

Table S2. Compilation of nstSGRs identified by parallel sRNA-Seq approach in the *P. aeruginosa* strains PAO1 and PA14.

nstSGR name ^e	class	PAO1				PA14				Notes ^d
		Genomic coordinates (left-right)	Flanking/ Involved <i>loci</i> ^a	# reads ^b	strand ^c	Genomic coordinates (left-right)	Flanking/ Involved <i>loci</i> ^a	# reads ^b	strand ^c	
Group A										
SPA0001	I	785400-785600	<i>phrD</i>	95	+					PhrD; RGP5
SPA0002	I	2568400-2569000	PA2326/PA2327	6	-					
SPA0003	I	3087500-3087800	PA2729/PA2730	36	+					RGP28
SPA0004	III	501100-501300	PA0445	150	+					
SPA0005	III	2556800-2557000	PA2319	149	-					
SPA0006	III	3044700-3044900	PA2690	151	+					
SPA0007	III	3843200-3843400	PA3434	150	+					
SPA0008	III	5383800-5384000	PA4797	150	+					
SPA0066	III	4473500-4473700	PA3993	149	-					
Group B										
SPA0009	I					278200-278400	PA14_03160/PA14_03170	7	+	RGP2
SPA0010	I					1924300-1924500	PA14_22090/PA14_22100	6	-	RGP33
SPA0011	I					2677700-2678200	PA14_30840/ <i>trbI</i>	11	+	RGP26
SPA0012	I					3515400-3515700	PA14_39480/PA14_39500	152	+	RGP52
SPA0013	I					3974900-3975200	PA14_44640/PA14_44650	5	-	RGP16
SPA0014	I					4401600-4401700	PA14_49480/PA14_49500	8	+	RGP47
SPA0015	I					5355400-5355700	PA14_60120/PA14_60130	10	-	RGP41; PAPI-1
SPA0016	I					6460900-6461400	PA14_72510/PA14_72520	5	-	
SPA0017	III					1315700-1316500	<i>trbL</i>	57	-	RGP36
SPA0018	III					1940100-1940300	PA14_22270	7	+	RGP33
SPA0019	III					3176100-3176300	PA14_35720	7	+	RGP23
SPA0020	III					4134300-4134700	PA14_46460	7	+	RGP14
SPA0021	III					5288100-5288500	PA14_59370	9	+	RGP41; PAPI-1
SPA0022	III					5303200-5303500	PA14_59580	5	-	RGP41; PAPI-1
SPA0023	III					5330700-5330900	PA14_59840	5	-	RGP41; PAPI-1
SPA0024	IV					2926400-2927500	PA14_33290/PA14_33300	3	+	RGP24; CRISPR-1
SPA0025	IV					2935700-2937400	PA14_33360	23	-	RGP24; CRISPR-2

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Group C										
SPA0026	I	580100-580200	<i>nirS/nirQ</i>	3	-	590077-590177	<i>nirS/nirQ</i>			
SPA0027	I	781000-781300	<i>toxR/PA0708</i>	11	+	4899097-4899397	PA14_55150/ <i>toxR</i>			
SPA0028	I	912700-912900	PA0836.1	5	-	4738703-4738903	PA53450			P5
SPA0029	I	1028100-1028200	PA0937/PA0938	6	+	4623357-4623457	PA14_52130/ <i>yaiL</i>			
SPA0030	I	1097000-1097300	PA1013.1/PA1014	5	-	4552631-4552931	PA14_51220/PA14_51230			
SPA0031	I	1135200-1135400	PA1047/PA1048	4	+	4514530-4514730	PA14_50810/PA14_50820			
SPA0032	I	1251200-1251300	<i>nrdB/PA1156</i>	5	-	4397712-4397812	<i>nrdA/nrdB</i>			
SPA0033	I	1474300-1474400	PA1361/PA1362	4	-	4160214-4160311	PA14_46670/ <i>norM</i>			
SPA0034	I	2031800-2031900	PA1869/PA1870	4	+	3601268-3601369	PA14_40300/PA14_40310			
SPA0035	I	2330400-2330600	<i>ada/PA2119</i>	5	-	3312492-3312692	PA14_37170 / <i>ada</i>			
SPA0036	I	2558300-2558900	PA2319/ <i>gntR</i>	2	-	3078836-3079153	<i>gntR/PA14_34670</i>			
SPA0037	I	2614800-2614900	PA2364/PA2365	7	+	3029702-3029801	PA14_34070/PA14_34080			
SPA0038	I	3116400-3116600	PA2754/ <i>eco</i>	11	+	2457373-2457573	<i>eco/PA14_28486</i>			
SPA0039	I	3261300-3261400	PA2906/ <i>cobI</i>	4	-	2307957-2308057	<i>cobL/PA14_26485</i>			
SPA0040	I	3489900-3490100	<i>purF/PA3109</i>	4	-	2078190-2078390	<i>cvpA/purF</i>			
SPA0041	I	4094900-4095000	<i>rpsB/map</i>	3	-	1463019-1463119	<i>map/rpsB</i>			
SPA0042	I	4780700-4780900	PA4270.1	4	-	745920-746120	<i>rplL/rpoB</i>			P26
SPA0043	I	5121600-5121800	PA4573/PA4574	4	-	5394065-5394265	PA14_60520/PA14_60530			
SPA0044	I	5325500-5325700	<i>pnp/rps0</i>	8	-	5597429-5597629	<i>rps0/pnp</i>			
SPA0045	I	5344900-5345100	PA4758.1	5	-	5616829-5617029	<i>carA/dapB</i>			P32
SPA0046	I	5439800-5439900	PA4844/ <i>dipZ</i>	5	+	5710452-5710552	<i>ctpL/dipZ</i>			
SPA0047	I	6110800-6111000	<i>aspA/PA5430</i>	5	-	6383723-6383923	<i>aspA/PA14_71670</i>			
SPA0048	II	990900-991100	<i>rsmA</i>	4	+	4660491-4660691	<i>rsmA</i>			
SPA0049	II	1182800-1183100	<i>fliC</i>	5	+	4466831-4467131	<i>fliC</i>			
SPA0050	II	3762700-3763000	<i>flgM</i>	6	+	1784235-1784535	<i>flgM</i>			
SPA0051	II	5337600-5337800	<i>ftsH</i>	5	-	5609529-5609729	<i>ftsH</i>			
SPA0052	II	5522100-5522300	<i>azu</i>	6	-	5792869-5793769	<i>azu</i>			
SPA0053	II	5813600-5813800	PA5165	4	+	6085771-6085971	PA14_68230			
SPA0054	III	176100-176200	<i>pcaG</i>	15	-	174851-175160	<i>pcaG</i>			

nstSGR name ^e	class	PAO1				PA14				Notes ^d
		Genomic coordinates (left-right)	Flanking/ Involved <i>loci</i> ^a	# reads ^b	strand ^c	Genomic coordinates (left-right)	Flanking/ Involved <i>loci</i> ^a	# reads ^b	strand ^c	
SPA0055	III	719900-720200	PA0667	8	+	730790-731290	PA14_08540/ <i>tyrZ</i>			
SPA0056	III	781400-782200	PA0708	14	+	4898197-4898997	PA14_55150			
SPA0057	III	782900-783600	PA0711	7	+	4896798-4897497	PA14_55117			
SPA0058	III	1027800-1028000	PA0937	4	-	4623557-4623757	<i>yaiL</i>			
SPA0059	III	2113600-2114100	PA1933	5	-	3518295-3518795	PA14_39520			
SPA0060	III	3348400-3348700	PA2990	4	-	2220645-2220945	<i>ugpQ</i>			
SPA0061	III	3349200-3349400	<i>sth</i>	8	+	2219945-2220145	<i>sth</i>			
SPA0062	III	3570600-3570800	PA3180	2	-	2003152-2003352	<i>mutT</i>			
SPA0063	III	3617500-3617600	PA3230	4	+	1951512-1951612	PA14_22410			
SPA0064	III	3865900-3866200	PA3459	4	-	1674746-1675046	<i>asnB</i>			
SPA0065	III	4245900-4246100	PA3788	4	-	1280381-1280581	PA14_15090			
SPA0067	III	5676000-5676200	<i>pilQ</i>	4	+	5947414-5947580	<i>pilQ</i>			
Group D										
SPA0068	I	332900-333100	PA0295/ <i>spul</i>	6	-	347000-347200	PA14_03855/PA14_03860	4	-	
SPA0069	I	586800-587000	<i>rsmY</i>	205	+	596800-597000	<i>rsmY</i>	99	+	RsmY
SPA0070	I	706700-706900	<i>vfr</i> /PA0653	12	-	717700-717800	<i>vfr</i> /PA14_08380	4	-	
SPA0071	I	883400-883600	PA0805/PA0806	5	-	4773800-4773900	PA14_53830/PA14_53840	5	+	
SPA0072	I	901500-901900	<i>ssrA</i>	1643	-	4749700-4750100	PA14_53560/PA14_53570	1595	+	tmRNA
SPA0073	I	1205000-1205100	PA1112.1	4	-	4444700-4445000	PA14_49990/PA14_50000	7	+	sRNA645
SPA0074	I	1557900-1558200	PA1429/ <i>lasR</i>	6	+	4086100-4086300	<i>lasR</i> /PA14_45970	8	-	
SPA0075	I	1668800-1669200	<i>ffs</i>	862		3974500-3974700	PA14_44640/PA14_44650	500	-	4.5S
SPA0076 ^f	I					3975600-3975800	PA14_44640/PA14_44650	555	-	4.5S
SPA0077	I	2473000-2473100	<i>bkdR/bkdA1</i>	8	+	3159700-3159900	<i>bkdA1/bkdR</i>	8	-	
SPA0078	I	2705600-2705800	PA2421/PA2422	6	-	2937800-2937900	PA14_33370/PA14_33380	7	+	
SPA0079	I	3123200-3123500	PA2763/PA2764	1893	-	2450500-2450700	PA14_28350/PA14_28360	2982	+	
SPA0080	I	3147500-3147600	PA2789/PA2790	7	+	2426600-2426800	PA14_28030/PA14_28040	25	-	
SPA0081	I	3442300-3442500	PA3069/PA3070	5	-	2129000-2129100	<i>moxR</i> /PA14_24440	5	+	
SPA0082	I	3705300-3705600	<i>phrS</i>	80	-	1841700-1842000	PA14_21260	120	+	PhrS; P20
SPA0083	I	3778000-3778200	<i>amiL</i>	28	-	1768500-1768600	PA14_20550/ <i>amiE</i>	3	+	AmiL
SPA0084	I	3958000-3958200	PA3535/PA3536	14	+	1599900-1600100	PA14_18620/PA14_18630	36	-	

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SPA0085	I	4057500-4057700	<i>rsmZ</i>	3494	-	1500300-1500500	<i>rpoS/fdxA</i>	8491	+	RsmZ
SPA0086	I	4388800-4389000	PA3919/PA1920	11	-	1135100-1135500	PA14_13170/PA14_13190	7	+	
SPA0087	I	4514400-4514700	PA4033/ <i>aqpZ</i>	10	+	1011600-1011900	<i>aqpZ</i> /PA14_11670	20	-	
SPA0088	I	4519000-4519100	PA4036/PA4037	4	-	1007000-1007300	PA14_11620/PA14_11630	4	+	
SPA0089	I	4536600-4536900	<i>ribC/ribD</i>	9	-	989600-989800	<i>ribD/ribC</i>	4	+	sRNA2315
SPA0090	I	4939100-4939300	PA4406.1	10	-	5102700-5102900	<i>lpxC/ftsZ</i>	3	-	72/101
SPA0091	I	4956300-4956700	<i>rnpB</i>	340	-	5119800-5120100	PA14_57460/PA14_57470	630	-	RnpB; sRNA2510
SPA0092	I	5308500-5309000	<i>crcZ</i>	100	+	5580500-5581300	<i>cbrB/pcnB</i>	120	+	CrcZ
SPA0093	I	5372500-5372600	PA4784/PA4785	10	-	5644200-5644400	PA14_63240/ <i>yfcY</i>	4	-	
SPA0094	I	5884300-5884600	<i>ssrS</i>	898	+	6156500-6156800	PA14_69030/PA14_69040	767	+	6S
SPA0095	I(PAO1)/III(PA14)	1997000-1997400	<i>cysI</i> /PA1839	8	+	3637200-3637500	PA14_40740	5	-	sRNA1059
SPA0096	I(PAO1)/V(PA14)	3114100-3114200	PA2751/PA2752	11	-	2459700-2460900	PA14_28520	41	+	
SPA0097	I(PAO1)/V(PA14)	3129600-3129700	PA2771/PA2770	15	+	2444300-2444400	PA14_28250	78	-	RGP43
SPA0098	II	410900-411500	PA0367	4	+	425649-426248	PA14_04820	3	+	
SPA0099	II	564700-564900	PA0506	3	+	574700-575000	PA14_06600	6	+	
SPA0100	II	648600-649000	PA0588	9	-	661400-661700	<i>prkA</i>	12	-	
SPA0101	II	1348400-1348600	PA1244	8	-	4286000-4286200	PA14_48150	7	+	
SPA0102	II	3549800-3550100	<i>rpsA</i>	8	-	2024000-2024200	<i>rpsA</i>	5	+	
SPA0103	II	3616900-3617100	PA3229	59	+	1951900-1952200	PA14_22420	3	-	
SPA0104	II	3889700-3899900	<i>rhII</i>	33	-	1651700-1651900	<i>rhII</i>	70	+	
SPA0105	II	3892800-3893300	<i>rhIA</i>	6	-	1648400-1649100	<i>rhIA</i>	17	+	
SPA0106	II	4622700-4622800	PA4133	11	+	904900-905200	<i>ccoN</i>	4	-	
SPA0107	II	5067700-5067900	PA4523	4	-	5231400-5231600	PA14_58690	3	-	
SPA0108	II	5165800-5166000	PA4606	2	-	5438300-5438500	PA14_60960	2	+	
SPA0109	II	5952700-5952900	<i>glnK</i>	9	-	6226000-6226100	<i>glnK</i>	13	-	
SPA0110	II	6162000-6162300	PA5473	3	+	6434900-6435100	PA14_72230	6	+	
SPA0111	III	182500-182700	<i>triC</i>	12	-	181400-181600	Pa14_01970	7	-	
SPA0112	III	410900-411500	PA0367	2	-	425649-426248	PA14_04820	5	-	
SPA0113	III	449000-449400	<i>gshB</i>	9	+	463700-464100	<i>gshB</i>	34	+	
SPA0114	III	2982700-2982900	<i>nuoA</i>	3	-	2599000-2599200	<i>nuoA</i>	11	+	

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SPA0115	III	3119200-3119700	PA2759	33	+	2454200-2454800	PA14_28410	88	-	
SPA0116	III	3127700-3127900	PA2769	20	+	2446100-2446200	PA14_28290	89	-	
SPA0117	III	3414600-3414800	<i>pyrD</i>	5	+	2154400-2154700	<i>pyrD</i>	8	-	
SPA0118	III	3761800-3762100	PA3350	14	-	1785200-1785400	<i>flgA</i>	5	+	
SPA0119	III	5680700-5681300	<i>ponA</i>	27	-	5951200-5952700	<i>ponA</i>	11	-	
SPA0120	III	6135900-6136000	<i>wbpZ</i>	5	+	6408800-6409000	<i>wbpZ</i>	9	+	
SPA0121	III	6171700-6172000	PA5480	14	-	6444600-6445100	PA14_72350	4	-	
SPA0122	III	6183500-6183700	PA5492	36	-	6456400-6456600	<i>engB</i>	73	-	
SPA0123	V	784000-784500	PA0713	17	+	4895600-4896200	PA14_55110	12	-	
SPA0124	V	1538600-1539000	PA1414	44	+	4105200-4105600	PA14_46160	197	-	
SPA0125	V	3108800-3109300	PA2747	9	-	2464700-2465200	PA_28600	12	+	
SPA0126	V	3710200-3710700	PA3309	14	+	1836400-1836900	PA14_21220	10	-	
SPA0127	V	5544700-5545000	PA4940	4	-	5816100-5816300	PA14_65260	4	-	
Group E										
SPA0128	I	99747-100047	<i>tha1/tssA1</i>			97400-97700	PA14_00980/PA14_00990	3	-	
SPA0129	I	517688-518088	PA0458/PA0459			530600-531100	<i>emrA/clpA</i>	4	+	
SPA0130	I	674110-674210	PA0611/PA0612			686800-686900	<i>prtR/PA14_07970</i>	3	+	
SPA0131	I	3813773-3813973	<i>hasAp/hasD</i>			1725300-1725500	<i>hasAP/hasD</i>	5	-	
SPA0132	I	3498188-3498388	<i>fimV/PA3116</i>			2069900-2070100	PA14_23810/ <i>fimV</i>	6	+	
SPA0133	I	3221081-3221181	PA2867/PA2868			2348200-2348300	PA14_26990 PA14_27000	3	-	
SPA0134	I	2966810-2967110	<i>icd/idh</i>			2614800-2615100	<i>idh/icd</i>	7	-	
SPA0135	I	2893791-2894091	PA2559/PA2560			2733300-2733600	PA14_31430/PA14_31440	3	+	
SPA0136	I	2341596-2341796	PA2127/ <i>cupA1</i>			3301600-3301800	PA14_37060/PA14_37070	4	+	
SPA0137	I	1720609-1720709	<i>gltA/sdhC</i>			3922800-3922900	<i>sdhC/gltA</i>	4	-	
SPA0138	I	1163027-1163327	<i>braC</i>			4486600-4486900	<i>braC</i>	5	+	
SPA0139	I	5282368-5282768	PA4702/PA4703			5554300-5554700	PA14_62250/PA14_62240	8	+	
SPA0140	II	8500-8700	PA0007			8500-8700	PA14_00080	7	+	
SPA0141	II	40479-40679	PA0039			40500-40700	PA14_00480	4	+	
SPA0142	II	141786-142186	PA0122			139700-140100	PA14_01490	17	+	
SPA0143	II	437564-437864	<i>pilU</i>			452300-452600	<i>pilU</i>	6	+	

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SPA0144	II	4507749-4507948	PA4026			1018300-1018500	PA14_11750	3	-	
SPA0145	II	3772836-3773036	<i>lecB</i>			1774200-1774400	<i>lecB</i>	6	-	
SPA0146	II	3649323-3649523	PA3261/PA3262			1897700-1897000	PA14_21830	4	+	
SPA0147	II	3332328-3332928	<i>rne</i>			2236400-2237000	<i>rne</i>	10	-	
SPA0148	II	2926236-2926636	<i>gacA</i>			2655300-2655700	<i>gacA</i>	4	+	
SPA0149	II	2059117-2059417	PA1888			3573000-3573300	PA14_40100	5	+	
SPA0150	II	1703023-1703223	<i>acnA</i>			3940300-3940500	<i>acnA</i>	5	+	
SPA0151	II	1226131-1226232	PA1134			4423700-4423800	PA14_49720	4	+	
SPA0152	II	0939003-940203	PA0861			4711400-4711600	PA14_53140	4	-	
SPA0153	II	5755147-5756347	<i>estA</i>			6028400-6028600	<i>estA</i>	5	-	
SPA0154	II	6106977-6107377	<i>adhA</i>			6379900-6380300	<i>adhA</i>	8	+	
SPA0155	III	131185-131585	<i>collI</i>			129100-129500	<i>collI</i>	4	-	
SPA0156	III	334675-334975	<i>spuA</i>			348800-349100	<i>spuA</i>	6	-	
SPA0157	III	380028-380328	<i>ptsP</i>			394200-394500	<i>ptsP</i>	3	-	
SPA0158	III	4751619-4751918	<i>bfrA</i>			774900-775200	<i>bfrA</i>	6	-	
SPA0159	III	4005030-4005330	PA3573			1552800-1553100	PA14_18090	11	-	
SPA0160	III	3501188-3500688	<i>leuB</i>			2067200-2067500	<i>leuB</i>	3	-	
SPA0162	III	2911211-2910811	<i>alkB1</i>			2672600-2672800	<i>alkB1</i>	3	-	
SPA0163	III	2818447-2818747	PA2500			2808600-2808900	PA14_32330	3	+	
SPA0164	III	1996877-1997277	PA1838/PA1839			3637400-3637800	PA14_40750	5	+	
SPA0165	III	1878304-1878604	PA1735			3756200-3756500	PA14_42100	4	+	
SPA0166	III	1558629-1558929	<i>lasR</i>			4085300-4085600	<i>lasR</i>	10	+	
SPA0167	III	1265312-1264912	PA1166/ <i>pcpS</i>			4383800-4384000	PA14_49330/ <i>pcpS</i>	3	-	
SPA0168	III	1096531-1096631	<i>purC</i>			4553300-4553400	<i>purC</i>	40	+	
SPA0169	III	1068967-1069257	PA0987			4583200-4583500	PA14_51540	5	+	RGP7
SPA0170	III	5001909-5002309	PA4473			5165500-5165900	PA14_58060	4	-	
SPA0171	III	5301669-5301869	PA4722			5573600-5573800	<i>aspC</i>	4	+	
SPA0172	III	5868087-5868387	PA5212/ <i>gcvP</i>			6140300-6140600	PA14_68840/ <i>gcvP1</i>	7	+	
SPA0173	III	5885587-5885887	PA5229			6157800-6158100	PA14_69050	6	-	
SPA0174	III	5925886-5926066	<i>argH</i>			6198100-6198300	<i>argH</i>	3	-	

nstSGR name ^e	class	PAO1				PA14				Notes ^d
		Genomic coordinates (left-right)	Flanking/ Involved <i>loci</i> ^a	# reads ^b	strand ^c	Genomic coordinates (left-right)	Flanking/ Involved <i>loci</i> ^a	# reads ^b	strand ^c	
SPA0175	III	5995982-5996181	PA5325			6268900-6269100	PA14_70300	4	-	
SPA0176	III	6176689-6176989	<i>ampDH2</i>			6449600-6449900	PA14_72400	4	+	
SPA0177	III	6218466-6218866	PA5525			6491700-6492100	PA14_72890	11	-	
SPA0178	V	4632556-4632856	PA4141			895000-895300	PA14_10360	15	-	
SPA0179	V	3235659-3236359	PA2883			2333200-2333600	PA14_26780	12	-	
SPA0181	V	3108471-3108771	PA2746/PA2747			2465200-2465500	PA14_28610	5	-	
SPA0182	V	1064311-1064707	PA0981/PA0982			4585500-4585900	PA14_51570	6	-	RGP7
SPA0184	V	5169142-5169442	PA4611			5441600-5441900	PA14_61010	7	-	

^a *Loci* (locus ID or gene name) either overlapping (class II, III and V) or flanking (class I) the nstSGRs.

^b Total number of cDNA reads identifying the nstSGR.

^c Upper (+) or lower (-) genomic DNA strand coincident with cDNA reads.

^d Names of annotated *P. aeruginosa* sRNAs; Region of Genomic Plasticity (RPG) containing the nstSGR.

^e Tested sRNAs are in boldface.

^f In PA14 this nstSGR contains a duplication of *ffs* gene for 4.5S between *loci* PA14_44640 and PA14_44650.