Supplementary Table 1: Prediction of sRNA binding motifs in genes differentially regulated in S. meliloti *hfq*- and *smc0113*- mutants

DOWN-REGULATED GENES

Target gene	smRNA	smRNA_motif_seq	Position of motif in smRNA	Position of motif in gene (3')	Length of motif	Gibbs Energy [ΔG; kcal/mol]	Enthalpy [ΔH; kcal/mol]	Entropy [ΔS; cal/(K·mol)]
SMc02597 **SodC**	sra21	CGCCCTTGCCGCC	162	368	13	-17.06	-106.6	-288.7
	sra06	TGCCGAAGCGGC	210	459	12	-14.57	-96.6	-264.47
	sra42	TGCCGCACAGGC	116	483	12	-14.5	-95.3	-260.53
	sra43	CGCCTGCCGTCA	774	377	12	-14.27	-95.8	-262.88
	sra63	ATGCGGGCCATT	1883	198	12	-12.21	-88.9	-247.25
	sra65	GCCGCGAAGGGC	450	93	12	-15.27	-98.3	-267.7
	sra13	CCGGCCGCGAA	28	90	11	-14.08	-89.1	-241.8
	sra33	AAGCGAGGAAG	201	212	11	-9.39	-81.6	-232.8
	sra47	GGAGGGCTGGC	760	42	11	-12.66	-83.7	-229.06
	sra48	GAGCGTGAAAA	38	308	11	-8.57	-82.8	-239.35
	sra49	TGCTCGGCATT	154	226	11	-10.45	-81.7	-229.73
	sra50	GCGGGCCATTG	141	200	11	-12.07	-86.1	-238.7
	sra53	CGTCGAGGGAC	187	116	11	-11.26	-86.2	-241.62
	sra61	GCCGGCATCGC	436	30	11	-13.66	-90.3	-247.11
	sra02	TTGCCGCCTG	113	373	10	-10.83	-76.5	-211.72
	sra10	AAGCTGTTGA	14	130	10	-7.17	-70.2	-203.22
	sra17	GCCCGGCCGC	598	88	10	-14.5	-82.4	-218.91
	sra19	GAAGGGCGGT	155	98	10	-10.35	-74.3	-206.18
	sra23	TTCGCCGGCA	204	243	10	-11.5	-76.8	-210.56
	sra25	CGAAGGGCGG	228	97	10	-11.29	-78.7	-217.36
	sra27	TCGGCAGGCC	16	335	10	-11.81	-76.3	-207.92
	sra28	GCATGTCGCC	1	185	10	-10.32	-78.8	-220.78
	sra34	CCTTGCCGCC	163	371	10	-11.51	-78.2	-215.01
	sra39	TCCTTCGGCA	187	331	10	-9.57	-72.4	-202.59
	sra41	GGCAAAATGC	111	249	10	-7.96	-75.3	-217.12
	sra45	GCCGTCGCCG	197	433	10	-13.18	-83.8	-227.69
	sra55	CGGCACCGAC	282	164	10	-11.47	-80.3	-221.92
	sra67	CGCAAGGTTC	50	151	10	-8.84	-76.9	-219.46
SMa2379 **KatB**	sra06	GAGCCGCGGAAGGTC	330	766	15	-17.25	-121.1	-334.83
	sra17	CGGGCCTTCCGGG	97	1515	13	-16.22	-102.7	-278.85
	sra29	AGGCCGGAATGCC	126	2059	13	-14.39	-99.4	-274.1
	sra10	GGTGCGGTCAGC	650	355	12	-13.62	-95.8	-264.98
	sra30	GCCGGCGCCGCC	182	1851	12	-18.43	-102.8	-272.03
	sra45	CTCGTAAGCGGG	28	1050	12	-11.81	-94.1	-265.31
	sra46	GCGCCGCCTTCC	93	1345	12	-15.27	-98.3	-267.7
	sra47	CCGCCGGCCTTG	743	547	12	-15.06	-96.8	-263.55
	sra63	CAAGCACAGAGA	2021	662	12	-9.75	-89	-255.52
	sra64	GTAGCGCTCGTC	679	1590	12	-12.05	-96.6	-272.6
	sra03	GCCGCCACGGC	307	1857	11	-15.05	-91.3	-245.84
	sra22	TCCATGCGGCC	572	508	11	-12.37	-84.2	-231.6
	sra27	CCGAAGTCGGC	10	1933	11	-11.71	-87.3	-243.74
	sra28	GCCGCAACGAA	116	43	11	-11.61	-87.3	-244.06
	sra34	GCAAAGGTTTC	254	1462	11	-8.02	-82.1	-238.84
	sra36	TCGTGGCCGCC	29	541	11	-13.86	-87.5	-237.43
	sra53	AGCGCTTCGGG	130	268	11	-12.44	-86.1	-237.5
	sra58	CCGCCTTCAGC	94	311	11	-11.79	-86.2	-239.92
	sra01	TGTCGTGGCC	324	539	10	-10.54	-76	-211.07
	sra05	CAACCGGGTC	134	1493	10	-9.76	-75.8	-212.94

	sra07	TCCGCGAACT	103	1006	10	-9.8	-74.9	-209.91
	sra11	AACCGGGTCG	50	1494	10	-10.4	-75.7	-210.53
	sra13	GCCGCGCTTG	136	753	10	-12.12	-82.6	-227.25
	sra14	GGCGCCGCCA	678	1854	10	-13.79	-80.7	-215.72
	sra16	GGCCGCCGGC	639	545	10	-14.5	-82.4	-218.91
	sra18	GACCAGATCA	205	3	10	-7.28	-70.6	-204.17
	sra19	GGTCGGGGTC	162	1242	10	-10.73	-75.6	-209.15
	sra25	GCCGCCTTCC	166	1347	10	-11.38	-77.9	-214.48
	sra26	GCGTTGAAGT	283	637	10	-8.17	-75.1	-215.8
	sra32	CCGCAGGCCG	443	324	10	-12.9	-80.9	-219.24
	sra33	TCGCGCGCGG	30	1480	10	-14.19	-85.6	-230.25
	sra38	GCCCAGGAAA	350	1735	10	-9.02	-71.7	-202.1
	sra39	CGGCGGCGCC	648	572	10	-14.78	-85	-226.4
	sra40	GCGGTCGGCA	548	15	10	-12.22	-79.5	-216.94
	sra42	GTCGAGACAA	57	799	10	-7.61	-73.8	-213.42
	sra48	GTGGTTGAAC	28	1203	10	-7.34	-74	-214.94
	sra49	CCTTCCGGGT	261	1351	10	-10.01	-72.5	-201.47
	sra50	CTTGGCAGCC	471	555	10	-10.04	-75.9	-212.36
	sra51	GCCCATATCG	606	231	10	-8.33	-74.5	-213.36
	sra52	CTCGACGGCG	43	567	10	-11.44	-82	-227.49
	sra55	TTGTCGGAGC	177	760	10	-9.15	-75	-212.32
	sra56	GTCCGGCCAG	55	1809	10	-11.07	-77.1	-212.9
	sra57	ACGCGCCGGC	65	1169	10	-14.05	-83.2	-222.94
	sra59	CCGCAAAGGC	124	98	10	-10.39	-78.1	-218.3
	sra60	TGGCCGGCGC	516	1849	10	-13.79	-80.7	-215.72
	sra61	CTCGTGGTTG	165	1200	10	-8.53	-76.1	-217.86
	sra62	GGTGCTCTTC	59	1311	10	-8.36	-74.4	-212.94
	sra65	TGCGACGGGA	393	2142	10	-11.05	-75.7	-208.43
	sra66	GCCCAGGAAA	836	1735	10	-9.02	-71.7	-202.1

SMc01700 ppiA	sra11	GGATATTTTCGC	1417	485	12	-8.14	-89.9	-263.61
	sra32	TGAAGCCCTTGA	102	344	12	-10.29	-86	-244.11
	sra38	GGGCGCGAGCAT	1322	147	12	-14.46	-95.9	-262.59
	sra50	CCTGGAAACCG	536	293	11	-10.14	-83.1	-235.25
	sra63	GCGGGCCATTC	1885	198	11	-11.93	-85.8	-238.17
	sra05	TGGACGAGCC	118	263	10	-10.26	-75.1	-209.07
	sra09	CTTAACGCTG	178	12	10	-7.32	-75.7	-220.48
	sra10	TTTTCGCCGG	38	490	10	-9.6	-76.5	-215.71
	sra17	AGCGAATTGG	573	552	10	-8.04	-73.5	-211.07
	sra19	CTCCGGCAAC	139	542	10	-9.95	-77	-216.18
	sra22	CATGCCTTCG	230	93	10	-8.72	-76.3	-217.88
	sra23	ATTCCGACGG	13	205	10	-9.05	-74.7	-211.68
	sra34	GACCTTGCCG	161	105	10	-9.95	-77	-216.18
	sra35	CCGACCTTAA	79	7	10	-7.43	-71.6	-206.91
	sra39	CGGCGAGCGC	107	527	10	-13.39	-85	-230.9
	sra40	TCCGGGCGCA	577	436	10	-12.61	-76.9	-207.28
	sra43	TCGCCTGCCG	773	385	10	-12.07	-78.9	-215.48
	sra45	CGATATCCGG	373	431	10	-8.09	-75	-215.72
	sra47	TTCGCCTGCC	132	384	10	-10.7	-76.2	-211.19
	sra53	CAAGGCTCCG	379	537	10	-9.81	-76.4	-214.71
	sra57	GTTGAGGAAG	243	132	10	-6.92	-72.5	-211.44
	sra60	GCCGCGGCCA	479	391	10	-13.79	-80.7	-215.72
	sra62	CGCGCTCGAA	96	218	10	-11.06	-81.1	-225.84
	sra64	ACGACGGGGC	620	454	10	-11.86	-77.6	-211.95
	sra65	GCGCCAAGGC	426	533	10	-11.86	-80	-219.69

SMc01946 livK	sra08	ACGCGGTGCCGC	196	1055	12	-16.25	-100.1	-270.37
	sra11	TCATCGACTTCT	1179	566	12	-8.74	-86.4	-250.39
	sra26	TCCGAAACGTCG	73	892	12	-11.45	-94.6	-268.08
	sra63	CGCCGATTGCCG	1106	104	12	-14.07	-99	-273.82
	sra10	CAGCGTGCCGT	769	318	11	-12.75	-88	-242.61
	sra19	GCGGCCGGGCT	87	280	11	-15.28	-88	-234.46
	sra27	CGTCCTTGAAA	190	638	11	-8.24	-81	-234.59
	sra39	GCCGGCGGCGC	646	246	11	-16.79	-94.8	-251.53
	sra47	GCGTCCTTGAA	272	637	11	-9.68	-82.9	-236.09
	sra49	TGTGCAGACCG	92	443	11	-10.95	-84.3	-236.49
	sra59	GCAACGGCGCC	468	670	11	-13.91	-91.2	-249.2
	sra64	CTTCTTGGTTT	163	573	11	-6.92	-77.9	-228.85
	sra66	GTCGTCGCCGA	549	900	11	-12.4	-88.6	-245.68
	sra02	CGGCGACCTT	29	626	10	-10.6	-76.9	-213.77
	sra03	TCCTTGAAAT	158	640	10	-5.65	-67	-197.8
	sra06	TGCAGGATGC	187	766	10	-9.27	-73.9	-208.38
	sra14	GGGATCCGAA	240	888	10	-8.68	-71.9	-203.8
	sra16	GCCGGCGGCG	643	246	10	-14.78	-85	-226.4
	sra17	GGATGCCGTT	544	770	10	-9.28	-74.2	-209.32
	sra21	CTTGTCGCCG	154	513	10	-10.2	-79.6	-223.77
	sra22	CCCGCAACGG	396	667	10	-11.57	-79.6	-219.35
	sra24	CACCCTGCTT	514	878	10	-9.04	-72.3	-203.98
	sra25	GAAGGGCCGC	218	203	10	-11.38	-77.9	-214.48
	sra30	GAGCTGCGCG	267	987	10	-11.87	-82.7	-228.36
	sra32	GCCATCGGCC	89	846	10	-11.41	-77.9	-214.38
	sra33	CGGACCAGTC	320	1011	10	-9.51	-75.9	-214.06
	sra37	GCGATATAGG	171	655	10	-6.69	-73	-213.81
	sra38	CCGATGCGGG	174	794	10	-11.32	-78.7	-217.26
	sra40	AGGCGCCCGC	516	662	10	-13.64	-80	-213.96
	sra41	GTCGTGAATG	66	615	10	-7.32	-75.7	-220.48
	sra43	TCATCGTCGC	213	386	10	-9.28	-77.3	-219.31
	sra45	GGTGCGGAAG	285	702	10	-9.95	-77	-216.18
	sra48	GGGCGACGGA	105	866	10	-11.73	-77.4	-211.73
	sra51	TCGGACCAGT	167	1010	10	-9.26	-71.5	-200.68
	sra53	CCGCAACGGC	411	668	10	-11.92	-81.4	-224.03
	sra57	TCTTGCGCGG	276	290	10	-10.94	-78.8	-218.78

SMb21647 agpA	sra10	TTTCGCCGGGCTT	39	17	13	-14.04	-99.9	-276.85
	sra27	GGAAAGCCCGCC	470	756	12	-13.54	-93.8	-258.77
	sra43	TCGTCGGCCTCG	142	1630	12	-13.9	-96	-264.71
	sra50	TGGAATCGCGCG	296	1931	12	-13.24	-97	-270.05
	sra56	TTCACCAGAGCC	159	793	12	-10.97	-88.7	-250.63
	sra57	GAGCCGCGCCGG	285	966	12	-16.68	-101	-271.87
	sra60	CTTTCGCCGGGC	334	16	12	-13.79	-96.4	-266.35
	sra02	CGTTCGTCCGG	11	889	11	-11.76	-88.7	-248.09
	sra03	CGGCAAAGGCA	70	2021	11	-11.36	-84.4	-235.5
	sra08	GCGGGGAAGCC	103	1243	11	-13.02	-85.9	-234.98
	sra17	GCTGGCGATGA	132	276	11	-11.01	-84.2	-235.98
	sra22	CGCCTTCGCGC	143	879	11	-13.89	-92.9	-254.76
	sra28	GCGGCCGCCAA	240	609	11	-14.31	-88.6	-239.54
	sra30	TGACGCGCGGG	70	947	11	-14.12	-90.1	-244.99
	sra31	GCGGCGCGCTT	64	991	11	-14.76	-92.3	-250
	sra32	CCGGCGGCAGC	229	1847	11	-14.9	-90.7	-244.39

	sra38	GGCGCGGGAAG	437	1361	11	-13.28	-88.5	-242.53
	sra39	GCGGCTGCTCG	421	1976	11	-13.52	-90.7	-248.85
	sra44	GTATTCGCGCA	55	1902	11	-9.98	-85.8	-244.48
	sra45	GCCGCTCGGCC	236	1835	11	-14.77	-90.4	-243.86
	sra53	GTCTTTGAGCC	84	660	11	-8.88	-82.3	-236.71
	sra55	AGCTCCCGCAC	66	868	11	-12.23	-84.5	-233.03
	sra61	TTCCGGCCGGC	431	1737	11	-13.82	-86.5	-234.34
	sra63	GGCGGCGCGCT	901	990	11	-15.91	-92.4	-246.63
	sra64	CCGCCATGGTG	471	827	11	-11.76	-85.3	-237.12
	sra01	CGATGCGTTT	55	2068	10	-8.4	-76.7	-220.22
	sra05	TTGGTGGTGG	111	217	10	-8.99	-71.8	-202.52
	sra06	CTGCTTGCCG	205	483	10	-10.28	-78.5	-219.95
	sra11	CGCCGTCCGA	957	1529	10	-11.99	-80	-219.29
	sra14	TCGCTCGTCA	365	258	10	-9.7	-75.7	-212.81
	sra16	GCCATTGCGA	71	1342	10	-9.62	-76.1	-214.36
	sra18	GCAAGATTAC	262	553	10	-5.89	-72.7	-215.4
	sra19	AGCGCCTTGA	252	1912	10	-9.89	-73.8	-206.07
	sra20	GCGAAAAGAT	24	1348	10	-6.8	-73.1	-213.76
	sra24	GTTCATATAT	255	1230	10	-3.4	-66.6	-203.79
	sra26	TCGGCGCGCC	128	134	10	-13.92	-83	-222.72
	sra29	GGTCGAGAGC	105	1086	10	-9.57	-76.8	-216.76
	sra47	TGCCGGCCTT	124	1802	10	-11.24	-73.8	-201.72
	sra48	GTCGCGCTGC	169	477	10	-12.02	-83.3	-229.82
	sra51	AATTTCTCCG	28	1873	10	-6.48	-71.3	-208.99
	sra58	CTTCAGCGAC	98	999	10	-8.59	-77	-220.57
	sra59	GACTCCACGA	16	1006	10	-8.71	-73.9	-210.18
	sra62	CCTCGATCAG	358	1550	10	-8.01	-74.3	-213.73
	sra65	CCGACGGTAT	35	202	10	-8.78	-74.2	-210.92

SMc02501 atpD	sra45	CGACCGGAACCGCG	83	1178	14	-17.29	-117.1	-321.81
	sra11	TGATAGAGGTCGT	861	844	13	-10.11	-93.9	-270.16
	sra42	ATCTGGCCCATGT	227	562	13	-11.97	-93.5	-262.88
	sra63	CCGAAGAGGCCGA	399	970	13	-14.03	-100.7	-279.45
	sra32	TGAAGCCCTTGA	102	113	12	-10.29	-86	-244.11
	sra38	TGGATGGCGCGG	1204	1087	12	-14.26	-94.8	-259.68
	sra43	CTTCGCATAGGG	29	993	12	-10.35	-90.8	-259.4
	sra10	CGCCGGACTCG	288	824	11	-13.09	-90	-247.98
	sra12	GCGACAGGAAA	118	191	11	-9.68	-82.9	-236.09
	sra17	TTGCGGGCGCG	60	211	11	-14.56	-91.2	-247.1
	sra19	GAACGAGGCGG	489	1298	11	-11.71	-87.3	-243.74
	sra23	CGGGCGACGGC	20	220	11	-14.83	-91.8	-248.18
	sra28	AGCCGCAACGA	115	1422	11	-11.9	-85	-235.68
	sra35	GCCGGGTCGGT	89	475	11	-13.51	-85.6	-232.45
	sra39	CCGGCTCGCCG	622	1133	11	-14.68	-91.2	-246.73
	sra40	CGCTTCCGTCG	470	1047	11	-11.95	-89.9	-251.32
	sra47	GCCTTCGTCAC	404	693	11	-10.37	-85.6	-242.55
	sra50	ACGATCATCGG	32	349	11	-9.36	-82.7	-236.47
	sra61	GCCTGCGAAGA	232	882	11	-10.98	-84.2	-236.08
	sra02	CGGCGACCTT	29	1208	10	-10.6	-76.9	-213.77
	sra03	AGTCGAGCGG	63	380	10	-10.35	-77	-214.88
	sra06	CGACTGGTCC	1	1056	10	-9.51	-75.9	-214.06
	sra07	TCGCGGGTCC	74	862	10	-11.73	-77.4	-211.73
	sra14	CGAAGAACGG	246	179	10	-8.6	-77.4	-221.82
	sra15	CCGCGATCGG	20	1187	10	-11.44	-81	-224.29
	sra16	TTCGAATGCG	670	1362	10	-8.27	-76.5	-219.99

	sra18	CAACTTCGAG	111	1289	10	-7.15	-75.1	-219.1
	sra21	CGCTCGATCT	21	202	10	-8.99	-76	-216.04
	sra22	GCCGCGAACG	39	1221	10	-12.04	-83.7	-231.06
	sra24	GAAGCTGCCT	63	1444	10	-9.09	-73.2	-206.69
	sra25	GCCGCCGAAG	223	966	10	-11.63	-80.5	-222.04
	sra26	TCTTCAGCGG	91	1109	10	-9.01	-74.4	-210.84
	sra27	TGCAGGGCCT	282	283	10	-10.88	-71.6	-195.77
	sra29	CAACGACTGT	51	1427	10	-7.87	-74.3	-214.19
	sra30	TCTTGCCGCC	175	983	10	-10.7	-76.2	-211.19
	sra36	GGGTCGACTG	201	305	10	-9.51	-75.9	-214.06
	sra41	CCGTAGCCGC	259	1418	10	-11.37	-80	-221.29
	sra46	CAGGCCGGTC	60	723	10	-11.07	-77.1	-212.9
	sra49	GCGACACTTC	242	323	10	-8.73	-77.6	-222.05
	sra51	AGCGGGCCGG	490	1114	10	-13.28	-78.2	-209.31
	sra53	CGCCGATGAC	558	1139	10	-10.09	-79.3	-223.14
	sra54	GCAACGACTG	483	1426	10	-8.87	-77.9	-222.58
	sra57	GCGGAAGATG	329	657	10	-8.59	-76	-217.34
	sra58	TCGAGCGCGA	115	422	10	-11.36	-79.2	-218.73
	sra60	GCCGGTGCCG	751	469	10	-13.05	-81.5	-220.69
	sra65	GAAGACGGAG	945	888	10	-8.12	-74.9	-215.3
	sra66	TTGGTCGTGG	715	535	10	-9.09	-74.1	-209.61

SMb20428 ehuB	sra47	CGCCGAGCCGCT	200	623	12	-15.81	-98.6	-266.93
	sra61	CGATGATCTTCG	191	68	12	-9.19	-92.4	-268.29
	sra06	GCGGGTTGCCT	12	443	11	-12.47	-84.4	-231.92
	sra11	CGGTCGCGCGG	30	331	11	-15.09	-94.4	-255.7
	sra16	GCCGCCATTGC	68	820	11	-12.41	-87.9	-243.4
	sra29	TTGCCTTTCTT	6	448	11	-7.68	-77.1	-223.82
	sra36	TGCAGGCCCGG	230	568	11	-13.59	-84.6	-228.95
	sra38	GGTCGTTCGCC	17	215	11	-11.85	-87.9	-245.2
	sra43	CGCCCGGCCTG	63	559	11	-14.55	-88.9	-239.73
	sra60	TCGGCAACGCC	315	616	11	-12.73	-87.4	-240.75
	sra63	CGACGGGGGCC	1343	188	11	-14.2	-87.4	-236
	sra64	CTCTGGCCATC	454	304	11	-9.88	-81.8	-231.89
	sra66	ATGGAGGCGAC	489	601	11	-10.67	-82.3	-230.95
	sra05	TTCTCCTCGG	4	364	10	-8.54	-72.3	-205.58
	sra10	GACCTTGCCA	88	672	10	-9.05	-72.7	-205.23
	sra14	GCGATGTCCT	0	415	10	-9.03	-74.3	-210.43
	sra17	GCGCCCGGCC	596	558	10	-14.5	-82.4	-218.91
	sra19	GTACCGCCGC	15	373	10	-11.51	-80.6	-222.75
	sra20	ATGTCCTTGT	108	418	10	-6.88	-68.3	-198.03
	sra27	GGCTCGATGA	486	64	10	-8.9	-74.1	-210.21
	sra32	CGTCGATGCG	564	269	10	-10.34	-81.9	-230.73
	sra33	AACGCCGAGC	132	621	10	-10.94	-78.7	-218.47
	sra37	CAGCATCTTC	308	288	10	-7.14	-73.7	-214.6
	sra39	TCGCAGCCTT	429	38	10	-9.89	-73.8	-206.07
	sra40	ATGCGCGCGA	260	724	10	-11.96	-80.5	-220.97
	sra46	GACGGCGGCA	241	504	10	-12.22	-79.5	-216.94
	sra50	ATCCGGCACC	725	312	10	-10.39	-74.3	-206.08
	sra51	TGGCGCCCGG	44	556	10	-13.44	-78.9	-211.07
	sra53	CGCCGCCCGG	225	377	10	-14.42	-83.2	-221.77
	sra55	CGAGCCGCTT	332	626	10	-10.8	-78.1	-217
	sra57	CGCCGCCCGG	307	377	10	-14.42	-83.2	-221.77
	sra59	ACCGGAGACC	530	666	10	-9.91	-73.2	-204.05
	sra62	AGATCTCGCG	159	638	10	-8.99	-76	-216.04

	sra65	GTAGCTCTTG	137	426	10	-6.85	-73.2	-213.93

SMc00421 **cysK1**	sra28	CGGAGCCGATCG	413	809	12	-13.35	-97	-269.71
	sra43	CACCAGTTCGGC	315	591	12	-12.15	-93.9	-263.59
	sra08	GCACCGTCGAA	181	23	11	-11.17	-86.2	-241.92
	sra10	CCGGCGTTTTC	32	79	11	-10.82	-87.1	-245.93
	sra11	GCGCGGCACCG	70	122	11	-15.32	-93.9	-253.36
	sra19	TGCGGCCGGGC	86	740	11	-15.44	-88.7	-236.22
	sra27	CCGAAGTCGGC	10	716	11	-11.71	-87.3	-243.74
	sra30	GCGGCCGCGAC	20	679	11	-15.18	-93.6	-252.84
	sra38	GGTGCCGATGC	170	396	11	-11.97	-86.8	-241.28
	sra39	TCCTGCCGGCG	642	74	11	-13.71	-86.9	-235.98
	sra52	CTCGACGGCGA	43	324	11	-12.26	-88	-244.21
	sra57	GAGCCGCGCCG	285	171	11	-15.03	-93	-251.38
	sra60	GCCGGTGCCGA	751	393	11	-13.86	-87.5	-237.43
	sra63	CGCCGATGCGG	1176	791	11	-13.57	-91.1	-249.99
	sra65	TCCAGATCTCC	500	443	11	-8.63	-77.7	-222.7
	sra01	GGCGCCGCCG	422	291	10	-14.78	-85	-226.4
	sra02	GCGGCCGCGA	240	679	10	-13.92	-83	-222.72
	sra05	TCTCCTCGGC	5	449	10	-9.98	-74.2	-207.06
	sra13	GCCGACCGGC	91	141	10	-12.92	-81.2	-220.17
	sra14	GGGCGCCGCC	677	290	10	-14.5	-82.4	-218.91
	sra16	TATCGCCGCC	64	108	10	-10.54	-77	-214.28
	sra17	CCGGCGGAAA	6	130	10	-10.71	-76.6	-212.44
	sra18	TTCGAGCTTG	115	831	10	-7.9	-74.3	-214.09
	sra20	CCACCTCTAT	58	101	10	-6.98	-68.7	-199.01
	sra25	GCCCTTTTCC	237	861	10	-8.57	-73.3	-208.71
	sra32	GCGTGATCTT	209	749	10	-7.93	-74.2	-213.67
	sra33	CGGCGTTTTC	362	80	10	-9.18	-79.1	-225.43
	sra34	TGCCGCCGGT	166	389	10	-12.74	-77.1	-207.5
	sra40	CTCGGGCATG	10	645	10	-9.84	-76.4	-214.61
	sra41	AAATGCCGAC	115	137	10	-8.18	-74.1	-212.56
	sra45	CGGTCCTTGA	380	799	10	-8.82	-73.2	-207.59
	sra46	CGCGCCGCCT	92	175	10	-13.91	-82.6	-221.49
	sra47	CACGCCTTCG	401	150	10	-10.2	-79.6	-223.77
	sra48	TCGACGGCGA	430	325	10	-11.16	-78	-215.49
	sra49	GGACCCGGGG	50	283	10	-11.94	-75	-203.33
	sra50	GCCGGGTTCT	433	487	10	-10.35	-74.3	-206.18
	sra53	TCGCCGCCTG	245	110	10	-12.07	-78.9	-215.48
	sra55	GCCGGCACCG	280	372	10	-13.05	-81.5	-220.69
	sra61	GCGGAAATGC	488	133	10	-9.17	-77.7	-220.96
	sra64	CTGGAGCGCG	634	117	10	-11.53	-80.9	-223.68
	sra66	GTCGTCGTGC	369	460	10	-10.24	-80.9	-227.82

UP-REGULATED GENES

Target gene	smRNA	smRNA_motif_seq	Position of motif in smRNA	Position of motif in gene (3')	Length of motif	Gibbs Energy [ΔG; kcal/mol]	Enthalpy [ΔH; kcal/mol]	Entropy [ΔS;cal/(K·mol)]
SMc00786 **dppA1**	sra16	CAGAAGACGAAAGTT	8	1510	15	-11.09	-113.1	-328.91
	sra07	CAGCGTGGCAATC	202	1548	13	-12.89	-103	-290.53
	sra11	CGGCACGGCGGGC	746	434	13	-18.61	-109.9	-294.34
	sra28	GTCGCTGCCAAG	149	1564	12	-12.34	-95.1	-266.83
	sra34	GGTTCGGATCGG	4	764	12	-11.78	-93.1	-262.19
	sra38	GCCGGCATCCTC	1258	507	12	-13.33	-93.9	-259.78

	sra12	GGTTGAGCTGG	171	995	11	-10.13	-82.7	-234
	sra25	CGAAGGGCGGC	228	695	11	-13.28	-88.5	-242.53
	sra37	CCATGCCCGCG	200	1169	11	-13.45	-88.8	-242.96
	sra48	CCGAGGATGAC	213	313	11	-9.79	-82.9	-235.72
	sra53	CTTCCACTGGC	734	1230	11	-10.13	-82.7	-234
	sra58	TGCCGGCCATC	29	1538	11	-12.37	-84.2	-231.6
	sra59	CCGCACCGTCG	252	323	11	-13.37	-90.9	-249.97
	sra60	CCGGTGCCGAG	752	976	11	-12.97	-87.7	-240.95
	sra63	GGCGACGTTGA	29	729	11	-11.17	-86.2	-241.92
	sra66	TGCACGAAGCC	376	49	11	-11.26	-85.1	-238.09
	sra04	GAGATAGGCG	30	723	10	-8.05	-74.6	-214.57
	sra06	CGCCTGCTTG	202	645	10	-10.28	-78.5	-219.95
	sra10	CGAGGAAGTT	427	275	10	-7.57	-72.4	-209.02
	sra14	TGATCGCGAA	318	869	10	-8.59	-74.6	-212.83
	sra19	TCGGTCTCCG	134	1387	10	-10.03	-75.6	-211.42
	sra21	GCGCTCGATC	20	1239	10	-10.16	-80.2	-225.84
	sra22	GTTGATCGCC	32	654	10	-8.73	-76.6	-218.82
	sra23	CGCGGCAGCG	110	1440	10	-13.52	-85.3	-231.42
	sra24	CGACCTTGTC	118	686	10	-8.4	-75.8	-217.32
	sra26	GCGGGCGTTC	111	441	10	-11.78	-81.1	-223.5
	sra27	CGGCAGGCCC	17	1161	10	-12.64	-78.3	-211.71
	sra30	TTTTCCGCCC	225	900	10	-9.36	-73.9	-208.08
	sra39	TTCGGCGAGC	105	1371	10	-10.81	-78.5	-218.25
	sra40	GCGAAAGGAC	782	967	10	-8.7	-76.6	-218.92
	sra41	TGCATCAGCT	436	421	10	-8.48	-71.5	-203.2
	sra43	GGGGCTTCGC	738	115	10	-11.38	-77.9	-214.48
	sra44	GCAGCTTGTC	33	1025	10	-8.82	-76.5	-218.21
	sra47	AAAGTCGCCG	41	30	10	-9.48	-76.8	-217.04
	sra57	ACTTCCACTG	54	1229	10	-7.51	-71.1	-205.04
	sra61	CGAGGATGAC	201	314	10	-8.15	-74.9	-215.21
	sra62	TGTTGATCGC	370	653	10	-8.07	-74.9	-215.47
	sra64	CGCTTCAGCT	523	1102	10	-9.33	-75.8	-214.32

SMc01525 dppA2	sra39	GCCGCCGAGGCGG	713	1591	13	-18.32	-109	-292.36
	sra47	GCCGGCCTTCGCC	125	513	13	-16.92	-106.3	-288.19
	sra51	GCGCGCTTGGCGC	37	160	13	-18.02	-112.8	-305.6
	sra40	GGTGATCGGATT	66	1296	12	-9.66	-88	-252.58
	sra55	GCGCGAGCCGCT	329	842	12	-16.16	-100.4	-271.6
	sra11	GGCGACCTCCG	896	81	11	-12.83	-87.4	-240.43
	sra14	GAACGGGCCAG	812	972	11	-11.59	-85	-236.68
	sra17	GTCACGGATTT	503	1051	11	-8.27	-80.9	-234.17
	sra26	CGGATTGCCGG	239	1302	11	-11.84	-86.6	-241.06
	sra29	CGGTCGAGAGC	104	1463	11	-11.46	-87.4	-244.85
	sra50	CGCCGGTGAGG	321	1208	11	-12.97	-87.7	-240.95
	sra54	GCCGGTTCGCC	121	901	11	-13.43	-89.1	-243.99
	sra58	TCGAGCGCGAG	115	838	11	-12.46	-89.2	-247.44
	sra60	TCGGCAACGCC	315	448	11	-12.73	-87.4	-240.75
	sra01	TCTTGTCCAC	339	1082	10	-7.52	-71.5	-206.3
	sra02	CCGGCGACCT	28	79	10	-11.72	-77	-210.49
	sra03	ATTGCCGGAG	80	1305	10	-9.14	-73.6	-207.84
	sra06	ACCGTCCAGC	123	1369	10	-10.39	-75.3	-209.29
	sra08	GTGCCGCCGA	201	1589	10	-12.22	-79.5	-216.94
	sra09	GCCTTTTCCG	111	1189	10	-8.8	-75.9	-216.33
	sra10	AGGCGGCAAG	915	1598	10	-10.69	-75.8	-209.94
	sra12	TCGTGGTTGC	18	349	10	-9.43	-75.9	-214.33

	sra16	GGTGATGATG	88	1497	10	-6.99	-72.5	-211.24
	sra18	CTTCTGCAGC	71	135	10	-8.68	-75.9	-216.73
	sra21	CGCGCGCGGT	137	358	10	-14.32	-85.8	-230.47
	sra23	GAGGTTTCGC	69	807	10	-8.7	-76.6	-218.92
	sra25	CGTTGAGATC	51	1412	10	-7.05	-74.8	-218.45
	sra27	GTTGCGCGCG	173	354	10	-12.52	-85.8	-236.27
	sra31	CGGCGCGCTT	65	158	10	-12.77	-82.5	-224.84
	sra32	GAACTCGAAA	548	1607	10	-6.48	-72.7	-213.5
	sra36	GCCGGACGAG	168	1424	10	-11.19	-79.4	-219.93
	sra38	TGTCGAGCTT	1012	1250	10	-8.35	-72.6	-207.15
	sra41	AAGGATTCGG	541	442	10	-7.58	-71.4	-205.78
	sra43	CGCATAGGGC	32	1137	10	-9.88	-76.7	-215.45
	sra45	GGCGGCCTTC	162	1179	10	-11.38	-77.9	-214.48
	sra46	CGTCCCCTTC	167	738	10	-9.48	-74.9	-210.94
	sra53	AGTTCCGGAA	175	211	10	-8.14	-70.4	-200.75
	sra57	CTCGGGTTTT	143	687	10	-7.82	-72.3	-207.91
	sra59	AGGATTCGGC	135	443	10	-9	-73.3	-207.31
	sra63	GCCGAAATCG	159	1014	10	-8.94	-78.2	-223.32
	sra65	TTGTCGTATT	335	1024	10	-5.73	-69.7	-206.24
	sra66	ATTCGGCAAC	211	446	10	-8.18	-74.1	-212.56

SMc02118 **aapJ**	sra02	AAGATCGCGGCC	259	811	12	-12.86	-93.7	-260.66
	sra21	CGCGCTCGATCT	19	56	12	-12.85	-96.4	-269.38
	sra06	CAGCGGACCGG	129	1	11	-12.97	-87.7	-240.95
	sra12	CGTCAAGCGTC	78	941	11	-10.61	-88.2	-250.16
	sra14	CGCCAACGAGA	683	992	11	-11.02	-85.6	-240.45
	sra17	CGTCGAATCCG	797	845	11	-10.38	-87.7	-249.3
	sra22	GGCCGGCGTCG	89	458	11	-14.83	-91.8	-248.18
	sra23	TTCCGACTGCC	216	116	11	-10.79	-83	-232.84
	sra26	ATCTTCAGCGG	90	64	11	-9.42	-81.6	-232.72
	sra27	CTGCAGCGCCG	69	747	11	-13.66	-91	-249.38
	sra33	AGCGCCGGAAA	397	751	11	-11.87	-84	-232.56
	sra43	GCGGCGGATGC	479	952	11	-13.66	-90.3	-247.11
	sra63	GGCGAGGCCGG	1018	891	11	-14.41	-88.6	-239.21
	sra65	TGGAGATGATC	280	359	11	-7.57	-77.6	-225.8
	sra01	ATCTCCGGCA	181	367	10	-9.45	-71.7	-200.7
	sra03	GATTGGCCTG	227	245	10	-8.49	-73.7	-210.26
	sra07	GGAAAGCGCT	122	757	10	-9.44	-75.4	-212.67
	sra10	TTGACCTTGC	86	790	10	-7.95	-72.6	-208.45
	sra24	CGTCACCCTG	511	323	10	-9.64	-76.2	-214.59
	sra28	TTGGCGGAGA	644	769	10	-9.57	-72.4	-202.59
	sra32	GGCGCCGGAA	43	588	10	-12.18	-78.5	-213.84
	sra37	GTCGAGTTCC	192	618	10	-8.27	-75.5	-216.78
	sra38	GCGTTGAGGC	286	46	10	-10.29	-78.8	-220.88
	sra39	CGGCGGCGCC	648	584	10	-14.78	-85	-226.4
	sra40	GCGCCGGAAA	193	589	10	-11.05	-78.4	-217.14
	sra45	GCCGTCGCCG	197	801	10	-13.18	-83.8	-227.69
	sra48	GAAACCGGCG	244	885	10	-10.31	-79.2	-222.13
	sra49	CGGCGGTGCG	235	9	10	-13.32	-84.1	-228.22
	sra50	GGCGCAGCGA	832	410	10	-12.42	-80.7	-220.16
	sra53	TTCACGTCGA	314	613	10	-8.4	-74.4	-212.8
	sra55	GCGGCGCCGG	37	586	10	-14.78	-85	-226.4
	sra57	GAAAGCGCTC	136	758	10	-8.89	-77.8	-222.17
	sra61	GGTTGTACTG	170	509	10	-6.93	-72.9	-212.69
	sra66	GTCGTCGTGC	369	559	10	-10.24	-80.9	-227.82

SMc00948 **glnA**	sra35	CAGCCGCCGATCGA	120	1234	14	-16.29	-113.1	-312.14
	sra01	AGGAGTCGATCTG	301	83	13	-10.9	-96.5	-275.98
	sra10	GGCTTTCGAGCG	837	146	12	-12.42	-96.4	-270.78
	sra14	CGTCGGCGAACA	270	1268	12	-13.05	-96.8	-270.03
	sra25	TGAAGGAGTCGA	135	80	12	-9.95	-87.2	-249.07
	sra47	GTTTCCGGATCG	72	1186	12	-10.66	-93	-265.48
	sra61	ACCCGGGACGAG	253	432	12	-13.44	-91.8	-252.66
	sra65	CAAAGGTCGGCT	46	560	12	-11.3	-90.5	-255.36
	sra16	CGCAGACGACA	217	1292	11	-11.06	-86.6	-243.57
	sra19	CCGCAGACGGT	4	172	11	-12.28	-85.9	-237.38
	sra27	CGGAAAGCCCG	469	533	11	-11.8	-86.6	-241.16
	sra38	CTGTCGAGCTT	1011	946	11	-9.42	-82.6	-235.95
	sra45	CTTGAAACCGG	385	954	11	-9.03	-83	-238.51
	sra53	CGAGCGCTTCG	128	152	11	-12.15	-91.1	-254.55
	sra60	CGAGCGCTTCG	701	152	11	-12.15	-91.1	-254.55
	sra63	CGTGCTGCAGC	482	1313	11	-12.3	-89.3	-248.25
	sra64	CGCTGCCACTT	68	759	11	-11.24	-84.7	-236.84
	sra66	CTTGGCCGTGC	662	1077	11	-12.07	-87.1	-241.91
	sra08	GCCGCCGATC	203	1236	10	-11.53	-80.2	-221.41
	sra09	AGGAGTTCGT	47	452	10	-8.02	-70.7	-202.09
	sra11	GGCATCGAAC	1192	726	10	-8.73	-76.6	-218.82
	sra21	GCCGCCCTTG	160	870	10	-11.51	-78.2	-215.01
	sra22	TGTCGCAGAA	125	1133	10	-8.5	-73.3	-208.95
	sra32	GCCCTTGACA	106	873	10	-9.05	-72.7	-205.23
	sra33	TGGGGTCGGT	272	1331	10	-10.6	-71.5	-196.36
	sra34	CGGACTTCGA	13	331	10	-8.92	-75.5	-214.68
	sra36	GTCGAAAACG	79	102	10	-7.63	-77.9	-226.58
	sra39	ACCGGATCGA	196	1120	10	-9.36	-72.8	-204.54
	sra40	GACGCCCAGC	858	738	10	-11.42	-78.9	-217.58
	sra43	CATCTTGTCG	170	702	10	-7.18	-75.1	-219
	sra48	GCATTCAGCG	458	478	10	-9.06	-78.1	-222.61
	sra49	CGGGGGCGGT	55	883	10	-13.08	-77	-206.1
	sra50	CCGTGTCGTC	564	917	10	-9.9	-79.1	-223.12
	sra51	GGCATGAAGG	147	637	10	-8.49	-73.7	-210.26
	sra55	AAACCGGATC	17	1118	10	-7.72	-72	-207.27
	sra58	GGATGCGGCA	60	371	10	-10.73	-76.2	-211.09
	sra62	TTGTCCATGG	445	226	10	-7.65	-70.8	-203.6

SMb21549 **thtR**	sra16	CCGCCGGCGGCG	641	463	12	-18.34	-103.6	-274.88
	sra61	TCGAGGATGACG	200	781	12	-10.87	-91.5	-259.99
	sra63	CCGCCGTCGAGG	828	490	12	-14.73	-98	-268.47
	sra02	CGGCGACCTTG	29	761	11	-11.84	-87.6	-244.27
	sra10	CGGGGCGGGCG	177	206	11	-16.06	-91.2	-242.26
	sra24	GCGACCTTGTC	117	763	11	-10.37	-85.6	-242.55
	sra38	TCCCGCCGGCG	1063	461	11	-15.21	-89.2	-238.56
	sra39	TGACGCCGGCC	571	350	11	-13.86	-87.5	-237.43
	sra40	GCGGCGTCGTA	366	469	11	-12.58	-89.2	-247.04
	sra47	CGCCGGCCTTG	744	353	11	-13.41	-88.8	-243.06
	sra50	GCAGCGAGCGC	835	853	11	-13.87	-92.5	-253.52
	sra51	TTCCTGCGGCT	546	402	11	-11.52	-81.8	-226.59
	sra60	AGCGCAGCGGC	636	364	11	-14.4	-90.1	-244.09
	sra65	GAGCGCAGCGG	954	363	11	-13.52	-90.7	-248.85
	sra11	GTTTGTCGCC	793	740	10	-8.98	-77.5	-220.93

sra17	CGGGCGCGCC	63	24	10	-14.78	-85	-226.4
sra19	GCGGGCTTAT	34	839	10	-9.18	-73.9	-208.68
sra22	GCCGGATCGG	544	31	10	-11.18	-78.4	-216.73
sra26	ATTCGCCTTG	173	810	10	-8.04	-73.5	-211.07
sra28	ATTGCCGCCA	163	479	10	-10.16	-73.7	-204.86
sra32	CGGCGGCAGC	230	654	10	-13.26	-82.7	-223.9
sra41	CGTGAATGCT	68	885	10	-8.06	-74.5	-214.21
sra43	TCGCATAGGG	31	704	10	-8.74	-72.9	-206.85
sra48	CGAGGATGAC	214	782	10	-8.15	-74.9	-215.21
sra53	GCCGTCGAGG	185	492	10	-11.19	-79.4	-219.93
sra55	CCGGGCGCGC	43	23	10	-14.78	-85	-226.4
sra58	GCCGGCCATC	30	332	10	-11.41	-77.9	-214.38
sra59	GACCCCGGAA	77	265	10	-10.03	-72.9	-202.72
sra64	CATGGTGGTG	475	69	10	-8.46	-73.8	-210.67