → →	**IGR**	SPy_0416	prtS: cell envelope proteinase	SPy_0421	hypothetical protein	143							1	YES	-
Spy_sRNA350644	350644	350709	66	no	1	→ → →	**5' UTR or 3' UTR**	SPy_0421	hypothetical protein	SPy_0422	metG: methionyl-tRNA synthetase	29							1	YES	
Spy_sRNA357085	357085	357104	20	no	1	→ → ←	**IGR**	SPy_0427	nrdE.1: ribonucleotide diphosphate reductase subunit alpha	SPy_0428	hypothetical protein	43							1	NO	-
Spy_sRNA374062	374062	374118	57	no	1	→ → ←	**3' UTR**	SPy_0456	mtsC: ABC transporter permease	SPy_0457	cyclophilin-type protein	17							1	YES	
Spy_sRNA374194	374138	374194	57	no	-1	→ ← ←	**3' UTR**	SPy_0456	mtsC: ABC transporter permease	SPy_0457	cyclophilin-type protein	34							1	YES	
Spy_sRNA382162	382162	382189	28	no	1	→ → →	**5' UTR or 3' UTR**	SPy_0464	hypothetical protein	SPy_0466	mrsA.2: methionin sulfoxide reductase A	168							1	YES	
Spy_sRNA391430	391385	391430	46	no	-1	← ← →	**IGR**	SPy_0478	hypothetical protein	SPy_0479	hypothetical protein	22							1	NO	-
Spy_sRNA392987	392987	393047	61	no	1		**as to CDS**	SPy_0481	transposase			220	SPync035						1	YES	+
Spy_sRNA413428	413428	413447	20	no	1	← → →	**5' UTR**	SPy_0513	pepQ: Xaa-Pro dipeptidase	SPy_0513	ccpA: catabolite control protein A	311							1	YES	
Spy_sRNA416968	416968	417051	84	**thrS T-box**	1	→ → →	**5' UTR**	SPy_0516	1,2-diacylglycerol 3-glucosyltransferase	SPy_0517	thrS: threonyl-tRNA synthetase	815	SPync037	2006/2008	x	SR418861	sRNASpy490434			YES	
Spy_sRNA450289	450289	450353	65	no	1	→ → →	**5' UTR or 3' UTR**	SPy_0556	hypothetical protein	SPy_0558	hypothetical protein	18	SPync038			SR452230 (NB)				YES	
Spy_sRNA471434	471434	471500	67	no	1	→ → →	**3' UTR**	SPy_0583	hypothetical protein	SPy_0583	ptsK: HPr kinase/phosphorylase	105					sRNASpy490493			NO	
Spy_sRNA477741	477693	477741	49	no	-1		**as to transcript**	SPy_0593	hypothetical protein			100	SPync040							NO	+
Spy_sRNA477714	477714	477761	48	no	1	→ → ←	**3' UTR**	SPy_0593	hypothetical protein	SPy_0595	lysS: lysyl t-RNA synthetase	125							1	NO	
Spy_sRNA477984	477934	477984	51	no	-1	→ ← ←	**3' UTR**	SPy_0593	hypothetical protein	SPy_0595	lysS: lysyl t-RNA synthetase	24							1	NO	
Spy_sRNA480642	480642	480690	49	no	1		**as to transcript**	SPy_0598	hypothetical protein			108							1	NO	+
Spy_sRNA480696	480654	480696	44	no	-1		**as to transcript**	SPy_0596	phosphoglycerate mutase			71	SPync041				sRNASpy490504			YES	+
Spy_sRNA482963	482817	482963	147	**TPP**	-1	← ← ←	**5' UTR**	SPy_0600	thiamine transporter	SPy_0601	N-acetylmuramoyl-L-alanine amidase	137	SPync042	2006	x	RNA484784				YES	+
Spy_sRNA500055	500055	500171	117	**yybP-ykoY**	1	→ → →	**5' UTR or 3' UTR**	SPy_0622	hypothetical protein	SPy_0623	pacL: calcium-transporting ATPase	76	SPync043			RNA501950		SSRC10		YES	+
Spy_sRNA516068	516068	516151	84	no	1	→ → →	**5' UTR or 3' UTR**	SPy_0642	(Fe-S)-binding protein	SPy_0643	prfB: peptide chain release factor 2	385	SPync044							YES	
Spy_sRNA529558	529558	529627	70	no (attP-L phage 370.1)	1	→ → ←	**IGR**	SPy_0654	hypothetical protein	SPy_0655	int1: integrase	28							1	YES	-
Spy_sRNA531081	531081	531168	88	no (310.1)	1		**as to transcript**	SPy_0655	int1: integrase			140	SPync046							YES	+
Spy_sRNA531147	531126	531147	22	no (310.1)	-1	← ← ←	**3' UTR**	SPy_0655	int1: integrase	SPy_0656	hypothetical protein	41	SPync047							YES	
Spy_sRNA532788	532742	532788	47	no (310.1)	-1		**as to transcript**	SPy_0659	hypothetical protein			68	SPync048						1	YES	+
Spy_sRNA542268	542254	542268	15	no (370.1)	-1	→ ← →	**IGR**	SPy_0671	hypothetical protein	SPy_0672	hypothetical protein	8							1	NO	+
Spy_sRNA544833	544833	544916	84	no (370.1)	1	→ → →	**5' UTR or 3' UTR**	SPy_0677	phage associated protein	SPy_0678	phage associated protein	33			x					YES	+
Spy_sRNA576081	576034	576081	48	no	-1	← ← ←	**5' UTR**	SPy_0717	rpmE2: 50S ribosomal protein L31	SPy_0720	hypothetical protein	257							1	YES	
Spy_sRNA579683	579683	579742	60	**L19**	1	→ → →	**5' UTR**	SPy_0723	transposase	SPy_0724	rplS: 50 ribosomal protein L19	330				SR540686				YES	
Spy_sRNA598538	598538	598655	118	**pelRNA**	1	→ → →	**5' UTR**	SPy_0737	epf: extracellular matrix binding protein	SPy_0738	sagA: streptolysine S associated protein	68	SPync053		x	SR559590 (NB)				YES	
Spy_sRNA614841	614841	614863	23	no	1	→ → →	**5' UTR or 3' UTR**	SPy_0754	atpE: ATP synthase F0F1 subunit C	SPy_0755	atpB: ATP synthase F0F1 subunit C	67							1	YES	
Spy_sRNA623726	623726	623928	203	**pheST T-box**	1	→ → →	**5' UTR**	SPy_0766	endA: nuclease	SPy_0768	pheS: phenylalanyl-t-RNA synthetase subunit alpha	87	SPync056				sRNA490592	SSRC13		YES	
Spy_sRNA639369	639369	639398	30	no	1	→ → →	**5' UTR**	SPy_0778	ABC transporter substrate binding protein	SPy_0779	rpsU: 30S ribosomal protein S21	823			x					YES	
Spy_sRNA644794	644794	644820	27	no	1	→ → →	**5' UTR**	SPy_0784	rmlD: dTDP-4-keto-L-rhamnose reductase	SPy_0784	hypothetical protein	27							1	YES	
Spy_sRNA658201	658201	658242	42	no	1	→ → →	**5' UTR**	SPy_0798	hypothetical protein	SPy_0799	pepT: peptidase T	344							1	YES	
Spy_sRNA661400	661400	661518	119	**L20**	1	→ → →	**5' UTR**	SPy_0803	cmk: cytidylate kinase	SPy_0804	infC: translation initiation factor IF-3	1091	SPync057	2006		SR622408				YES	

Spy_sRNA676268	676268	676322	55	**L21**	1	→ → →	**5' UTR**	SPy_0818	capsule biosynthesis protein	SPy_0819	rplU: 50S ribosomal protein L21	207							1	YES	
Spy_sRNA678476	678456	678476	21	no	-1		**as to CDS**	SPy_0824	capsular polysaccharide biosynthesis protein			15							1	NO	-
Spy_sRNA680207	680207	680277	71	**PyrR1**	1	→ → →	**5' UTR**	SPy_0827	pseudouridine synthase D	SPy_0830	pyrR: pyrimidine regulatory protein PyrR	252	SPync059	2006		SR641213		SSRC14		YES	+
Spy_sRNA684274	684274	684376	103	no	1	→ → →	**3' UTR**	SPy_0833	carA: carbamoyl phosphate synthase small subunit	SPy_0835	carB: carbamoyl phosphate synthase large subunit	566							1	NO	
Spy_sRNA694150	694150	694234	85	no	1	→ → →	**IGR**	SPy_0841	RNA binding protein	SPy_0843	hypothetical protein	23							1	YES	+
Spy_sRNA704619	704619	704683	65	no	1	→ → →	**5' UTR**	SPy_0852	apbA: 2-dehydropantoate 2-reductase	SPy_0853	transcriptional repressor	76	SPync061							YES	
Spy_sRNA713953	713953	714006	54	no	1	→ → →	**5' UTR or 3' UTR**	SPy_0865	hypothetical protein	SPy_0866	papS: tRNA CCA pyrophosphorylase	34							1	NO	
Spy_sRNA717625	717625	717745	121	no	**1**	→ → →	**IGR**	SPy_0867	ABC transporter ATP binding protein	SPy_0870	fms: peptide deformylase	11	SPync062	2006	x					NO	-
Spy_sRNA728180	728180	728195	16	no	1		**as to CDS**	SPy_0880	mvaS.1, 3-hydroxy-3-methylglutaryl-coenzyme A			21							1	YES	+
Spy_sRNA737945	737945	738003	59	no	1	→ → →	**5' UTR or 3' UTR**	SPy_0889	rpiA: ribose 5 phosphate isomerase A	SPy_0890	deoB: phosphopentomutase	80							1	YES	
Spy_sRNA744487	744487	744600	114	**PyrR2**	1	→ → →	**5' UTR**	SPy_0899	hypothetical protein	SPy_0900	pyrF: orotidine 5'-phosphate decarboxylase	21	SPync065		x					YES	-
Spy_sRNA746178	746178	746201	24	no	1	→ → →	**IGR**	SPy_0901	pyrE: orotate phosphoribosyltransferase	SPy_0902	amiC: amydase	501							1	YES	
Spy_sRNA763180	763165	763180	16	no	-1		**as to CDS**	SPy_0918	exfoliative toxin			7							1	NO	
Spy_sRNA773110	773110	773132	23	no	1	→ → →	**5' UTR**	SPy_0929	nth: endonuclease III	SPy_0930	hypothetical protein	22							1	YES	
Spy_sRNA776304	776281	776304	24	no	-1		**as to CDS**	SPy_0933	glucose-1-phosphate thymidyl transferase			14							1	NO	-
Spy_sRNA779816	779816	779907	92	no (370.3)	**1**	← → ←	**IGR**	SPy_0937	int3: Integrase	SPy_0938	hypothetical protein	405	SPync067		x					YES	+
Spy_sRNA780010	779922	780010	89	no (370.3)	-1	← ← ←	**3' UTR**	SPy_0937	int3: Integrase	SPy_0938	hypothetical protein	291	SPync069							YES	
Spy_sRNA783335	783320	783335	16	no (370.3)	-1	← ← →	**5' UTR**	SPy_0944	hypothetical protein	SPy_0945	hypothetical protein	42							1	YES	
Spy_sRNA784641	784505	784641	137	no (370.3)	-1		**as to CDS**	SPy_0947	hypothetical protein (end of SPy_0948)			46							1	NO	-
Spy_sRNA792465	792419	792465	47	no (370.3)	**-1**	→ ← →	**IGR**	SPy_0965	hypothetical protein	SPy_0967	hypothetical protein	49	SPync070				sRNASpy491489c			YES	+
Spy_sRNA800369	800301	800369	69	no (370.3)	**-1**		**as to transcript**	SPy_0978	hypothetical protein			878	SPync071							YES	+
Spy_sRNA825970	825970	826113	144	no	1	← → →	**IGR**	SPy_1013	fbp: fibronectin-binding protein-like protein A	SPy_1016	hypothetical protein	32	SPync073							YES	
Spy_sRNA854545	854347	854545	199	**tracrRNA**	**-1**	→ ← →	**IGR**	SPy_1044		SPy_1046	Cas9	262	SPync074	2006	x	RNA772970 (NB)	sRNASpy490822 (NB)			YES	
Spy_sRNA860730	860730	861240	511	**crRNA**	**1**	→ → →	**IGR**	SPy_1049	Csn2	SPy_1052		1396	SPync075				sRNASpy490827			YES	
Spy_sRNA878614	878614	878634	21	no	1	→ → →	**5' UTR**	SPy_1068	uvrC: excinuclease ABC subunit B	SPy_1069	NAD(P)H- dependente quinone reductase	163							1	YES	
Spy_sRNA882398	882398	882494	97	**L10**	1	← → →	**5' UTR**	SPy_1071	trmE: tRNA modification GTPase	SPy_1072	rplJ: 50S ribosomal protein L10	105	SPync076	2006	x	SR800747	sRNASpy490845c			YES	
Spy_sRNA883534	883534	883570	37	no	1	→ → →	**3' UTR**	SPy_1073	rplL: 50S ribosomal protein L7/L12	SPy_1075	hypothetical protein	103	SPync077	2006		SR801894				YES	
Spy_sRNA896885	896864	896885	22	no	-1		**as to CDS**	SPy_1096	folyl-polyglutamate synthetase			12							1	YES	-
Spy_sRNA921480	921480	921541	62	no	1	← → →	**5' UTR**	SPy_1124	hypothetical protein	SPy_1125	GTP pyrophosphokinase	141							1	YES	
Spy_sRNA924338	924322	924338	17	no	-1		**as to CDS**	SPy_1128	eutD phosphotransacetylase			29							1	YES	+
Spy_sRNA930739	930739	930908	170	**purine**	1	→ → →	**5' UTR**	SPy_1135	guanosine 5'-monophosphate oxidoreductase	SPy_1136	xpt: xanthine phosphoribosyltransferase	39	SPync081	2006	x	RNA849201				YES	+
Spy_sRNA946822	946787	946822	36	no	-1	← → →	**5' UTR**	SPy_1151	ldh: L-lactate dehydrogenase	SPy_1152	gyrA: DNA gyrase subunit A	217							1	YES	
Spy_sRNA946941	946941	946976	36	no	1	← → →	**5' UTR**	SPy_1151	ldh: L-lactate dehydrogenase	SPy_1152	gyrA: DNA gyrase subunit A	1587							1	YES	
Spy_sRNA950946	950946	951203	258	no	1	→ → →	**IGR**	SPy_1155	hypothetical protein	SPy_1156	hypothetical protein	34	SPync082			SR869300				YES	
Spy_sRNA956690	956690	956719	30	no	1	→ → →	**5' UTR**	SPy_1163	Smf familly DNA processing protein	SPy_1164	topA: DNA topoisomerase I	38	SPync083							YES	
Spy_sRNA979619	979619	979634	16	no	1		**as to CDS**	SPy_1193	hypothetical protein			68							1	YES	-
Spy_sRNA992257	992231	992257	27	no	-1	← ← ←	**5' UTR**	SPy_1206	ABC transporter ABC binding protein	SPy_1208	hypothetical protein	28							1	YES	
Spy_sRNA996147	995997	996147	151	**asd**	-1	← ← ←	**IGR**	SPy_1211	hypothetical protein	SPy_1212	cardiolipin synthetase	1056	SPync084	2006		SR914400 (NB)	RNASpy490957c (NB)			YES	
Spy_sRNA1023066	1022983	1023066	84	no	-1	← ← ←	**5' UTR or 3' UTR**	SPy_1239	pepN: lysyl aminopeptidase	SPy_1240	phoU: phosphate uptake regulatory protein	29							1	YES	
Spy_sRNA1032107	1032107	1032123	17	no	1		**as to CDS**	SPy_1251	tRNA pseudouridine synthase B			37							1	YES	+
Spy_sRNA1041038	1040988	1041038	51	no	-1	← ← ←	**3' UTR**	SPy_1259	transcriptional regulator	SPy_1260	hypothetical protein	28							1	NO	
Spy_sRNA1046169	1046102	1046169	68	no	-1	← ← →	**5' UTR**	SPy_1267	pcrA: DNA helicase II	SPy_1270	Na(+)- linked D alanine glycine permease	730							1	YES	
Spy_sRNA1046345	1046345	1046593	249	**glycine**	1	← → →	**5' UTR**	SPy_1267	pcrA: DNA helicase II	SPy_1270	Na(+)-linked D-alanine glycine permease	399	SPync087	2006	x	RNA964800	sRNASpy491007c			YES	+
Spy_sRNA1062281	1062265	1062281	17	no	-1	← ← →	**IGR**	SPy_1284	dnaE: DNA polymerase III	SPy_1285	GntR family transcriptional regulator	22							1	NO	
Spy_sRNA1062296	1062296	1062318	23	no	1	← → →	**5' UTR**	SPy_1284	dnaE: DNA polymerase III	SPy_1285	GntR family transcriptional regulator	479							1	YES	
Spy_sRNA1063616	1063602	1063616	15	no	-1		**as to CDS**	SPy_1287	ABC transporter permease			155							1	YES	+
Spy_sRNA1065030	1065030	1065377	348	**tmRNA**	1	← → →	**IGR**	SPy_1289	putative membrane-associated alkaline phosphatase	SPy_1290	hypothetical protein	1509		2006		RNA983400	sRNASpy491023c			YES	+
Spy_sRNA1085297	1085252	1085297	46	no	-1	← ← ←	**IGR**	SPy_1306	malX: maltose/maltodextrine binding protein	SPy_1308	esterase	29						SSRC24		NO	
Spy_sRNA1093376	1093376	1093397	22	no	1	← → →	**5' UTR**	SPy_1314	uvrB: excinuclease ABC subunit B	SPy_1315	hypothetical protein	1981							1	YES	
Spy_sRNA1106573	1106490	1106573	84	no	-1	← ← ←	**IGR**	SPy_1333	ogbE: essential GTPase	SPy_1335	hypothetical protein	28		2006						YES	
Spy_sRNA1108142	1108081	1108142	62	no	-1		**as to CDS**	SPy_1336	transposase			30							1	NO	
Spy_sRNA1109453	1109404	1109453	50	no	-1	→ ← ←	**3' UTR**	SPy_1339	hypothetical protein	SPy_1340	hypothetical protein	16							1	YES	
Spy_sRNA1110925	1110800	1110925	126	no	**-1**	← ← →	**IGR**	SPy_1340	major facilitator superfamily permease	SPy_1343	hypothetical protein	82	SPync090		x					YES	+
Spy_sRNA1126903	1126628	1126903	276	**metK2 riboswitch**	**-1**	← ← ←	**5' UTR**	SPy_1359	metK: S-adenosylmethionine synthetase	SPy_1361	inlA: internalin A precursor	55	SPync091			RNA1083000 (NB)				YES	+
Spy_sRNA1153040	1152787	1153040	254	**alaS T-box**	-1	← ← ←	**5' UTR**	SPy_1389	alaS: alanine tRNA synthetase	SPy_1390	prsA	185			x					YES	
Spy_sRNA1156523	1156470	1156523	54	no	-1	← ← ←	**3' UTR**	SPy_1392	oxalate:formate antiporter	SPy_1393	pepB oligopeptidase	46							1	NO	
Spy_sRNA1167444	1167444	1167461	18	no	1		**as to CDS**	SPy_1408	comEC: competence protein			68							1	NO	+
Spy_sRNA1173936	1173866	1173936	71	no	-1	← ← ←	**3' UTR**	SPy_1414	cation (K) transport protein	SPy_1415	deaD: ATP dependant RNA helicase	125				SR1131900				NO	
Spy_sRNA1178332	1178312	1178332	21	no	-1	← ← ←	**5' UTR**	SPy_1419	hypothetical protein	SPy_1420	murF: Dala Dala adding enzyme	26							1	YES	
Spy_sRNA1185490	1185448	1185490	43	no	-1	← ← →	**5' UTR**	SPy_1429	gpmA: phosphoglyceromutase	SPy_1432	pyrD: dihydroorotate deshydrogenase 1A	95							1	YES	
Spy_sRNA1186876	1186760	1186876	117	no	**-1**	→ ← ←	**IGR**	SPy_1432	pyrD: dihydroorotate dehydrogenase 1A	SPy_1434	heavy metal-transporting ATPase	23	SPync095		x					YES	+
Spy_sRNA1212757	1212757	1212799	43	no (370.2)	1	← → ←	**IGR**	SPy_1469	hypothetical protein	SPy_1470	hypothetical protein	37							1	YES	+
Spy_sRNA1219348	1219348	1219389	42	no (370.2)	1	← → ←	**IGR**	SPy_1484	xis: excisionase	SPy_1485	Cro-like repressor protein	6	SPync096		x					NO	
Spy_sRNA1221370	1221286	1221370	85	no (370.2)	-1		**as to transcript**	SPy_1487	hypothetical protein			136	SPync097				sRNASpy491489c			NO	+
Spy_sRNA1221305	1221305	1221338	34	no (370.2)	1	→ → →	**3' UTR**	SPy_1487	hypothetical protein	SPy_1488	int2: integrase	84	SPync098							NO	
Spy_sRNA1222613	1222580	1222613	34	no (370.2)	-1	→ ← ←	**3' UTR**	SPy_1488	int2: integrase	SPy_1489	hlpA: histone like DNA binding protein	116			x					YES	+
Spy_sRNA1232985	1232966	1232985	20	no	-1	← ← ←	**5' UTR**	SPy_1502	folD	SPy_1503	phosphomannomutase	15							1	YES	
Spy_sRNA1238146	1238104	1238146	43	no	-1	← ← ←	**3' UTR**	SPy_1507	amino acid ABC transporter permease	SPy_1508	hypothetical protein	81			x					NO	
Spy_sRNA1260092	1259959	1260092	134	no	**-1**	← ← →	**IGR**	SPy_1531	dpr: Dps-like peroxide resistance protein	SPy_1532	leader peptidase family protein	219	SPync100							YES	+

Spy_sRNA1267683	1267601	1267683	83	no	-1	← ← ←	**5' UTR**	SPy_1539	asnA: asparagine synthetase	SPy_1541	arcC: carbamate kinase	21							1	YES	
Spy_sRNA1280820	1280782	1280820	39	no	-1	← ← ←	**IGR**	SPy_1556	two component response regulator	SPy_1557	msrA	809							1	YES	
Spy_sRNA1295825	1295682	1295825	144	**valS T-box**	-1	← ← ←	**IGR**	SPy_1570	hypothetical protein	SPy_1571	hypothetical protein	105	SPync103	2006		SR1251900 (NB)	sRNASpy491217c	SSRC29		YES	
Spy_sRNA1298670	1298633	1298670	38	no	-1		**as to CDS**	SPy_1576	3-deoxy-7-phosphoheptulonate synthase			11							1	NO	-
Spy_sRNA1300419	1300419	1300496	78	no	1	→ → ←	**IGR**	SPy_1577	aroB: 3-dehydroquinate synthase	SPy_1580	acetate kinase	90						SSRC30		NO	+
Spy_sRNA1329429	1329429	1329561	133	no	1	→ → →	**3' UTR**	SPy_1608	hypothetical protein	SPy_1610	hypothetical protein	29	SPync104	2006			sRNASpy491243	SSRC31		NO	
Spy_sRNA1330456	1330388	1330456	69	no	-1	→ ← ←	**IGR**	SPy_1610	hypothetical protein	SPy_t10	tRNA-Glu	357							1	YES	
Spy_sRNA1365555	1365437	1365555	119	**RNase P bact b**	-1	← ← ←	**IGR**	SPy_1644	methyltransferase	SPy_1646	cell division initiation protein	686		2006/2008		RNA1320100	sRNASpy1275c			YES	+
Spy_sRNA1369722	1369666	1369722	57	no	-1	→ ← ←	**3' UTR**	SPy_1649	pbp1A	SPy_1651	pepC: cystein aminopeptidase	34							1	NO	
Spy_sRNA1373789	1373724	1373789	66	no	-1	← ← ←	**3' UTR**	SPy_1653	nicotinate phosphoribosyltransferase	SPy_1654	aapA: aminoacid permease	15							1	NO	
Spy_sRNA1379849	1379787	1379849	63	no	-1	← ← ←	**5' UTR or 3' UTR**	SPy_1659	ATP-dependente RNA helicase	SPy_1662	mraY	32							1	YES	
Spy_sRNA1400292	1400175	1400292	118	no	-1	← ← ←	**3' UTR**	SPy_1684	glpK: glycerol kinase	SPy_1686	hypothetical protein	110				SR1355150				YES	
Spy_sRNA1404921	1404703	1404921	219	**glyQS T-box**	-1	← ← ←	**IGR**	SPy_1689	glyQ: glycine--tRNA ligase alpha chain	SPy_1691	hypothetical protein	446	SPync107				sRNASpy491311c (NB)			YES	
Spy_sRNA1424223	1424164	1424223	60	no	-1	→ ← ←	**3' UTR**	SPy_1718	esterase	SPy_1719	rbfA: ribosome binding factor A	30							1	NO	
Spy_sRNA1424640	1424598	1424640	43	no	-1	← ← ←	**5' UTR**	SPy_1719	rbfA: ribosome binding factor A	SPy_1721	infB: translation Initiation Factor IF-2	16	SPync109				sRNASpy491336c			YES	
Spy_sRNA1430184	1430139	1430184	46	no	-1	← ← ←	**IGR**	SPy_1725	hypothetical protein	SPy_t51	tRNA-ser	224		2006		SR1385110				YES	
Spy_sRNA1431858	1431841	1431858	18	no	-1	← ← ←	**5' UTR**	SPy_1727	hypothetical protein	SPy_1728	ABC transporter permease	94							1	YES	
Spy_sRNA1438545	1438488	1438545	58	no	-1	← ← →	**IGR**	SPy_1736	hypothetical protein	SPy_1737	hypothetical protein	35							1	NO	
Spy_sRNA1439780	1439780	1439805	26	no	1	→ → →	**5' UTR**	SPy_1737	hypothetical protein	SPy_1738	manL	88						SSRC34		YES	
Spy_sRNA1443306	1443306	1443490	185	**serS T-box**	1	→ → →	**5' UTR**	SPy_1741	hypothetical protein	SPy_1742	serS: seryl-tRNA synthetase	1849	SPync111			RNA1439100 (NB)	sRNASpy491357			YES	
Spy_sRNA1486297	1486297	1486313	17	no	1		**as to CDS**	SPy_1794	ABC transporter permease			10							1	NO	
Spy_sRNA1525787	1525735	1525787	53	no	-1	← ← ←	**3' UTR**	SPy_1837	mutS2: DNA mismatch repair protein	SPy_1839	hypothetical protein	50	SPync113							NO	
Spy_sRNA1537282	1537282	1537345	64	no	1	← → →	**5' UTR**	SPy_1851	C3-degrading proteinase	SPy_1852	hypothetical protein	374							1	YES	
Spy_sRNA1539542	1539484	1539542	59	no	-1	← ← ←	**IGR**	SPy_1854	glpF.2: glycerol uptake facilitator protein	SPy_1856	norA: antibiotic resistance protein NorA	72	SPync114		x					NO	
Spy_sRNA1551952	1551952	1551975	24	no	1	← → →	**IGR**	SPy_1869	udp: uridine phosphorylase	SPy_1870	GntR family transcriptional regulator	19	SPync115							YES	
Spy_sRNA1555761	1555761	1555844	84	no	1	← → →	**5' UTR**	SPy_1874	glycoprotein endopeptidase	SPy_1875	hypothetical protein	86	SPync116							YES	
Spy_sRNA1566698	1566651	1566698	48	no	-1	← ← ←	**5' UTR**	SPy_1888	rpmB: 50S ribosomal protein L28	SPy_1889	fba: fructose-bisphosphate aldolase	7408			x					YES	
Spy_sRNA1567948	1567930	1567948	19	no	-1	← ← ←	**5' UTR**	SPy_1889	fba: fructose bisphosphate aldolase	SPy_t52	tRNA-Leu	22	SPync117							YES	
Spy_sRNA1571135	1571079	1571135	57	no	**-1**	← ← ←	**IGR**	SPy_1894	pyrG: CTP synthetase	SPy_1895	rpoE: DNA-directed RNA polymerase subunit delta	26	SPync118	2006	x	SR1568180	sRNASpy491561c			NO	+
Spy_sRNA1571806	1571783	1571806	24	no	-1	← ← ←	**5' UTR**	SPy_1895	rpoE: DNA-directed RNA polymerase subunit delta	SPy_1896	RopA: peptidyl-prolyl cis/trans isomerase	502							1	YES	
Spy_sRNA1610157	1610073	1610157	85	**L13**	-1	← ← ←	**5' UTR**	SPy_1932	rplM: 50S ribosomal protein L13	SPy_1934	transcription regulator	83							1	YES	
Spy_sRNA1620465	1620415	1620465	51	no	**-1**	← ← ←	**5' UTR**	SPy_1946	pnpA: polynucleotide phosphorylase/polyadenylase	SPy_1947	translaldolase	318	SPync120							YES	-
Spy_sRNA1663522	1663522	1663724	203	**6S RNA**	1	→ → →	**IGR**	SPy_1992	recombination factor protein RarA	SPy_t56	tRNA-Lys	5354	SPync121		x	RNA1660600				YES	+
Spy_sRNA1663576	1663557	1663576	20	**6S RNA R1**	-1	→ ← →	**IGR**	SPy_1992	recombination factor protein RarA	SPy_t56	tRNA-Lys	6								NO	
Spy_sRNA1663625	1663608	1663625	18	**6S RNA R2**	-1	→ ← →	**IGR**	SPy_1992	recombination factor protein RarA	SPy_t56	tRNA-Lys	3								NO	
Spy_sRNA1680670	1680499	1680670	172	no	-1	← ← →	**IGR**	SPy_2010	C5A peptidase	SPy_2013	IS1562 transposase	105		2006	x	SR1678800 (NB)		SSRC39		YES	
Spy_sRNA1696383	1696383	1696417	35	no	1	← → ←	**IGR**	SPy_2034	hypothetical protein	SPy_2037	foldase prsA	13	SPync123							YES	
Spy_sRNA1696464	1696449	1696464	16	no	-1	→ ← ←	**IGR**	SPy_2034	hypothetical protein	SPy_2037	foldase prsA	284							1	YES	
Spy_sRNA1696905	1696822	1696905	84	no	-1	→ ← ←	**IGR**	SPy_2034	hypothetical protein	SPy_2037	foldase prsA	51							1	YES	
Spy_sRNA1699993	1699935	1699993	59	no	-1	← ← ←	**5' UTR**	SPy_2039	speB: pyrogenic exotoxin B	SPy_2040	hypothetical protein	13	SPync125							NO	
Spy_sRNA1713593	1713446	1713593	148	no	-1	← ← ←	**5' UTR or 3' UTR**	SPy_2058	secE: preprotein translocase subunit secE	SPy_2059	pbp2a: penicillin-binding protein 2A	139	SPync128							YES	
Spy_sRNA1718031	1717943	1718031	89	no	-1		**as to CDS**	SPy_2063	hypothetical protein			46	SPync130							NO	+
Spy_sRNA1721621	1721494	1721621	128	**csRNA**	**-1**	→ ← ←	**IGR**	SPy_2066	dipeptidase	SPy_2070	molecular chaperon groEL	95	SPync131	2006		SR1719800 (NB)				YES	+
Spy_sRNA1727859	1727819	1727859	41	no	-1	← ← ←	**3' UTR**	SPy_2074	ctsR	SPy_2077	csp: cold shock protein	103					sRNASpy491718c			NO	
Spy_sRNA1750524	1750472	1750524	53	no	-1	← ← ←	**5' UTR**	SPy_2095	pepO: endopeptidase O	SPy_2096	dexS: dextran glucosidase	44							1	YES	
Spy_sRNA1755445	1755320	1755445	126	no	**-1**	→ ← ←	**IGR**	SPy_2099	trehalose operon transcriptional repressor	SPy_2102	transcriptional regulator MarR family	2176	SPync133			SR1754950 (NB)	sRNASpy491738			YES	+
Spy_sRNA1760295	1760181	1760295	115	no	-1	← ← ←	**5' UTR or 3' UTR**	SPy_2107	oxidoreductase	SPy_2110	nrdD: anaerobic ribonucleoside triphosphate reductase	46	SPync134							NO	
Spy_sRNA1764396	1764315	1764396	82	no	-1	← ← ←	**5' UTR**	SPy_2111	hypothetical protein	SPy_2112	hypothetical protein	62							1	YES	
Spy_sRNA1774740	1774740	1774779	40	no (370.4)	1	← → ←	**IGR**	SPy_2122	int4: integrase	SPy_2125	repressor protein	46	SPync135		x					NO	+
Spy_sRNA1775122	1775002	1775122	121	no (370.4)	-1	← ← ←	**IGR**	SPy_2122	int4: integrase	SPy_2125	repressor protein	102	SPync136							YES	+
Spy_sRNA1778807	1778712	1778807	96	no (370.4)	-1		**as to transcript**	SPy_2129	hypothetical protein			334	SPync137							YES	+
Spy_sRNA1786666	1786666	1786750	85	no (370.4)	1	→ → ←	**IGR**	SPy_2147	hypothetical protein	SPy_2148	mutS: DNA mismatch repair protein MutS	206							1	YES	+
Spy_sRNA1794883	1794883	1794900	18	no	1		**as to CDS**	SPy_2155	hypothetical protein			6							1	NO	
Spy_sRNA1797333	1797303	1797333	31	no	-1	← ← ←	**5' UTR**	SPy_2156	aspS: aspartyl-tRNA synthetase	SPy_2157	hisS: histidyl-tRNA synthetase	34							1	YES	
Spy_sRNA1811977	1811890	1811977	88	no	-1	← ← ←	**5' UTR**	SPy_2178	rpsD: 30S ribosomal protein S4	SPy_2180	transposase	78	SPync138							YES	
Spy_sRNA1820593	1820515	1820593	79	no	**-1**	← ← ←	**IGR**	SPy_2186	phosphohydrolase	SPy_2188	mnmA: tRNA specific thiouridylase MnmA	472	SPync139	2006	x	SR1806601 (NB)				YES	
Spy_sRNA1839037	1838982	1839037	56	no	-1	← ← ←	**5' UTR**	SPy_2205	hypothetical protein	SPy_2206	guaB: inosine 5'-monophosphate dehydrogenase	14							1	NO	
Spy_sRNA1842269	1842185	1842269	85	**trsA T-box**	-1	← ← →	**5' UTR**	SPy_2207	tryptophanyl-tRNA synthetase	SPy_2209	hyp. membrane spanning protein	55		2006/2008	x					YES	+
Spy_sRNA1849261	1849261	1849323	63	no	1	← → →	**IGR**	SPy_2214	transposase	SPy_t10	tRNA-arginine	1491							1	YES	-
Spy_sRNA1851592	1851576	1851592	17		-1		**as to transcript**	SPy_2216	htrA serine protease			6	SPync141							NO	

Table S2. Novel putative regulatory RNAs identified by visual inspection the sRNA sequencing data using the Integrative Genome Viewer (IGV)
For each identified putative sRNA, the identifier, coordinates, size, predicted function (Rfam database), strand, predicted location, transcriptional direction (middle arrow), surrounding genes located upstream and downstream, coverage (number of cDNA reads calculated using SAMtools), and a comparison with previous screens are indicated. sRNAs confirmed by Northern blot analysis are indicated. Validated elements with a putative function, sRNAs and asRNAs are highlighted in green, blue and in orange, respectively. Note that the sRNAs described in this table were expressed in three independent libraries of *S. pyogenes* SF370 sRNAs (data not shown). NB, Northern blot.

Table S3: List of Strains, Plasmids and Oligos used in this study

Strain	Relevant characteristics	Source
Streptococcus pyogenes		
WT		
EC904	SF370 (M1 serotype) (WT)	ATCC 700294
Δ*rnc*		
EC1636	EC904Δ*rnc*	[21]
Δ*rny*		
EC2058	EC904Δ*rny*	this study
Δ*ciaR*		
EC1732	EC904Δ*ciaR*	this study
E. coli		
RDN204	TOP10, Host for cloning	Invitrogen

Plasmids	Relevant characteristics	Source
Vectors for *S. pyogenes*		
pEC85	*repDEG*-pAMβ1, pJH1-*aphIII*, ColE1	Bernhard Roppenser
pEC214	pWV01-*repA*ts, pJH1-*aphIII*, P*clpB*-*βgal*, ColE1	Lab collection
pEC454	pUC19Ωlox66-*erm*-lox71	Lab collection
pEC455	pEC85ΩP*gyrA*-*cre* recombinase	Lab collection
Plasmids used for the overexpression of CiaR		
pET21	f1, pBR322	Novagen
pEC1455	pET21Ω*ciaR*	This study
Plasmids used for the construction of Δ*ciaR*		
pEC277	pEC214Ω*ciaR*koup-*ciaR*kodw	This study

Purpose	Primer code	Sequence 5’-3’[a]	F/R[b]	Usage[c]
Primers used for Northern blots of putative sRNAs				
Spy_sRNA93359	OLEC1023	*CTGACTTTATCAGTGTGATTTAACTGCTGT*	R	NB
Spy_sRNA195261	OLEC1024	*GAAGATAGGTGCCCAGGAGATTTATGAAAA*	R	NB
Spy_sRNA318404	OLEC1026	*CTCAGCAAACAATGTGGTTGATGGTGACTC*	R	NB
Spy_sRNA542268	OLEC3160	*CTGAGCTACGCCCCCTCTGTCCTTTGTC*	R	NB
Spy_sRNA544833	OLEC3161	*AGTTTGATCGTAGTTAAAGTTGGCGACTAA*	R	NB
Spy_sRNA694150	OLEC3162	*TAAACTTGCTTCAACACCACTGTTTTATAA*	R	NB
Spy_sRNA779816	OLEC1033	*CGAGGCAAATCTAGTATAGTAAAAACCTGC*	R	NB
Spy_sRNA1110925	OLEC1036	*GCAAGTCCATCAAAGTTCACTAAATAATAA*	R	NB
Spy_sRNA1126903	OLEC1037	*GTTCCCCAAATGAAGTCAACAACGTCTCAA*	R	NB
Spy_sRNA1186876	OLEC1039	*GCTAAACCAATGATCATAATAGTAAACATA*	R	NB
Spy_sRNA1212757	OLEC3163	*AAAAAGCCAGCTCACAGCTGACTCCTTAGT*	R	NB
Spy_sRNA1222613	OLEC3164	*AAAGCCCACTGCACAGGCTACAACGCTTGT*	R	NB
Spy_sRNA1260092	OLEC1040	*GACCTAATCCTATTCGACAATAACGGAATA*	R	NB
Spy_sRNA1300419	OLEC3165	*TTTCTCATTAAGGCTTTTTAGACGAAATAA*	R	NB
Spy_sRNA1571135	OLEC1041	*GAGAGCTTTTGCCTGACCTCATAAAGAGGT*	R	NB
Spy_sRNA1721621	OLEC1043	*GATAGCATTAGTTTAAGACGATACTTCTAC*	R	NB
Spy_sRNA1755445	OLEC1044	*GAGTTTCCCCATTATCAACTGTGTTATTGT*	R	NB
Spy_sRNA1774740	OLEC3166	*AAGTTTTCCACGCTCGCAAGGTCTTAAAAA*	R	NB
Spy_sRNA1775122	OLEC3167	*ACCGTCCCACACTTTAGCCAATCGTGGACG*	R	NB
Spy_sRNA1786666	OLEC3168	*TTACACAATGAGTTCAGCAGGCAAGAACTA*	R	NB
Primers used for Northern blots of putative asRNAs				
Spy_sRNA392987	OLEC3145	*AATCCTGTATAGTAGAGTTGCGACACTTAC*	R	NB
Spy_sRNA477741	OLEC3146	*CCTTTTAACCTGGTGATGACATCGCTAGGT*	R	NB
Spy_sRNA480642	OLEC4058	*TTGATCTCTTACTGACAAGACACTCACTTT*	R	NB
Spy_sRNA480696	OLEC4057	*AAAGTGAGTGTCTTGTCAGTAAGAGATCAA*	R	NB
Spy_sRNA531081	OLEC4893	*TTTTTACTATACTAGATTCGCCTCACGCTC*	R	NB
Spy_sRNA532788	OLEC4056	*CTGTAAAATAGCAGTTTACGGGACAGACAG*	R	NB
Spy_sRNA728180	OLEC4064	*CCGTGCGCCTTTTAG*	R	NB
Spy_sRNA800369	OLEC1034	*GAAATAACAAATACCGTCTAGCTCTCGGTC*	R	NB
Spy_sRNA924338	OLEC4067	*TGTTCGTCCAGCTCTTC*	R	NB
Spy_sRNA1032107	OLEC4069	*GCCGTCTTAGTCTCCC*	R	NB
Spy_sRNA1063616	OLEC4070	*CTCCCTGATCGCTGG*	R	NB
Spy_sRNA1167444	OLEC4071	*TGGGCGCCCTTTCTTTT*	R	NB
Spy_sRNA1221370	OLEC4060	*AGAGCGTGAGGCGAATCTAGTATAGTAAAA*	R	NB
Spy_sRNA1718031	OLEC4061	*TCCTAGCCTTTTGAGTTTATCTGTTTTCAT*	R	NB
Spy_sRNA1778807	OLEC4062	*GCGACCAAACTTCCAAGCCTTTAATTAGTA*	R	NB
Primers used for Northern blots of known sRNAs				
SRP	OLEC431	*TGTTTCATCATAACTCCCAT*	F	NB
	OLEC432	*CCTCTTAGCCTAAATAAAAA*	R	NB
tmRNA	OLEC448	*TTTGGGGTTGTTACGGATTC*	F	NB
	OLEC449	*AACATATTTGTCTACGTCCA*	R	NB
RNase P	OLEC375	*TAGCTTAACCTATTATGCAA*	F	NB
	OLEC376	*AGGGATGTGCATACACATTA*	R	NB
6S RNA	OLEC653	*ACATTGCTGTGGCATACGA*	F	NB
	OLEC654	*TGAGCCCGCGCAGTATAA*	R	NB
T-box-tsrA	OLEC468	*AAAAAGTCCCCACGCTATTA*	F	NB
	OLEC469	*TGTACTGAGACCGTCAAGTC*	R	NB
yybP-YkoY	OLEC352	*AGATAGCAGTAAATCATCTGA*	F	NB
	OLEC353	*GTTGTTCAAATAAAAAGACC*	R	NB
PyrR	OLEC709	*ATAATAGTTTAAATTTAGACA*	F	NB
	OLEC710	*CTATAATGTGTCAATATCTCA*	R	NB
glycine	OLEC435	*TTTTTGAGGTATGATAGTCC*	F	NB
	OLEC436	*ATTTAACGAGTGCTATCATC*	R	NB
purine	OLEC437	*TGATATGGAGTTAGCTAGGA*	F	NB
	OLEC438	*CAAAGCCAGAAACTATAAGA*	R	NB
TPP	OLEC397	*CCATAAGAAGGACTAAACCA*	F	NB
	OLEC398	*TAAAACCCCTTATCCTTGAC*	R	NB
FMN	OLEC433	*GTCAGTAGCTGACGCTTTTA*	F	NB
	OLEC434	*GATATCGCAGAAAGTATACC*	R	NB
Loading controls for Northern blots				
5S rRNA	OLEC288	*CTAAGCGACTACCTTATCTCA*	R	NB
Primers used for CiaR overexpression (Cloning in pEC21a)				
CiaR	OLEC1471	GGTGGTCATATG*ATGATAAAAATATTATTA*	F	PCR

	OLEC1472	TGATCTCGAG*TTCATTGTTTTTTAGAATATATCC*	R	PCR
Primers used for amplification of the CiaR-binding promoter regions				
Spy_sRNA195261	OLEC1574	*GGTTTAGGTAAACCGCTTTTTAGG*	F	PCR
	OLEC1575	*TTTGGCGTGGAAACTAGCTCTCTC*	R	PCR
Spy_sRNA1721621	OLEC1627	*GGAATGACATTAGTATACTAGATAAG*	F	PCR
	OLEC1628	*TAACCGTTGCTATCACCAGATTCA*	R	PCR
pepV	OLEC1603	*GGACAATTAGTTAAATGTAATGTC*	F	PCR
	OLEC1604	*GGTTGTCATTATACTCTCCTTATTC*	R	PCR
SP_0570	OLEC1607	*GTGACATGATAACTCCTTTATCTA*	F	PCR
	OLEC1608	*TTCTCTGAAAGAGCAACTATTGTT*	R	PCR
htrA	OLEC1611	*CCTTTGTACAAAGGTCTTTATTAG*	F	PCR
	OLEC1612	*GCATGTTTTGTCCTCCGAATTATT*	R	PCR
pepO	OLEC1615	*TGATAAGTTGTCATTCGTATCTCC*	F	PCR
	OLEC1616	*CAATTGAGATAAGTTATTTTAGCT*	R	PCR
pcrA	OLEC1619	*AAGGATTCATGCTTTCTCCTTAAT*	F	PCR
	OLEC1620	*AGGAATCTCTTTACTTTTGGGGTC*	R	PCR
pbp2A	OLEC1623	*CTCATAACGTTATTATACCACTATG*	F	PCR
	OLEC1624	*ATTCAAACGGAATTTGCACATCAC*	R	PCR
negative control	OLEC1303	GAAATTAATACGACTCACTATAG*GCATCCTAAAAAGCGGTTTACCTAAACCG*	F	PCR
	OLEC1523	*AAAAACCTAACCAGCCGGTTAACTGG*	R	PCR
Primers used for construction of pEC455				
P*gyrA* from *Streptococcus agalactiae*	OLEC1852	*GGTTCGTATGGCTCAGTGGT*	F	PCR
	OLEC1853	*GTTCTCTTTCGCTTCCATCGT*	R	
cre recombinase from pNZ5348	OLEC1933	*CAGTGAAGAAAAGGGGCATTTTTTAATGGTATCCAATTTACTGACCGTACAC*	F	PCR
	OLEC1934	*AAAGAGCTCCTAATCGCCATCTTCCAGCAGG*	R	
Primers used for construction of ∆*rny*				
Up fragment	OLEC1998	*ATGATGATCAATGATTTTGAAAAAAGAGAAAATG*	F	PCR
	OLEC1999	*TATAATGTATGCTATACGAACGGTAGTTTGTACCTCAATATATTCTAGATTTCATTAA*	R	
Dw fragment	OLEC2000	*ATAGCATACATTATACGAACGGTAAAAAAGAGGAATTATCCTCTTTTTCTTTATGA*	F	PCR
	OLEC2501	*CAAGTGCCTGAAGTGTTGACTTC*	R	
PCR checking	OLEC2502	*TAATGAAATCTAGAATATATTGAGGTACAAAC*	F	PCR
	OLEC2503	*GACAGCTTCACGTTTAGCTGAAG*	R	
	OLEC2785	*TCGCAATCGTTGAAAATCAT*	F	SEQ
	OLEC2786	*CGAACGGTAGTTTGTACCTCAA*	R	SEQ
Primers used for construction of ∆*ciaR*				
Up fragment	OLEC1350	GGGCTG*GGATCCCGCTTGGTTTTAGCCAACCAAATG*	F	PCR
	OLEC1351	*ATCTCTTTTTTTAATTTGTTCATGTCTCTACCTCAATTGTTCT*	R	
Dw fragment	OLEC1352	*AGAACAATTGAGGTAGAGACATGAACAAATTAAAAAAAGAGAT*	F	PCR
	OLEC1353	TTTGGG*GAATTCTTTAGCAACTAGTTCATAATTCTC*	R	
PCR checking	OLEC1363	*TTATCTTACAGATTATGCGGTTTGG*	F	SEQ
	OLEC1364	*CTAGTCATGAATTAAGGACCCC*	F	SEQ

[a] *italic*, sequence annealing to the template; underlined, restriction site;.

[b] F, forward primer; R, reverse primer.

[c] NB, probe for Northern blot; SEQ, sequencing.

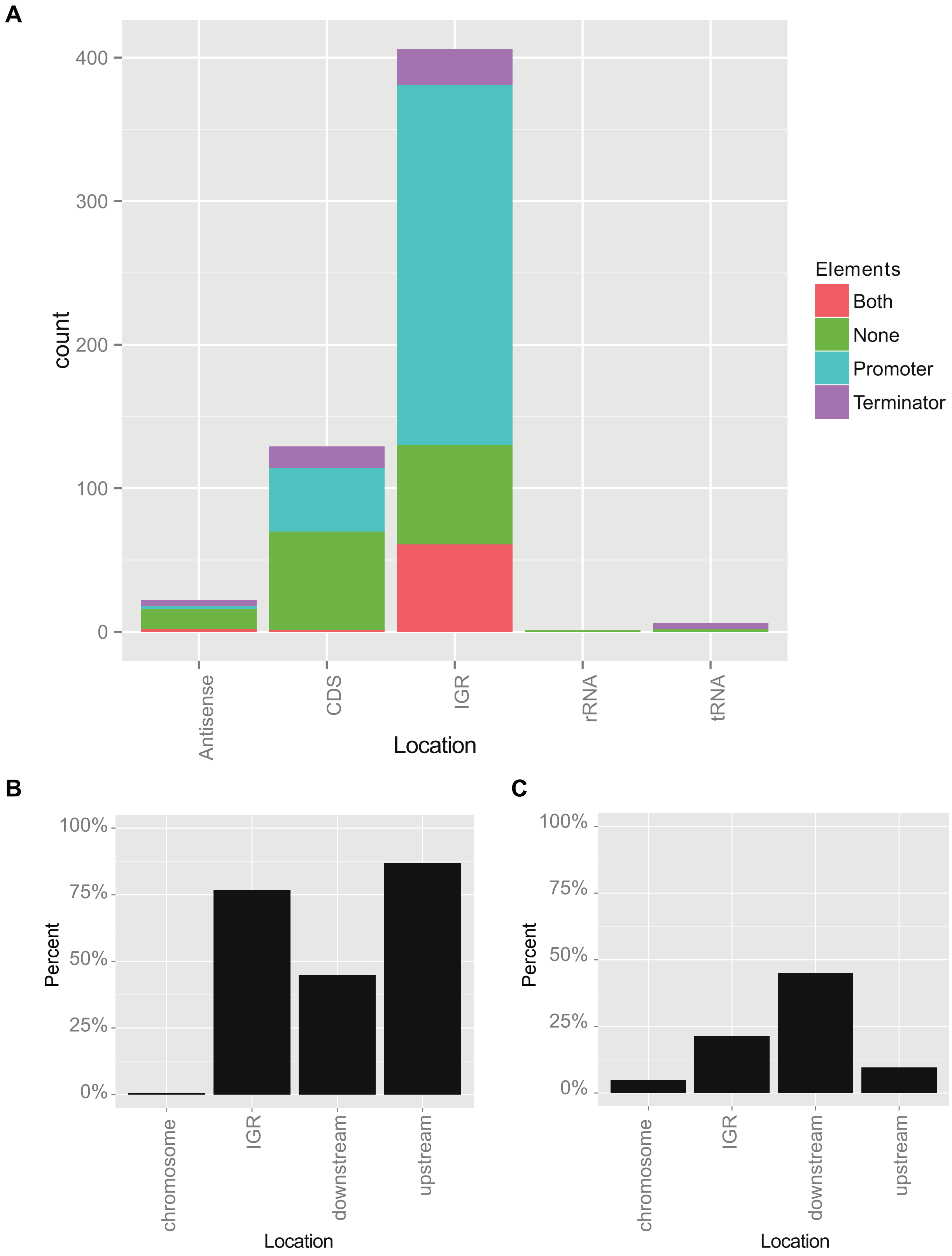


Figure S1. sRNA categories

The bars in **A** represent the distribution of reads in the different annotated regions on the genome. Antisense indicates putative sRNAs that are transcribed opposite to the three annotated regions: CDS, rRNA and tRNA. The colors of the bars represent the number of the predicted RNAs that had a promoter upstream (blue), a terminator downstream (purple), both a promoter and a terminator (red), or no promoter and no terminator (green). The bars in **B** represent the percent of sRNAs that had a predicted promoter located right upstream of the sRNA sequence. The bars in **C** represent the percent of sRNAs that had a predicted terminator located downstream of the sRNA sequence. Chromosome shows the percent locations on the chromosome that fit the same criteria. CDS: coding sequence.

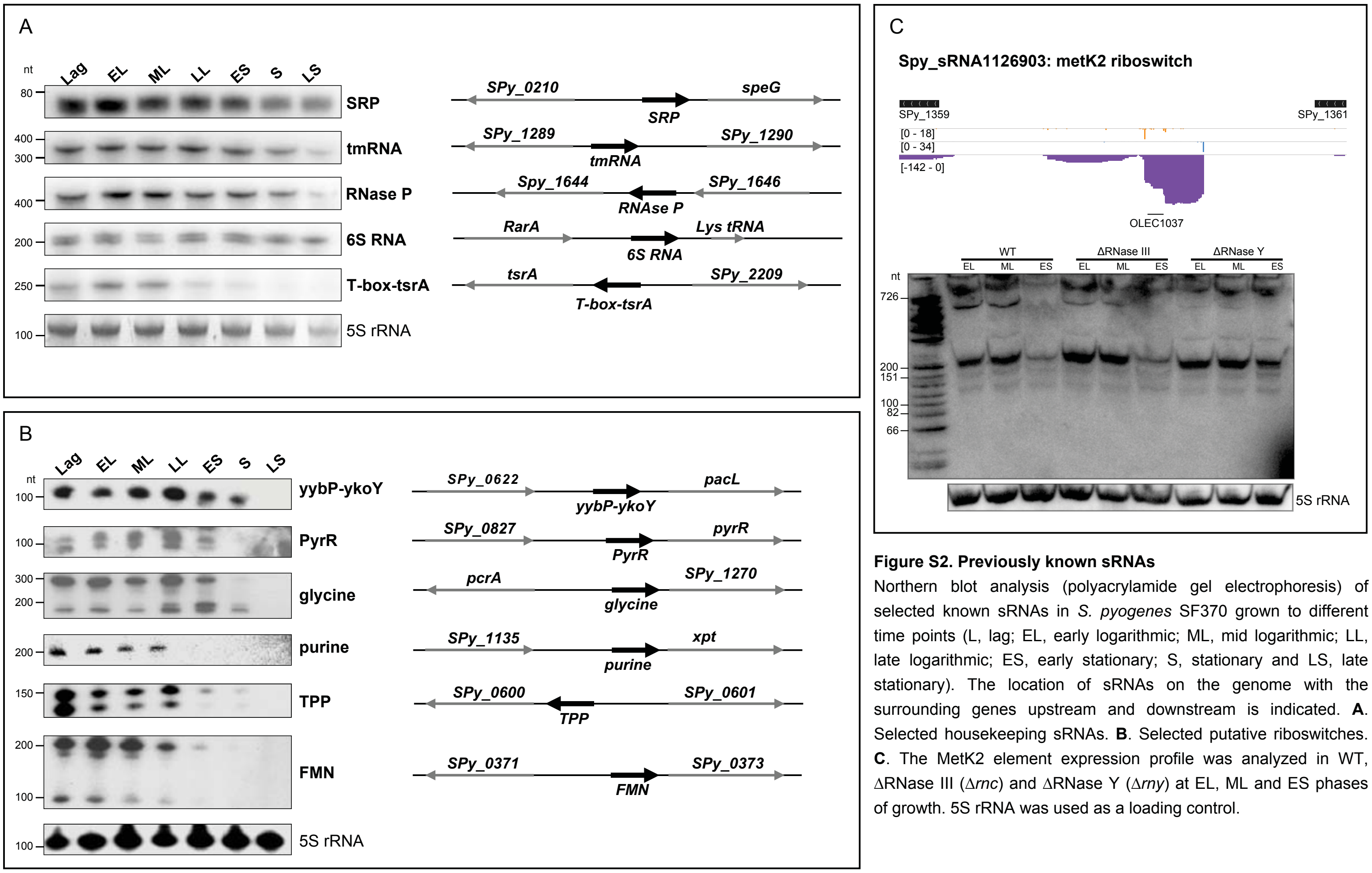


Figure S2. Previously known sRNAs

Northern blot analysis (polyacrylamide gel electrophoresis) of selected known sRNAs in *S. pyogenes* SF370 grown to different time points (L, lag; EL, early logarithmic; ML, mid logarithmic; LL, late logarithmic; ES, early stationary; S, stationary and LS, late stationary). The location of sRNAs on the genome with the surrounding genes upstream and downstream is indicated. **A**. Selected housekeeping sRNAs. **B**. Selected putative riboswitches. **C**. The MetK2 element expression profile was analyzed in WT, ΔRNase III (Δ*rnc*) and ΔRNase Y (Δ*rny*) at EL, ML and ES phases of growth. 5S rRNA was used as a loading control.

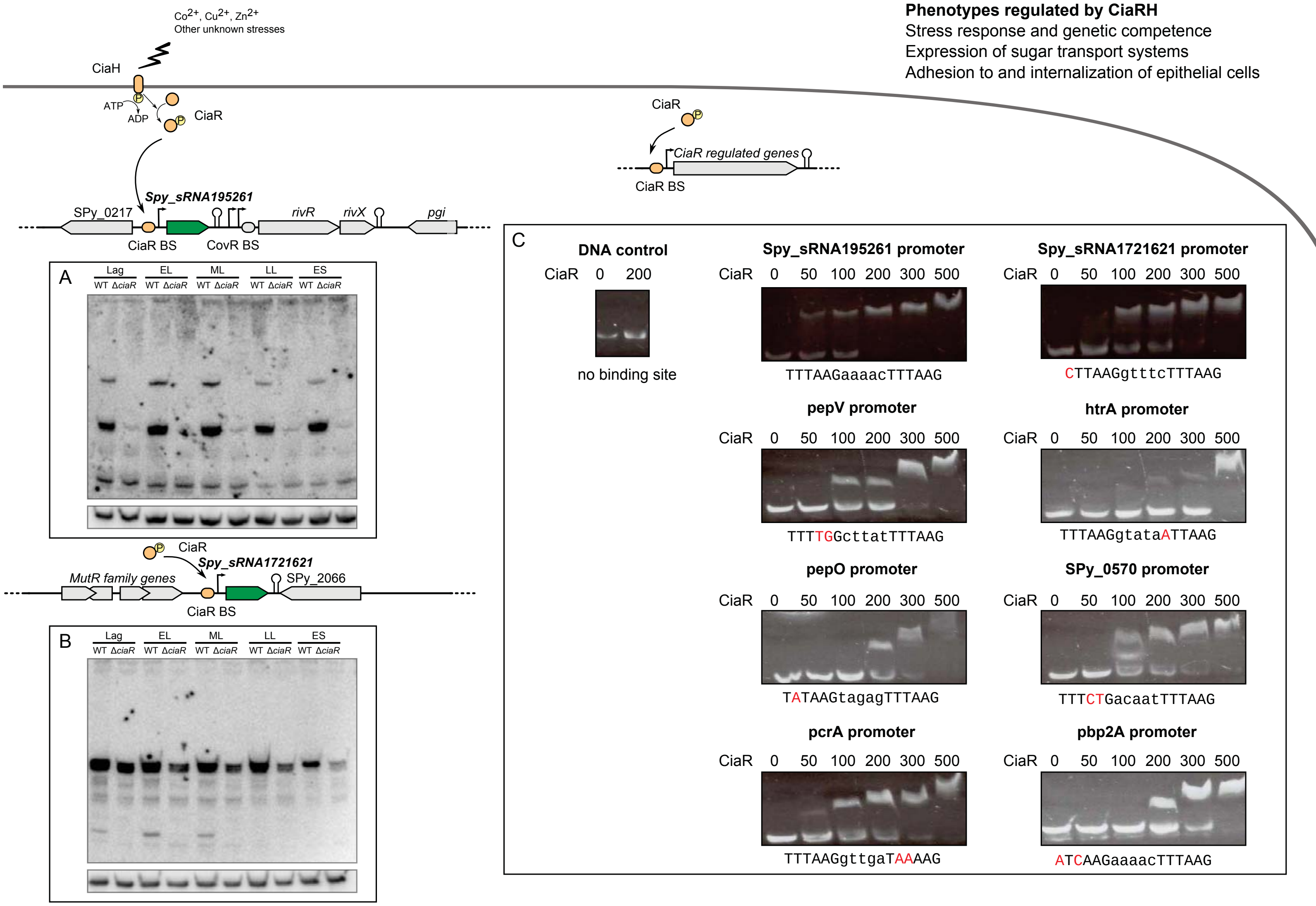
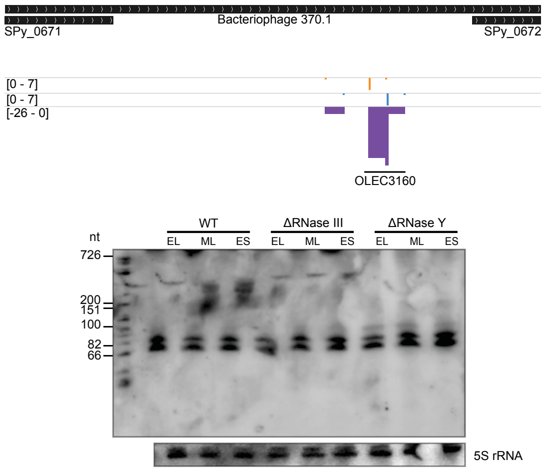

Co2+, Cu2+, Zn2+
Other unknown stresses
CiaH
ATP
ADP
P
CiaR
Phenotypes regulated by CiaRH
Stress response and genetic competence
Expression of sugar transport systems
Adhesion to and internalization of epithelial cells
CiaR
CiaR regulated genes
CiaR BS
Spy_sRNA195261
SPy_0217
rivR
rivX
pgi
CiaR BS
CovR BS
A
Lag
EL
ML
LL
ES
WT ΔciaR
CiaR
Spy_sRNA1721621
MutR family genes
SPy_2066
CiaR BS
B
Lag
EL
ML
LL
ES
WT ΔciaR
C
DNA control
CiaR 0 200
no binding site
Spy_sRNA195261 promoter
CiaR 0 50 100 200 300 500
TTTAAGaaaacTTTAAG
Spy_sRNA1721621 promoter
CiaR 0 50 100 200 300 500
CTTAAGgtttcTTTAAG
pepV promoter
CiaR 0 50 100 200 300 500
TTTTGGcttatTTTAAG
htrA promoter
CiaR 0 50 100 200 300 500
TTTAAGgtataATTAAG
pepO promoter
CiaR 0 50 100 200 300 500
TATAAGtagagTTTAAG
SPy_0570 promoter
CiaR 0 50 100 200 300 500
TTTCTGacaatTTTAAG
pcrA promoter
CiaR 0 50 100 200 300 500
TTTAAGgttgaTAAAAG
pbp2A promoter
CiaR 0 50 100 200 300 500
ATCAAGaaaacTTTAAG

Figure S3. csRNAs in *S. pyogenes*

The drawing represents the cytosol (lower part) separated from the extracellular environment (upper part) by the cell wall/membrane delineated by a grey line. The two identified csRNAs of *S. pyogenes* SF370 are depicted in green. The two-component system CiaRH is represented in orange. CiaH is the sensor anchored in the membrane and CiaR is a transcriptional regulator binding to a specific DNA sequence that is located upstream of the csRNAs and other genes in the genome. Northern blot analysis (polyacrylamide gel electrophoresis) of **A**. Spy_sRNA195261 and **B**. Spy_sRNA1721621 csRNA expression in WT and Δ*ciaR* strains grown to different growth phases (lag; EL, early logarithmic; ML, mid logarithmic; LL, late logarithmic and ES, early stationary). 5S rRNA is used as loading control. In the presence of CiaR, csRNA expression is up-regulated at all phases of growth. **C.** Electrophoretic mobility shift assays of various putative CiaR binding promoter regions containing the TTTAAG-N_5-TTTAAG. Molar ratios of CiaR to promoter fragment are indicated for each lane. No shift was observed with the control DNA that does not contain the consensus sequence. Spy_sRNA195261 and Spy_sRNA1721621 promoter fragments (top) are bound by CiaR. Spy_sRNA195261 promoter contains a perfect CiaR binding motif and shows stronger binding than the Spy_sRNA1721621 promoter region with a single mismatch to the consensus sequence. Note, that as observed by Northern blot analysis (**A** and **B**), CiaR had a stronger regulatory effect on Spy_sRNA195261. Promoter regions of genes with degenerated CiaR-binding motifs (bottom) are bound by CiaR with varying affinities suggesting potential regulation of those genes by CiaRH.

Spy_sRNA542268



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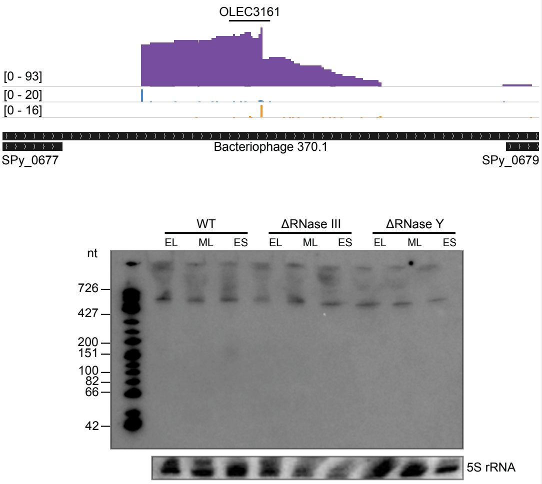

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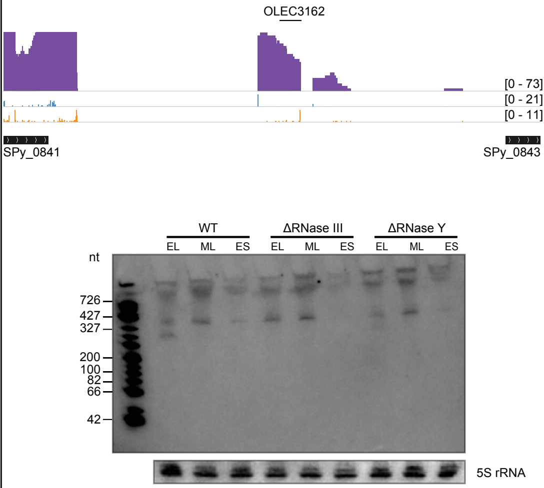

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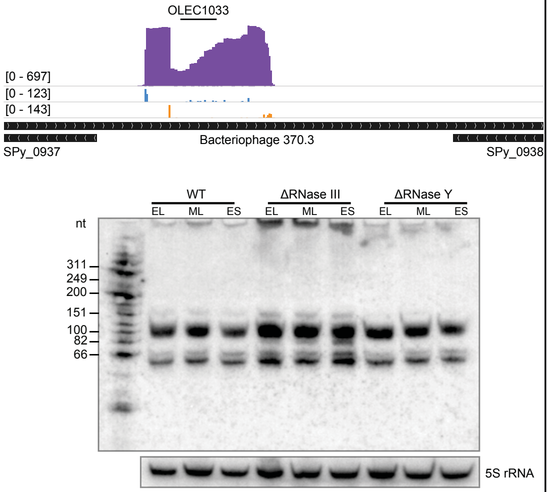

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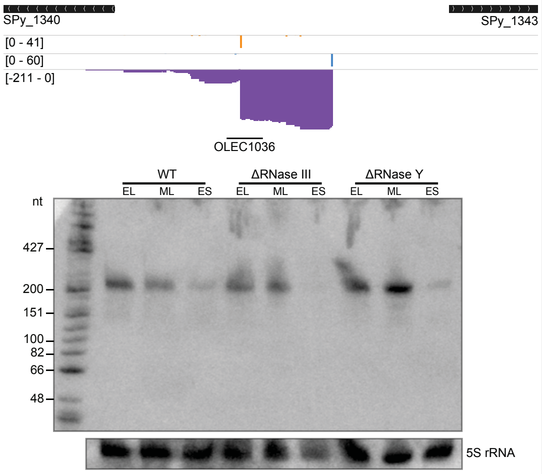
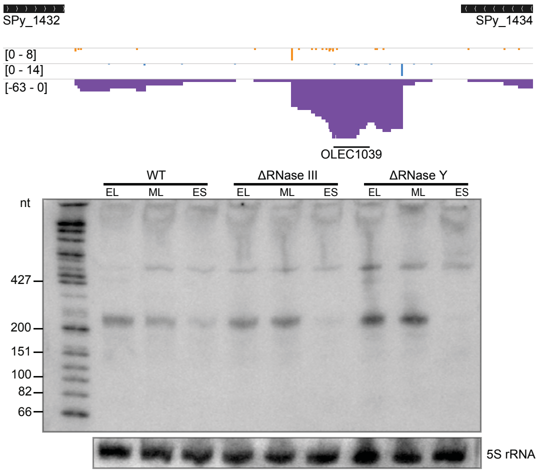


Spy_sRNA1186876



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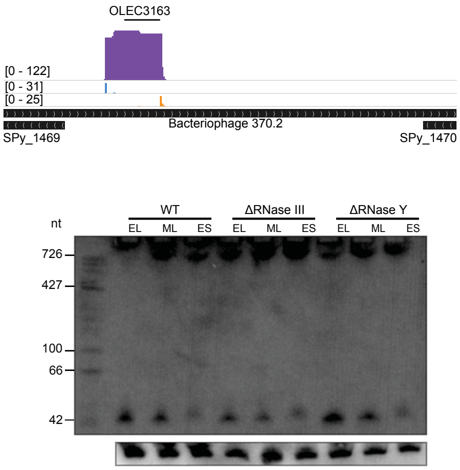

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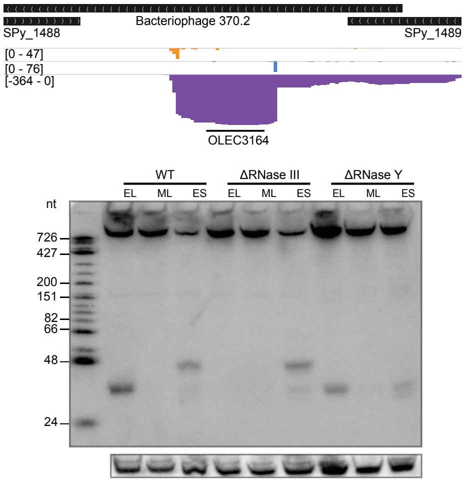

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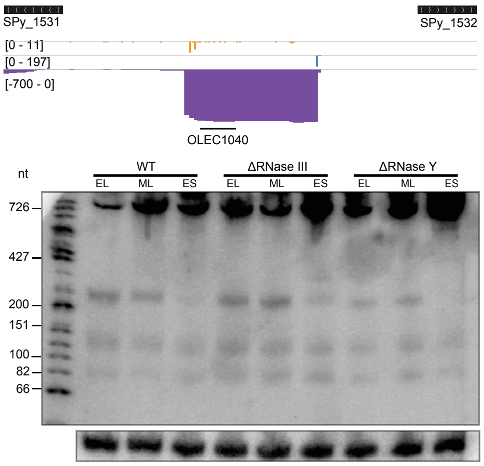
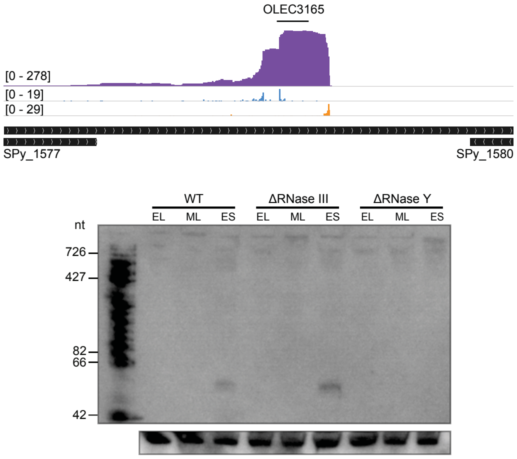
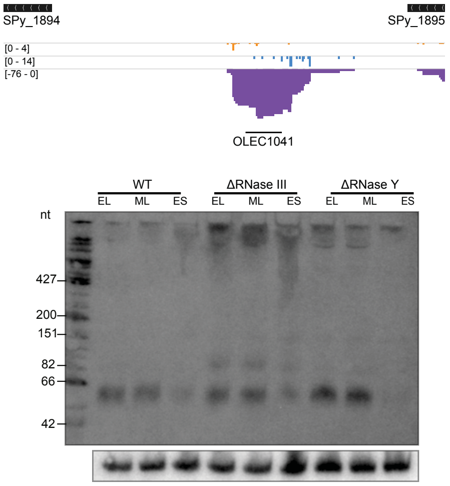


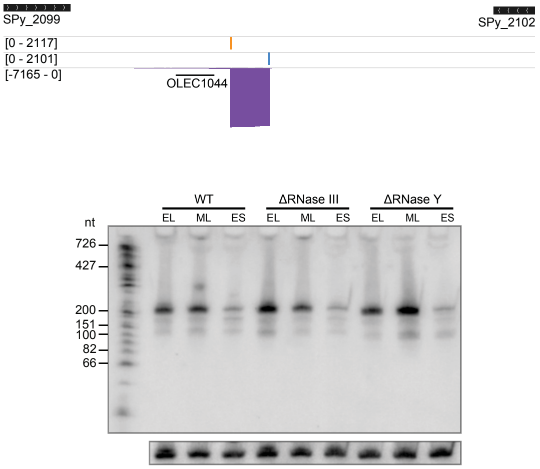
Spy_sRNA1300419



Spy_sRNA1571135



Spy_sRNA1755445



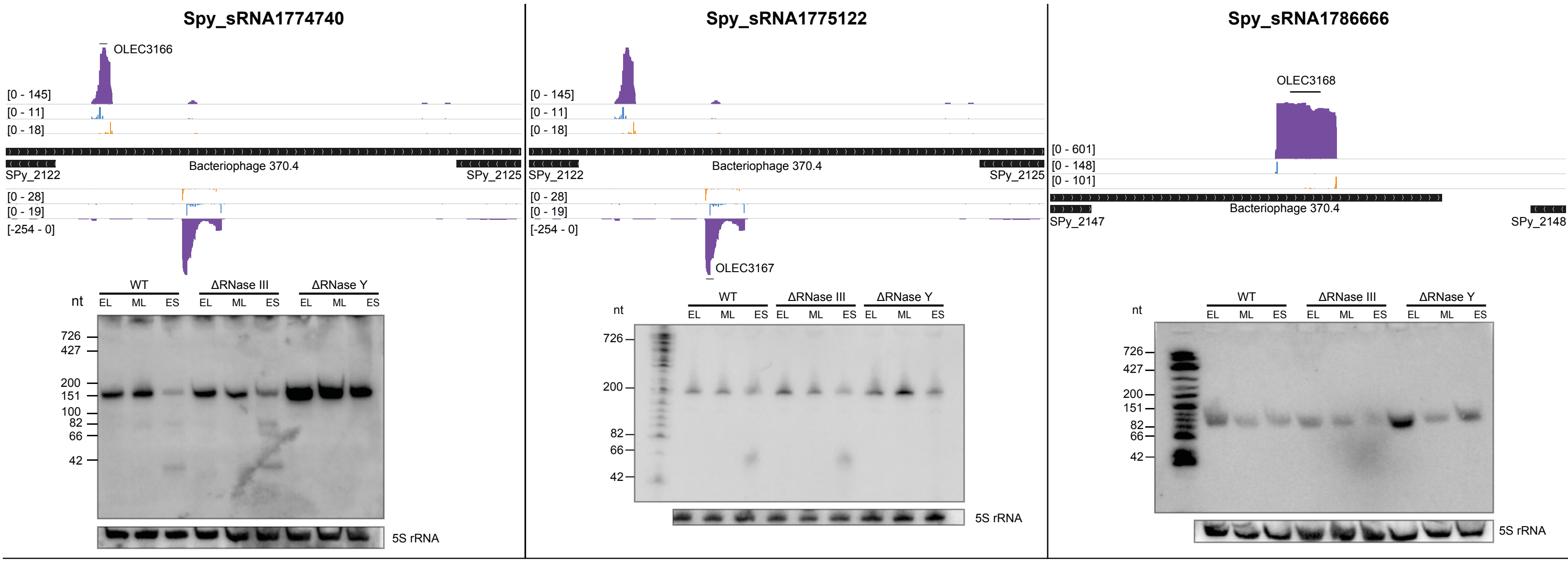
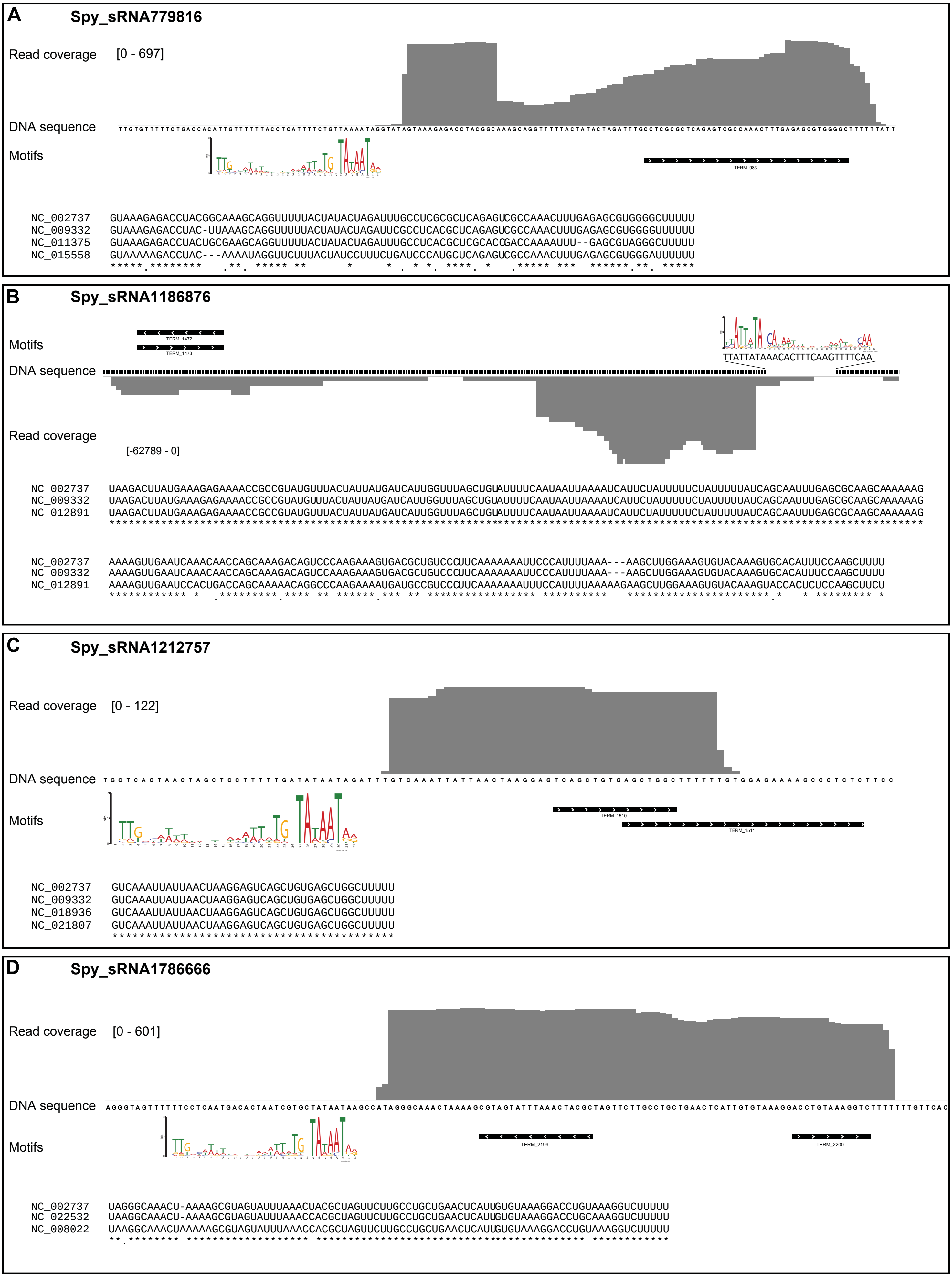


Figure S4. Expression profiles of experimentally validated sRNAs

Expression profiles of selected sRNAs and surrounding loci were captured using the Integrative Genomics Viewer (IGV) software. The sequence coverage was calculated using BEDTools-Version-2.15.0 and the scale is given in number of reads per million. The distribution of reads starting (5') and ending (3') at each nucleotide position is indicated in blue and orange, respectively. Transcripts from the positive strand are represented above the locus drawn in black and transcripts from the negative strand are represented below. The positions of the primers used in Northern blot analysis (OLEC) are indicated. Polyacrylamide Northern blot expression profile was analyzed in WT (SF370), ΔRNase III (Δ*rnc*) and ΔRNase Y (Δ*rny*) strains by using total RNA from early logarithmic (EL), mid logarithmic (ML) and early stationary (ES) phases of growth. The approximate size of bands was estimated according to the ΦX174 DNA/HinfI Marker (Fermentas®). 5S rRNA specific hybridization pattern was used as a reference.



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NC_011375   GUAAAGAGACCUACUGCGAAGCAGGUUUUUACUAUACUAGAUUUGCCUCACGCUCGCACCGACCAAAAUUU--GAGCGUAGGGCUUUUU
NC_015558   GUAAAAAGACCUAC---AAAAUAGGUUCUUUACUAUCCUUUCUGAUCCCAUGCUCAGAGUCGCCAAACUUUGAGAGCGUGGGAUUUUUU
            *****.********   .**. ***** **      *     * . * *. ****. *   .***** ***  ******.**. *****
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NC_002737   UAAGACUUAUGAAAGAGAAAACCGCCGUAUGUUUACUAUUAUGAUCAUUGGUUUAGCUGUAUUUUCAAUAAUUAAAAUCAUUCUAUUUUUCUAUUUUUAUCAGCAAUUUGAGCGCAAGCAAAAAG
NC_009332   UAAGACUUAUGAAAGAGAAAACCGCCGUAUGUUUACUAUUAUGAUCAUUGGUUUAGCUGUAUUUUCAAUAAUUAAAAUCAUUCUAUUUUUCUAUUUUUAUCAGCAAUUUGAGCGCAAGCAAAAAG
NC_012891   UAAGACUUAUGAAAGAGAAAACCGCCGUAUGUUUACUAUUAUGAUCAUUGGUUUAGCUGUAUUUUCAAUAAUUAAAAUCAUUCUAUUUUUCUAUUUUUAUCAGCAAUUUGAGCGCAAGCAAAAAG
            *****************************************************************************************************************************

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NC_012891   AAAAGUUGAAUCCACUGACCAGCAAAAACAGGCCCAAGAAAAUGAUGCCGUCCCUUCAAAAAAAAUUUCCAUUUUAAAAAGAAGCUUGGAAAGUGUACAAAGUACCACUCUCCAAGCUUCU
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NC_009332   GUCAAAUUAUUAACUAAGGAGUCAGCUGUGAGCUGGCUUUUU
NC_018936   GUCAAAUUAUUAACUAAGGAGUCAGCUGUGAGCUGGCUUUUU
NC_021807   GUCAAAUUAUUAACUAAGGAGUCAGCUGUGAGCUGGCUUUUU
            ******************************************
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NC_002737   UAGGGCAAACU-AAAAGCGUAGUAUUUAAACUACGCUAGUUCUUGCCUGCUGAACUCAUUGUGUAAAGGACCUGUAAAGGUCUUUUU
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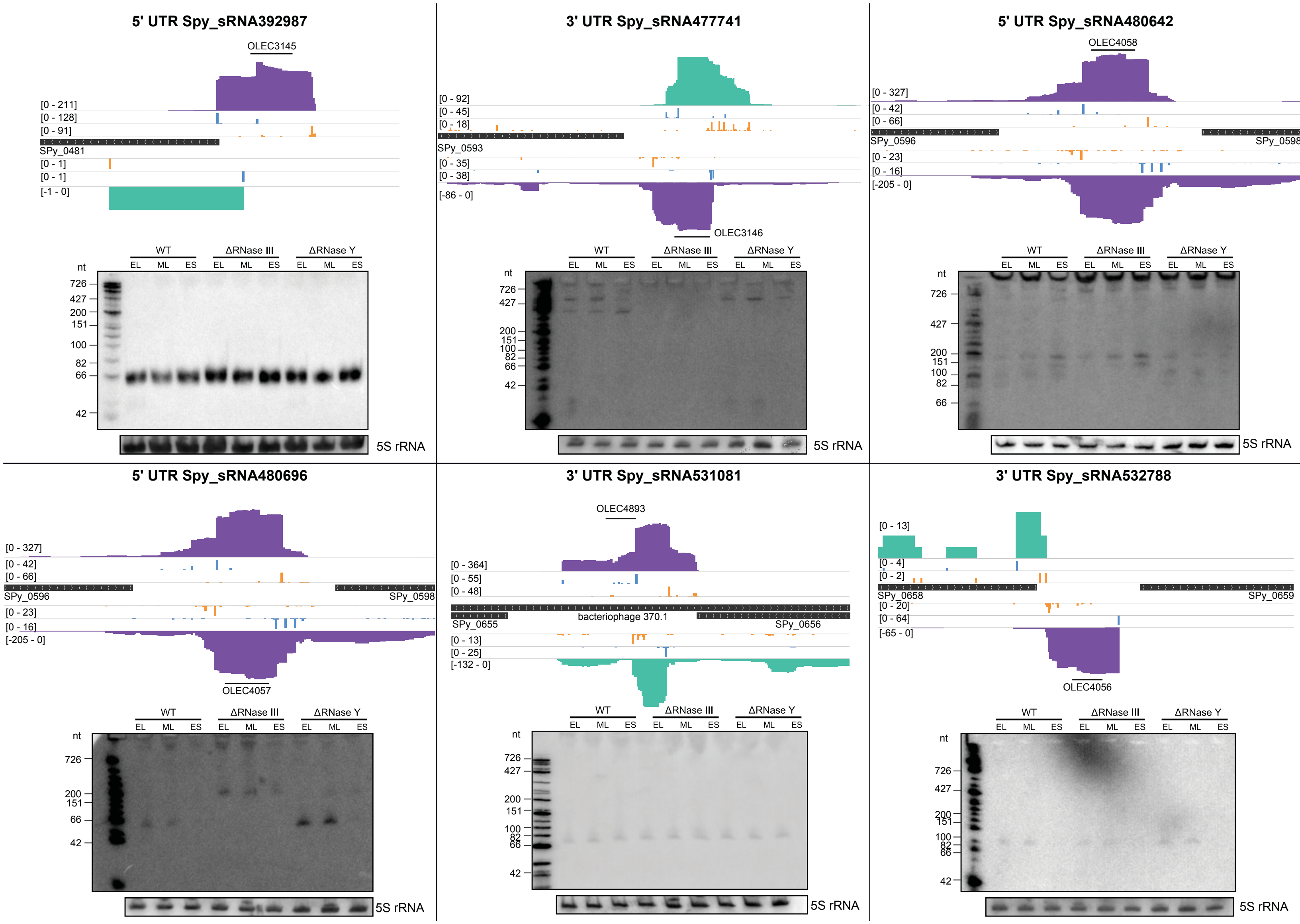
NC_008022   UAAGGCAAACUAAAAAGCGUAGUAUUUAAACCACGCUAGUUCUUGCCUGCUGAACUCAUUGUGUAAAGGACCUGUAAAGGUCUUUUU
            **.******** ******************* ****************************************** ************
```

Figure S5. Expression profiles and sequence conservation of selected sRNAs

sRNA sequencing expression profiles of four selected sRNAs captured using the Integrative Genomics Viewer (IGV) software. The sequence coverage was calculated using BEDTools-Version-2.15.0 and the scale is given in number of reads per million. For each sRNA, the predicted promoter region (logo obtained by MEME v 4.9.1) and terminator region (using TransTermHP v2.07 [83] (downloaded from http://transterm.cbcb.umd.edu/tt/Streptococcus_pyogenes_M1_GAS.tt)) are indicated. sRNA homologues from other streptococcal strains were aligned using MAFFT (mafft-ginsi) (v7.220) [82]. See also Figure 2 for Northern blot analyses and sRNA structure predictions.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OLEC3145
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[0 - 128]
[0 - 91]
SPy_0481
[0 - 1]
[0 - 1]
[-1 - 0]
WT
ΔRNase III
ΔRNase Y
EL
ML
ES
nt
726
427
200
151
100
82
66
42
5S rRNA
3' UTR Spy_sRNA477741
[0 - 92]
[0 - 45]
[0 - 18]
SPy_0593
[0 - 35]
[0 - 38]
[-86 - 0]
OLEC3146
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OLEC4058
[0 - 327]
[0 - 42]
[0 - 66]
SPy_0596
SPy_0598
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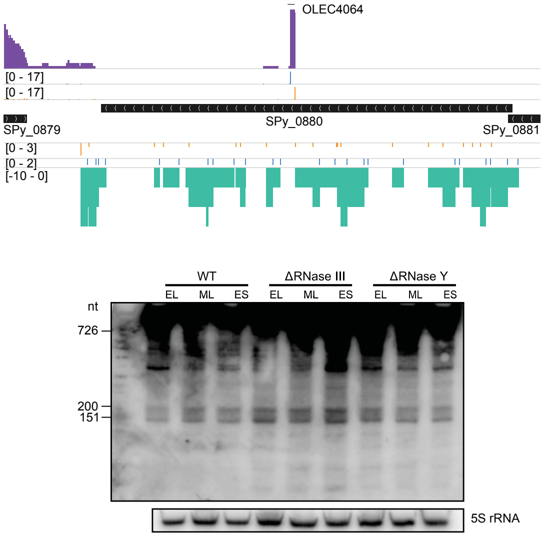
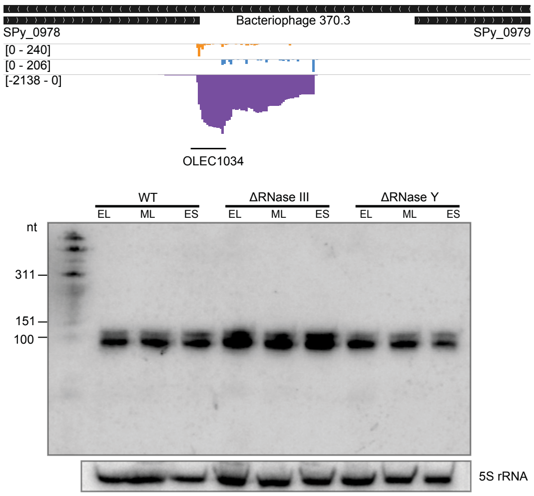


3' UTR Spy_sRNA800369



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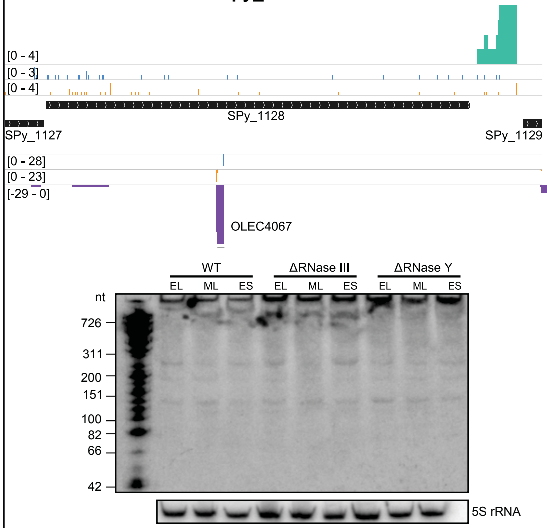
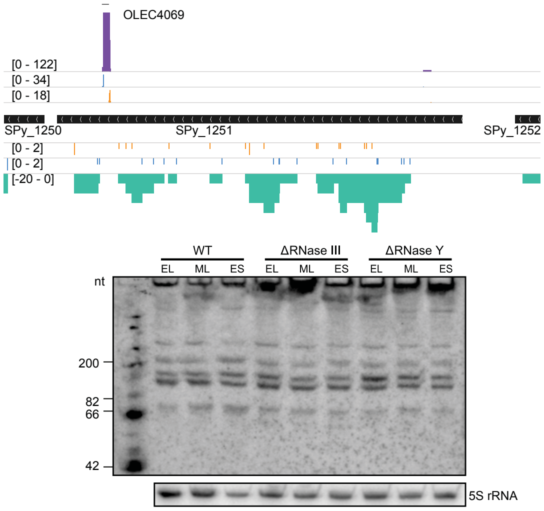


CDS Spy_sRNA1032107



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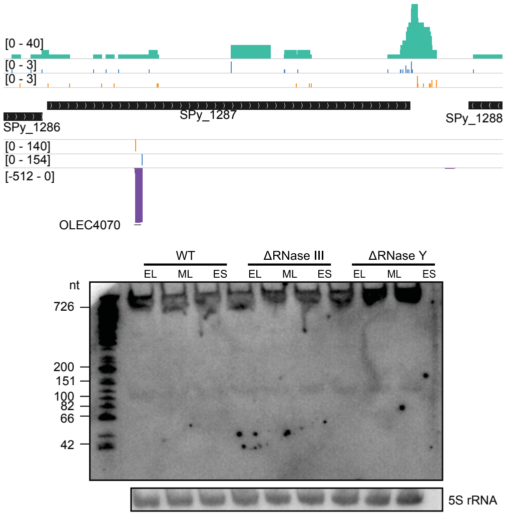

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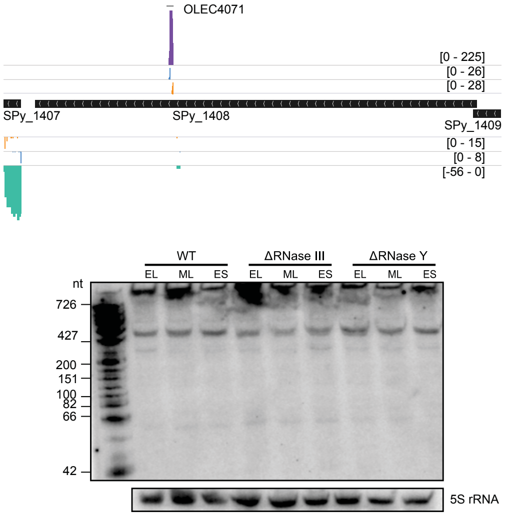

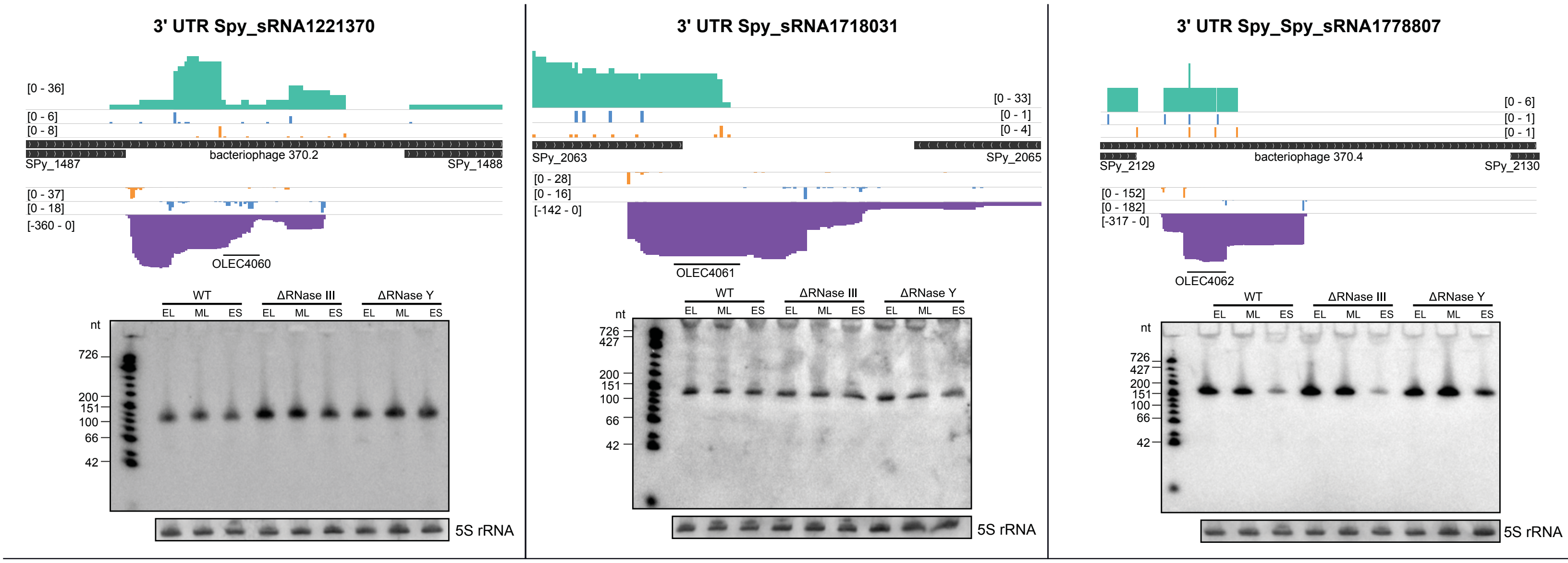

Figure S6. Expression profiles of experimentally validated asRNAs

Expression profiles of selected asRNAs and surrounding loci were captured using the Integrative Genomics Viewer (IGV) software. The sequence coverage was calculated using BEDTools-Version-2.15.0 and the scale is given in number of reads per million. The putative asRNAs are represented in purple and the other transcripts are shown in green. The distribution of reads starting (5') and ending (3') at each nucleotide position is indicated in blue and orange, respectively. Transcripts from the positive strand are represented above the locus drawn in black and transcripts from the negative strand are represented below. The positions of the primers used in Northern blot analysis (OLEC) are indicated. Northern blot expression profiling (polyacrylamide gel electrophoresis) was analyzed in WT (SF370), ΔRNase III (Δ*rnc*) and ΔRNase Y (Δ*rny*) strains grown to early logarithmic (EL), mid logarithmic (ML) and early stationary (ES) phases. The approximate size of fragments was estimated according to the ΦX174 DNA/HinfI Marker (Fermentas®). 5S rRNA specific hybridization pattern was used as a reference.

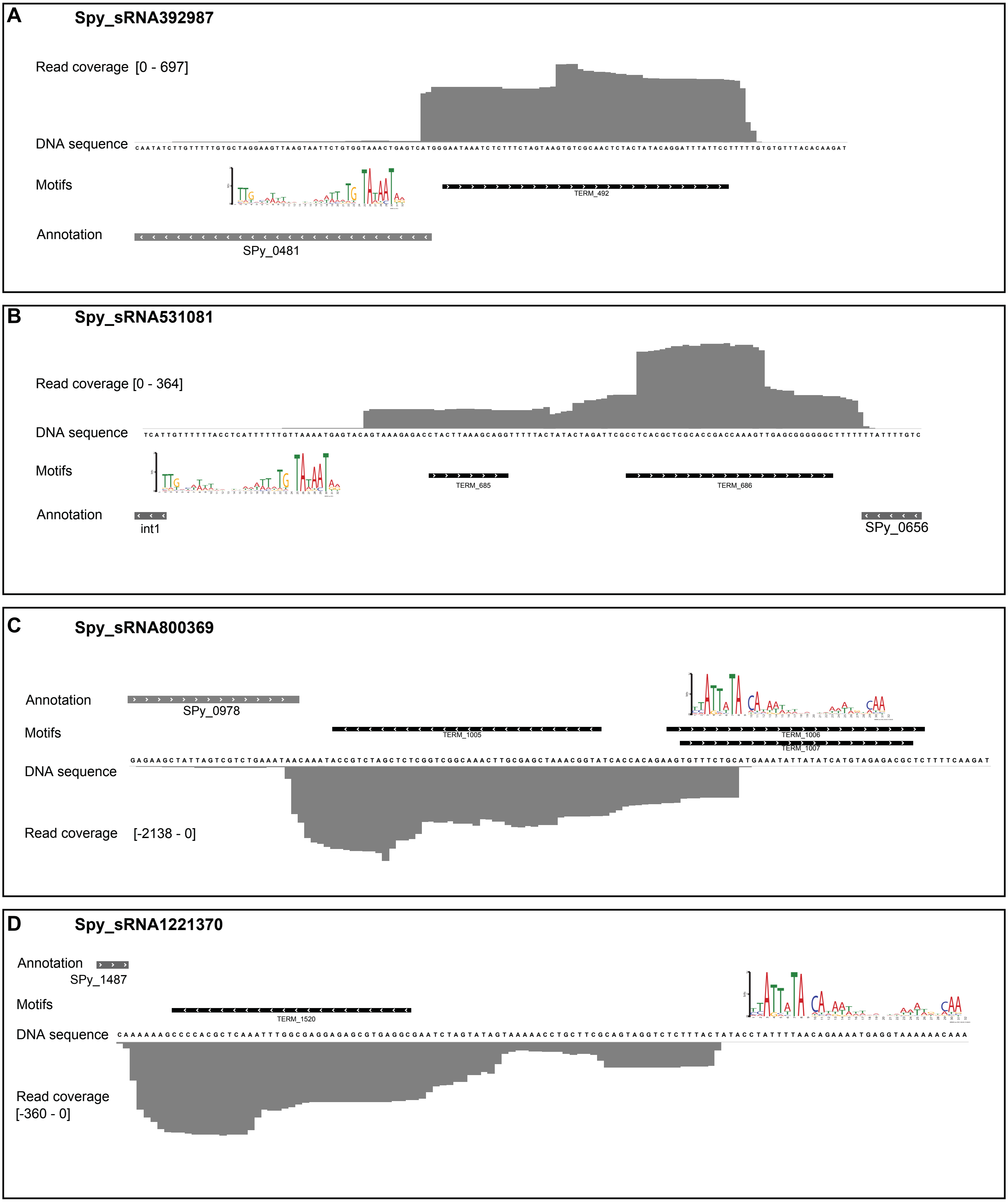
A
Spy_sRNA392987
Read coverage [0 - 697]
DNA sequence
CAATATCTTGTTTTTGTGCTAGGAAGTTAAGTAATTCTGTGGTAAACTGAGTCATGGGAATAAATCTCTTTCTAGTAAGTGTCGCAACTCTACTATACAGGATTTATTCCTTTTTGTGTGTTTACACAAGAT
Motifs
TERM_492
Annotation
SPy_0481
B
Spy_sRNA531081
Read coverage [0 - 364]
DNA sequence
TCATTGTTTTTACCTCATTTTTTGTTAAAATGAGTACAGTAAAGAGACCTACTTAAAGCAGGTTTTTACTATACTAGATTCGCCTCACGCTCGCACCGACCAAAGTTGAGCGGGGGGCTTTTTTTATTTTGTC
Motifs
TERM_685
TERM_686
Annotation
int1
SPy_0656
C
Spy_sRNA800369
Annotation
SPy_0978
Motifs
TERM_1005
TERM_1006
TERM_1007
DNA sequence
GAGAAGCTATTAGTCGTCTGAAATAACAAATACCGTCTAGCTCTCGGTCGGCAAACTTGCGAGCTAAACGGTATCACCACAGAAGTGTTTCTGCATGAAATATTATATCATGTAGAGACGCTCTTTTCAAGAT
Read coverage [-2138 - 0]
D
Spy_sRNA1221370
Annotation
SPy_1487
Motifs
TERM_1520
DNA sequence
CAAAAAAGCCCCACGCTCAAATTTGGCGAGGAGAGCGTGAGGCGAATCTAGTATAGTAAAAACCTGCTTCGCAGTAGGTCTCTTTACTATACCTATTTTAACAGAAAATGAGGTAAAAAACAAA
Read coverage
[-360 - 0]

Figure S7. Expression profiles of selected asRNAs

sRNA sequencing expression profiles of four selected asRNAs captured using the Integrative Genomics Viewer (IGV) software. The sequence coverage was calculated using BEDTools-Version-2.15.0 and the scale is given in number of reads per million. For each sRNA, the predicted promoter region (logo obtained by MEME v 4.9.1) and terminator region (using TransTermHP v2.07 [83] (downloaded from http://transterm.cbcb.umd.edu/tt/Streptococcus_pyogenes_M1_GAS.tt)) are indicated.

```
Spy_sRNA392987
NC_002737.1     atgggaataaatctctttctagt-aagtgtcgcaactctactatacaggatttattcctttt
NC_020540.2     atgggaataaatctctttctagt-aagtgtcgcaactctactatacaggatttattcctttt
NC_018936.1     atgggaataaatctctttctagt-aagtgtcgcaactctactatacaggatttattcctttt
NC_017596.1     atgggaataaatctctttctagt-aagtgtcgcaactctactatacaggatttattcctttt
NC_017596.1     atgggaataaatctctttctagt-aagtgtcgcaactctactatacaggatttattcctttt
NC_007297.1     atgggaataaatctctttctagt-aagtgtcgcaactctactatacaggatttattcctttt
NC_018712.1     atgggaataaatctctttctagt-aagtttcgcaactctactatacaggatttattcctttt
NC_018712.1     atgggaataaatctctttctagtgaggtctcgcaactctactatacaggatttattcctttt
NC_017053.1     atgggaataaatctctttctagt-aagtttcgcaactctactatacaggatttattcctttt
NC_017040.1     atgggaataaatctctttctagt-aagtttcgcaactctactatacaggatttattcctttt
NC_012891.1     atgggaataaatctctttctagtgaagtgtcgcaactctactatacaggatttattcctttt
NC_012891.1     atgggaataaatctctttctagtgaggtctcgcaactctactatacaggatttattcctttt
NC_008022.1     atgggaataaatctctttctagt-aagtttcgcaactctactatacaggatttattcctttt
NC_004606.1     atgggaataaatctctttctagt-aagtgtcgtaactctactatacaggatttattcctttt
NC_004070.1     atgggaataaatctctttctagt-aagtgtcgtaactctactatacaggatttattcctttt
NC_011375.1     atgggaataaatctctttctagtgaagtgtcgtaactctactatacaggatttattcctttt
NC_004116.1     atgggaataaatctctttctagtgaagtctcgcaactctactatacaggatttattcctttt
                ********************** *.** ***.*****************************
```

```
Spy_sRNA531081
NC_002737.1     agtaaagagacctact-taaagcagg-tttttactatactag-attcgcctcacgctcgcaccgaccaaagttg---agcggggggcttttttt
NC_002737.1     agtaaagagacctactgcgaagcagg-tttttactatactag-attcgcctcacgctctcctcg-ccaaatttg---agcgtggggc-tttttt
NC_007432.1     agtaaagag-cctact-taaagcagg-tttttactatactag-attcgcctcacgctcgcaccgaccaaagttg---agcgtggggcttttttt
NC_012471.1     agtaaagagacctactgcgaagcaggttttttactatacagg-atttgcctcacgctcgcaccgaccaaagttg---agcgtggggc-tttttt
NC_008024.1     agtaaagagacctact-taaagcagg-tttttactatactagaattcgcctcacgctcagactcgccaaagtttgagagcgtggggc-tttttt
NC_008024.1     agtaaagagacctactgcgaagcagg-tttttactatactag-attcgcctcacgctctcctcg-ccaaatttg---agcgtggggc-tttttt
NC_008022.1     agtaaagagacctact-taaagcagg-tttttactatactagaattcgcctcacgctcagactcgccaaagtttgagagcgtggggc-tttttt
NC_008021.1     agtaaagagacctact-taaagcagg-tttttactatactagaattcgcctcacgctcagactcgccaaagtttgagagcgtggggc-tttttt
NC_017596.1     agtaaagagacctactgcgaagcagg-tttttactatactag-attcgcctcacgctctcctcg-ccaaatttg---agcgtggggc-tttttt
NC_004606.1     agtaaagagacctactgcgaagcagg-tttttactatactag-attcgcctcacgctctcctcg-ccaaatttg---agcgtggggc-tttttt
NC_004070.1     agtaaagagacctactgcgaagcagg-tttttactatactag-attcgcctcacgctctcctcg-ccaaatttg---agcgtggggc-tttttt
NC_003485.1     agtaaagagacctactgcgaagcagg-tttttactatactag-attcgcctcacgctctcctcg-ccaaatttg---agcgtggggc-tttttt
NC_003485.1     agtaaagagacctact-taaagcagg-tttttactatactag-attcgcctcacgctcagagtcgccaaactttgagagcgtggggt-tttttt
NC_017053.1     agtaaagagacctactgcaaagcagg-tttttactatactag-attcgcctcacgctcagaccg-ccaagtttg-aaagcgtggggc-tttttt
NC_009332.1     agtaaagagacctact-taaagcagg-tttttactatactag-attcgcctcacgctcagagtcgccaaactttgagagcgtggggt-tttttt
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NC_020540.2     -----------------------ggt-tgtttcttatactag-atccgcctcacgctcgcaccgaccaaagttg---aacgtgtggc-tttttt
NC_018936.1     -----------------------ggt-tgtttcttatactag-atccgcctcacgctcgcaccgaccaaagttg---aacgtgtggc-tttttt
NC_007297.1     -----------------------ggt-tgtttcttatactag-atccgcctcacgctcgcaccgaccaaagttg---aacgtgtggc-tttttt
                                       .*  * *** .***** .* **..***********    .  ****. **    *.** * **. ******
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Spy_sRNA800369
NC_002737.1     gcagaaacacttctgtggtgataccgtttagctcgcaagtttgccgaccgagagctagacggtatttgttatttcagacgactaatagct
NC_017596.1     gcagaaacacttctgtggtgataccgtttagctcgcaagtttgccgaccgagagctagacggtatttgttatttcagacgactaatagct
                ******************************************************************************************
```

```
Spy_sRNA1221370
NC_002737.1     gtaaagagacctactgcgaagcagg-tttttactatactagattcgcctcacgctctcctcg-ccaaatttg---agcgtggggcttttt
NC_002737.1     gtaaagagacctact-taaagcagg-tttttactatactagattcgcctcacgctcgcaccgaccaaagttg---agcggggggcttttt
NC_017596.1     gtaaagagacctactgcgaagcagg-tttttactatactagattcgcctcacgctctcctcg-ccaaatttg---agcgtggggcttttt
NC_008024.1     gtaaagagacctactgcgaagcagg-tttttactatactagattcgcctcacgctctcctcg-ccaaatttg---agcgtggggcttttt
NC_004606.1     gtaaagagacctactgcgaagcagg-tttttactatactagattcgcctcacgctctcctcg-ccaaatttg---agcgtggggcttttt
NC_004070.1     gtaaagagacctactgcgaagcagg-tttttactatactagattcgcctcacgctctcctcg-ccaaatttg---agcgtggggcttttt
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NC_003485.1     gtaaagagacctact-taaagcagg-tttttactatactagattcgcctcacgctcagagtcgccaaactttgagagcgtggggtttttt
NC_012471.1     gtaaagagacctactgcgaagcagg-tttttactatactagatttgcctcacgctcgcaccgaccaaaattt--gagcgtagggcttttt
NC_012471.1     gtaaagagacctactgcgaagcaggttttttactatacaggatttgcctcacgctcgcaccgaccaaagttg---agcgtggggcttttt
NC_011375.1     gtaaagagacctactgcgaagcagg-tttttactatactagatttgcctcacgctcgcaccgaccaaaattt--gagcgtagggcttttt
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NC_009332.1     gtaaagagacctact-taaagcagg-tttttactatactagattcgcctcacgctcagagtcgccaaactttgagagcgtggggtttttt
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NC_021486.1     ----------------------------tttattgtac-agttttgcctcacgctctcctcg-ccaaatttg---agcgtggggcttttt
                                            ****.*.***  * .*.***********    .  ****. **    **** .***.*****
```

Figure S8. Sequence conservation of selected asRNAs

asRNA homologues from other streptococcal strains were aligned using MAFFT (mafft-ginsi) (v7.220) [82]. See also Figure 4 for Northern blot analyses and sRNA structure predictions.