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Supplemental Material to:

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Genome-wide profiling of Hfq-binding RNAs uncovers extensive post-transcriptional rewiring of major stress response and symbiotic regulons in *Sinorhizobium meliloti*

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Table S1. Reads mapping and statistics

	C-wt	C-SinI	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
Raw reads	3,831,151	4,160,695	4,369,818	4,131,614	3,902,689	3,921,397	4,286,578
Mapped reads	2,972,437	3,881,916	4,044,659	3,764,945	3,674,853	3,703,621	3,077,688
Unmapped reads	858,714	278,779	325,159	366,669	227,836	217,776	1,208,890
Uniq. mapped reads	1,250,199	906,528	1,028,776	1,155,531	1,178,600	326,838	1,413,343

Table S2.- Hfq-associated sRNAs.

	CoIP-RNA[2]				GenDB annotation[2]		Enrichment in CoIP-RNA					RPKM values				
sRNA name[1]	start	stop	S[3]	R[4]	start	stop	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
asRNAs																
SMa_asRNA_118	189091	189189	+	A	189091	189189	14.64	1.86	33.15	25	132.09	2277.89	104.9	1885.48	1514.36	6196.36
SMa_asRNA_140	239340	239436	-	A	239340	239436	1.18	6.07	1.4	1.33	12.17	30.06	71.37	52.48	31.54	430.36
SMa_Hfq_asRNA_1	239740	240305	+	A	239740	240305	27.62	8.59	13.72	13.25	8.98	501.47	59.63	272.83	281.1	146.26
SMa_Hfq_asRNA_2	374508	374614	+	A	374508	374614	0.35	1.31	1.35	1.5	6.09	18.17	32.35	63.44	57.19	257.89
SMa_Hfq_asRNA_3	487642	487829	+	A	487642	487829	2.07	17.72	5.4	9	11.26	15.51	64.44	76.72	130.2	135.49
SMa_Hfq_asRNA_4	533706	533826	+	A	533706	533826	4.15	4.72	6.6	1	0.46	40.17	14.3	301.52	25.29	11.69
SMa_asRNA_326	589878	589974	-	A	589878	589974	3.67	0.2	15.6	3	0.91	841.76	8.92	446.1	63.08	14.59
SMa_asRNA_335	597898	597995	+	A	597898	597995	11.4	0.47	3.6	2	0.91	1081.13	8.83	95.24	31.22	14.44
SMa_asRNA_355	632618	632715	-	A	632618	632715	5.51	0.49	6.6	2	1.22	753.82	17.66	181.81	31.22	21.66
SMa_Hfq_asRNA_5	706270	706376	-	A	706270	706376	7.05	0.94	3.9	2	1.22	299.78	8.09	95.15	28.59	19.84
SMa_asRNA_407	724748	724927	+	A	724748	724927	2.59	4.72	0.8	2	8.52	21.6	14.42	14.14	34	161.16
SMa_asRNA_414	734101	734197	-	A	734101	734197	5.96	3.54	2.2	7.11	2.5	450.94	98.14	279.91	977.82	262.59
SmelA053	890286	890432	-	A	890286	890432	0.52	10.19	0.4	1	0.3	46.29	400.32	40.4	104.07	24.07
SMa_Hfq_asRNA_6	920333	920826	+	A	920333	920826	4.38	3.67	12.96	2.4	29.7	35.42	10.51	183.78	30.97	348.04
SMa_Hfq_asRNA_7	1072934	1073041	+	A	1072934	1073041	1.66	1.89	1.2	3	10.04	27	8.01	23.57	56.66	209.64
SMa_Hfq_asRNA_8	1193706	1194042	+	A	1193706	1194042	1	0.57	7.2	0.67	2.74	77.88	15.41	178.76	9.08	54.59
SMa_asRNA_664	1253036	1253207	+	A	1253036	1253207	3.96	19.44	8.43	1.44	14.91	847.7	1630.18	1243.1	213.46	1809.99
SMa_asRNA_672	1256049	1256148	-	A	1256049	1256148	2.49	1.89	11.4	6	0.91	48.6	8.65	313.93	152.98	14.15
SMa_asRNA_677	1257730	1257827	+	A	1257730	1257827	0.69	0.94	9.6	7	2.74	39.67	17.66	268.39	187.32	57.76
SMa_Hfq_asRNA_9	1265440	1265688	+	A	1265440	1265688	0.5	0.94	0.8	4	6.19	19.52	13.9	23.85	135.16	170.49
SMa_asRNA_687	1279352	1279450	-	A	1279352	1279450	2.9	1.89	7.1	0.67	1.01	58.91	8.74	599.92	30.91	64.32
SMc_Hfq_asRNA_1	161179	161355	-	C	161179	161355	2.76	1.84	2.49	28.57	4	126.31	29.34	134.22	1711.31	179.88
SMc_Hfq_asRNA_2	169553	169658	-	C	169553	169658	1.78	1.35	7.4	1.33	1.42	45.85	8.16	288.16	28.86	40.05
SMc_Hfq_asRNA_3	198030	198330	-	C	198030	198330	4.15	1.89	8.1	2	2.13	29.06	2.88	149.4	30.49	30.56
SMc_Hfq_asRNA_4	323142	323356	+	C	323142	323356	1.15	1.05	8.1	1	1.98	18.08	4.03	209.16	14.23	39.49
SMc_asRNA_1015	819242	819343	+	C	819242	819343	1.87	15.59	1.5	1	2.59	76.24	271.5	74.86	30	110.99

Table S2. Cont.

	CoIP-RNA[2]				GenDB annotation[2]		Enrichment in CoIP-RNA					RPKM values				
sRNA name[1]	start	stop	S[3]	R[4]	start	stop	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc_Hfq_asRNA_5	852502	852767	+	C	852502	852767	0.99	0.41	6.6	0.67	0.3	36.54	3.25	207.33	11.5	5.32
SMc_Hfq_asRNA_6	1100620	1100832	+	C	1100620	1100832	2.76	3.15	1.8	2.67	18.87	13.69	4.06	31.87	43.09	305.61
SMc_Hfq_asRNA_7	1124662	1124768	-	C	1124662	1124768	2.76	4.72	10.8	2	2.13	27.25	16.18	277.54	28.59	39.68
SMc_Hfq_asRNA_8	1198526	1198720	+	C	1198526	1198720	6.22	4.72	1	1.33	11.36	24.92	4.44	17.4	15.69	199.56
SMc_asRNA_1280	1409124	1409234	+	C	1409124	1409234	0.41	0.4	0.34	1.43	5.09	52.54	15.59	53.51	248.08	739.41
SMc_Hfq_asRNA_9	1426071	1426411	+	C	1426071	1426411	8.29	12.28	13.65	1.5	2.13	54.16	30.45	223.93	17.94	26.97
SMc_Hfq_asRNA_10	1426437	1426679	+	C	1426437	1426679	23.85	7.09	8.8	1.33	1.83	88	7.12	150.14	12.59	23.29
SMc_asRNA_1306	1460765	1460889	-	C	1460765	1460889	1.38	3.15	0.45	3.5	5.78	38.88	34.62	13.58	146.86	209.43
SMc_Hfq_asRNA_11	1505764	1505870	+	C	1505764	1505870	0.52	40.38	1	2	8.32	90.84	3032.95	31.72	57.19	264.5
SMc_asRNA_1331	1517149	1517246	+	C	1517149	1517246	6.22	9.45	8.85	1.5	3.35	49.59	26.49	502.15	62.44	151.62
SMc_Hfq_asRNA_12	1577074	1577386	-	C	1577074	1577386	4.47	6.91	7.8	15.33	46.26	83.85	49.77	103.01	215.05	513.14
SMc_asRNA_1392	1677067	1677165	+	C	1677067	1677165	1.3	1.77	7.2	1.33	0.41	39.27	17.48	299.96	30.91	7.15
SMc_asRNA_1473	1851839	1851939	+	C	1851839	1851939	1.68	1.35	2.52	0.8	8.28	153.98	42.84	168.01	30.29	469.36
SMc_Hfq_asRNA_13	1882475	1882605	+	C	1882475	1882605	2.9	1.89	5.7	1	0.61	44.52	6.61	239.64	23.36	16.2
SmelC457	1963705	1963962	+	C	1963705	1963962	10.19	43.62	16.43	8.75	52.09	61026.84	102130.97	87773.3	50578.6	228821.38
SMc_Hfq_asRNA_14	2054843	2055169	-	C	2054843	2055169	6.22	0.86	2.4	1	0.56	95.12	2.65	121.95	46.78	21.64
SMc_asRNA_1560	2060655	2060788	-	C	2060655	2060788	0.74	1.01	0.45	3	8.67	29.02	12.92	12.66	114.16	295.69
SMc_Hfq_asRNA_15	2130094	2130200	-	C	2130094	2130200	2.07	31.72	2.7	2	11.26	54.51	372.04	63.44	28.59	238.05
SMc_Hfq_asRNA_16	2262599	2262713	-	C	2262599	2262713	4.15	1.89	5.04	1.6	0.49	76.07	7.53	302.5	79.82	18.46
SmelCR256	2520774	2520857	+	C	2520774	2520857	1.19	6.95	1.08	1.16	0.9	694.31	1596.87	898.97	1019.87	614.89
SMc_Hfq_asRNA_17	2804585	2804704	-	C	2804585	2804704	1.38	3.15	9.6	2	1.22	8.1	7.21	197.97	25.5	23.58
SMc_asRNA_1951	2987843	2987940	+	C	2987843	2987940	3.96	1.68	9.37	1.48	3.49	1428.29	229.6	3099.49	499.53	945.8
SMc_Hfq_asRNA_18	3030604	3030759	+	C	3030604	3030759	1.66	2.83	0.96	1.6	17.77	43.62	27.74	38.07	58.84	657.65
SmelCR308	3109149	3109209	+	C	3109149	3109209	2.49	4.72	0.45	1	8.07	79.67	56.75	69.55	150.47	1217.9
SMc_Hfq_asRNA_19	3154182	3154287	-	C	3154182	3154287	2.26	0.86	7	2	0.41	100.87	8.16	272.15	57.73	6.67
SMc_Hfq_asRNA_20	3170205	3170330	+	C	3170205	3170330	0.47	0.43	10.8	2	0.61	30.86	6.87	235.68	24.28	5.62
SMc_Hfq_asRNA_21	3176950	3177118	+	C	3176950	3177118	0.5	5.86	1.68	4	1.1	69.02	337.97	65.27	162.94	33.49

Table S2. Cont.

	CoIP-RNA[2]				GenDB annotation[2]		Enrichment in CoIP-RNA					RPKM values				
sRNA name[1]	start	stop	S[3]	R[4]	start	stop	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc_Hfq_asRNA_22	3196375	3196780	+	C	3196375	3196780	11.06	6.82	23.4	16	7.67	232.23	53.29	407.51	293.9	115.02
SMc_asRNA_2170	3431298	3431533	+	C	3431298	3431533	2.95	5.97	5.1	1.27	3.15	218.29	172.35	668.7	168.54	338.78
SMc_asRNA_2194	3501869	3502070	+	C	3501869	3502070	0.86	1.14	1.67	0.67	5.41	293.53	149.95	100.81	30.29	276.71
SMc_asRNA_2214	3548012	3548123	-	C	3548012	3548123	4.67	3.54	6.6	1	2.03	69.43	15.45	492.41	54.64	120.03
SMc_asRNA_2215	3548232	3548328	-	C	3548232	3548328	4.67	2.36	7.05	1.5	1.07	80.17	8.92	402.36	63.08	43.77
SMc_asRNA_2223	3568619	3568716	-	C	3568619	3568716	0.07	0.49	4.8	2	10.14	9.92	44.15	199.13	62.44	353.77
SMc_asRNA_2239	3615739	3615976	+	C	3615739	3615976	1.98	4.65	4.95	13	13.92	245.05	225.44	231.72	655.63	541.06
SMb_Hfq_asRNA_1	87365	87725	-	B	87365	87725	5.77	256.43	8.2	9	18.7	379.66	6633.16	575.83	678.03	1081.89
SMb_Hfq_asRNA_2	277846	278321	-	B	277846	278321	1.13	1.29	0.27	1.27	9.68	10.21	3.64	7.13	38.57	258.64
SMb_Hfq_asRNA_3	369388	369450	-	B	369388	369450	4.15	56.7	1.2	5	10.96	46.29	315.94	40.4	194.26	393.08
SMb_Hfq_asRNA_4	405276	405337	-	B	405276	405337	0.69	7.87	2.8	1.33	8.12	15.68	125.62	177.9	49.35	445.07
SMb_asRNA_2537	611474	611570	-	B	611474	611570	1.04	1.57	8.4	1.33	0.61	20.04	8.92	358.63	31.54	14.59
SMb_Hfq_asRNA_5	635910	636057	+	B	635910	636057	1.9	0.79	10.5	3	2.13	65.68	5.85	194.92	41.35	28.68
SMb_asRNA_2599	708857	708981	+	B	708857	708981	5.47	2.15	14.4	5.33	4.67	217.73	27.69	481.93	171.34	124.53
SmelBR041	785108	785152	-	B	785108	785152	23.42	8.28	15.16	23.07	134.62	33394.59	4596.25	14273.05	23457.08	104307.46
SMb_asRNA_2627	805768	805865	+	B	805768	805865	2.59	1.18	8.6	4	1.01	138.86	17.66	363.63	156.1	28.88
SMb_asRNA_2687	936656	936755	+	B	936656	936755	0.46	1.05	0.15	9.25	4.41	9.72	8.65	8.48	1101.46	403.3
SMb_Hfq_asRNA_6	956076	956255	+	B	956076	956255	4.74	4.05	12	2	2.43	81	24.04	183.83	17	27.52
SMb_Hfq_asRNA_7	998847	998967	-	B	998847	998967	2.59	2.36	2.6	2.67	11.77	32.13	7.15	84.15	75.86	333.31
SMb_asRNA_2767	1104414	1104510	-	B	1104414	1104510	15.34	1.89	0.03	0.78	0.04	360.75	8.92	26.24	883.19	29.18
SMb_asRNA_2781	1116527	1116647	+	B	1116527	1116647	0.69	32.29	0.13	1.11	1.29	8.03	286.08	7.01	101.14	105.25
SMb_asRNA_2782	1116728	1116825	+	B	1116728	1116825	0.57	23.19	0.36	1.2	7.18	19.84	468.02	17.32	62.44	418.75
SMb_Hfq_asRNA_8	1284907	1285044	-	B	1284907	1285044	1.56	12.99	0.22	0.91	5.64	14.09	62.71	18.44	88.68	517.84
SMb_asRNA_2913	1318963	1319217	+	B	1318963	1319217	6.92	22.19	2.91	1.58	4.95	709.01	889.16	1061.41	611.92	1487.23
SMb_asRNA_2914	1321782	1321879	+	B	1321782	1321879	1.04	2.36	1.35	1.5	5.63	9.92	8.83	69.26	62.44	259.91
SmelB128	1331218	1331295	+	B	1331218	1331295	1.24	20.32	0.28	0.65	1.72	137.08	943.07	163.17	392.26	861.75
SMb_asRNA_2941	1381268	1381364	-	B	1381268	1381364	1.04	4.72	0.3	4.5	9.28	10.02	26.77	8.75	252.34	437.66

Table S2. Cont.

	CoIP-RNA[2]				GenDB annotation[2]		Enrichment in CoIP-RNA					RPKM values				
sRNA name[1]	**start**	**stop**	**S[3]**	**R[4]**	**start**	**stop**	**Hfq-log**	**Hfq-stat**	**Hfq-cold**	**Hfq-heat**	**Hfq-salt**	**Hfq-log**	**Hfq-stat**	**Hfq-cold**	**Hfq-heat**	**Hfq-salt**
SMb_asRNA_2951	1403234	1403330	-	B	1403234	1403330	0.78	6.5	0.1	0.67	6.14	20.04	89.22	8.75	94.63	875.31
SMb_asRNA_2952	1406453	1406549	-	B	1406453	1406549	3.87	4.09	4.4	8.67	16.84	270.56	107.06	183.69	378.51	598.13
SMb_Hfq_asRNA_9	1440135	1440297	-	B	1440135	1440297	0.52	1.18	11.2	1.33	1.62	5.96	5.31	286.29	18.77	30.39
trans-sRNAs																
SmelA001	1002	1054	+	A	1002	1054	1.33	0.77	3.5	0.42	5.28	1137.09	244.93	2225.22	230.91	2763.42
SmelC412 (AbcR1)	1698818	1698948	-	C	1698818	1698948	21.02	115.33	37.3	59.32	69.43	84232.61	180604.98	293490.92	504954.04	449094.94
SmelC289	1398278	1398426	-	C	1398278	1398426	14.33	30.62	7.08	19.55	39.04	379658.83	316929.17	139837.16	417648.36	633796.48
SmelC151	843451	843524	+	C	843451	843524	5.35	20.15	9.41	1	10.5	15263.48	22477.09	72302.92	8269.24	66269.94
SmelC073	424110	424268	+	C	424110	424268	3.57	177.87	11.2	10.57	18.5	22216.06	433158.7	14434.57	14720.81	19606.49
SmelC689	3046710	3046789	+	C	3046710	3046789	26.5	113.22	15.76	28.52	283.2	12721.43	21245.64	6395.3	12506.2	94633.79
SmelCR165	1491158	1491215	+	C	1491158	1491215	5.71	0.28	1.52	0.3	1.58	6167.36	104.45	3876.6	791.28	3318.13
SmelC671	2986421	2986520	+	C	2986421	2986520	8.51	26.35	2.87	0.47	41.39	38832.55	46991.38	3767.18	642.52	44737.9
SmelC411 (AbcR2)	1698618	1698731	-	C	1698618	1698731	2.24	221.46	1.06	14.37	59.55	7298.74	282865.32	3334.32	49141.79	154840.05
SmelA075	1220693	1220808	+	A	1220693	1220808	9.29	1.17	0.81	10.57	21.25	2882.57	134.29	3167.11	44575.49	68137.55
SmelC025	206861	206977	-	C	206861	206977	1.35	0.33	0.22	2.71	5.77	3755.19	347.64	3016.76	40794.93	65934.48
SMc_ncRNA_328	3432973	3433069	-	C	3432973	3433069	50.06	24.3	22.5	10.25	15.37	1683.51	312.26	2615.37	1261.7	1466.14
SmelCR249	2436657	2436725	+	C	2436657	2436725	4.6	1.31	2.92	3.6	5.11	2577.99	275.93	2385.54	3148.3	3435.17
SmelC339	1527765	1527858	+	C	1527765	1527858	1.79	14.2	9.46	0.62	7.35	1954.4	6076.23	1841.35	97.65	1174.22
SMc_ncRNA_330	3433149	3433246	-	C	3433149	3433246	50.29	10.04	25.2	12	19.17	1914.3	141.29	1445.85	718.07	902.48
SMc_ncRNA_320	3406544	3406641	+	C	3406544	3406641	8.84	6.22	5.79	4.57	7.39	793.49	211.94	1160.15	967.84	1220.15
SmelCR154	1402390	1402495	+	C	1402390	1402495	1.3	1.21	5.27	2.14	16.35	192.57	65.31	976.53	404.1	2503.1
SMc_ncRNA_324	3413409	3413506	-	C	3413409	3413506	1.84	0.79	6.66	1.6	4.38	148.78	17.66	952.36	218.54	512.61
SMb_ncRNA_373	613314	613456	-	B	613314	613456	13.35	3.84	8.24	0.91	4.32	693.34	72.62	890	85.58	380.98
SMc_Hfq_ncRNA_6	1825885	1826007	+	C	1825885	1826007	0.89	315.91	3.66	1.9	11.33	1588.44	220628.52	876.06	472.62	2243.43
SmelC181	923658	923856	-	C	923658	923856	0.87	34.01	1.41	0.43	3.24	1475.14	22596.15	737.61	230.62	1397.31
SmelA060	1021534	1021641	+	A	1021534	1021641	1.69	623.52	0.27	31.65	77.18	6201.18	894602.34	652.06	84706.14	156995.78
SmelA035	552854	552983	+	A	552854	552983	11.46	144.1	1.6	14.53	15.38	1644.97	8114.82	515.61	5107.21	4120.07

Table S2. Cont.

	CoIP-RNA[2]				GenDB annotation[2]		Enrichment in CoIP-RNA					RPKM values				
sRNA name[1]	start	stop	S[3]	R[4]	start	stop	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc_ncRNA_302	3367250	3367346	-	C	3367250	3367346	12.81	0.26	8.55	1.5	2.28	4509.41	26.77	489.84	63.08	102.12
SMc_ncRNA_199	683509	683606	+	C	683509	683606	7.05	1.89	6.24	0.8	0.85	158.7	8.83	441.55	31.22	43.32
SmelB126	1325476	1325586	+	B	1325476	1325586	0.36	342.87	0.35	11.96	54.03	1961.57	737775.55	420.41	15628.87	53741.35
SmelC483	2098461	2098583	-	C	2098461	2098583	0.34	0.14	2.29	0.37	5.33	260.79	35.18	413.89	49.75	799.58
SMc_ncRNA_326	3430139	3430235	-	C	3430139	3430235	8.04	1.77	2.51	1.45	0.66	300.63	17.84	393.62	220.8	80.24
SmelC165	910182	910297	+	C	910182	910297	2.61	0.7	3.13	15.11	71.69	276.53	22.38	336.46	1767.19	6459.37
SmelC435	1823103	1823231	+	C	1823103	1823231	7.65	178.26	0.65	5.29	41.13	2049.55	18723.56	335.44	2988.47	17781.8
SMa_ncRNA_83	706600	706696	-	A	706600	706696	5.8	0.36	6.4	1.33	1.01	1082.26	17.84	271.16	31.54	29.18
SmelAR018	224583	224642	-	A	224583	224642	0.91	0.59	1.09	1.64	7.03	97.2	14.42	268.68	407.95	1485.84
SmelC601	2625313	2625439	-	C	2625313	2625439	0.04	7.23	0.08	1.16	2.96	76.54	5662.6	253.87	4240.1	8273.23
SmelA072	1161766	1161873	+	A	1161766	1161873	1.05	345.81	0.17	12.53	47.15	2232.07	289709.68	243.54	20199.16	57848.14
SMa_ncRNA_52	344734	344832	+	A	344734	344832	9.8	5.15	1.93	8.67	7.71	500.74	96.16	239.97	1174.4	807.6
SmelCR278	2761185	2761252	-	C	2761185	2761252	3.11	6.3	0.67	4.11	8.52	114.36	89.09	237.07	1619.8	2611.66
SMc_Hfq_ncRNA_7	2241875	2242065	-	C	2241875	2242065	0.62	1.89	7.2	2	1.52	10.18	13.59	208.78	48.06	33.34
SMa_ncRNA_107	962683	962779	-	A	962683	962779	0.86	1.97	4.4	6	6.9	40.08	35.69	183.69	252.34	240.71
SMc_Hfq_ncRNA_4	1635208	1635315	-	C	1635208	1635315	7.47	1.42	7.2	5	6.39	315.01	16.03	180.69	113.32	131.03
SMc_Hfq_ncRNA_5	1734353	1734540	+	C	1734353	1734540	1.3	1.18	7.2	10.67	2.23	72.39	23.02	157.96	244.12	37.64
SMa_Hfq_ncRNA_1	198840	198991	-	A	198840	198991	1.24	2.83	1.93	4.67	10.62	12.79	11.39	156.3	402.58	726.16
SmelC570	2504181	2504263	-	C	2504181	2504263	1.53	7.46	0.4	1	1.14	152.25	302.37	153.34	405.49	375.08
SMa_ncRNA_167	1328352	1328451	+	A	1328352	1328451	0.46	0.35	1.02	0.4	6.57	77.76	17.31	135.75	30.6	757.07
SMa_Hfq_ncRNA_6	706407	706476	-	A	706407	706476	17.63	2.36	3.6	2	0.61	458.24	12.36	133.33	43.71	10.11
SmelB075	800730	800793	-	B	800730	800793	0.96	17.4	0.94	4.57	2.17	561.95	4070.1	132.57	717.1	265.33
SMc_Hfq_ncRNA_1	485164	485270	+	C	485164	485270	1.74	6.61	2.55	1	0.76	181.69	274.99	126.87	28.59	26.45
SmelC434	1821211	1821366	+	C	1821211	1821366	2.14	6.43	0.43	1.37	2.68	1009.41	1187.16	119.66	411.87	634.97
SMc_ncRNA_210	1099201	1099351	+	C	1099201	1099351	0.82	6.01	0.15	1.49	1.15	160.93	475.69	112.38	1215.74	721.6
SmelC416	1718814	1718919	-	C	1718814	1718919	0.09	60.02	0.1	0.91	10.86	45.85	14303.64	112.06	1154.57	10713.26
SmelC466	1979801	1979975	-	C	1979801	1979975	0.2	0.13	0.21	0.12	7.1	72.21	14.84	111.51	52.45	3157.66

Table S2. Cont.

	CoIP-RNA[2]				GenDB annotation[2]		Enrichment in CoIP-RNA					RPKM values				
sRNA name[1]	start	stop	S[3]	R[4]	start	stop	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SmelC600	2625202	2625346	+	C	2625202	2625346	0.65	2.98	0.67	0.78	5.68	33.52	65.65	111.18	126.6	814.89
SmelC092	525012	525073	+	C	525012	525073	0.44	2.36	0.9	1	15.62	31.36	83.75	109.48	98.7	1746.03
SMa_ncRNA_6	14244	14353	+	A	14244	14353	4.15	18.51	0.9	2.4	0.79	203.24	361.9	107.99	305.96	77.19
SmelB047	545360	545471	-	B	545360	545471	0.81	256.41	0.07	9.58	51.12	243.01	31023.15	90.91	15024.92	61006.57
SmelCR230	2237604	2237674	+	C	2237604	2237674	1.02	18.65	0.6	1.25	16.97	492.86	3595.69	83.65	172.37	2212.32
SMc_ncRNA_256	2070690	2070798	+	C	2070690	2070798	1.24	1.89	2.2	1.33	8.12	17.84	7.94	77.84	28.07	253.16
SMa_Hfq_ncRNA_5	643567	643692	-	A	643567	643692	8.92	0.94	2.4	2	1.42	324.01	6.87	74.07	48.57	33.69
SMa_Hfq_ncRNA_7	989029	989149	+	A	989029	989149	2.37	2.02	1.32	1.2	9.74	56.23	14.3	70.12	50.57	461.95
SmelA052	882393	882521	+	A	882393	882521	0.74	10.12	0.82	0.75	5.17	67.82	395.8	65.77	47.44	367.48
SMc_Hfq_ncRNA_8	3095011	3095064	-	C	3095011	3095064	0.58	6.24	0.37	1.25	1.6	108	512.83	62.85	226.64	262.05
SMc_Hfq_ncRNA_2	1184098	1184204	-	C	1184098	1184204	0.92	1.05	2.4	3	9.74	27.25	8.09	55.51	57.19	204.99
SMb_Hfq_ncRNA_2	476454	476505	+	B	476454	476505	0.96	25.08	0.27	2.44	0.61	93.46	1131.68	48.95	588.39	108.85
SmelC067	411084	411173	-	C	411084	411173	0.83	1.42	0.72	1.2	5.23	32.4	19.23	47.14	67.99	330.19
SMc_ncRNA_251	1965348	1965445	+	C	1965348	1965445	5.53	6.3	1.2	26.67	1.62	69.43	26.49	43.29	1217.6	50.54
SMc_ncRNA_202	791769	791866	-	C	791769	791866	0.19	0.3	1.2	1.33	6.29	19.84	8.83	43.29	31.22	216.59
SmelCR205	1822907	1822965	+	C	1822907	1822965	1.04	87.41	0.22	5.64	5.26	16.48	1070.75	43.14	1555.74	1127.27
SmelCR197	1770021	1770081	-	C	1770021	1770081	0.24	6.63	0.4	2	2.43	159.35	1858.49	41.73	250.79	266.78
SmelCR070	775030	775111	+	C	775030	775111	0.15	0.7	0.6	2.8	5.84	11.85	31.66	41.39	223.87	405.54
SmelB008	65071	65147	+	B	65071	65147	0.39	5.46	0.01	0.47	1.96	63.12	404.6	33.06	3695.38	11853.63
SMa_ncRNA_165	1319143	1319271	+	A	1319143	1319271	2.76	4.72	0.22	0.25	9.09	22.61	13.42	32.89	23.72	1305.39
SMa_Hfq_ncRNA_4	552893	553025	-	A	552893	553025	5.18	8.27	1.2	10.67	6.29	65.78	39.04	31.9	345.07	159.6
SMa_Hfq_ncRNA_3	240685	240791	+	A	240685	240791	1.04	3.15	0.75	1	5.02	18.17	24.26	31.72	28.59	211.6
SMa_ncRNA_120	1021704	1021801	+	A	1021704	1021801	1.04	7.09	1.2	3	10.96	9.92	44.15	25.97	62.44	252.69
SMa_Hfq_ncRNA_8	1086740	1086846	-	A	1086740	1086846	1.38	11.02	0.8	4.67	7.71	9.08	48.53	23.79	171.57	244.66
SmelC500	2180099	2180274	-	C	2180099	2180274	0.67	2.81	0.75	2.5	5.48	60.75	103.26	19.28	69.54	140.7
SmelC781	3539507	3539650	+	C	3539507	3539650	0.15	17.12	0.05	0.72	10.6	47.25	2367.84	17.68	382.45	4530.24
SMc_ncRNA_263	2179479	2179575	-	C	2179479	2179575	0.92	1.05	0.6	1.33	6.29	30.06	8.92	17.49	31.54	218.83

Table S2. Cont.

	CoIP-RNA[2]				GenDB annotation[2]		Enrichment in CoIP-RNA					RPKM values				
sRNA name[1]	**start**	**stop**	**S[3]**	**R[4]**	**start**	**stop**	**Hfq-log**	**Hfq-stat**	**Hfq-cold**	**Hfq-heat**	**Hfq-salt**	**Hfq-log**	**Hfq-stat**	**Hfq-cold**	**Hfq-heat**	**Hfq-salt**
SMb_Hfq_ncRNA_1	242108	242215	+	B	242108	242215	0.83	31.18	0.45	4	1.98	9	256.42	15.71	198.31	78.62
SMc_Hfq_ncRNA_3	1398540	1398649	+	C	1398540	1398649	0.52	1.18	0.3	0.67	5.78	8.84	7.87	15.43	27.81	360.2
SmelC507	2206348	2206579	+	C	2206348	2206579	0.17	52.82	0.13	2	0.42	37.71	5084.24	14.63	290.14	45.75
SmelC139	816486	816553	-	C	816486	816553	0.37	45.9	0.01	3.19	2.62	57.18	3448.89	12.48	11428.58	7158.66
SMc_ncRNA_262	2153309	2153455	+	C	2153309	2153455	1.99	12.99	0.03	3.43	0.15	145.47	382.66	11.54	1873.24	57.76
SmelA054	911299	911374	+	A	911299	911374	0.14	0.52	0.4	5.33	9.94	25.58	45.55	11.16	281.81	446.87
SMc_ncRNA_275	2475875	2475972	+	C	2475875	2475972	0.46	13.39	0.6	2	0.91	29.76	441.53	8.66	31.22	14.44
SMa_Hfq_ncRNA_2	239707	239949	-	A	239707	239949	0.13	6.3	0.18	1.6	12.11	8	224.36	6.98	88.14	576.52

[1]New *S. meliloti* sRNAs discovered in this work are shaded. sRNAs with putative RpoH (H1, H2 or H1/2), RpoE2 and RpoN (σ^{54}) promoters are indicated in blue, red and green color, respectively.

[2] Coordinates acording to the annotation of the *S. meliloti* 1021 genome

[3]S, coding strand

[4]R, replicon. A, pSymA; B, pSymB; C, chromosome

Table S3.- Hfq-bound mRNAs.

	CoIP-RNA[2]						Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
Transport											
SMa0081	42785	43461	+	42785	43441	ABC transporter, permease	0.61	0.87	9.43	2.86	4.78
SMa0082	43471	44286	+	43471	44286	ABC transporter, PSBP	6.33	3.23	2.31	0.4	1.16
SMa0104	52944	54556	+	52944	54536	ABC transporter, PSBP	3.01	7.32	6.06	0.05	0.2
SMa0157	87263	88324	-	87283	88287	ABC transporter, PSBP	2.57	16.71	2.77	0.87	3.26
SMa0252	140349	141373	+	140349	141353	TRAP-type PSBP	13.37	2.83	5.21	0.34	3.44
SMa0302	167410	168978	-	167430	168956	ABC transporter, PSBP	5.96	2.66	1.52	9.18	2.79
SMa0391	211227	212489	+	211336	212469	ABC transporter, ATP-binding protein	2.43	1.17	2.27	10.1	1.19
SMa0392	212503	213638	+	212503	213618	ABC transporter, PSBP	7.8	4.64	3.09	7.67	0.79
SMa0466	251991	253645	+	252021	253625	ABC transporter, PSBP	8.51	29.43	3.97	3.58	3.25
SMa0495	269279	270196	-	269299	270117	ABC transporter, PSBP	9.85	1.35	7.73	19.56	14.27
SMa0503	273422	274098	+	273422	274078	ABC transporter, permease	0.25	1.51	1.54	1	7.74
SMa0709	384094	385385	+	384120	385385	ABC transporter, PSBP	2.49	3.78	11.8	6	8.72
SMa0799	435861	436891	+	435861	436871	ABC transporter, PSBP	5.18	7.48	2.35	1.69	1.03
SMa1087	594293	596597	+	594396	596597	Cation transport ATPase	0.8	0.04	7.29	2.19	0.8
SMa1120	609243	610181	+	609267	610181	ABC transporter, ATP-binding protein	90.12	0.64	23.92	3.87	1.26
SMa1122	610188	612551	+	610188	612551	Putative permease	11.44	0.32	4.27	2.25	0.46
SMa1155	630151	632927	+	630205	632907	Cation transport P-type ATPase	3.68	0.18	12.48	4	3.77
SMa1185	652157	652984	+	652157	652984	NosY permease	2.6	0.13	29	1.33	1.01
SMa1328	724513	725889	-	724533	725855	Permease	0.54	15.11	0.49	2.79	2.17
SMa1337	731195	732664	+	731337	732644	ABC transporter, PSBP	3.11	3.85	2.3	1.89	5.13
SMa1374	754635	755594	-	754635	755594	ABC transporter, permease	0.47	0.27	5.64	0.8	1.83
SMa1375	756573	758077	-	756593	758077	ABC transporter, PSBP	8.45	2.36	14.2	2.83	2.74
SMa1379	759671	761221	-	759691	761166	ABC transporter, PSBP	3.99	1.57	6.42	2.62	2.29
SMa1462	805568	806478	-	805588	806478	ABC transporter, PSBP	6.06	2.54	7.8	4.29	1.22
SMa1646	917347	918389	-	917367	918389	ABC transporter, ATP-binding protein	5.58	1.24	7.63	2	10.79
SMa1668	934971	936563	+	935142	936563	ArcD2 arginine/ornithine antiporter	0.37	6.41	0.29	1.15	3.41
SMa1755	997793	998998	-	997813	998865	ABC transporter, PSBP	2.91	1.65	1.8	6.58	2.19
SMa1860	1054935	1056565	+	1054935	1056545	ABC transporter, PSBP	2.07	292.1	3.72	6.2	2.56
SMa1862	1056583	1057587	+	1056637	1057587	ABC transporter permease	2.07	63.78	0.3	2	0.91
SMa2127	1201708	1203258	-	1201708	1203258	ABC transporter, ATP-binding protein	0.83	0.71	5.2	1.33	2.13
SMa2199	1231870	1232834	-	1231890	1232780	ABC transporter, PSBP	4.51	2.05	6	1.75	5.86
SMa2337	1304774	1306139	+	1304824	1306119	RhtX rhizobactin transporter	0.41	0.94	0.37	0.46	13.34

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMa2339	1317985	1319117	+	1317985	1319097	Siderophore biosynthesis protein	0.69	0.39	0.11	0.12	7.14
SMa2414	1315674	1317985	+	1315745	1317985	RhtA rhizobactin transporter	0.55	0.31	0.1	0.08	7.18
SMb20015	21392	22348	-	21392	22348	putative sugar ABC transporter	0.52	0.62	7.2	2	1.95
SMb20018	25072	26134	-	25092	26114	probable sugar transport ATP-binding protein	1.15	3.77	9.62	0.9	1.75
SMb20058	68748	69548	+	68748	69548	ABC transporter, ATP-binding protein	2.38	0.96	5.24	0.89	0.47
SMb20263	268445	269344	+	268518	269324	putative ABC transporter periplasmic amino acid- binding protein	7	0.52	12.84	0.66	3.74
SMb20284	288541	289707	-	288561	289661	putative ABC transporter periplasmic spermidineputrescine-binding protein	5.15	2.43	1.23	4.9	1.89
SMb20289	294213	295636	-	294233	295582	putative permease protein	0.76	0.99	3.3	1.5	6.85
SMb20295	301924	302915	+	301924	302895	putative ABC transporter	5.57	8.45	2.43	1.36	5.34
SMb20315	316605	317769	+	316763	317749	ABC transporter, permease	0.44	0.25	1.05	1.33	19.43
SMb20316	317775	318850	+	317829	318830	ABC transporter, PSBP	5.83	1.35	2.17	1.48	21.75
SMb20370	382623	383323	+	382623	383303	putative ATP-binding transport protein	5.18	14.65	4.54	7.43	16
SMb20383	394220	395367	-	394240	395313	putative ABC transporter	21.82	29.1	77.7	63.67	108.75
SMb20417	431083	431964	+	431083	431964	probable glycerol-3-phosphate ABC transporter permease protein	2.52	58.38	3.8	0.44	5
SMb20428	443289	444160	+	443289	444140	Cystine-binding periplasmic protein precursor	0.78	7.68	0.71	1	2.45
SMb20442	453269	454281	+	453287	454261	TRAP-type PSBP	0.88	2.36	1.96	1.26	5.41
SMb20484	499666	500847	+	499835	500827	putative ABC transporter periplasmic sugar- binding protein	2.31	2.89	3.92	0.96	6.02
SMb20508	530432	531489	-	530452	531435	probable sugar ABC transporter	5.36	6.3	0.6	0.43	0.48
SMb20538	562331	563698	+	562392	563678	probable sugar ABC transporter	2.32	8.89	1.8	0.91	5.7
SMb20611	1626557	1627989	-	1626577	1627935	C4-dicarboxylate transport protein	7.2	0.38	0.75	0.38	1.27
SMb20620	1639412	1640475	-	1639432	1640475	putative sugar ABC transporter	2.59	1.67	5.08	0.31	0.98
SMb20634	1653907	1655162	-	1653927	1655162	putative sugar uptake ABC transporter PSBP precursor	1.94	3.25	7.63	0.57	1.91
SMb20660	1460912	1462336	-	1460932	1462236	putative sugar uptake ABC transporter PSBP precursor	1.58	15.69	5.04	0.8	1.83
SMb20673	1474322	1475965	-	1474322	1475902	putative sugar uptake ABC transporter ATP- binding protein	3.04	7.34	0.36	6.92	10.11
SMb20706	1508244	1509077	+	1508281	1509057	putative amino acid uptake ABC transporter PSBP precursor	4.75	0.94	36.34	0.53	13.06
SMb20714	1517030	1518129	+	1517084	1518109	ABC transporter, permease	13.43	24.18	2.17	1.38	26.64
SMb20720	1524513	1525483	+	1524513	1525463	putative sugar uptake ABC transporter PSBP precursor	2.72	1.3	5.7	0.5	1.22
SMb20856	1260885	1261927	-	1260905	1261873	ABC transporter, PSBP	1.48	1.01	4.89	3.43	23.04
SMb20893	1300065	1301299	-	1300085	1301299	ABC transporter, permease	2.03	2	4.23	1	5.88
SMb20895	1303007	1304243	-	1303027	1304094	ABC transporter, PSBP	0.69	0.93	1.04	1.44	7.67
SMb20902	1311579	1312743	+	1311686	1312723	ABC transporter, PSBP	1.44	13.08	1.09	0.62	7.61
SMb20931	1154816	1156074	+	1154870	1156054	ABC transporter, PSBP	1.59	10.28	2.25	1	1.01
SMb21114	755247	756592	-	755267	756592	NrtA nitrate transport protein	0.91	1.18	0.27	5.27	1.99

Table S3.- Cont.

	CoIP-RNA[2]						Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMb21131	770163	771044	-	770163	771044	ABC-type sulfate transport system, periplasmic component	0.82	8.73	1.81	0.77	1.02
SMb21135	774326	775258	+	774396	775238	ABC transporter, PSBP	8.71	1.89	0.19	4.15	0.42
SMb21144	888494	889496	+	888559	889476	putative choline uptake ABC transporter PSBP precursor	1.1	11.66	0.69	0.86	1.35
SMb21151	895555	896804	+	895555	896784	ABC transporter, PSBP	5.66	7.19	4.76	3.87	2.43
SMb21196	944982	946636	+	945018	946616	ABC transporter, PSBP	4.52	6.37	5.78	0.38	1.64
SMb21215	968075	969756	-	968095	969702	putative dipeptide uptake ABC transporter PSBP precursor	2.19	0.35	6.9	0.17	0.58
SMb21220	782613	783548	-	782613	783494	ABC transporter, permease	0.61	0.56	1.56	1.2	7.79
SMb21221	783717	785029	-	783737	784975	ABC transporter, PSBP	14.15	1.48	4.89	4.71	7.04
SMb21330*	998495	998766	+	998537	998746	hypothetical protein with amino acid permeases signature	0.18	35.68	0.1	1.49	6.03
SMb21343	1008768	1009772	-	1008768	1009772	ABC transporter, permease	0.52	0.47	1.4	1.33	6.9
SMb21353	1018467	1019464	-	1018487	1019464	ABC transporter, PSBP	1.45	17.8	1.92	1.4	1.46
SMb21375	1039944	1040926	-	1039964	1040926	ABC transporter, permease	0.41	0.94	0.11	0.36	12.28
SMb21376	1040923	1042488	-	1040923	1042434	ABC transporter, ATP-binding protein	1.86	0.5	0.16	0.13	352.15
SMb21377	1042516	1043502	-	1042536	1043426	ABC transporter, PSBP	9.53	5.36	0.65	2.99	555.95
SMb21430	1360613	1361737	-	1360613	1361683	putative iron ABC transporter permease protein	0.25	0.31	2.25	0.5	7.56
SMb21431	1361790	1362232	-	1361810	1362232	possibly C terminus of iron ABC transporter PSBP	1.17	0.59	1.48	0.27	12.13
SMb21432	1362235	1362965	-	1362235	1362942	putative iron uptake ABC transporter PSBP precursor	0.79	0.43	0.88	0.53	8.3
SMb21461	1387331	1388639	-	1387351	1388613	putative sugar uptake ABC transporter PSBP precursor	4.78	3.94	0.84	7.63	2.1
SMb21506	1431320	1433038	-	1431320	1432936	probable exopolysaccharide transport protein	1.53	1.25	6.93	0.18	0.61
SMb21507	1433011	1433815	+	1433139	1433795	putative amino acid exporter	0.52	3.15	0.15	1.67	5.43
SMb21526	1050876	1051993	+	1050954	1051973	ABC transporter, PSBP	8.55	10.34	6	4	8.03
SMb21572	1110834	1111950	+	1110929	1111930	putative amino acid uptake ABC transporter PSBP precursor	23.7	25.84	6.04	59.65	12.8
SMb21604	1144842	1146157	-	1144862	1146124	putative sugar uptake ABC transporter PSBP precursor	10.26	26.36	8.82	2	5.95
SMb21644	1672399	1674089	-	1672419	1674089	AgpD	1.04	1.07	5.6	2.67	2.03
SMb21647	1676336	1678555	-	1676356	1678437	periplasmic alpha-galactoside binding protein	1.62	0.94	17.56	0.36	1.66
SMc00052	1087406	1087825	+	1087406	1087825	Probable Na(+)/H(+) antiporter	1.01	0.18	5.44	0.37	0.91
SMc00056	1090244	1090615	+	1090244	1090615	Probable Na(+)/H(+)-antiporter	1.56	0.51	7	1.33	0.81
SMc00078	1011516	1012711	-	1011536	1012642	Putative methionine ABC transporter, PSBP	31.67	3.36	11.82	8.28	2.42
SMc00139	2031433	2032386	+	2031583	2032386	Amino acid transport system permease	7.65	0.24	11.4	2.92	2.92
SMc00140	2030457	2031340	+	2030538	2031320	Putative amino-acid binding periplasmic protein	5.24	0.64	2.77	3.96	1.53
SMc00265	1833337	1834401	-	1833357	1834367	Putative oxobutyric acid and 3-methyl oxovaleric acid ABC transporter, PSBP	3.19	9.75	4.5	0.13	0.95
SMc00245	1812104	1813815	-	1812104	1813690	Putative ABC transporter ATP-binding protein	21.73	4.8	25.33	11.82	2.8
SMc00671	2908957	2909868	+	2909011	2909868	Histidine ABC transporter, permease	0.83	0.47	5.05	3.29	0.25

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc00672	2907840	2908894	+	2907840	2908874	Histidine ABC transporter, periplasmic solute- binding protein	7.17	5.39	17.58	19.35	0.32
SMc00770	783174	784368	+	783254	784348	Probable putrescine-binding periplasmic protein	9.32	2.09	4.59	3.38	3.41
SMc00771	784397	785611	+	784466	785611	Probable putrescine transport ATP-binding protein	2.65	0.67	2.97	4.86	14.46
SMc00784	805282	806393	-	805302	806345	Fe3+ ABC transporter	6.4	23.62	2.53	1.07	19.66
SMc01094	464397	465625	-	464417	465625	Putative multidrug efflux system transmembrane protein	3.93	4.72	1.64	10.77	0.42
SMc01496	2633056	2634427	-	2633076	2634386	Putative C6 polyol ABC transporter, PSBP	2.47	5.45	3.3	1.07	137.46
SMc01497	2632014	2632960	-	2632014	2632886	Putative C6 polyol ABC transporter, permease component	0.62	0.33	1	0.19	10.7
SMc01498	2631158	2632008	-	2631178	2632008	Putative C6 polyol ABC transporter, permease component	1.95	0.29	1.25	0.67	12.78
SMc01499	2630146	2631147	-	2630146	2631147	Putative C6 polyol ABC transporter, ATP-binding component	1.92	0.26	1.4	0.4	31.86
SMc01510	2619659	2620467	+	2619659	2620447	Putative hemin transport system ATP-binding ABC transporter	0.3	1.01	0.13	0.44	8.12
SMc01511	2618550	2619650	+	2618550	2619650	Putative hemin transport system permease transmembrane protein	1.3	1.48	0.13	0.3	5.07
SMc01512	2617595	2618545	+	2617595	2618545	Putative hemin binding periplasmic transmembrane protein	0.59	1.86	0.17	0.25	7.58
SMc01513	2616470	2617557	+	2616470	2617537	Putative hemin transport protein	1.63	9.74	0.11	0.11	4.61
SMc01525	2607411	2609109	-	2607431	2609071	Putative dipeptide binding periplasmic protein	25.64	2.23	10.68	8.8	9.12
SMc01597	2390461	2392082	-	2390481	2392028	Putative amino-acid permease	18.27	14.35	4.76	10.12	1.75
SMc01605	2394103	2395268	+	2394145	2395248	Putative periplasmic binding ABC transporter	7.58	11.22	6.83	5.43	1.91
SMc01631	2423322	2424486	+	2423387	2424466	ABC transporter ATP-binding protein	3.98	13.99	5	17.05	7.88
SMc01632	2424518	2425701	+	2424518	2425681	Substrate-binding periplasmic protein precursor	2.9	16.42	2.28	7.87	2.23
SMc01642	2436766	2438409	+	2436820	2438409	ABC transporter, PSBP, mediates the uptake of proline betaine	7.13	2.07	3.63	2.89	2.65
SMc01647	2442860	2444523	+	2442914	2444503	Probable ABC transporter	5.39	2.99	2.33	0.35	2.65
SMc01652	2449136	2450388	+	2449208	2450368	Putative putrescine and agmatine ABC transporter, PSBP	11.83	1.84	3.71	2.59	1.61
SMc01657	2455049	2457272	+	2455078	2457252	Putative ferrichrome-iron receptor precursor protein	1.04	1.42	0.1	0.36	11.64
SMc01659	2458016	2459169	+	2458016	2459149	Putative ABC transporter, periplasmic component	0.55	1.74	0.18	0.31	10.49
SMc01826	2649289	2650178	+	2649289	2650158	Putative uracil and uridine ABC transporter, permease component	3.02	3.5	18.82	9.12	12.67
SMc01827	2650188	2651200	+	2650188	2651180	Putative uracil and uridine ABC transporter, ATP- binding component	10.18	2.8	14.38	13.41	1.13
SMc01869	2340687	2342158	+	2340828	2342138	Probable MFS permease	1.64	1.24	2.07	0.44	6.9
SMc01946	2668369	2669561	-	2668389	2669507	Putative leucine-specific binding protein precursor	11.69	3.07	28.79	6.94	2.26
SMc01948	2669972	2670717	-	2669992	2670717	Probable branched-chain amino acid transport ATP-binding ABC transporter	2.48	0.43	11.53	1.11	1.19
SMc01950	2671601	2672986	-	2671601	2672986	ABC-type branched-chain amino acid transport system, permease component	1.38	0.23	7.89	0.79	0.62
SMc01951	2672991	2674046	-	2672991	2673893	Probable branched-chain amino acid transport permease ABC transporter	19.4	6.39	46.8	8.34	10.16
SMc01966	2688018	2689155	-	2688038	2689117	Putative spermidine/putrescine-binding periplasmic ABC transporter	2.49	2.73	2.67	6	2.37
SMc01977	2701474	2702756	+	2701474	2702736	Sugar-binding periplasmic protein precursor	4.15	8.11	2.29	8.17	1.65
SMc02021	2724206	2725378	-	2724226	2725260	Putative organic acid ABC transporter, PSBP	1.56	11.81	0.92	0.46	1.73

Table S3.- Cont.

	CoIP-RNA[2]						Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc02025	2728693	2730257	-	2728713	2730257	Periplasmic dipeptide transport protein precursor	2.25	0.66	6.37	2.5	2.13
SMc02033	2738642	2739918	-	2738662	2739849	Sugar-binding periplasmic protein precursor.	1.59	0.62	3.18	1.4	100.13
SMc02079	1635529	1636959	+	1635650	1636939	Long-chain fatty acid transport protein precursor	4.6	5.44	13.11	0.58	1.33
SMc02084	1627335	1627760	+	1627335	1627760	Probable biopolymer transport transmembrane protein	0.93	0.71	0.71	0.24	6.48
SMc02085	1626219	1627328	+	1626342	1627328	Probable biopolymer transport transmembrane protein	0.41	0.47	0.35	0.12	5.39
SMc02118	1592063	1593200	-	1592083	1593108	Probable general L-amino acid-binding periplasmic ABC transporter	34.66	25.47	13.29	16.44	11.86
SMc02119	1590785	1592032	-	1590785	1591978	Probable general L-amino acid transport permease ABC transporter	23.24	6.2	14.49	6.2	6.58
SMc02120	1589626	1590780	-	1589626	1590780	Probable general L-amino acid transport permease ABC transporter	5.15	0.95	12.53	2.06	7.81
SMc02121	1588811	1589622	-	1588831	1589607	Probable general L-amino acid transport ATP- binding ABC transporter	11.46	4.14	26.01	6.62	7.15
SMc02161	534624	535979	+	534724	535959	Probable MFS permease	1.2	0.15	1.7	1.33	5.38
SMc02146	566599	567769	+	566715	567749	Phosphate binding periplasmic protein	3.49	6.25	0.37	4.62	0.5
SMc02167	527060	527700	+	527060	527680	Putative fructose transport system kinase	0.74	1.69	0.18	0.17	5.77
SMc02171	523795	524937	+	523892	524917	Putative fructose ABC-type transport system, periplasmic component	1.33	17.97	0.09	0.35	7.55
SMc02219	581426	582369	+	581426	582349	Putative amino acid-binding periplasmic protein precursor	0.19	7.96	0.07	1.69	0.09
SMc02258	623300	624079	-	623300	624025	Amino-acid ABC transporter permease	3.79	0.65	6.45	6.5	4.57
SMc02259	624113	624915	-	624133	624915	Putative periplasmic binding ABC transporter	10.94	1.63	14.01	29.4	3.9
SMc02260	624932	625829	-	624952	625806	Amino-acid transport ATP-binding protein	17.52	4.56	18.23	34.11	61.37
SMc02324	695030	696093	+	695084	696073	ABC transporter , periplasmic rhamnose binding protein	2.25	5.53	3.97	0.75	3.42
SMc02337	2757705	2759210	-	2757705	2759210	ABC sugar transporter, fused ATP-binding domains	0.87	0.5	1	2	7.3
SMc02356	2777440	2778686	+	2777494	2778666	Putative branched chain amino acid binding periplasmic ABC transporter	3.6	2.24	21.19	7.75	4.41
SMc02378	1132381	1133453	+	1132435	1133433	Probable glycine betaine ABC transporter, PSBP	29.24	1.73	9.62	0.71	3.55
SMc02379	1133568	1134561	+	1133654	1134541	Probable glycine betaine ABC transporter, permease	67.94	12.68	51.02	8.07	19.24
SMc02417	2789060	2790811	+	2789229	2790791	Putative allantoin and other purine derivative ABC transporter, PSBP	3.28	1.97	7.8	10	14.61
SMc02471	3325288	3326675	-	3325308	3326612	Putative periplasmic binding ABC transporter	2.43	6.19	2.56	0.84	3.81
SMc02484	3310806	3311506	-	3310806	3311450	Amino acid efflux protein	1.49	0.38	8.23	1.71	1.22
SMc02514	3277157	3278941	+	3277197	3278921	Putative glycerol- 3-phosphate and glycerol ABC transporter, PSBP	2.43	32.48	1.21	1.9	2.27
SMc02518	3273913	3274983	+	3273913	3274983	Putative glycerol- 3-phosphate and glycerol ABC transporter, ATP-binding	11.06	17.72	6.17	17.71	9.74
SMc02519	3272819	3273909	+	3272819	3273889	Putative glycerol- 3-phosphate and glycerol ABC transporter, ATP-binding	4.47	3.63	1.85	6.36	1.83
SMc02616	109181	110598	-	109201	110598	Amino acid transporter	0.69	12.86	0.82	0.5	0.53
SMc02737	2591057	2592119	+	2591143	2592099	Putative choline ABC transporter, PSBP	18.48	1.52	6.97	2.11	2.52
SMc02772	22130	23124	+	22130	23104	Putative D-fucose, pyruvic acid or L-fucose ABC transporter, permease	1.31	6.71	1.2	0.31	2.29
SMc02774	19363	20451	+	19442	20431	Putative D-fucose, pyruvic acid or L-fucose ABC transporter, PSBP	10.37	20.72	15.23	2.54	20.88
SMc02832	180119	182085	-	180139	181998	Putative taurine, valine, isoleucine and leucine ABC transporter, PSBP	4.88	4.98	2.45	2.44	7.2

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc02871	226852	227691	-	226852	227691	Putative ABC transporter	13.43	7.19	6.31	2	2.27
SMc02873	228900	230231	-	228920	230179	Probable ABC transporter	14.88	7.38	5.14	1.85	0.75
SMc03061	757652	759152	+	757756	759132	Alpha-glucosides ABC transporter, PSBP	2.35	0.69	7.72	0.24	0.43
SMc03062	759311	760394	+	759384	760394	Alpha-glucosides ABC transporter, permease component	0.78	0.04	5.12	0.14	0.24
SMc03065	763243	764351	+	763243	764331	Alpha-glucosides ABC transporter, ATP binding component	2.49	0.07	14	0.15	0.43
SMc03196	3159884	3160735	+	3159930	3160715	Putative molybdate-binding periplasmic ABC transporter	2.19	5.1	0.61	2.96	0.93
SMc03807	3471607	3472982	+	3471607	3472962	Probable ammonium transporter	8.9	5	4.42	4.5	38.88
SMc03269	3386367	3387985	+	3386367	3387965	Periplasmic dipeptide transport protein precursor	8.07	3.02	5.07	1.86	3.42
SMc03813	3480131	3481164	-	3480151	3481164	Putative periplasmic binding ABC transporter	1.58	7.09	3.9	1.75	6.16
SMc03972	2967677	2968972	-	2967677	2968834	Putative multidrug efflux system transmembrane protein	2.39	0.62	2.54	0.85	7.84
SMc03814	3481183	3482210	-	3481203	3482210	Sugar transport system permease	1.12	6.54	0.75	1.3	1.95
SMc03991	2988000	2989888	+	2988054	2989868	Probable ABC transporter ATP-binding transmembrane protein	6.93	0.27	11.63	0.69	0.96
SMc04036	3038922	3040625	+	3038922	3040625	Putative amino acid or peptide ABC transporter, ATP-binding component	1.56	9.3	3.75	5.75	5.55
SMc04037	3040644	3042158	+	3040644	3042158	Putative amino acid or peptide ABC transporter, PSBP	2.45	17.16	3.17	8.22	1.52
SMc04087	3626509	3628033	+	3626622	3628013	MFS-type transport protein	0.68	1.89	5.26	0.35	1.93
SMc04127	147683	149342	+	147807	149342	Sugar ABC transporter, ATP-binding protein	3.19	2.27	5.51	3.8	4.64
SMc04135	136542	137892	-	136542	137825	Putative amino acid or peptide ABC transporter, PSBP	1	3.97	1.01	2.21	8.39
SMc04251	2077346	2078650	-	2077366	2078472	Probable periplasmic mannitol-binding protein	5.41	5.03	11.19	0.33	1.21
SMc04147	121668	123596	+	121792	123576	Putative amino-acid permease	2.19	12.6	7.27	5.25	4.72
SMc04259	2087727	2089009	-	2087747	2088982	Putative gentiobiose, salicin, and cellobiose ABC transporter, PSBP	0.72	13.69	0.97	0.37	0.99
SMc04289	2209107	2210396	-	2209127	2210266	Solute-binding protein	2.51	17.8	1.5	2.5	3.2
SMc04293	2110798	2112414	-	2110798	2112414	Putative peptide-binding periplasmic ABC transporter	2.65	19.7	12.35	2.35	0.93
SMc04294	2112436	2113376	-	2112456	2113376	Putative peptide ABC transporter	1.08	4.52	9.47	1.11	4.19
SMc04407	3613811	3615828	-	3613831	3615780	MFS-type transport protein	1.56	297.33	1.22	1.36	5.09
SMc04439	2130901	2131868	+	2130955	2131848	Putative ABC-transporter ATP-binding protein	19.98	1.17	5.31	0.62	2.61
Small and macromolecule metabolism. Energy production and conversion											
SMa0005	4454	5446	+	4454	5446	formate dehydrogenase-O, iron-sulfur subunit	2.47	26.43	0.72	0.8	0.61
SMa0034	19453	21178	-	19453	21108	Serralysin-like metalloprotease	5.99	0.93	2.12	0.46	0.56
SMa0059	30703	31488	-	30703	31488	dehydrogenase related to short chain alcohol dehydrogenases	0.75	1.72	1.8	1.5	11.41
SMa0101	51213	52907	+	51262	52887	Amidohydrolase	3.8	9.28	9.79	0.15	0.31
SMa0187	102630	103622	+	102649	103602	dehydrogenase related to short chain alcohol dehydrogenases	1.09	35.81	1.12	2.31	1.35
SMa0233	129280	130741	-	129300	130691	OtsA trehalose-6-phosphate synthase	0.76	9.95	0.1	0.76	1.76
SMa0680	364033	366401	-	364053	366401	decarboxylase (lysine, ornithine, arginine)	3.07	0.34	5.6	2	1.01

Table S3.- Cont.

	CoIP-RNA[2]						Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMa0693	375551	376957	+	375708	376937	ArcA1 arginine deiminase	1	0.03	15.3	2	4.57
SMa0695	376973	377977	+	376973	377977	ArcB, ornithine carbamoyltransferase, catabolic	6.55	0.87	3.86	1.14	2.09
SMa0697	377980	378974	+	377980	378954	ArcC carbamate kinase	8.84	0.41	4.8	1.67	1.22
SMa0943	526345	528126	+	526469	528106	arylsulfatase	15.21	28	33.97	2.25	3.5
SMa1084	591045	593494	-	591065	593440	phosphoketolase	6.48	0.1	20.7	2	1.13
SMa1126	613754	614892	-	613774	614892	Protease	3.02	0.04	17.31	2.57	0.43
SMa1128	614926	616295	-	614946	616274	DegP4 protease like protein	3.35	0.04	127.8	19	4.87
SMa1131	616449	618092	-	616469	618064	Metallo-beta-lactamase superfamily protein	0.96	0.01	18.07	4	0.68
SMa1156	632953	634100	-	632973	634046	Alcohol dehydrogenase, Zn-dependent class III	3.29	0.11	12.18	0.92	1.03
SMa1166	639848	640965	+	639902	640945	Protein containing an alpha/beta hydrolase fold	0.59	0.03	6.69	2.29	0.78
SMa1182	647969	649888	+	647969	649888	NosZ nitrous oxide reductase	12.18	0.11	115	7.33	5.07
SMa1183	649888	651249	+	649888	651249	NosD nitrous oxidase accessory protein	6.83	0.1	17.28	1.33	0.85
SMa1184	651246	652160	+	651246	652160	NosF ATPase	2.96	0.11	38.8	2.67	1.62
SMa1186	652981	653538	+	652981	653538	NosL copper chaperone	6.32	0.24	5.91	0.57	0.96
SMa1188	653531	654555	+	653531	654535	NosX accesory protein	4.67	0.26	8.8	1.33	2.03
SMa1232	676000	676721	-	676020	676721	NapC membrane-bound tetraheme cytochrome c subunit	0.42	2.67	11.8	3.33	1.42
SMa1233	676725	677228	-	676725	677228	NapB periplasmic nitrate reductase cytochrome c- type subunit	1.66	6.07	3.48	1.6	0.61
SMa1236	677198	679702	-	677198	679702	NapA periplasmic nitrate reductase	1.99	12.53	6.93	1.41	1.29
SMa1239	679677	679964	-	679677	679964	NapD component of periplasmic nitrate reductase	7.41	2.92	5	1.33	1.22
SMa1243	680890	681394	-	680910	681353	Azu1 pseudoazurin	23.42	0.22	46.35	3.75	2.51
SMa1269	693888	695803	-	693908	695803	NorD accessory protein for nitric oxide reductase	5.3	0.87	2.1	0.75	1.14
SMa1272	695808	696626	-	695808	696626	NorQ accessory protein for nitric oxide reductase	5.88	0.47	0.6	1.43	0.43
SMa1283	700220	700926	+	700220	700906	NnrU-like protein	2.77	0.08	5.55	0.5	0.53
SMa1296	706835	707950	-	706855	707877	Alcohol dehydrogenase, Zn-dependent class III	2.83	0.04	12.12	1.2	0.85
SMa1353	740057	741046	-	740057	740944	Isomerase	2.65	17.48	1.9	1.22	1.52
SMa1450	799175	800385	-	799195	800385	Thiolase	1.73	0.31	5.55	0.2	0.68
SMa1495	824518	825724	+	824592	825704	Aminotransferase	4.03	9.45	7.26	0.6	0.91
SMa1593	887977	889161	-	887977	889107	oxidoreductase, fragment	0.45	1.64	0.26	0.57	9.3
SMa1670	936579	937858	+	936579	937838	ArcA2 arginine deiminase	0.33	7.16	0.39	0.71	0.17
SMa1727	974581	975536	+	974626	975516	alpha/beta hydrolase fold protein	5.08	0.71	6.75	4.17	3.2
SMa1857	1053951	1054885	+	1054005	1054865	hydrolase	1.87	105.36	2.23	4	5.83
SMa1939	1101611	1103220	-	1101631	1103166	oxidoreductase	1.46	7.83	2.29	2.37	2.95
SMa2033	1149810	1150732	+	1149915	1150712	Transglycosylase	0.41	0.93	0.54	1.26	6.7

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMa2141	1210145	1211025	-	1210165	1211025	formyltetrahydrofolate deformylase	1.51	1.72	1.65	6	5.02
SMa2217	1241610	1242935	+	1241610	1242935	decarboxylase	2.44	1.11	0.22	7.31	0.61
SMa2219	1242938	1243531	+	1242938	1243531	decarboxylase	1.08	0.52	0.9	5.14	0.74
SMa2349	1323007	1323708	+	1323061	1323708	oxidoreductase	0.49	8.34	0.26	2.29	1.65
SMa2351	1323705	1324655	+	1323705	1324655	oxidoreductase	1.04	42.52	0.23	0.46	1.12
SMa2353	1324660	1326878	+	1324660	1326858	oxidoreductase	0.76	12.6	0.4	0.57	1.36
SMa2400	1306158	1307591	+	1306236	1307591	RhbA rhizobactin biosynthesis protein	0.52	1.18	0.05	0.31	6.67
SMa2402	1307588	1309075	+	1307588	1309075	RhsB L-2,4-diaminobutyrate decarboxylase	0.65	1.77	0.07	0.17	5.2
SMa2404	1309062	1310819	+	1309062	1310819	RhbC rhizobactin biosynthesis protein	0.89	0.84	0.09	0.36	7.59
SMa2406	1310812	1311402	+	1310812	1311402	RhbD rhizobactin biosynthesis protein	2.76	6.3	0.5	0.67	7.81
SMa2408	1311399	1312769	+	1311399	1312769	RhbE rhizobactin biosynthesis protein	0.74	0.67	0.29	0.38	5.91
SMb20019	26186	27342	-	26206	27342	dihydrolipoyllysine-residue succinyltransferase	0.95	9.48	3.94	1.39	0.53
SMb20020	27345	29444	-	27345	29423	pyruvate dehydrogenase (acetyl-transferring)	1.31	39.59	1.23	1.45	0.15
SMb20059	69552	70331	+	69552	70331	SAM-dependent methyltransferase	1.28	0.29	6.14	1.24	0.75
SMb20076	83911	85001	+	83965	84981	3-oxoacyl-[acyl-carrier-protein] reductase	0.28	62.37	0.02	0.58	1.93
SMb20094*	101390	103018	-	101410	102993	phospholipase D	0.22	29.72	0.07	2.72	3.54
SMb20103	113255	115096	+	113274	115076	probable FAD-dependent oxidoreductase	0.79	5.31	6.32	0.27	0.61
SMb20115	126376	128169	-	126396	128117	putative dihydroxy-acid dehydratase protein	1.81	9.6	1.8	4.75	6.54
SMb20170	188359	189533	+	188406	189533	probable glutathione-dependent formaldehyde dehydrogenase protein	6.53	4.49	6.94	1.14	0.52
SMb20171	189530	190372	+	189530	190372	carboxylesterase	7.04	1.73	4.96	0.16	0.08
SMb20172	190386	190816	+	190386	190796	putative cytochrome c protein	4.04	5.3	13.75	0.67	0.71
SMb20173	190920	192799	+	190974	192779	putative methanol dehydrogenase protein, large subunit	2.9	12.11	4.04	0.23	0.38
SMb20174	192804	193388	+	192858	193388	putative cytochrome c protein	7.07	8.92	3.19	0.53	0.32
SMb20196	204389	205324	-	204389	205324	probable CbbX protein	0.4	14.36	0.35	0.74	0.58
SMb20197	205336	205725	-	205336	205725	putative ribulose-1,5-bisphosphate carboxylase small subunit protein	0.3	12.49	3	2.67	2.43
SMb20198	205747	207227	-	205767	207227	putative ribulose-1,5-bisphosphate carboxylase large subunit protein	0.78	30.42	1	1	1.22
SMb20199	207240	208339	-	207260	208339	putative fructose-1,6-bisphosphate aldolase protein	0.83	24.25	1.5	1.5	0.46
SMb20200	208342	210426	-	208342	210426	putative transketolase protein	0.57	21.26	1.3	1	0.41
SMb20202	211317	212420	-	211317	212366	putative D-fructose-1,6-bisphosphatase protein	0.34	6.7	4.3	1	1.32
SMb20204	213638	213807	+	213692	213787	putative pyrroloquinoline quinone synthesis protein A	3.33	6.73	2.8	0.57	1.04
SMb20207	215504	215800	+	215504	215800	putative pyrroloquinoline quinone synthesis protein D	2.76	26.77	6.45	1.5	1.37
SMb20216	224060	225180	+	224114	225160	epoxide hydrolase	1.01	6.45	1.5	1.5	1.22
SMb20238	242383	243197	-	242403	243197	3-demethylubiquinone-9 3-O-methyltransferase	0.44	30.04	0.2	1.24	0.87

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMb20239	243200	244240	-	243200	244240	putative dTDP-glucose 4,6-dehydratase protein	0.49	33.91	0.28	2.92	4.21
SMb20243	247592	248743	-	247592	248743	putative glycosyltransferase protein	0.27	11.3	0.04	1.09	2.25
SMb20245*	249858	251095	-	249858	250964	UDP-glucose 4-epimerase	1.95	35.02	0.13	3.25	12.57
SMb20246	251182	252290	+	251298	252290	putative oxidoreductase	0.24	32.35	0.06	1.08	0.62
SMb20247	252295	253328	+	252295	253308	probable oxidoreductase	0.26	22.05	0.25	1.26	1.92
SMb20249*	255207	256341	+	255238	256341	putative myo-inositol-1-phosphate synthase	0.26	17.72	0.11	1.27	6
SMb20270	275427	276482	+	275434	276462	probable proline racemase	1.22	0.39	5.31	0.42	0.58
SMb20384	395399	396390	-	395419	396390	membrane dipeptidase	49.97	6.14	25.45	20.08	26.86
SMb20404	416859	419119	+	416859	419099	putative aldehyde dehydrogenase protein	0.59	20.25	0.33	3.09	0.66
SMb20423	437134	438566	-	437134	438510	adenosylmethionine-8-amino-7- oxononanoatetransami nase	7.39	7.09	0.87	2.55	1.43
SMb20465	477045	478189	-	477065	478135	probable glucokinase	1.15	5.51	0.19	1.47	6.47
SMb20482	496696	498503	+	496696	498483	probable D-alanine-D-alanine-ligase	1.12	6	0.33	0.22	3.06
SMb20489	505347	506819	+	505347	506819	probable carbohydrate kinase	0.82	0.17	5.45	0.67	3.86
SMb20490	506812	507530	+	506812	507510	L-fuculose-phosphate aldolase	3.65	0.63	6.22	0.91	3.54
SMb20574	1586795	1589466	+	1586819	1589446	(1->4)-alpha-D-glucan 1-alpha-D-glucosylmutase	0.29	7.17	0.14	5.1	5.96
SMb20575	1589440	1590569	-	1589460	1590515	3-carboxy-cis,cis-muconate cycloisomerase protein	0.2	1.57	0.37	1	5.78
SMb20584	1598685	1599394	+	1598712	1599374	putative oxidoreductase	5	32.73	3.26	3.83	2.36
SMb20585	1599530	1601349	+	1599584	1601329	putative gamma-glutamyltranspeptidase protein	1.09	5.59	1.13	0.43	1.11
SMb20587	1602284	1603198	+	1602338	1603198	Beta-ketoadipate succinyl-CoA transferase	0.72	9.61	0.22	0.53	0.42
SMb20588	1603212	1603997	+	1603212	1603997	Beta-ketoadipate succinyl-CoA transferase	1.53	25.86	2.3	1.33	0.81
SMb20589	1603997	1605219	+	1603997	1605199	acetyl-CoA C-acyltransferase	0.4	6.57	0.7	1	1.07
SMb20704*	1505405	1506941	+	1505461	1506921	putative glycogen synthase protein	0.96	25.44	0.03	1.8	1.63
SMb20745	1533856	1534946	-	1533876	1534910	glutamate-ammonia ligase	2.98	0.23	12.87	0.89	31.11
SMb20755	1545142	1546728	+	1545196	1546728	putative propionyl-CoA carboxylase beta chain protein	7.51	9.19	8.12	1.13	1.67
SMb20772	1564594	1565686	-	1564614	1565660	probable pyridoxal phosphate biosynthetic protein PdxA	0.89	0.45	1.95	2	11.11
SMb20821	609947	610821	+	610001	610801	putative 3-methyl-2-oxobutanoate hydroxymethyltransferase	0.92	52.9	1.19	3.16	89.23
SMb20825	615982	616813	+	616023	616793	putative acetyltransferase, cysElacA/lpxA/nodL family protein	2.73	1.15	9.93	1.56	2.1
SMb20932	1156100	1157580	-	1156120	1157517	glucan endo-1,3-beta-D-glucosidase	2.14	7.68	0.56	0.81	0.94
SMb20993	1228662	1230045	+	1228814	1230025	acyl-CoA dehydrogenase	3.75	9.14	5.45	1.67	3.55
SMb21009	1242295	1243914	-	1242315	1243808	probable glycerol kinase, similar to sugar kinases protein	1.06	0.52	5.1	3.67	10.75
SMb21094	736482	737976	+	736510	737976	probable argininosuccinate lyase protein	10.69	1.82	3.6	39.33	13.8
SMb21100	742000	742898	+	742000	742878	probable polysaccharide deacetylase	0.28	18.16	0.57	4.63	1.63
SMb21148	892577	893774	+	892614	893774	probable oxidoreductase	4.92	1.83	2.85	19.15	2.42

Table S3.- Cont.

	CoIP-RNA[2]						Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMb21186	935333	936673	-	935353	936621	putative 4-aminobutyrate aminotransferase protein	7.8	0.66	10.22	2.71	2.57
SMb21202	953899	954905	+	953953	954885	probable dioxygenase	1.24	52.92	0.09	0.71	0.22
SMb21203	954932	955608	+	954986	955588	putative esteraselipase/thioesterase protein	1.44	15.2	0.44	0.55	0.5
SMb21213	966517	967196	+	966517	967176	putative serinethreonine protein phosphatase	1.41	1.7	6.2	1.33	1.32
SMb21217	779808	780743	-	779808	780743	Sugar amine kinase	2.59	2.36	1.2	3.33	6.49
SMb21239	804362	805620	+	804362	805600	putative pectate lysase	10.93	3.22	17.69	3.26	2.41
SMb21246	814934	815646	+	814934	815626	undecaprenyl-phosphate galactose phosphotransferase	1.48	1.35	5.28	0.8	0.97
SMb21256	826662	828169	-	826682	828115	probable UDP-glucose/GDP-mannose dehydrogenase	0.91	0.16	6.95	0.38	0.56
SMb21302	884993	885494	+	885019	885474	putative fucose operon fucU protein	1.29	0.86	7.8	2.4	2.86
SMb21304	885931	886771	+	885957	886751	putative NG,NG-dimethylarginine dimethylaminohydrolase (dimethylargininase)	9.53	3.77	11.68	10.46	3.14
SMb21354	1019475	1020928	-	1019495	1020904	putative glucuronate isomerase (uronic isomerase) protein	1.18	3.91	2.68	2.92	20.6
SMb21364	1027620	1029193	-	1027640	1029193	putative membrane-anchored oxidoreductase	0.15	7.09	1.11	1.71	1.65
SMb21368	1031581	1032564	+	1031581	1032564	putative cytochrome c oxidase chain II protein	0.78	4.13	0.45	1	7.46
SMb21373	1037696	1038996	-	1037716	1038996	probable tagatose 6-phosphate kinase	0.28	0.63	0.21	0.43	6.65
SMb21374	1038999	1039940	-	1038999	1039940	fructokinase	0.62	0.94	0.08	0.27	7.83
SMb21417	1346712	1347782	+	1346712	1347782	putative CDP-glucose 4,6-dehydratase protein	0.61	0.21	7.48	0.46	0.84
SMb21418	1347789	1349041	+	1347789	1349021	putative NDP-hexose 3-C-methyltransferase protein	1.07	0.22	6.22	0.55	1.6
SMb21446*	1374614	1376744	-	1374614	1376710	isoamylase	0.24	5.01	0.23	1.45	3.54
SMb21447*	1376831	1378678	+	1376853	1378658	4-alpha-D-{(1->4)-alpha-D- glucano}trehalosetrehal ohydrolase	0.26	14.37	0.14	3.05	4.52
SMb21449*	1379371	1380231	-	1379391	1380113	probable glutathione S-transferase protein	0.85	12.46	0.69	2	14.43
SMb21474	1399297	1400099	+	1399297	1400079	putative dehydrogenase, possibly 3-oxoacyl-[acyl- carrier protein] reductase	0.57	14.5	0.07	0.85	4.38
SMb21487	1408262	1409471	+	1408363	1409451	putative cytochrome o ubiquinol oxidase chain II protein	1.94	0.05	11.64	0.11	0.27
SMb21488	1409489	1411498	+	1409489	1411498	putative cytochrome o ubiquinol oxidase chain I protein	1.91	0.04	5.27	0.06	0.17
SMb21489	1411495	1412127	+	1411495	1412127	putative cytochrome o ubiquinol oxidase chain III protein	2.56	0.07	8.01	0.32	0.38
SMb21504	1429228	1429983	-	1429228	1429983	putative protein, slightly similar to carbohydrate deacetylase	1.5	0.9	6	0.67	0.71
SMb21543	1074851	1078315	+	1074957	1078295	putative hemolysin-adenlyate cyclase protein	1.86	47.12	0.66	1.69	1.9
SMb21581	1120648	1121814	+	1120703	1121794	putative glycosyltransferase, similar to smb20117 protein	0.74	21.26	0.07	2.78	2.12
SMb21634	1662466	1662989	-	1662486	1662989	ADP-dependent short-chain-acyl-CoA hydrolase	0.76	7.03	3.2	2.33	1.72
SMb21635	1662986	1665052	-	1662986	1665052	aldehyde dehydrogenase (NAD+)	0.37	18.51	0.96	0.4	0.67
SMb21636	1665083	1666179	-	1665103	1666179	probable phenylacetic acid degradation oxidoreductase	0.57	12.97	1.6	1.67	0.91
SMb21637	1666188	1666732	-	1666208	1666732	putative phenylacetic acid degradation protein	0.27	6.91	2.1	2	0.61
SMb21639	1667527	1667811	-	1667527	1667811	putative phenylacetic acid degradation protein	1.33	31.55	4.2	0.86	0.7
SMb21640	1667831	1668892	-	1667831	1668829	putative phenylacetic acid degradation protein	0.66	8.64	1.8	1.28	0.74

Table S3.- Cont.

	CoIP-RNA[2]						Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMb21648	1678706	1680341	-	1678726	1680198	MelA	1.13	0.67	9.87	0.67	0.68
SMc00036	1050740	1051434	+	1050794	1051414	Putative glutathione S-transferase	1.83	0.83	5.34	0.8	1.1
SMc00045	1069331	1069854	+	1069385	1069834	Probable Cytochrome c556	5.04	5.88	7.01	0.95	0.99
SMc00086	1069902	1070890	+	1069956	1070870	Putative diheme cytochrome C-type signal peptide protein	3.84	1.05	5.87	0.52	0.93
SMc00093	1039273	1040942	-	1039293	1040942	Choline dehydrogenase CHD oxidoreductase flavoprotein FAD membrane	4.45	0.29	1.6	5.22	0.51
SMc00103	1062702	1063487	-	1062702	1063364	Putative (S)-2-haloacid dehalogenase IVA	13.1	1.47	3.16	7.32	7.5
SMc00117	1084354	1084802	-	1084374	1084781	Probable peptide methionine sulfoxide reductase	6.13	3.49	0.22	1.77	0.45
SMc00149	2020170	2021696	+	2020255	2021676	Probable fumarate hydratase class II	8.86	3.3	3.08	1.01	0.66
SMc00165	1999787	2000682	-	1999807	2000628	Probable oxidoreductase	2.32	9.45	1.46	0.86	0.78
SMc00180	1983591	1984575	+	1983644	1984555	Probable coproporphyrinogen III oxidase, aerobic protein	1.92	0.27	6.45	0.2	0.49
SMc00225	1061895	1062688	-	1061915	1062688	Probable trans-aconitate methyltransferase	2.07	0.3	1.45	7.36	1.05
SMc00246	1813817	1814838	-	1813837	1814814	Probable quinone oxidoreductase	19.61	6.85	11.54	10.99	7.78
SMc00321	273485	274440	+	273485	274420	Probable tRNA pseudouridine synthase B	1.25	0.22	6	0.35	1.61
SMc00365	319240	320396	+	319294	320376	Probable phenylalanyl-tRNA synthetase alpha chain	10.85	0.42	4.51	0.23	1.05
SMc00374	328131	329155	-	328151	329101	Putative oxidoreductase transmembrane protein	0.95	5.13	0.37	0.62	8.67
SMc00414	363378	364047	-	363378	363980	Phospholipid N-methyltransferase	1.54	10.21	0.54	1.64	2.82
SMc00463	1961433	1961804	-	1961433	1961804	Probable dihydroneopterin aldolase dhna lyase folate biosynthesis protein	6.9	2.06	9.02	2.37	1.01
SMc00465	1960902	1961446	-	1960922	1961446	Probable7,8-dihydro-6-hydroxymethylpterin-pyropho sphokinaseprotein	6.1	0.67	5.77	0.31	0.61
SMc00480	1937035	1938323	+	1937089	1938303	Probable isocitrate dehydrogenase [NADP] protein	51.08	4.31	13.1	7.58	9.64
SMc00495	1915686	1916569	+	1915805	1916569	Probable phosphoribosylaminoimidazole- succinocarboxamide synthase	5.37	5.1	4.75	0.64	1.02
SMc00553	1222891	1223651	-	1222911	1223651	Probable NAD/NADP dependent oxidoreductase	2.76	5.09	2.38	1.03	2.12
SMc00605	1276321	1276949	-	1276341	1276949	Glutathione S-transferase family protein	5.39	2.02	2.05	0.35	0.66
SMc00615	1286874	1287972	-	1286874	1287944	5'-phosphoribosyl-5-aminoimidazole synthetase	0.66	0.35	5.08	0.71	1.04
SMc00637	2940486	2942011	-	2940506	2941936	Phosphoglucosamine mutase	19.45	13.67	14.19	8.97	15.47
SMc00640	2936883	2938127	-	2936903	2938081	Putative phosphoserine aminotransferase	1.43	5.56	0.9	0.55	0.69
SMc00673	2906392	2907822	+	2906417	2907802	Hydrolase	1.46	1.35	7.74	5.21	1.66
SMc00768	779960	781338	-	779980	781269	Probable isocitrate lyase	0.81	231.51	0.65	0.55	1.05
SMc00779	799009	800267	+	799009	800247	Probable FAD-linked oxidoreductase	2.36	6.04	2.8	0.76	1.65
SMc00781	801290	802832	+	801316	802812	Methylmalonate-semialdehyde dehydrogenase	2.36	5.1	1.27	0.99	0.82
SMc00815	836121	837734	+	836212	837714	Probable inosine-5'-monophosphate dehydrogenase	0.83	0.05	6.12	0.35	7.74
SMc00817	838252	839201	+	838306	839181	Probable carboxymethylenebutenolidase	1.09	9.9	6.48	0.8	2.31
SMc00860	927485	928545	-	927505	928521	Putative octaprenyl-diphosphate synthase	12.62	1.43	12.41	2.88	5.98
SMc00867	919560	920342	-	919580	920230	Probable ribonuclease HII protein	0.7	2.19	0.85	1.75	5.75

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc00880	906261	907094	-	906261	907031	Probable 3-oxoacyl-(acyl carrier protein) reductase	3.11	9.76	1.72	11.86	3.28
SMc00883	903790	904694	-	903810	904694	Probable regucalcin	5.01	3.26	1.7	2.98	0.78
SMc00893	889665	890395	+	889665	890375	Probable phosphoglycolate phosphatase	1.63	0.36	6.3	2	4.26
SMc00894	888315	889648	+	888315	889628	Putative 3-deoxy-D-manno-octulosonic-acid transferase	1.26	0.09	5.31	1.59	3.04
SMc00896	887162	888000	+	887162	887980	Inositol monophosphatase family protein	5.33	1.05	1.84	2.25	3.1
SMc00923	859650	860329	+	859674	860309	Probable DNA-3-methyladenine glycosylase I	3	0.87	6.57	1.37	4.65
SMc00943	1770218	1770880	-	1770238	1770837	WrbA1 flavoprotein	7.02	12.39	1.87	1.56	7.35
SMc00948	1774729	1776189	+	1774760	1776169	Glutamine synthetase I	3.36	1.59	2.49	0.79	5.94
SMc00956	1786128	1786922	+	1786128	1786922	Probable exodeoxyribonuclease III	1.95	10.84	2.53	2.89	7.85
SMc00982	954956	956321	+	955077	956321	Putative dioxygenase Rieske 2Fe-2S family protein	11.26	0.14	3.09	0.77	0.42
SMc01030	1555923	1556993	+	1555947	1556993	Pyruvate dehydrogenase E1 component alpha subunit	6.49	0.43	4.53	2.76	1.61
SMc01035	1561049	1562514	+	1561049	1562494	Probable dihydrolipoamide dehydrogenase	4.02	0.23	5.29	2.75	2.23
SMc01047	1576163	1577046	+	1576163	1577026	D-alanine aminotransferase	10.17	0.39	7.18	1.05	1.86
SMc01093	465657	466543	-	465677	466492	Putative esterase/lipase	3.55	6.07	1.78	6.41	1.34
SMc01126	424347	426717	-	424367	426652	NADP-dependent malic enzyme protein	4.54	0.7	6.96	2.27	2.44
SMc01134	416442	416805	+	416474	416785	Probable integration host factor beta-subunit	3.61	5.69	5.86	12.36	36.9
SMc01135	415364	416390	+	415411	416370	Putative protease IV transmembrane protein	2.1	1.67	2.11	15.2	9.53
SMc01165	383832	385858	-	383852	385804	Putative sugar kinase	0.63	6.15	0.65	1.27	3.26
SMc01169	1759723	1760907	-	1759743	1760861	Probable alanine dehydrogenase oxidoreductase	6.47	1.59	0.33	4.1	0.86
SMc01172	1757646	1758563	+	1757700	1758563	Putative 3-mercaptopyruvate sulfurtransferase	7.13	2.16	7.46	2	2.24
SMc01173	1756753	1757522	+	1756753	1757502	Probable alanyl-tRNA synthetase	6.15	2.05	2.71	1.3	0.93
SMc01202	1727315	1728028	-	1727335	1727952	Putative lipoprotein	1.63	0.84	1.3	1.52	5.8
SMc01208	1720404	1720938	+	1720429	1720938	Putative peptidyl-prolyl cis-trans isomerase B	23.24	6.3	4.5	0.75	1.55
SMc01227	1697011	1698152	-	1697031	1698152	Putative glycerol trinitrate (GTN) reductase	3.67	3.3	0.16	6.19	0.66
SMc01336	1441614	1444499	-	1441634	1444408	Probable ribonuclease E	13.85	0.38	10.84	1.81	2.98
SMc01343	1436883	1437373	-	1436903	1437349	Putative 3-dehydroquinate dehydratase	28.1	2.41	28.3	2.22	15.14
SMc01344	1436403	1436879	-	1436403	1436879	Probable biotin carboxyl carrier protein of acetyl-CoA carboxylase (bccp)	59.93	2.53	24.35	1.96	6.35
SMc01345	1435047	1436396	-	1435047	1436396	Probable biotin carboxylase	9.44	0.21	4.08	0.43	1.17
SMc01423	2268825	2269484	-	2268825	2269484	Probable nitrile hydratase subunit beta protein	0.66	1.02	5.7	6	2.28
SMc01471	2318423	2319115	+	2318496	2319095	Probable electron transport protein SCO1/SenC, cytochrome C oxidase	7.01	374.01	15.89	10.69	29.27
SMc01500	2629356	2630149	-	2629376	2630149	Probable sorbitol dehydrogenase (L-iditol 2- dehydrogenase)	0.91	0.25	4.03	0.57	14
SMc01501	2627865	2629349	-	2627865	2629349	Probable mannitol 2-dehydrogenase	0.53	0.18	2.22	0.59	7.91
SMc01502	2627174	2627868	-	2627194	2627868	Hydrolase phosphatase	1.64	1.21	3.29	0.52	9.09

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc01524	2609099	2610246	-	2609119	2610219	Putative dipeptidase	6.96	1.4	7.97	4.21	10.4
SMc01582	2386279	2387444	-	2386299	2387444	Putative alcohol dehydrogenase	2.57	1.75	5.58	2.77	0.7
SMc01616	2406458	2407416	-	2406478	2407416	Putative D-erythrulose-1-phosphate dehydrogenase	0.46	0.2	9	1.2	1.34
SMc01619	2409552	2410607	-	2409552	2410607	Oxidoreductase	0.36	0.14	11.4	1.5	1.07
SMc01620	2410621	2412135	-	2410621	2412135	Putative erythritol phosphate dehydrogenase	0.5	0.28	6.38	0.55	1.33
SMc01621	2412144	2412832	-	2412164	2412832	Putative L-fuculose phosphate aldolase	0.2	0.1	11.4	1.6	1.22
SMc01622	2412842	2413879	-	2412842	2413879	Oxidoreductase	0.28	0.08	6.5	1	1.52
SMc01658	2457282	2458013	+	2457282	2458013	Putative ferric iron reductase	0.25	0.57	2	2	38.96
SMc01661	2459969	2461580	-	2459989	2461536	Probable trimethylamine methyltransferase	5.94	10.24	11.01	3.14	1.96
SMc01662	2461597	2464064	-	2461617	2464064	Probable sarcosine dehydrogenase	2.23	1.9	6.94	2.5	0.27
SMc01666	2469586	2470924	+	2469621	2470904	Putative methionine gamma-lyase	2.27	13.61	1.33	2.21	2.24
SMc01720	482266	482652	-	482266	482652	Probable ribonuclease P protein component (protein C5)	34.12	0.67	12.98	1.39	3.69
SMc01790	1335415	1336679	-	1335435	1336679	Putative glycosyltransferase	1.7	0.49	5.4	1	0.61
SMc01814	2635706	2637114	+	2635733	2637094	Probable glutamate synthase small chain	10.34	24.28	17.77	12.29	53.64
SMc01820	2643533	2644940	+	2643670	2644920	Putative N-carbamyl-L-amino acid amidohydrolase	8.52	6.31	4.93	18.02	15.19
SMc01905	1364597	1367191	+	1364751	1367171	Probable ATP-dependent protease LA protein	3.69	5.1	0.4	1.82	0.64
SMc01918	1382176	1383480	+	1382176	1383480	NADH-quinone oxidoreductase subunit F 1	5.97	0.29	6.24	2.03	1.01
SMc01967	2689268	2690461	-	2689288	2690346	Putative agmatinase	3.57	1.02	4.94	13.4	4.25
SMc01972	2695775	2697108	-	2695795	2697108	Putative gamma-glutamylputrescine oxidoreductase	1.02	0.42	0.89	0.7	6.36
SMc01982	2706278	2707370	+	2706406	2707350	Probable alternative cytochrome C oxidase polypeptide II transmembrane protein	0.64	15.93	0.8	3.11	3.01
SMc01983	2707384	2709165	+	2707384	2709165	Probable alternative cytochrome C oxidase polypeptide I transmembrane protein	0.42	8.43	0.16	0.8	1.46
SMc01985	2709873	2710595	+	2709873	2710595	Cytochrome c oxidase subunit III	0.16	6.47	0.6	1	2.13
SMc02026	2730261	2731117	-	2730281	2731117	Putative beta-lactamase precursor protein	2.3	1.31	8	4.67	8.32
SMc02034	2740350	2741197	-	2740370	2741143	Putative oxidoreductase	2.26	37.63	0.93	0.9	0.91
SMc02035	2741351	2742465	-	2741371	2742411	Malate/L-lactate dehydrogenase family protein	1	14.94	0.08	0.67	0.12
SMc02047	1673622	1674841	-	1673622	1674761	Probable aminomethyltransferase (glycine cleavage system T protein)	1.36	7.38	1.26	5.74	0.59
SMc02048	1673243	1673605	-	1673243	1673605	Probable glycine cleavage system H	2.63	8.3	0.58	3.14	0.36
SMc02049	1670359	1673243	-	1670379	1673243	Probable glycine dehydrogenase decarboxylating protein	2.19	7.09	1.27	3.65	0.26
SMc02062	1655208	1655881	+	1655208	1655861	L-isoaspartyl protein carboxyl O- methyltransferase (PCMT)	0.86	0.72	6.52	0.33	0.61
SMc02089	1619930	1621119	+	1619930	1621099	Probable lipid-A-disaccharide synthase	3.71	0.2	5.65	0.25	0.51
SMc02110	1599323	1599821	+	1599468	1599821	Putative ATP-dependent Clp protease adapter protein clpS 1	9.14	4.54	1.16	2.93	3.3
SMc02122	1587257	1588230	+	1587398	1588210	Probable ferredoxin--NADP reductase	6.52	1.59	1.86	1.23	1.22
SMc02162	532666	534499	-	532686	534386	Long-chain-fatty-acid-CoA ligase	2.39	9.08	3.51	2.46	2.42

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc02227	587880	590113	-	587900	590113	Putative fatty oxidation complex alpha subunit	2.89	6.4	0.18	1.28	2.12
SMc02253	618134	618585	-	618154	618459	Putative salycilate biosynthesis protein	1.12	0.21	5.12	0.16	0.16
SMc02254	618674	619698	-	618694	619698	Putative quinol oxidase subunit II transmembrane protein	0.7	0.14	5.98	0.26	0.16
SMc02271	638297	639120	-	638317	639120	Short-chain dehydrogenases/reductases (SDR) family protein	0.93	0.2	5.55	0.33	1.07
SMc02322	691858	694012	-	691858	693957	Hypothetical oxidoreductase	1.94	8.12	1.76	0.53	2.31
SMc02341	2762122	2763575	-	2762142	2763575	Carbohydrate kinase	0.73	1.11	11.7	3	2.74
SMc02355	2776720	2777393	+	2776720	2777373	Putative isochorismatase family protein	0.83	0.76	6.41	7.75	1.14
SMc02364	1111502	1111977	+	1111502	1111957	Cytochrome C-type biogenesis transmembrane protein	0.52	0.35	5.8	2	1.93
SMc02479	3318478	3319524	-	3318498	3319460	Probable malate dehydrogenase	5.03	0.6	1.13	2.25	0.92
SMc02480	3317268	3318464	-	3317268	3318464	Probable succinyl-CoA synthetase beta chain	5.19	1.36	2.25	1.7	1.01
SMc02483	3311686	3313013	-	3311706	3312959	Probable E2 component of 2-oxoglutarate dehydrogenase complex	3.54	0.36	6.52	1.71	1.29
SMc02486	3309537	3310309	-	3309557	3310309	Putative oxidoreductase	2.54	0.37	18.97	1.85	4.78
SMc02487	3308094	3309520	-	3308114	3309520	Probable E3 component of 2-oxoglutarate dehydrogenase complex	4.15	1.47	6.2	1.78	1.17
SMc02499	3293573	3295122	-	3293593	3295122	Probable ATP synthase subunit alpha	6.55	0.27	5.27	0.26	1.32
SMc02520	3271216	3272800	+	3271269	3272780	Putative glycerol-3-phosphate dehydrogenase	0.95	1.18	1.11	17.14	3.22
SMc02521	3270353	3271158	+	3270374	3271138	Glycerol-3-phosphate regulon repressor	9.54	9.45	3.71	13.27	4.76
SMc02525	3266153	3267729	-	3266173	3267729	Putative NAD-dependent formate dehydrogenase beta subunit	0.76	5.61	1.3	0.87	1.66
SMc02562	52443	54113	+	52483	54093	Phosphoenolpyruvate carboxykinase	0.91	25.99	0.53	0.61	0.1
SMc02569	57889	58685	-	57909	58685	Probable imidazole glycerol phosphate synthase subunit HisF	2.27	0.35	7.29	0.71	0.91
SMc02610	103574	104524	+	103599	104504	Amidophosphoribosyl transferase-like protein	0.75	10.31	0.35	2.08	0.52
SMc02612	105243	106591	+	105243	106571	Glutamate synthase family protein	1.54	11.58	1.13	1.62	0.68
SMc02645	1175167	1176477	+	1175221	1176477	Putative cyclopropane-fatty-acyl-phospholipid synthase	1.8	11.53	0.04	1.44	0.19
SMc02654	1168355	1168794	+	1168355	1168774	Probable holo-acyl-carrier protein synthase	2.67	0.16	0.92	5.07	0.72
SMc02660	1201811	1202328	+	1201811	1202308	Putative acyltransferase	3.23	2.83	6.67	2	2.36
SMc02689	2537867	2539435	-	2537887	2539395	Probable aldehyde dehydrogenase	5.08	3.48	6.35	1	3.7
SMc02720	2568457	2569089	-	2568477	2569064	CLP protease proteolytic subunit	5.02	2.33	0.87	0.9	0.47
SMc02755	46260	47765	-	46280	47680	Probable adenosylhomocysteinase	6.64	1.02	3.44	1.1	3.04
SMc02775	18314	19353	+	18314	19333	Putative L-fucose dehydrogenase (D-threo aldose 1- dehydrogenase)	2.28	3.15	3.49	2	5.98
SMc02819	2375998	2376921	-	2376018	2376785	Putative ribonuclease	2.35	1.15	1.41	2.57	6.31
SMc02841	191420	192326	-	191440	192312	Putative methylated-DNA--protein-cysteine methyltransferase transcript. regulator	0.61	6.83	2.19	0.79	0.29
SMc02885	241278	241951	-	241298	241951	Probable peptide methionine sulfoxide reductase	2.36	9.67	0.27	1.2	0.23
SMc03010	708133	709182	+	708133	709182	Protein-glutamate methylesterase	1.23	0.06	7.08	0.8	1.1
SMc03070	769253	770831	-	769253	770728	Glucose-6-phosphate 1-dehydrogenase	9.04	1.77	4.92	1.81	19.78

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc03101	3242093	3242739	-	3242113	3242601	Putative carbon monoxide dehydrogenase small subunit	0.95	1.94	1.14	1.23	6.47
SMc03102	3239666	3242065	-	3239666	3242011	Putative carbon monoxide dehydrogenase large subunit transmembrane protein	1.41	15.37	1.73	0.54	1.33
SMc03109	3231029	3232009	-	3231049	3231945	Probable manno(fructo)kinase	1.61	0.24	15.13	1.67	1.12
SMc03163	3121878	3123228	-	3121898	3123208	Probable xylose isomerase	5.32	1.92	5.27	0.89	1.69
SMc03164	3123283	3124757	-	3123303	3124757	Putative xylulose kinase	6.62	4.27	3.84	0.8	1.4
SMc03187	3151678	3152456	-	3151698	3152456	Probable precorrin-4 C11-methyltransferase	0.9	0.19	5.66	0.86	0.7
SMc03188	3152475	3153790	-	3152495	3153736	Probable precorrin-6Y C5,15-methyltransferase (decarboxylating) protein	0.75	0.13	5.17	0.92	0.28
SMc03195	3158982	3159854	-	3159002	3159727	Probable uracil-DNA glycosylase	1.08	2.21	1.27	8.36	2.05
SMc03201	3164747	3166128	+	3164896	3166128	Probable 2-oxoisovalerate dehydrogenase alpha subunit	1.3	8.37	3.65	0.62	3.23
SMc03204	3168434	3169848	+	3168434	3169828	Probable E3 component of branched-chain alpha-keto acid dehydrogenase	0.67	2.11	5.69	0.18	1.41
SMc03211	3175429	3176675	+	3175543	3176655	Putative 4-hydroxyphenylpyruvate dioxygenase	0.74	22.66	0.2	2.52	0.36
SMc03252	3366166	3367110	-	3366186	3367034	Putative glutamate 5-kinase	8.22	0.08	11.19	3.4	0.94
SMc03253	3367392	3368269	-	3367412	3368254	Putative L-proline 3-hydroxylase	2.2	0.01	4.9	6.2	0.44
SMc03267	3383364	3384420	+	3383404	3384420	Putative dipeptidase	3.48	6.3	0.6	2.32	2.69
SMc03767	3433254	3434526	-	3433274	3434392	Putative arylsulfatase regulatory protein.	5.71	1.22	3.95	3.02	2
SMc03773	3439793	3440425	+	3439793	3440425	Putative acetyltransferase	7.26	1.18	2.02	0.37	1.7
SMc03786	3451446	3451951	-	3451466	3451951	Probable bacterioferritin (Bfr) (cytochrome B-1) (cytochrome B-557) protein	3.92	5.12	1.64	1.03	0.9
SMc03834	3500693	3501056	-	3500713	3501027	Putative pterin-4-alpha-carbinolamine dehydratase	1.77	15.4	1.87	4.67	4.73
SMc03861	3525478	3526220	+	3525478	3526200	Probable tRNA guanine-N1-methyltransferase	2.35	0.31	5.12	0.42	0.45
SMc03882	3548929	3549671	-	3548949	3549596	Putative glutathione S-transferase	4.29	0.15	5.1	0.45	0.56
SMc03885	3551544	3552619	+	3551544	3552599	Putative histidinol-phosphate aminotransferase	0.68	0.08	6.58	0.67	0.42
SMc03922	3067709	3069939	+	3067709	3069919	Probable 1,4-alpha-glucan branching enzyme (glycogen branching enzyme)	1.83	0.33	5.61	1.57	1.7
SMc03929	3078302	3079480	-	3078322	3079446	Putative zinc-type alcohol dehydrogenase transmembrane protein	1.89	0.33	5.02	0.32	0.51
SMc03938	3088812	3090232	-	3088832	3090232	Probable NAD(P) transhydrogenase subunit beta transmembrane protein	3.08	0.08	6.59	0.06	0.33
SMc03939	3090242	3090652	-	3090242	3090652	Probable NAD(P) transhydrogenase subunit alpha part 2 transmembrane protein	18.4	0.97	21.46	0.34	1.39
SMc03950	3090654	3092049	-	3090654	3091802	NAD(P) transhydrogenase subunit alpha part 1	2.72	0.15	10.53	0.16	0.72
SMc03983	2980233	2981384	+	2980339	2981364	Probable fructose-bisphosphate aldolase class I	3.71	27.02	2.47	1.97	0.68
SMc04001	2997136	2997636	+	2997136	2997636	Probable phosphoribosylaminoimidazole carboxylase catalytic subunit	10.05	1.67	15.43	1.71	1.54
SMc04013	3009340	3010517	+	3009360	3010517	Putative para-aminobenzoate synthase component 1	1.69	0.17	5.7	1.67	1.72
SMc04019	3016823	3017921	+	3016873	3017901	Probable ferrochelatase	0.81	0.37	5.79	0.65	0.2
SMc04029	3031953	3033073	+	3032007	3033053	Putative low specificity L-threonine aldolase	0.93	0.25	9.94	1.71	2.52
SMc04047	3052166	3052629	-	3052186	3052629	Probable pseudoazurin (blue copper protein)	4.34	129.5	1	1.11	5.28
SMc04048	3052656	3053017	-	3052676	3053017	Putative cytochrome C	3.04	103.72	0.87	0.22	3.21

Table S3.- Cont.

	CoIP-RNA[2]						Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc04049	3053070	3054343	-	3053090	3054289	Putative sulfite oxidase	1.39	174.77	0.52	0.23	1.73
SMc04095	3637934	3639915	-	3637954	3639861	Putative acyl-CoA synthetase	1.15	7.17	0.88	0.46	0.66
SMc04124	151452	151910	+	151452	151910	Putative cytidine deaminase	1.46	1.51	6.23	2.77	1.69
SMc04146	123668	126195	-	123688	126141	Putative phosphoketolase	0.67	11.14	0.41	1.12	2.43
SMc04149	117754	119111	+	117754	119091	Flavin-containing monooxygenase family protein / FMO family protein	1.78	51.63	2.2	1.67	3.45
SMc04153	113789	114958	+	113825	114958	Putative aminomethyltransferase	1.87	69.65	2.26	16.1	8.46
SMc04172	2161394	2162823	+	2161394	2162803	Adenylate/guanylate cyclase	0.73	9.37	0.33	1.7	2.75
SMc04252	2078744	2079819	-	2078764	2079792	Probable oxidoreductase	5.03	1.01	2.97	0.8	0.79
SMc04268	2096393	2097351	-	2096413	2097351	LpxXL C28-acyltransferase	1.16	0.26	5.63	0.89	1.01
SMc04277	2101114	2101644	-	2101114	2101590	Putative (3R)-hydroxymyristoyl-[acyl carrier] dehydratase transmembr. protein	3.43	7.42	1.52	0.54	1.03
SMc04278	2101742	2102133	-	2101762	2102049	Acyl carrier protein for transfer of long hydroxylated fatty acids to lipid A	2.98	0.52	2.59	0.66	5.43
SMc04290	2109844	2110817	-	2109864	2110817	Probable amidase	0.66	7.52	1.41	0.24	0.21
SMc04302	2116207	2116871	-	2116227	2116871	Probable Cob(I)alamin adenosyltransferase	5.34	1.67	7.91	1	1.79
SMc04322	2223890	2224959	+	2223890	2224939	Putative oxidoreductase	11.15	48.9	2.67	7.17	4.59
SMc04342	2147101	2148117	+	2147155	2148117	Methyltransferase	6.66	0.26	1.61	0.37	0.27
SMc04346	2230722	2231761	-	2230742	2231761	Ketol-acid reductoisomerase	9.11	0.82	0.74	1.41	0.05
SMc04397	3601170	3602704	-	3601190	3602704	Putative L-sorbosone dehydrogenase, NADP dependent protein	1.57	5.01	1.48	2.53	0.59
SMc04444	3263034	3265913	-	3263034	3265913	Probable NAD-dependent formate dehydrogenase alpha subunit	0.97	8.6	2.28	1.16	2.69
Regulation of transcription: transcription factors and signal transduction											
SMa0662	350905	351644	-	350925	351560	Transcriptional regulator, CAP/Crp family	7.26	1.69	4.63	3.14	1.83
SMa0806	441520	442106	+	441631	442086	SyrB3 regulator	8.45	11.77	3.81	3.11	1.47
SMa1179	645644	647963	+	645676	647943	NosR regulatory protein	0.84	0.03	23.65	1.33	0.71
SMa1207	661849	662589	-	661869	662549	Transcriptional regulator, CAP/Crp family	0.48	0.01	27.9	2.5	0.76
SMa1480	813927	814922	+	814015	814902	Transcriptional regulator, LysR family	3.72	1.11	6.71	4.57	2.2
SMa1505	830315	831188	+	830383	831168	Transcriptional regulator, GntR family	4.84	2.41	3.47	13.42	3.2
SMa1548	854157	857457	+	854222	857437	Diguanylate cyclase/phosphodiesterase	0.63	10.44	1.02	2.18	4.68
SMa1558	862096	864222	+	862096	864222	Sensor histidine kinase	1.47	6.4	1.17	2.6	2.04
SMa1586	879839	880366	-	879859	880314	SyrB2 regulator	36.48	16.97	11.6	9.4	5.06
SMa1698	957908	958406	-	957928	958383	SyrB1 regulator	4.8	5.65	4.64	2.29	2.35
SMa2215	1240743	1241607	+	1240832	1241587	Transcriptional regulator, GntR family	1.12	2.54	0.18	5.95	0.64
SMa5007	550324	550724	-	550344	550724	Possible transcriptional regulator	6.22	9.07	0.02	2.01	0.28
SMb20014	20357	21378	-	20377	21378	probable transcriptional regulator	0.82	0.8	7.8	1.5	2.28
SMb20162	179966	180786	+	180077	180766	probable transcriptional regulator	1.18	2.88	7.32	1.4	2.28

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMb20294	301194	301915	+	301194	301895	putative transcriptional regulator	1.13	5.41	1.36	0.96	3.74
SMb20367	379510	380306	-	379530	380222	putative transcriptional regulator protein	0.9	1.6	1.34	2.29	5.48
SMb20455	467338	468026	-	467358	467972	putative transcriptional regulator protein	0.75	12.89	0.49	2.31	0.48
SMb20480	494013	494815	+	494013	494795	putative transcriptional regulator protein	5.18	1.05	0.5	0.27	7.45
SMb20613	1630003	1631405	+	1630003	1631385	C4-dicarboxylate transport transcriptional regulatory protein	0.98	0.42	7.13	2.44	3.92
SMb20773	1565787	1566564	+	1565858	1566544	putative transcriptional regulator, GntR family protein	1.12	1.52	2.22	5.41	3.9
SMb20933*	1157673	1160420	+	1157697	1160420	putative two-component sensor histidine kinase protein	0.35	24.67	0.03	1.31	2.37
SMb20934	1160417	1160973	+	1160417	1160953	putative two-component response regulator protein	1.04	33.07	0.1	1.33	5.71
SMb21117	758115	758628	-	758135	758593	putative transcriptional regulator protein	1.48	7.42	0.82	1.77	2.14
SMb21200	950500	951863	-	950520	951863	putative two-component response regulator protein	0.95	6.12	0.68	0.2	2.37
SMb21291	867040	868108	-	867060	868007	putative transcriptional regulator, lysR family protein	41.88	16.97	26.51	16.75	12.82
SMb21372	1036526	1037658	-	1036546	1037604	putative transcriptional regulator, LacI family protein	1.32	2.79	0.76	0.45	6.06
SMb21419	1349024	1350024	-	1349044	1349931	putative transcriptional regulator, araC family protein	4.34	1.77	1.35	15.6	2.8
SMb21571	1110151	1110851	+	1110205	1110831	putative transcriptional regulator TetR family protein	1.46	0.62	0.55	7.95	3.72
SMb21579	1119447	1119965	+	1119502	1119945	putative transcriptional regulator, merR family protein	3.17	13.9	0.37	2.81	1.52
SMb22017	1655147	1656259	-	1655147	1656175	Mutated LacI family transcriptional regulator	1.34	0.47	5.17	0.92	4.07
SMc00131	2038070	2038601	-	2038090	2038578	Transcription regulator AsnC family	5.52	1.25	9.08	0.39	1.1
SMc00347	302509	302995	-	302529	302936	Putative regulator of nucleoside diphosphate kinase	3.86	8.59	1.17	0.58	0.44
SMc00720	2861658	2862152	-	2861678	2862037	Putative 2-component receiver domain protein	3.48	10.84	4.58	0.37	1.67
SMc00888	895194	896984	+	895248	896984	Putative 2-component receiver domain protein	1.26	0.14	12.72	0.8	1.1
SMc00947	1774230	1774697	+	1774339	1774677	Nitrogen regulatory protein PII	1.57	0.68	4.83	2.16	11.45
SMc01042	1568272	1569420	+	1568272	1569420	Nitrogen assimilation regulatory protein	1.04	0.42	1	6.43	3.44
SMc01043	1569417	1570891	+	1569417	1570871	Nitrogen assimilation regulatory protein	2.12	0.39	1.2	7.21	3.04
SMc01110	445312	445874	+	445435	445854	Transcription regulator	24.13	3.9	4.58	7.74	4.04
SMc01141	409754	410314	-	409774	410238	Probable nitrogen regulatory IIA protein	3.98	9.16	1.98	2.24	3.47
SMc01225	1699124	1700153	-	1699144	1700040	Transcription regulator LysR family	3.36	1.18	6.05	2.95	4.53
SMc01585	2520885	2521227	+	2520992	2521207	Putative cold shock transcription regulator	2.86	5.38	1.35	1.26	0.26
SMc01768	1314360	1314982	+	1314450	1314962	Transcription regulator MarR family	4.75	45.61	18.42	0.38	4.64
SMc01819	2642730	2643536	-	2642750	2643391	Transcription regulator TetR family	27.74	34.59	26.68	18.31	8.05
SMc01836	2660070	2660407	+	2660070	2660387	Putative DNA-binding protein	7.03	2.54	0.45	0.94	1.14
SMc01908	1370272	1370786	-	1370272	1370745	Transcription regulator MarR family	1.24	3.93	0.97	1.87	6.09
SMc01945	2667610	2668103	+	2667667	2668083	Organic hydroperoxide resistance transcriptional regulator	0.75	6.87	0.47	0.87	2.49
SMc02036	2742434	2743290	+	2742563	2743270	Putative transcription regulator	0.69	7.48	0.21	0.88	0.22

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc02151	560227	560667	-	560247	560579	Virulence-associated protein	5.13	2.76	5.14	2.37	3.5
SMc02172	522311	523608	-	522311	523540	Transcriptional regulator, ROK family	1.17	14.76	0.07	1.55	1.72
SMc02248	610614	611335	+	610668	611315	Transcriptional regulatory protein	2.48	5.99	11.63	1.23	1.5
SMc02620	111736	112553	+	111802	112533	Putative HTH-type transcriptional regulator	5.05	4	6.82	1.05	2.59
SMc03060	756348	757503	-	756368	757438	Transcriptional regulator	7.26	0.52	13.52	2.33	1.8
SMc03150	3176725	3177642	-	3176745	3177458	Transcription regulator LuxR family	2.2	6.5	2.17	4.89	4.67
SMc03165	3124767	3125858	-	3124767	3125804	Transcription regulator LacI family	5.2	5.3	4.38	1.2	5.3
SMc03210	3174913	3175494	-	3174933	3175412	Transcription regulator, AsnC family	1.44	8.66	0.57	1.17	1.07
SMc03806	3471166	3471599	+	3471241	3471579	Probable nitrogen regulatory protein PII 2	1.04	1.42	0.8	0.67	6.19
SMc03820	3486734	3487470	-	3486754	3487437	Putative transcription regulator	5.65	27.96	4.59	6.35	7.7
SMc03880	3547909	3548546	+	3547948	3548526	Polyhydroxyalkanoate and exopolysaccharide biosynthesis transcript. regulator	18.2	4.57	22.28	23.58	22.57
SMc04297	2114253	2114867	-	2114253	2114867	Putative response regulator	0.52	2.95	6.45	1.5	0.61
SMc05011	3359808	3360048	+	3359852	3360028	Putative bacteriophage DNA-binding transcription regulator	5.73	24.46	0.09	2.22	0.46
Regulation of transcription: ECFs and alternative σ factors											
SMb21484*	1405275	1405859	+	1405318	1405839	RpoE5 (σ24)	0.19	8.27	0.01	1.67	2.43
SMc01419	2267073	2267627	+	2267073	2267627	RpoE1	0.43	5.7	1.8	3	3.65
SMc01504*	2624260	2625164	+	2624350	2625144	Receiver domain	0.57	64.44	0.01	1.38	1.72
SMc01505*	2624022	2624246	-	2624022	2624189	Anti-sigma factor	0.57	9.92	0.05	1.54	2.47
SMc01506*	2623440	2624014	-	2623460	2624014	RpoE2 (σ24)	0.69	56.45	0.11	2.84	3.09
SMc03873*	3538486	3539426	-	3538506	3539372	RpoH2 (σ32)	0.94	13.89	0.03	1.06	1.12
SMc04051	3055204	3055806	-	3055204	3055740	RpoE4 (σ24)	1.11	53.84	1.05	0.67	0.56
SMc01139	411244	412876	-	411264	412808	RpoN (σ54)	2.12	0.86	1.53	6.16	3.6
SMc01140	410393	411076	-	410413	410985	Probable σ54 modulation protein	4.31	12.28	0.82	3.08	4.32
Nodulation and nitrogen fixation											
SMa0615	328632	329404	+	328632	329384	FixO3 cytochrome-c oxidase subunit	1.14	6.1	0.31	1.45	0.73
SMa0617	329568	330449	+	329568	330449	FixP3 Diheme c-type cytochrome	0.26	5.51	0.22	0.87	0.71
SMa0773	419144	420714	+	419284	420714	NoeA host specific nodulation protein	5.57	1.77	3.96	0.8	7.18
SMa0815	445875	447573	-	445895	447520	NifA transcriptional activator	6.06	0.51	2.59	1.91	1.55
SMa0827	454495	456071	+	454549	456051	NifD nitrogenase molybdenum-iron protein alpha chain	5.39	0.94	5.93	1.33	2.1
SMa0851	468179	468996	-	468199	468942	NodH sulfotransferase	5.81	0.63	0.48	0.58	0.63
SMa1208	662603	662790	-	662623	662790	FixS1 nitrogen fixation protein	1.57	0.17	40.5	2	0.61
SMa1209	662787	665060	-	662787	665060	FixI1 ATPase	0.82	0.03	50.2	4	16.43
SMa1210	665057	665560	-	665057	665560	FixH nitrogen fixation protein	3.17	0.04	67.5	1	1.37

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMa1211	665557	667162	-	665557	667131	FixG iron sulfur membrane protein	0.77	0.02	27.16	2.18	0.77
SMa1213	667340	668229	-	667360	668229	FixP1 di-heme c-type cytochrome	2.87	0.05	101.4	7	2.43
SMa1214	668233	668385	-	668233	668385	FixQ1 nitrogen fixation protein	8.37	0.17	23.1	2	0.61
SMa1216	668398	669129	-	668398	669129	FixO1 cytochrome C oxidase subunit	2.05	0.05	31.2	5	0.76
SMa1220	669143	670819	-	669143	670762	FixN1 cytochrome c oxidase subunit 1	1.51	0.01	58.08	3.2	0.97
SMb20879*	1285191	1285705	-	1285211	1285663	putative protein required for attachment to host cells	4.26	62.67	0.26	1.44	8.85
SMc01521	2611709	2612133	+	2611709	2612113	Repressor of nitrogen fixation genes, negatively autoregulated	7.31	4.05	1.2	1.71	1.39
SMc05009	2594996	2595537	+	2595019	2595537	Nodulation protein NolR inactivated by a frameshift	0.45	10.01	5.63	1.19	10.33
Quorum sensing, motility, chemotaxis and EPS II biosynthesis											
SMb21307	969800	970797	-	969820	970797	hypothetical protein WgeH (formerly ExpE8)	1.56	0.33	8.8	0.19	0.84
SMb21309	972161	974377	-	972161	974377	putative membrane protein WgeF (formerly ExpE6)	1.12	0.22	5.19	0.04	1.05
SMb21310	974386	975090	-	974386	975090	putative membrane protein WgeE (formerly ExpE5)	1.65	0.24	5.51	0.15	1.24
SMb21323	992615	993807	+	992615	993787	putative protein WgaF (formerly ExpA6)	11.53	0.34	14.02	0.24	5.49
SMc00168	1996835	1997527	+	1996863	1997507	N-acyl-L-homoserine lactone synthetase (SinI)	0.97	10.93	0.15	0.03	0.04
SMc03004	702118	703793	+	702172	703773	IcpA/McpE internal chemotaxis protein	0.99	0.11	5.6	0.44	1.01
SMc03005	703799	704092	+	703799	704092	conserved hypothetical protein contains an anti-anti-sigma domain	5.94	0.18	11.7	7	1.22
SMc03006	704096	704481	+	704096	704461	Chemotaxis regulator protein	7.33	0.34	1.6	0.44	0.68
SMc03007	704482	706758	+	704482	706758	Chemotaxis protein (sensory transduction histidine kinase)	1.54	0.08	11.25	1.5	1.98
SMc03011	709182	709571	+	709182	709571	Response regulators with a CheY-like receiver domain	5.24	0.41	7.56	0.8	2.43
SMc03013	710149	710543	+	710149	710523	conserved hypothetical protein	4.19	0.21	6.6	1.5	1.37
SMc03014	711451	713282	+	711589	713262	Flagellar M-ring transmembrane protein	1.3	0.39	7.68	2.4	1.95
SMc03019	717304	718415	-	717324	718361	Flagellar motor switch protein	1.2	0.19	5.4	0.6	0.73
SMc03020	718429	719081	-	718449	719081	Flagellar motor switch protein	0.35	0.2	6.2	1.33	1.01
SMc03022	720050	720956	-	720050	720928	Chemotaxis (motility protein A) transmembrane	2.07	0.75	12	2	1.22
SMc03030	726091	726899	+	726091	726879	Flagellar basal-body rod protein	0.92	0.2	6.9	1.5	0.91
SMc03034	729052	729762	+	729052	729762	Flagellar L-ring protein precursor (basal body L- ring protein)	0.98	0.18	9.6	2.67	0.61
SMc03037	731156	732489	+	731285	732469	Flagellin A	1.13	0.37	6.33	0.2	0.97
SMc03038	732695	734016	+	732812	733996	Flagellin B	2.99	1.54	7.72	0.18	0.91
SMc03039	734146	735487	+	734262	735467	Flagellin D	0.89	0.29	8.93	0.44	1.66
SMc03040	735635	736770	+	735785	736750	Flagellin C	3.38	24.65	2.39	0.32	7.35
SMc03044	740239	741666	+	740239	741666	FliK hook length control protein	1.97	0.23	15	2	3.04
SMc03047	743180	744422	+	743202	744422	Flagellar hook protein	1.12	0.07	6.83	1.23	0.94
SMc03048	744491	745924	+	744506	745924	Putative flagellar hook-associated protein	1.11	0.1	15.48	1.6	0.85

Table S3.- Cont.

	CoIP-RNA[2]						Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc03049	745927	746984	+	745927	746964	Putative flagellar hook-associated protein	0.49	0.19	7.4	0.67	0.71
SMc03051	747346	747795	+	747346	747795	Putative flagellin synthesis repressor protein	2.45	0.43	6.48	0.8	1.46
Translation											
SMb20049	60280	62291	+	60310	62271	putative elongation factor G protein	0.98	9.36	1.32	0.2	1.25
SMb21157	901188	901637	+	901228	901617	putative translation initiation inhibitor protein	2.81	1.12	0.84	5.65	0.42
SMc00323	276550	276975	+	276686	276955	Probable 30S ribosomal protein S15	28.38	12.09	8.08	5.94	13.54
SMc00357	312171	312840	+	312251	312820	Probable elongation factor P	1.94	0.3	6.47	0.24	0.72
SMc00363	318407	318727	+	318504	318707	Probable 50S ribosomal protein L35	94.28	1.04	6.7	6.72	10.29
SMc00364	318744	319168	+	318744	319148	Probable 50S ribosomal protein L20	37.82	1	8.6	2.92	1.79
SMc00403	354073	355401	-	354093	355382	probable Sun protein (FMU protein)	3.83	0.26	11.16	0.56	1.12
SMc00565	1236088	1236710	-	1236108	1236683	Probable 50S ribosomal protein L9	8.97	0.13	5.92	0.59	1.89
SMc00567	1237846	1238114	-	1237866	1238114	Putative 30S ribosomal protein S18	8.71	0.48	6.96	0.7	1.88
SMc00568	1238120	1238804	-	1238140	1238589	Putative 30S ribosomal protein S6	7.67	0.24	5.06	0.49	1.48
SMc01152	398018	398424	+	398138	398404	30S ribosomal protein S20	6.84	0.82	24.18	0.95	6.86
SMc01290	1487883	1488373	+	1487883	1488353	Probable 50S ribosomal protein L15	25.95	0.34	5.73	1	1.1
SMc01291	1487666	1487869	+	1487666	1487869	Probable 50S ribosomal protein L30	68.91	1.03	10.82	0.51	1.17
SMc01292	1487084	1487653	+	1487084	1487653	Probable 30S ribosomal protein S5	136.66	4.44	9.89	1.09	1.21
SMc01293	1486588	1486970	+	1486588	1486950	Probable 50S ribosomal protein L18	27.78	2.56	5.18	0.54	3.82
SMc01294	1486020	1486575	+	1486042	1486575	Probable 50S ribosomal protein L6	17.76	0.56	3.92	0.81	0.94
SMc01295	1485603	1486021	+	1485603	1486001	Probable 30S ribosomal protein S8	5.33	0.09	2.57	0.51	0.66
SMc01296	1485285	1485590	+	1485285	1485590	Probable 30S ribosomal protein S14	14.18	0.32	2.51	0.74	0.58
SMc01297	1484693	1485270	+	1484693	1485250	Probable 50S ribosomal protein L5	9.04	0.14	2.74	0.27	0.58
SMc01298	1484389	1484700	+	1484389	1484700	Probable 50S ribosomal protein L24	33.27	0.88	3.76	0.38	0.45
SMc01299	1483889	1484374	+	1484006	1484374	Probable 50S ribosomal protein L14	27.27	10.08	12.64	1.18	10.65
SMc01300	1483591	1483847	+	1483591	1483827	Probable 30S ribosomal protein S17	55.59	0.51	7.97	1.75	1
SMc01301	1483377	1483577	+	1483377	1483577	Probable 50S ribosomal protein L29	78.29	1.3	1.86	0.74	0.41
SMc01302	1482932	1483364	+	1482951	1483364	Probable 50S ribosomal protein L16	106.19	0.81	10.56	2.04	0.68
SMc01303	1482199	1482932	+	1482199	1482912	Probable 30S ribosomal protein S3	44.45	0.6	9.81	1.43	1.34
SMc01304	1481810	1482199	+	1481810	1482199	Probable 50S ribosomal protein L22	36.23	0.19	9.47	2.35	0.59
SMc01305	1481529	1481807	+	1481529	1481807	Probable 30S ribosomal protein S19	36.23	0.3	2.16	0.46	0.2
SMc01306	1480677	1481513	+	1480677	1481513	Probable 50S ribosomal protein L2	10.77	0.1	3.7	0.72	0.36
SMc01307	1480340	1480653	+	1480340	1480633	Probable 50S ribosomal protein L23	24.18	0.31	2.9	1.1	0.39
SMc01308	1479723	1480343	+	1479723	1480343	Probable 50S ribosomal protein L4	12.39	0.09	2.82	0.51	0.35

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc01309	1478970	1479710	+	1479024	1479710	Probable 50S ribosomal protein L3	86.81	0.76	9.81	2.71	0.83
SMc01310	1478536	1478921	+	1478593	1478901	Probable 30S ribosomal protein S10	40.26	0.96	13.01	2.36	2.01
SMc01311	1477261	1478470	+	1477275	1478450	Probable elongation factor TU protein	6.78	0.28	2.66	0.87	0.74
SMc01312	1475104	1477223	+	1475104	1477203	Probable elongation factor G	7.55	0.14	3.04	0.32	0.27
SMc01313	1474604	1475094	+	1474604	1475074	Probable 30S ribosomal protein S7	7.42	0.31	1.16	0.27	0.15
SMc01318	1463666	1464066	+	1463666	1464046	Probable 50S ribosomal protein L7/L12 (L8)	5.61	0.19	4.33	0.21	2.3
SMc01803	1350259	1350746	-	1350279	1350746	Probable 30S ribosomal protein S9	114.91	5.92	53.7	3.31	2.43
SMc01804	1350749	1351318	-	1350749	1351213	Probable 50S ribosomal protein L13	476.29	5.32	56.73	4.42	3.76
SMc02310	682222	682559	+	682276	682539	Probable translation initiation factor IF-1 protein	5.48	0.68	1.97	0.31	1.09
SMc03770	3438825	3439379	+	3438988	3439359	Probable 50S ribosomal protein L21	41.47	3.37	51.8	5.12	9
SMc03772	3439361	3439682	+	3439393	3439662	Probable 50S ribosomal protein L27	45.88	1.47	24.15	2.01	2.86
SMc03859	3524375	3524788	+	3524394	3524768	Probable 30S ribosomal protein S16	5.08	0.41	1.74	0.44	0.46
SMc03863	3527112	3527814	+	3527261	3527794	Probable 50S ribosomal protein L19	142.1	16.53	58.4	5.07	19.29
SMc03881	3548580	3548884	-	3548600	3548785	Probable 50S ribosomal protein L32	8.42	0.69	6.44	0.87	5.35
SMc04320	2222629	2222885	+	2222629	2222865	30S ribosomal protein S21	6.37	1.01	6.58	0.07	2.3
SMc04434	482666	482921	-	482686	482820	Probable 50S ribosomal protein L34	47.75	4.3	51.99	6.67	110
Stress responses. Chaperones											
SMa0124	66172	67826	-	66192	67826	60 kDa chaperonin	6.34	2.5	5.35	0.17	0.23
SMa1118	608662	609230	+	608683	609210	HspC2 heat shock protein	508.78	2.82	67.02	19.75	2.27
SMa2379	1342262	1344598	-	1342282	1344465	KatB catalase/peroxidase	3.84	9.18	1.73	1.83	0.52
SMb20007*	10127	12291	+	10154	12271	KatC	0.33	61.42	0.19	2.24	1.99
SMb20054	63000	63910	-	63020	63847	chloride peroxidase	1.04	108.67	1.68	1.6	0.73
SMb20227	232785	233417	+	232839	233417	NdiA1	0.41	49.14	0.09	1.47	4.93
SMb20228	233410	233829	+	233410	233829	putative nutrient deprivation-induced protein	0.69	229.94	0.05	1.75	2.33
SMb20229	233826	234820	+	233826	234800	NdiB	0.28	60.95	0.06	1.81	4.2
SMb20964	1192333	1193041	+	1192362	1193021	peroxidase	2.6	18.75	0.97	2.44	2.35
SMb21566	1104585	1106249	-	1104605	1106233	putative heat shock protein groEL	9.79	0.57	0	1.42	0
SMb22023	1106260	1106691	-	1106280	1106594	10 kDa chaperonin	9.39	3.08	0	0.26	0
SMc00040	1057488	1058020	+	1057578	1058000	Putative organic hydroperoxide resistance protein	2.21	33.53	0.21	1.36	0.54
SMc00819	840208	841815	+	840311	841795	Catalase	0.92	45.41	0.25	3.83	0.36
SMc00913	869135	870826	-	869135	870772	60 KD chaperonin A	6.29	0.2	0.03	3.05	0.08
SMc01106	448813	449320	-	448833	449264	Probable small heat shock protein	6.71	0.83	0.07	0.39	0.11
SMc01758	1303815	1305570	-	1303835	1305463	60 KD chaperonin B (GroEL) protein	2.53	61.23	0.17	0.63	0.44

Table S3.- Cont.

	CoIP-RNA[2]						Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc02597*	1197360	1197928	+	1197390	1197908	Putative superoxide dismutase CU-ZN precursor transmembrane protein	0.52	5.91	0.09	0.82	6.13
SMc02857	209659	211709	+	209764	211689	Heat shock protein 70 (HSP70) chaperone	9.24	3.36	0.06	0.32	0.06
SMc03876	3541479	3542152	-	3541499	3541930	Heat shock protein 15 (HSP15).	1.33	0.14	5.82	0.43	0.93
Cell division. DNA replication, recombination and repair											
SMb20008	12297	13384	+	12297	13364	DNA ligase (ATP)	0.17	8.66	0.6	1.2	1.22
SMb20045	56536	57560	-	56556	57560	probable replication protein B	0.72	1.48	1.43	1.47	8.25
SMb20686	1489737	1490711	+	1489827	1490711	putative DNA ligase	4.58	30.34	1.27	1.44	1.68
SMb21445	1373459	1374621	-	1373479	1374621	putative DNA topoisomerase I	0.28	10.74	0.18	1.46	6.09
SMb21448	1378691	1379406	+	1378745	1379386	putative DNA polymerase related protein	0.92	32.02	0.47	2.44	5.07
SMb21522	1446088	1446371	-	1446108	1446371	putative cell division inhibitor protein	0.69	5.41	2.07	0.17	1.65
SMb21523	1446368	1447183	-	1446368	1447183	putative cell division inhibitor protein	2.3	13.03	2.44	0.16	1.72
SMb21524	1447261	1448047	-	1447281	1448030	putative cell division inhibitor protein	5.06	7.01	3.5	0.27	3.14
SMc00299	1871586	1872394	+	1871586	1872374	Probable DNA repair protein	1.24	0.79	5.8	0.83	1.22
SMc00760	1948158	1949313	-	1948178	1949263	DNA strand exchange and recombination protein	4.08	6.37	1.87	2.2	2.31
SMc01722	479457	480151	-	479477	480130	Hypothetical GTP-binding protein	2.52	1.38	7.84	0.75	2.36
SMc01874	2334374	2336220	-	2334394	2336166	Cell division protein	1.88	7.32	1.9	1.02	0.29
SMc02050	1668541	1670112	+	1668617	1670092	Probable trigger factor	7.93	0.37	4	0.25	0.82
SMc02566	55241	55935	+	55295	55915	Probable DNA repair system specific for alkylated DNA protein	1.69	11.02	1.47	0.7	1.61
SMc03246	3358510	3359808	+	3358559	3359788	Phage-related integrase	9.82	14.34	0.07	1.95	0.14
SMc03789	3455857	3457470	-	3455857	3457470	Putative DNA polymerase	0.64	1.96	1.71	3.4	7.7
SMc03959*	2951570	2954244	+	2951627	2954224	Probable ATP-dependent DNA ligase	0.44	18.26	0.24	3.53	2.76
SMc04187	2175636	2177155	-	2175636	2177069	DNA packaging protein GP2	0.64	3.27	0.51	2.43	8.74
SMc04296	2214096	2215210	-	2214116	2215156	Cell division protein ftsz	2.6	4.5	1.83	5.65	0.9
SMc05018	3417237	3419215	-	3417257	3419215	Putative DNA or RNA helicase	1.26	0.84	5.62	1.05	0.93
Other membrane and surface functions											
SMa0669	356020	357269	+	356020	357249	HlyD-family protein	2	0.13	8.4	1.5	1.52
SMa1303	712238	713410	-	712238	713410	VirB10-like transmembrane secretion protein	1.52	1.26	1.14	6.6	0.97
SMa1313	716412	717133	-	716432	717133	VirB5 type IV secretion protein	0.52	1.77	0.09	8.32	0.67
SMa1319	719850	720149	-	719850	720149	VirB2 type IV secretion protein	2.07	4.72	0.07	6.18	0.27
SMa1905	1082691	1085171	+	1082806	1085151	MrcB penicillin binding protein B	3.39	1.32	5.04	0.67	1.2
SMb20775	1567264	1570887	+	1567285	1570887	hypothetical exported protein, TonB-dependent receptor protein	0.42	0.35	5.45	1.27	1.22
SMb20815	602766	604453	-	602786	604453	similar to protein involved in assembly of outer membrane proteins	5.35	3.37	3.73	3.01	2.48
SMb20831	622953	623980	-	622973	623926	RkpR	5.65	13.3	5.44	2.69	6.55

Table S3.- Cont.

	CoIP-RNA[2]						Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMb20946	1172839	1173606	-	1172859	1173539	exopolysaccharide production protein	0.94	7.47	0.22	2.18	1.59
SMb21006	1241039	1241288	-	1241039	1241260	hypothetical membrane protein	0.89	1.57	1.8	2	8.32
SMb21303	885495	885943	+	885495	885923	hypothetical membrane-anchored protein	3.2	0.52	9.44	2.45	4.12
SMb21362	1025607	1026131	+	1025671	1026111	hypothetical membrane-anchored protein	0.41	6.61	0.6	2	6.24
SMc00088	1033159	1033646	-	1033179	1033592	Hypothetical/unknown transmembrane protein	7.33	0.52	8.19	0.47	0.39
SMc00130	995679	995819	+	995679	995819	Hypothetical transmembrane protein	3.05	0.83	5.29	0.37	1.07
SMc00135	2034596	2035401	-	2034616	2035347	Hypothetical transmembrane protein	21.05	10.63	3.82	19	2.36
SMc00250	1820555	1820793	+	1820609	1820773	Hypothetical transmembrane protein	4.07	1.67	6.15	3.67	9.23
SMc00455	1082618	1083421	+	1082739	1083401	Probable HlyIII	0.63	11.77	1.12	1.59	2.91
SMc00506	1905825	1906735	-	1905845	1906654	Hypothetical transmembrane protein	0.46	6.79	0.57	0.74	2.72
SMc00764	775134	775404	+	775244	775384	Hypothetical/unknown transmembrane protein	0.86	8.96	0.48	2.51	4.28
SMc00796*	817036	817245	+	817061	817225	Hypothetical transmembrane protein	0.31	8.27	0.03	2.27	2.19
SMc00799	819127	819719	-	819147	819719	Hypothetical transmembrane protein	0.31	15.12	0.02	0.81	4.41
SMc00800*	819810	820413	-	819830	820273	Hypothetical transmembrane protein	0.23	41.41	0.02	0.98	1.14
SMc00816	837775	838211	+	837775	838191	Conserved hypothetical transmembrane protein	1.9	0.52	6.07	0.5	0.99
SMc00830	851046	852366	+	851078	852346	Hypothetical transmembrane protein	0.81	0.03	6.48	0.36	0.33
SMc00885*	900972	901788	-	900992	901630	Hypothetical transmembrane signal peptide protein	0.28	27.36	0.02	1.19	1.91
SMc00971	969964	970932	-	969984	970907	Probable pirin-related protein	3.15	5.92	1.94	0.9	2.16
SMc00990	943588	944858	-	943608	944804	Putative fosmidomycin resistance antibiotic resistance transmembrane protein	1.52	0.2	6.73	0.29	2
SMc01036*	1562544	1562841	+	1562570	1562821	Hypothetical transmembrane protein	1.13	6.05	1	1.29	5.99
SMc01102	454174	455399	-	454194	455399	Hypothetical transmembrane protein	0.57	0.29	0.52	1.16	6
SMc01264*	1512504	1512993	-	1512524	1512877	Hypothetical transmembrane protein	0.56	5.41	0.18	1.01	1.99
SMc01274	1501555	1501952	-	1501575	1501952	Protein CrcB homolog	1.73	0.63	5.3	2	1.12
SMc01289	1488535	1489929	+	1488589	1489929	Preprotein translocase subunit SecY	6.25	0.13	3.03	0.58	0.65
SMc01342	1437469	1438302	-	1437489	1438256	Putative outer membrane protein	5.96	0.91	3.63	0.65	1.07
SMc01410	2253125	2253418	+	2253179	2253418	Putative lipoprotein transmembrane	1.43	14.47	0.31	1.49	0.99
SMc01418	2266664	2267089	+	2266715	2267089	hypothetical signal peptide protein	0.53	19.78	0.58	1.17	0.57
SMc01459	2305422	2306297	+	2305476	2306297	Hypothetical transmembrane protein	0.66	7.14	0.47	1.83	0.32
SMc01488	2247620	2248191	-	2247640	2248137	Hypothetical transmembrane protein	1.56	3.1	20.67	4	1
SMc01489	2253436	2253809	+	2253436	2253789	hypothetical signal peptide protein	0.47	8.23	0.39	1.91	1.03
SMc01508	2621064	2621515	+	2621064	2621495	Hypothetical transmembrane protein	0.58	27.56	0.02	0.67	2.13
SMc01509*	2620514	2621036	+	2620654	2621016	Hypothetical transmembrane protein	0.47	63.74	0.01	1.12	3.65
SMc01519	2612639	2613033	+	2612639	2613013	Hypothetical transmembrane protein	0.63	0.18	6.3	1.67	1.83

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc01581	2517634	2517935	+	2517634	2517915	Hypothetical transmembrane protein	5.92	2.7	3.36	3	0.3
SMc01714	490525	491138	+	490630	491118	Hypothetical transmembrane protein	1.78	28.35	2.55	2	2.55
SMc01721	480462	482269	-	480482	482269	Putative inner-membrane transmembrane protein	7.23	0.17	4.35	0.39	0.6
SMc01723	478789	479402	-	478809	479348	Hypothetical transmembrane protein	6.22	11.29	2.77	1.04	1.77
SMc01729	473140	474074	+	473140	474054	Hypothetical transmembrane protein	0.46	0.12	5.63	0.52	0.42
SMc01776	1321935	1322520	-	1321955	1322458	Auxin-binding protein	1.35	5.18	2.61	0.7	12.49
SMc01794	1340713	1341320	-	1340713	1341288	Putative polysaccharide export system periplasmic transmembrane protein	1.27	0.57	6.83	0.19	0.67
SMc01907	1367837	1370105	+	1367896	1370085	Hypothetical transmembrane protein	1.04	0.79	5.47	1	1.37
SMc01947	2669602	2669966	-	2669622	2669966	Conserved hypothetical transmembrane protein	7.34	11.33	23.76	5.19	59.39
SMc01986	2710607	2710986	+	2710607	2710966	Hypothetical transmembrane protein	1.15	66.15	1	2	1.42
SMc02058	1659763	1660219	+	1659867	1660199	Probable YajC protein	1.86	0.23	5.37	0.31	0.59
SMc02066	1651446	1652154	+	1651507	1652154	Putative Sec-independent translocase transmembrane protein	2.25	0.52	5.54	1.48	0.53
SMc02072	1644321	1647199	+	1644342	1647179	Hypothetical transmembrane protein	1.73	9.38	2.65	0.83	0.61
SMc02156	539741	540615	+	539798	540595	Putative major antigenic peptide PEB	0.41	7.29	0.21	0.62	0.92
SMc02200	545971	546552	-	545971	546495	Hypothetical transmembrane protein	1.58	6.75	0.74	1.81	4.12
SMc02232	597475	598621	+	597695	598621	Hypothetical transmembrane protein	0.91	0.76	5.14	0.42	0.77
SMc02234	598621	599444	+	598621	599424	Hypothetical transmembrane protein	1.01	1.1	5.35	0.73	0.83
SMc02274	648247	649697	+	648325	649677	Capsule polysaccharide exporter	4.26	0.25	5.53	0.18	1.56
SMc02401	1153162	1153684	-	1153182	1153658	Hypothetical transmembrane protein	0.36	4.59	0.42	11.65	2.4
SMc02432	2812118	2814130	+	2812170	2814110	Hypothetical transmembrane protein	2.27	0.16	5.43	0.35	2.14
SMc02446	2829202	2829449	-	2829222	2829395	Putative pilus assembly protein	2.26	5.04	7.8	0.67	0.3
SMc02447	2829453	2829945	-	2829473	2829793	Conserved hypothetical transmembrane protein	0.94	1.79	5.59	0.09	1.08
SMc02571	1200492	1201814	+	1200492	1201814	Putative secretion membrane fusion protein	2.18	1.65	13.95	3	3.5
SMc02573	60108	60581	-	60108	60581	Hypothetical transmembrane protein	1.22	0.42	5.36	0.4	1.26
SMc02617	110613	110774	-	110613	110774	Conserved hypothetical transmembrane protein	4.15	281.12	0.6	2	2.43
SMc02619	111180	111551	-	111180	111497	Conserved hypothetical transmembrane protein	1.48	50.62	2.7	5	3.35
SMc02638	1182547	1183053	+	1182571	1183053	Hypothetical transmembrane protein	1.62	9.24	0.37	2	3.86
SMc02820	166109	167583	+	166163	167563	Putative pilus assembly protein	2.38	0.99	5.28	0.53	0.53
SMc02853	203994	205223	+	204256	205203	Hypothetical transmembrane protein	4.91	1.04	10.22	3.42	4.28
SMc02884	240001	241111	-	240021	241013	Probable membrane lipoprotein	3.44	1.68	6.92	2.87	1.88
SMc02942	2946801	2947460	-	2946821	2947351	Peptidoglycan-associated lipoprotein	1.5	14.41	3.2	0.23	2.2
SMc02989	3109282	3109514	-	3109302	3109514	Conserved hypothetical transmembrane protein	7.65	0.65	4.26	0.29	0.35
SMc03941	3092100	3092437	-	3092120	3092344	Conserved hypothetical transmembrane protein	1.22	0.63	5.83	0.59	0.27

Table S3.- Cont.

	CoIP-RNA[2]						Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc04050	3054414	3055207	-	3054434	3055207	Hypothetical transmembrane protein	0.3	7.81	1.62	1.54	1.31
SMc04114	160646	160913	+	160711	160893	Putative pilin subunit	18.48	22.39	10.52	0.54	5.34
SMc04182	2172259	2172671	-	2172279	2172617	Hypothetical transmembrane protein	1.13	3.87	1.35	1.5	7.91
SMc04183	2172962	2173848	-	2172982	2173794	Hypothetical transmembrane protein	1.46	6.67	4.95	3	60.72
SMc04184	2174286	2174587	-	2174306	2174533	Hypothetical transmembrane protein	1.04	3.94	1.5	2	9.13
SMc04189*	2177556	2177853	-	2177576	2177731	Hypothetical transmembrane protein	0.69	8.92	0.05	1.92	4.41
SMc04194*	2181009	2181248	+	2181031	2181228	Putative transmembrane protein	0.49	8.32	0.06	1.64	1.72
SMc04248	2073286	2073901	+	2073326	2073901	Hypothetical transmembrane protein	6.57	1.57	6.92	0.75	2.61
Hfq operon											
SMc01048	1577073	1577369	+	1577127	1577369	Probable RNA binding protein	17.78	1.85	15.17	2.97	6.1
SMc01049	1577376	1578793	+	1577376	1578773	Putative GTP-binding protein	4.34	0.29	6.98	0.87	1.13
hypothetical proteins											
SMaORF11	375058	375366	-	375078	375335	hypothetical protein	0.91	0.04	16.2	2.67	0.81
SMaORF15	699623	699793	+	699638	699793	hypothetical protein	9.36	0.11	24.6	4.5	0.76
SMaORF16	699810	700208	+	699810	700208	hypothetical protein	6.3	0.04	24.48	2.4	2.43
SMaORF21	1082421	1082652	+	1082462	1082632	hypothetical protein	3.39	5.88	8.2	1.11	4.87
SMaORF7	314177	314460	-	314197	314442	hypothetical protein	6.5	19.84	5.7	10	128.43
SMa0017	11452	12083	+	11506	12063	hypothetical protein	1.52	0.81	6.2	1.67	1.52
SMa0121	65471	65658	-	65491	65658	hypothetical protein	1.61	3.36	5.88	2.98	4.11
SMa0123	65709	66166	-	65729	66112	hypothetical protein	4.15	3.54	9.74	0.38	0.46
SMa0134	71046	71671	-	71066	71671	conserved hypothetical protein	1.12	147.11	0.01	3.19	1.23
SMa0136	72217	74306	+	72274	74286	conserved hypothetical protein	0.37	5.7	0.43	0.55	2.6
SMa0164	90721	91037	+	90721	91017	hypothetical protein	11.3	10.43	24.9	1.4	12.6
SMa0166	91039	91589	+	91039	91569	conserved hypothetical protein	3.62	0.8	5.93	0.52	1.74
SMa0229	127945	128527	+	128085	128507	conserved hypothetical protein	0.27	6.36	0.37	0.45	1.66
SMa0232	128673	129298	+	128727	129278	conserved hypothetical protein	0.36	45.59	0.65	0.56	0.61
SMa0279	156780	157465	-	156800	157411	conserved hypothetical protein	0.59	2.7	0.48	1.6	5.48
SMa0359	193562	193807	-	193562	193807	conserved hypothetical protein	2.16	1.85	34.2	6	5.17
SMa0414	224751	226495	+	224805	226475	conserved hypothetical protein	0.93	7.56	1.09	1.43	2.03
SMa0541*	289805	290248	+	289833	290228	conserved hypothetical protein	0.83	89.3	0.03	2.03	1.93
SMa0543	290313	290977	+	290367	290957	hypothetical protein	0.86	21.66	0.05	2.7	1.45
SMa0609	325226	325801	+	325226	325801	hypothetical protein	10.37	4.72	1.95	4.5	1.22
SMa0610	325807	326687	+	325807	326667	hypothetical protein	5.18	0.89	2.33	0.89	3.18

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMa0633	340377	340876	-	340397	340783	hypothetical protein	4.05	0.18	22.05	3	1.98
SMa0636	341244	342172	+	341499	342152	conserved hypothetical protein	0.53	0.01	16.2	1	1.42
SMa0667	355474	356016	+	355528	356016	conserved hypothetical protein	1.14	0.06	12.6	1.33	1.42
SMa0670	357305	358233	+	357359	358213	conserved hypothetical protein	13.91	0.26	8.31	1.54	1.5
SMa0687	371770	372399	-	371790	372296	hypothetical protein	9.23	0.47	6.12	0.6	0.67
SMa0689	372465	373435	-	372485	373435	conserved hypothetical protein	15.67	0.56	26.8	2.67	1.62
SMa0690	373436	374889	-	373456	374856	conserved hypothetical protein	20.44	0.67	13.55	2	0.91
SMa0809	442266	442987	+	442329	442967	hypothetical protein	8.46	1.93	5.72	1	1.78
SMa0888	495150	496014	+	495196	496014	conserved hypothetical protein	0.78	2.07	2.25	2	5.63
SMa0937	520741	523052	-	520761	522920	conserved hypothetical protein	0.32	7.5	3.06	1.2	1.34
SMa0945	528169	528764	+	528169	528744	conserved hypothetical protein	6.08	9.45	42.8	2.67	6.49
SMa1043	573878	574182	+	573878	574162	conserved hypothetical protein	6.29	1.92	3.02	2.14	0.33
SMa1045	574201	574542	+	574255	574542	hypothetical protein	4.67	2.36	8	2	0.61
SMa1060	579966	581353	-	579986	581353	conserved hypothetical protein	2.22	7.51	2.6	2.15	4.91
SMa1077	588561	589103	+	588601	589083	Nex18 Symbiotically induced conserved protein	5.83	12.37	1.34	2.51	1.46
SMa1082	590330	591001	-	590350	590970	conserved hypothetical protein	1.99	0.02	53.85	7	1.98
SMa1086	593600	594315	-	593620	594294	conserved hypothetical protein	3.21	0.02	17.4	6.4	1.34
SMa1089	596594	596797	+	596594	596797	hypothetical protein	4.06	0.41	5.83	1.14	0.26
SMa1091	596794	597317	+	596794	597297	hypothetical protein	1.96	0.13	10.95	2.5	2.13
SMa1093	598230	598636	+	598284	598616	hypothetical protein	11.92	0.79	5.47	1.25	0.91
SMa1095	598750	599132	+	598804	599112	hypothetical protein	9.51	1.11	7.5	2	1.22
SMa1132	618385	618902	+	618493	618882	hypothetical protein	1.12	0.03	7.62	1.8	0.43
SMa1146	623712	626454	+	623735	626434	conserved hypothetical protein	1.36	0.02	8.07	2.22	2.1
SMa1147	626479	627356	+	626512	627336	conserved hypothetical protein	1.25	0.03	8.14	1.71	0.7
SMa1149	627414	628327	+	627474	628307	conserved hypothetical protein	5.9	0.07	27.48	5.6	1.7
SMa1153	628931	629661	+	628967	629641	conserved hypothetical protein	2.54	0.02	20.2	6	1.83
SMa1154	629707	630149	+	629734	630129	conserved hypothetical protein	7.18	0.21	2.77	1	1.75
SMa1169	641608	642023	+	641662	642003	hypothetical protein	0.66	0.02	14.8	2	2.43
SMa1176	643856	644451	-	643876	644394	hypothetical protein	1.15	0.16	7.27	2	4.53
SMa1200	660498	661087	-	660518	661033	conserved hypothetical protein	5.07	0.37	14.2	1.33	2.43
SMa1201	661232	661779	-	661252	661632	hypothetical protein	0.74	0.05	12.3	4	2.13
SMa1231	675099	675976	+	675132	675956	conserved hypothetical protein	2.7	0.68	6.87	1.5	1.88
SMa1256	687697	688227	-	687697	688227	conserved hypothetical protein	5.3	0.52	1.04	1.64	0.5

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMa1259	688231	689589	-	688231	689589	conserved hypothetical protein	3.09	0.24	6.17	0.86	2.61
SMa1501	828335	829269	-	828355	829269	conserved hypothetical protein	1.31	5.77	0.49	2.87	0.3
SMa1503	829280	830309	-	829300	830166	conserved hypothetical protein	1.64	5.97	0.1	1.32	0.13
SMa1507	831222	832336	+	831222	832316	conserved hypothetical protein	12.55	6.34	0.78	12.21	0.23
SMa1697	957048	957729	-	957068	957667	conserved hypothetical protein	10.57	2.09	4.79	0.94	1.58
SMa1750	992835	994311	+	992912	994291	conserved hypothetical protein	1.49	9.27	1.23	1.97	4.71
SMa1765	1003466	1003971	-	1003486	1003971	conserved hypothetical protein	0.66	9.03	0.48	1.95	1.78
SMa1793	1016898	1017382	+	1016940	1017362	conserved hypothetical protein	1.75	15.63	0.51	3.71	6
SMa1835	1041063	1042050	-	1041083	1041973	conserved hypothetical protein	1.14	9.45	2.4	1.71	2.52
SMa1918	1092261	1092560	+	1092279	1092560	conserved hypothetical protein	1.9	12.6	0.4	1	1.37
SMa1927	1095973	1097039	+	1096027	1097019	conserved hypothetical protein	2.35	6.45	1.56	0.46	2.16
SMa1957	1112285	1113228	+	1112318	1113208	conserved hypothetical protein	1.94	0.63	0.33	5.4	0.7
SMa2011	1138651	1138997	+	1138651	1138977	hypothetical protein	5.18	46.07	0.3	2.14	14.96
SMa2023	1144189	1145041	+	1144230	1145021	Conservative hypothetical protein	3.92	8.14	0	2.97	0.01
SMa2049	1158381	1159631	+	1158529	1159611	conserved hypothetical protein	1.04	0.89	3.33	0.89	5.34
SMa2055	1161154	1161479	+	1161208	1161459	hypothetical protein	5.66	0.86	3.15	1.5	0.3
SMa2061	1162567	1164041	+	1162596	1164041	conserved hypothetical protein	0.61	5.28	0.1	1.19	2.13
SMa2071	1168535	1168800	-	1168555	1168746	conserved hypothetical protein	0.52	83.27	0.05	3.71	3.83
SMa2129	1203271	1204455	-	1203291	1204310	conserved hypothetical protein	2.14	2.05	10.26	2	8.46
SMa2201	1232872	1233316	-	1232892	1233272	conserved hypothetical protein	3.26	1.35	2.8	2	6.49
SMa2221	1243528	1244241	+	1243528	1244241	conserved hypothetical protein	2.59	3.54	0.6	8.5	0.23
SMa2229	1248057	1248616	-	1248077	1248562	conserved hypothetical protein	2.44	3.61	2.77	3.5	5.33
SMa2239	1254231	1255058	+	1254259	1255038	conserved hypothetical protein	6.7	2.6	5.88	1.89	1.91
SMa2241	1255074	1256341	+	1255074	1256321	conserved hypothetical protein	8.64	3.46	13.83	2.78	3.69
SMa2243	1256319	1257338	-	1256339	1257265	conserved hypothetical protein	6.43	0.85	6	1.19	0.72
SMa2315	1291230	1291817	+	1291278	1291817	hypothetical protein	2.38	7.09	0.88	5.85	2.11
SMa2361	1331739	1332750	+	1331764	1332750	conserved hypothetical protein	7.65	4.9	2.5	1.87	1.59
SMa5002	71692	72109	-	71712	72026	conserved hypothetical protein	1.04	238.6	0.04	4.52	2
SMa5019	204395	204993	+	204550	204993	conserved hypothetical protein	0.32	0.73	0.6	1.6	5.23
SMa5034	1339039	1339781	+	1339095	1339781	conserved hypothetical protein	0.87	1.22	5.4	2.18	2.27
SMbORF12	1115785	1116277	+	1115934	1116257	hypothetical protein	0.27	34.29	0.05	1.85	1.05
SMbORF15	1380844	1381226	-	1380864	1381079	hypothetical protein	0.54	82.07	0.14	1.23	14
SMbORF18	1581755	1581882	-	1581755	1581859	hypothetical protein	0.83	1.89	4.2	2	22.83

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMbORF6	575694	576029	-	575714	575896	hypothetical protein	0.55	22.13	0.18	2.31	1.52
SMbORF8	585229	586183	+	585318	586163	hypothetical protein	1.56	0.55	5.36	0.82	1.15
SMb20025	36075	37144	+	36147	37124	conserved hypothetical protein	0.54	8.54	0.36	0.67	5.64
SMb20026	37267	37792	+	37331	37792	conserved hypothetical protein	4.9	15.46	3.87	1.33	25.63
SMb20041	51626	52253	+	51703	52233	hypothetical protein	0.3	22.78	0.07	1.22	2.76
SMb20063	72756	73072	+	72756	73052	conserved hypothetical protein	1	7.56	1.03	1.62	0.58
SMb20065*	73929	74390	+	73972	74370	hypothetical protein	0.33	32.33	0.04	1.75	1.99
SMb20066	74483	74742	+	74537	74722	hypothetical protein	1.66	126.62	0.12	2.4	3.26
SMb20074	83357	83646	+	83384	83626	hypothetical protein	0.52	32.78	0.03	1.5	6.36
SMb20075	83675	83886	+	83675	83866	hypothetical protein	2.07	236.24	0.05	0.67	2.33
SMb20081	92715	93445	-	92735	93445	conserved hypothetical protein	0.32	12.96	0.3	1.55	1.22
SMb20082	93442	94399	-	93442	94344	hypothetical protein	0.26	31.3	0.09	3.2	2.47
SMb20083*	94443	94811	+	94552	94791	hypothetical protein	0.64	20.53	0.45	3.83	17.2
SMb20163	180811	181980	+	180811	181980	conserved hypothetical protein	1.04	2.81	7	2	2.23
SMb20167	185402	186288	-	185422	186234	hypothetical protein	1.56	6.6	0.62	1.25	1.52
SMb20180	197742	198241	+	197742	198221	hypothetical protein	4.69	6.57	20.1	14	28.91
SMb20236	241677	242095	+	241731	242075	hypothetical protein	0.65	15.67	0.6	4	0.87
SMb20240	244260	245378	-	244260	245378	conserved hypothetical protein	0.32	10.9	0.6	3.6	15.58
SMb20241	245375	246460	-	245375	246460	conserved hypothetical protein	0.28	15.12	0.11	0.94	1.65
SMb20242	246457	247587	-	246457	247587	conserved hypothetical protein	0.69	17.32	0.1	1.33	3.65
SMb20250	256338	256957	+	256338	256937	conserved hypothetical protein	0.57	12.89	0.16	1.45	5.81
SMb20251	257005	257991	+	257009	257971	hypothetical protein	0.52	28.35	0.13	1.57	9.96
SMb20254*	260389	260704	-	260409	260684	hypothetical protein	1.18	6.07	0.6	10	9.74
SMb20255*	260739	261354	-	260759	261310	hypothetical protein	1.91	18.9	0.51	3.14	6.78
SMb20269	273692	275403	+	273692	275383	conserved hypothetical protein	0.76	0.07	5.82	0.5	0.46
SMb20273	278639	278865	-	278659	278844	hypothetical protein	0.41	2.16	0.18	1.84	5.3
SMb20292	299388	300533	-	299408	300391	hypothetical immunogenic protein	6.02	3.6	3.81	4.71	3.89
SMb20293*	300570	301082	+	300703	301062	hypothetical protein	0.28	7.24	0.1	1.33	6.15
SMb20340*	345295	345548	+	345349	345528	hypothetical protein	5.39	205.05	0.64	2.12	4.15
SMb20341	345679	345938	+	345733	345918	hypothetical protein	2.49	40.63	0.48	1.6	5.36
SMb20454*	466799	467273	+	466834	467253	conserved hypothetical protein	0.32	21.08	0.02	3.1	2.14
SMb20475	487989	488532	-	487989	488483	conserved hypothetical protein	0.84	24.32	0.9	2	6.09
SMb20534	557533	558362	-	557553	558362	hypothetical protein	2.07	1.42	1.44	1.2	5.48

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMb20607	1621026	1621490	-	1621026	1621490	conserved hypothetical protein	1.09	3.6	2.1	1	5.02
SMb20614	1631490	1633571	-	1631510	1633528	hypothetical protein	1.7	0.09	5.53	0.16	0.72
SMb20647	1448307	1448693	-	1448327	1448578	hypothetical protein	1.25	9.55	0.4	0.13	2.07
SMb20675	1477146	1477741	-	1477166	1477741	conserved hypothetical protein	12.74	4.72	2.77	2	0.42
SMb20724	1529171	1530169	+	1529225	1530169	conserved hypothetical exported protein	4.4	11.17	1.51	0.29	1.72
SMb20771	1563532	1564592	-	1563552	1564538	conserved hypothetical protein	2.26	1.29	2.35	1.82	5.59
SMb20835	627105	628120	-	627125	628120	conserved hypothetical protein	4.48	1.36	5.75	2.1	4.84
SMb20886	1291425	1292871	+	1291462	1292871	conserved hypothetical protein	2.86	1.42	4.47	2.56	8.5
SMb20889	1294728	1295518	-	1294748	1295452	hypothetical glycine-rich protein	1.89	20.19	0.38	1.7	1.71
SMb20897	1305414	1305886	+	1305414	1305866	hypothetical protein	2.37	2.7	0.9	1.5	5.93
SMb20907	1317258	1317583	+	1317258	1317563	hypothetical protein	1.15	2.89	7.8	2	4.46
SMb20908*	1317768	1318151	-	1317788	1318126	hypothetical protein	0.46	7.35	1.11	2.86	7.22
SMb21013	636603	637129	-	636623	637090	hypothetical protein	3.2	2.86	5.45	2.15	2.81
SMb21030	650627	651096	-	650647	651096	hypothetical protein	10.02	38.59	3.12	4.4	4.14
SMb21161	905250	906703	+	905250	906683	conserved hypothetical protein	1.18	0.63	5.52	4	1.22
SMb21253	823674	824464	+	823674	824444	hypothetical protein	2.95	1.15	8.62	0.75	0.61
SMb21332*	999469	1000089	+	999572	1000069	hypothetical protein	1.04	29.53	0.12	0.62	2.08
SMb21334	1000578	1001413	+	1000632	1001393	hypothetical exported glutamine-rich protein	0.41	23.94	0.14	2	7.07
SMb21399	1330848	1331272	-	1330868	1331272	hypothetical protein	3.73	1.89	1	2	9.33
SMb21402	1332640	1333952	+	1332769	1333932	hypothetical calcium binding protein	2.45	0.4	7.7	0.76	1.57
SMb21403	1335187	1335833	+	1335358	1335813	hypothetical protein	3.52	8.42	8.8	4.67	13.8
SMb21407	1338042	1338880	+	1338042	1338860	conserved hypothetical protein	0.52	49.61	0.21	2.12	5.3
SMb21440	1369931	1370513	+	1370059	1370493	hypothetical protein	1.61	10.28	1.48	2.17	5.63
SMb21441	1371025	1371485	-	1371045	1371485	conserved hypothetical protein	0.54	86.45	0.03	2.8	1.24
SMb21442	1371498	1371947	-	1371498	1371947	hypothetical protein	0.2	147.39	0.01	4.78	3.54
SMb21443	1371979	1372367	-	1371999	1372313	hypothetical protein	0.38	87.62	0.14	2	4.98
SMb21444*	1372300	1373094	+	1372331	1373074	hypothetical protein	1.45	101.58	0.26	3	22.43
SMb21450	1380254	1380867	+	1380308	1380847	conserved hypothetical protein	1.04	27.17	0.38	1.45	2.27
SMb21452*	1381205	1381576	+	1381221	1381556	putative chaperone	0.44	51.3	0.24	1.47	5.15
SMb21454	1381803	1382137	-	1381823	1382137	hypothetical protein	0.75	22.55	0.18	1.7	2.18
SMb21456	1383771	1384280	-	1383791	1384228	hypothetical protein	0.57	17.21	0.74	2.88	0.85
SMb21470	1397681	1398016	+	1397735	1398016	hypothetical protein	0.65	1.77	0.6	6.55	5.31
SMb21471	1397994	1398262	+	1397994	1398242	hypothetical protein	0.46	15.75	0.17	0.95	0.58

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMb21473	1398866	1399300	+	1398866	1399300	conserved hypothetical protein	0.52	48.82	0.06	1.86	5.65
SMb21480	1403354	1403634	-	1403374	1403634	conserved hypothetical protein	0.41	46.3	0.04	0.82	2.56
SMb21481	1403628	1404158	-	1403628	1404104	conserved hypothetical protein	0.5	74.94	0.02	0.82	2.35
SMb21482	1404381	1404757	-	1404401	1404703	hypothetical protein	1.3	23.03	0.09	1.16	2.34
SMb21483*	1404776	1405077	-	1404796	1405077	hypothetical protein	0.11	29.44	0.06	2.12	3.56
SMb21485	1406188	1406702	+	1406242	1406682	hypothetical protein	0.22	0.75	0.3	1.8	5.11
SMb21544	1078366	1078838	+	1078420	1078818	hypothetical exported protein	1.89	12.46	1.2	2.18	2.93
SMb21573	1111973	1113030	+	1112027	1113010	hypothetical exported protein	2.24	8.13	0.21	1.23	2.21
SMb21630	1657730	1658991	-	1657750	1658991	conserved hypothetical protein	23.64	0.92	8.31	0.98	1.14
SMb21668	1026223	1026499	+	1026252	1026479	hypothetical protein	2.07	10.39	1.54	1.14	8.35
SMb21681	1318311	1318603	+	1318407	1318583	hypothetical protein	2.71	32.29	1.13	1.73	4.54
SMb21682	1321481	1321686	+	1321481	1321666	hypothetical protein	2.49	1.89	1.2	2	9.33
SMb21683	1331288	1331593	-	1331308	1331481	hypothetical protein	4.09	37.6	0.96	17.33	62.78
SMb21687	1405905	1406119	+	1405905	1406099	hypothetical protein	0.83	27.4	0.21	1.5	6.36
SMb21696	672636	673517	+	672636	673517	hypothetical protein	0.59	2.7	1	5.33	8.72
SMcORF14	1718937	1719188	-	1718957	1719088	hypothetical protein	0.73	12.13	0.14	0.97	0.88
SMcORF17	1769008	1769310	+	1769051	1769290	hypothetical protein	1.02	6.23	2.8	1.46	0.84
SMcORF19	1923643	1923905	+	1923643	1923885	hypothetical protein	7.37	15.22	3.14	3.69	1.57
SMcORF22	2695440	2695699	-	2695460	2695609	hypothetical protein	2.8	0.3	10.32	1.35	5.32
SMcORF23	2916649	2916955	-	2916669	2916929	hypothetical protein	0.69	12.6	0.24	5.06	3.54
SMcORF7	1104180	1104372	-	1104200	1104340	hypothetical protein	1.2	22.71	0.76	0.3	0.09
SMc00003	985149	986308	+	985233	986288	Putative chaperone protein	3.11	14.95	4.11	0.57	1.39
SMc00048	1081587	1082083	+	1081641	1082063	conserved hypothetical protein	3.15	6.58	0.73	1.27	1.12
SMc00049	1082124	1082488	+	1082124	1082468	hypothetical protein	4.51	9.45	0.46	0.86	1.07
SMc00063	1098804	1099144	+	1098840	1099124	hypothetical protein	0.85	43.6	0.11	1.47	2.9
SMc00079	1012751	1013520	-	1012771	1013466	conserved hypothetical protein	4.38	0.07	6	0.84	2.42
SMc00134	2035528	2036433	+	2035586	2036413	conserved hypothetical protein	3.08	0.61	6.55	1.33	2.43
SMc00141	2027950	2029985	-	2027970	2029985	hypothetical protein	6.32	27.97	1.15	2.94	3.88
SMc00198	2030030	2030296	-	2030050	2030202	hypothetical/unknown protein	3.05	28.63	0.79	2.4	2.95
SMc00242	1808963	1810116	-	1808983	1810116	hypothetical signal peptide protein	24.63	12.3	6.15	2.05	3.83
SMc00252	1821842	1822181	-	1821862	1822161	hypothetical protein	0.24	7.15	0.22	0.93	1.46
SMc00254	1823652	1824133	+	1823706	1824113	conserved hypothetical protein	2.07	1278.87	0.22	4	75.48
SMc00255	1824443	1824768	+	1824443	1824748	hypothetical protein	1.51	7.73	3.36	1.33	1.91

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc00276	1845653	1846548	-	1845673	1846548	conserved hypothetical protein	5.1	1.09	3.33	2	0.95
SMc00291	1860437	1861966	+	1860627	1861946	conserved hypothetical protein	1.23	1.08	5.71	0.48	3.39
SMc00336	291247	292873	-	291267	292847	hypothetical protein	1.05	1.96	5.22	0.24	1.07
SMc00338	293363	293910	-	293383	293910	conserved hypothetical protein	1.45	10.63	0.99	2.06	0.37
SMc00360	315744	316492	-	315764	316384	conserved hypothetical protein	9.64	3.65	5.16	5.99	7.67
SMc00367	323138	323599	-	323158	323517	conserved hypothetical protein	0.59	5.4	0.02	0.9	0.04
SMc00371*	325747	326297	-	325767	326258	conserved hypothetical protein	1.07	182.72	0.03	4.84	2.53
SMc00400	349912	351059	-	349932	351059	hypothetical signal peptide protein	2.21	0.94	2.22	1	12.23
SMc00402	352638	353993	-	352658	353938	hypothetical signal peptide protein	1.39	0.94	1.24	0.16	5.29
SMc00431	379419	379897	-	379439	379843	conserved hypothetical protein	0.83	1.89	0.75	1.5	5.33
SMc00472	1950626	1951647	+	1950695	1951627	conserved hypothetical protein	5.07	0.37	4.62	0.13	0.53
SMc00487	1923344	1923635	+	1923402	1923635	conserved hypothetical protein	4.97	5.84	2.69	6.43	6.84
SMc00496	1915242	1915698	-	1915262	1915576	hypothetical protein	2.67	4.84	5.26	1.38	1.66
SMc00521	1893346	1893773	+	1893346	1893753	conserved hypothetical protein	3.03	0.55	5.15	0.32	1.24
SMc00591	1263519	1263875	+	1263574	1263855	Hypothetical/unknown signal peptide protein	9.07	8.71	0.44	8.69	0.3
SMc00596	1268581	1269104	-	1268601	1269104	conserved hypothetical protein	6.22	4.13	1.5	2	12.58
SMc00651	2924671	2925419	+	2924797	2925399	hypothetical protein	1.26	14.17	3.25	0.63	1.12
SMc00665*	2914461	2914689	-	2914481	2914669	hypothetical/unknown protein	0.32	13.81	0.07	2.67	7.3
SMc00689	2888418	2889988	+	2888546	2889988	hypothetical protein signal peptide	3.13	6.83	2.03	2.03	1.14
SMc00705	2874211	2875081	-	2874231	2875034	Conserved hypothetical signal peptide protein	2.3	5.64	0.98	1.67	0.56
SMc00767	779609	779974	-	779629	779868	hypothetical protein	2.59	278.76	0.6	1	2.43
SMc00777	797279	797795	+	797329	797775	conserved hypothetical protein	14.47	0.13	0.02	0.17	0.1
SMc00795*	816082	816374	-	816102	816350	conserved hypothetical protein	0.57	94.82	0.03	4.57	1.78
SMc00798	818820	819142	+	818874	819122	conserved hypothetical protein	0.58	13.08	0.48	0.28	2.95
SMc00814	834994	836041	+	835041	836021	hypothetical signal peptide protein	1.87	14.17	0.21	1.03	1.9
SMc00823	843911	844326	+	843911	844306	hypothetical protein	2.28	7.09	0.4	2.12	1.56
SMc00850	937447	937985	+	937447	937965	conserved hypothetical protein	1.27	0.13	5.6	0.27	0.93
SMc00866	920371	921587	-	920391	921548	hypothetical protein	0.86	0.97	1.77	1.68	10.8
SMc00895	888006	888297	+	888041	888277	conserved hypothetical protein	11.16	1.12	7.31	2.05	6.39
SMc00902	881183	881763	+	881183	881743	conserved hypothetical protein	1.94	0.21	5.25	1	1.01
SMc00939	1767976	1768491	-	1767996	1768385	conserved hypothetical protein	1.81	6.5	2.31	3.54	2.48
SMc00940*	1768571	1768920	-	1768591	1768842	hypothetical protein	2.37	121.49	0.13	2.44	3.92
SMc00942	1769621	1770017	-	1769641	1769883	conserved hypothetical protein	4.3	8.92	2.88	1.67	2.92

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc00959*	1785806	1786124	+	1785948	1786124	hypothetical/unknown protein	1.75	8.21	0.83	2.78	3.55
SMc00987	947998	948652	-	948018	948584	conserved hypothetical protein	3.26	8.94	10.2	0.53	2.34
SMc01002	1529012	1529514	+	1529066	1529494	conserved hypothetical protein	1.7	7.56	0.64	1.58	0.5
SMc01016	1541086	1541587	-	1541106	1541537	hypothetical protein	1.67	7.61	0.85	2.31	0.79
SMc01029	1555406	1555830	+	1555529	1555810	conserved hypothetical protein	2.09	6.41	11.85	2.4	7.22
SMc01051	1581592	1582445	-	1581612	1582445	conserved hypothetical protein	3.11	0.75	5.92	1	1.22
SMc01068	1521785	1522128	-	1521805	1522074	hypothetical/unknown protein	2.34	5.43	6.9	1	2.33
SMc01091	467531	467748	-	467551	467694	hypothetical protein	7.26	2.36	6.09	0.57	0.61
SMc01107	448507	448829	-	448527	448784	conserved hypothetical protein	2.35	7.6	1.28	1.09	0.42
SMc01159*	391073	391978	+	391073	391978	hypothetical protein	3.3	9.93	1.16	2.27	1.12
SMc01265	1510718	1512265	+	1510718	1512265	conserved hypothetical protein	0.86	26.62	0.34	2.75	2.76
SMc01266	1509389	1510705	+	1509389	1510705	conserved hypothetical protein	0.45	29.96	0.19	1.26	1.62
SMc01267*	1507355	1509384	+	1507415	1509364	conserved hypothetical protein	1.11	68.46	0.26	1.67	1.47
SMc01277	1499081	1499886	-	1499101	1499886	hypothetical protein	1.42	0.63	6.85	1	1.42
SMc01325	1458322	1459160	+	1458475	1459140	hypothetical/unknown protein	0.24	0.21	0.91	0.48	5.71
SMc01349	1432697	1433214	+	1432697	1433194	conserved hypothetical protein	1.53	0.17	5.08	0.67	1.06
SMc01445	2289052	2289290	-	2289072	2289290	hypothetical protein	3.2	50.25	0.35	3.75	7.41
SMc01446	2289323	2289585	-	2289343	2289585	hypothetical protein	2.76	46.2	0.34	5.37	8.37
SMc01456	2300337	2300807	+	2300353	2300787	hypothetical protein	1.39	6.71	1.22	1.33	3.36
SMc01467*	2314631	2315123	-	2314651	2315040	conserved hypothetical protein	0.35	15.49	0.04	1.37	2.59
SMc01514	2615641	2616173	-	2615661	2616095	conserved hypothetical protein	7.11	36.45	0.47	0.17	31.4
SMc01515	2614674	2615620	-	2614694	2615620	hypothetical protein signal peptide	2.95	5.3	0.27	0.37	16.8
SMc01541	2476579	2477780	-	2476599	2477780	conserved hypothetical protein	1.78	1.35	10.2	1.33	1.62
SMc01542	2477790	2478025	-	2477810	2478025	hypothetical protein	3.07	0.41	13.05	2.5	4.87
SMc01545	2481516	2481934	-	2481536	2481880	hypothetical protein	1.56	1.18	7.68	2	2.68
SMc01549	2488524	2489192	-	2488544	2489170	hypothetical protein peptide signal	0.82	5.1	0.76	2.18	1.33
SMc01550	2490159	2490672	+	2490185	2490652	conserved hypothetical protein	2.52	1.85	8.33	1.18	1.43
SMc01557	2498282	2498699	-	2498302	2498658	hypothetical signal peptide protein	1.16	12.44	0.3	1.88	0.98
SMc01559	2499408	2499930	-	2499428	2499850	conserved hypothetical protein	1.48	10.91	1.53	1.11	0.88
SMc01590*	2522953	2523623	+	2522971	2523603	hypothetical protein	0.15	21.23	0.02	1.98	3.25
SMc01602	2393048	2393979	+	2393081	2393959	conserved hypothetical protein	2.41	13.49	4.93	10.47	20.09
SMc01617	2407430	2408275	-	2407430	2408275	conserved hypothetical protein	0.46	0.19	11.4	4	4.57
SMc01701	510966	511597	-	510986	511570	conserved hypothetical protein	0.65	0.26	6.18	0.8	1.03

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc01703	509437	509888	-	509457	509888	conserved hypothetical protein	0.1	0.14	16	8	3.86
SMc01748	2613082	2613396	+	2613136	2613396	hypothetical protein	0.77	1.05	7.2	1.25	1.07
SMc01759	1305576	1305846	-	1305596	1305814	conserved hypothetical protein	0.56	5.63	0.02	0.75	0.06
SMc01788	1332481	1332736	-	1332501	1332716	hypothetical protein	0.98	221.09	2	6.11	17.69
SMc01910	1372292	1375773	+	1372292	1375753	hypothetical protein	1.28	0.12	5.57	0.14	0.81
SMc01911	1375788	1376260	+	1375842	1376240	conserved hypothetical protein	3.16	8.1	3.63	1.3	0.79
SMc01929	1394904	1396591	+	1394904	1396571	hypothetical protein	2.84	0.26	5.07	0.2	0.2
SMc01930	1396630	1397054	+	1396630	1397034	hypothetical protein	1.28	0.55	9.37	0.5	0.46
SMc01995	2659618	2660086	+	2659700	2660086	conserved hypothetical protein	12.44	2.51	1.08	2.22	0.9
SMc02090	1619046	1619933	+	1619046	1619933	conserved hypothetical protein	1.44	0.51	7.1	0.42	0.71
SMc02153	555359	556690	-	555359	556690	conserved hypothetical protein	1.2	0.16	5.59	0.63	0.96
SMc02154	551813	554713	-	551813	554713	hypothetical protein	1.73	0.1	5.27	0.51	0.63
SMc02155	548950	551798	-	548970	551798	hypothetical protein	2.3	0.31	5.18	0.49	0.57
SMc02173	521858	522306	-	521878	522306	conserved hypothetical protein	1.04	8.66	0.26	1.43	7.3
SMc02202	542113	542975	+	542113	542955	hypothetical protein	8.05	10.39	0.91	2.41	1.43
SMc02203	547672	548831	+	547672	548811	conserved hypothetical protein	7.31	4.68	4.82	5.38	1.73
SMc02226	587292	587829	+	587336	587809	conserved hypothetical protein	0.75	1.72	0.8	1	6.7
SMc02277	652153	652411	+	652179	652391	hypothetical/unknown protein	1.78	7.48	5.2	1.3	0.78
SMc02312	683262	683494	+	683262	683474	conserved hypothetical protein	3.07	12.31	3.66	0.46	5.34
SMc02313	684818	685302	-	684838	685302	hypothetical protein	5.68	2.74	0.05	0.36	0.08
SMc02319	689827	690035	-	689847	690035	hypothetical/unknown protein	6.22	2.07	0.9	0.78	1.39
SMc02354	2775866	2776733	+	2775918	2776733	conserved hypothetical protein	0.69	1.57	2.45	5.69	0.94
SMc02392	1145047	1145517	+	1145231	1145497	hypothetical protein	7.93	28.56	51.98	1.56	26.73
SMc02405	1157064	1157563	+	1157064	1157543	conserved hypothetical protein	8.37	0.65	10.8	1.52	4.67
SMc02407	1162858	1163549	-	1162858	1163436	conserved hypothetical protein	2.66	5.39	2.4	1.33	2.11
SMc02434	2817118	2817914	-	2817138	2817782	hypothetical protein	48.26	4.9	30.92	1.78	4.86
SMc02441	2825670	2826118	-	2825690	2826118	conserved hypothetical protein	6.03	2.53	1.32	3.45	2.56
SMc02552*	1208625	1208841	-	1208645	1208794	hypothetical/unknown protein	47.36	3.27	2.8	5.09	7.8
SMc02556	1206297	1206678	-	1206297	1206566	conserved hypothetical protein	1.96	8	0.93	1.13	2.02
SMc02564	54694	55210	+	54717	55190	conserved hypothetical protein	1.54	9.4	2.67	1.02	2.08
SMc02589	79804	81084	-	79804	81030	conserved hypothetical protein	0.94	1.5	4.07	0.44	5.68
SMc02642	1179035	1179564	+	1179230	1179544	hypothetical protein	2.9	5.08	0.3	2.94	5.05
SMc02656	1167314	1167512	+	1167340	1167492	hypothetical/unknown protein	6.87	0.56	0.05	3.89	0.22

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc02699	2547792	2548042	+	2547837	2548022	conserved hypothetical protein	0.48	10.93	0.57	1.05	3.27
SMc02727	2578361	2579421	+	2578415	2579401	hypothetical protein	0.55	6.93	0.27	1.45	3.15
SMc02732	2585353	2585805	-	2585373	2585777	conserved hypothetical protein	3.49	1.1	8.13	1.63	2.73
SMc02803	3643515	3644060	+	3643515	3644060	conserved hypothetical protein	1.39	0.46	6.75	0.78	1.76
SMc02845	194399	194883	+	194438	194863	Putative resistance protein	1.14	0.94	0.09	0.49	9.61
SMc02847	196034	196422	+	196034	196402	hypothetical protein	3.18	0.63	2.92	0.67	5.6
SMc02848	196549	197265	-	196569	197240	conserved hypothetical protein	1.04	5.8	3.04	0.2	1.08
SMc02860	214165	214858	-	214165	214800	hypothetical protein	2.91	4.09	2.19	2.69	9.88
SMc02906	262066	262456	+	262113	262436	conserved hypothetical protein	7.35	2.15	2.55	3.31	2.49
SMc03066	764395	764863	+	764433	764843	conserved hypothetical protein	2.57	0.14	5.81	0.16	0.32
SMc03093	3255763	3256388	-	3255783	3256262	conserved hypothetical protein	1.18	1.1	0.4	0.73	7.53
SMc03149	3178489	3179114	+	3178543	3179094	hypothetical protein	3.06	2.25	8.83	1.43	2.09
SMc03151	3109511	3110232	-	3109511	3110209	conserved hypothetical protein	8.61	0.42	1.21	0.57	0.33
SMc03249	3362726	3363037	-	3362726	3362983	hypothetical protein	4.15	6.3	10.8	6	3.96
SMc03251	3364872	3365953	-	3364892	3365899	hypothetical protein	2.76	0.1	5.47	3.25	1.14
SMc03288	3405993	3406387	+	3406047	3406367	hypothetical/unknown protein	4.15	1.05	9.2	3.33	3.45
SMc03289	3406781	3407037	-	3406801	3406983	hypothetical/unknown protein	0.8	13.81	0.3	0.33	1.67
SMc03766	3431997	3432818	-	3431997	3432764	hypothetical protein	14.52	1.32	11.15	4.14	2.37
SMc03787	3451917	3452260	-	3451917	3452228	hypothetical protein	0.47	0.29	0.4	0.73	6.05
SMc03790	3457313	3458298	-	3457313	3458266	conserved hypothetical protein	1.92	1.55	0.83	2.19	5.6
SMc03844	3509082	3509580	-	3509102	3509512	conserved hypothetical protein	1.27	6.89	1.04	2.22	1.8
SMc03852	3516889	3517502	-	3516909	3517502	hypothetical protein signal peptide	0.54	0.34	8.1	3.25	2.51
SMc03956	2948979	2950069	-	2948999	2950069	hypothetical signal peptide protein	5.14	4.46	6.16	2.53	1.65
SMc03988	2986144	2986352	+	2986144	2986332	hypothetical protein	20.38	10.07	42.4	14.67	22.72
SMc04000	2996764	2997122	+	2996919	2997122	hypothetical protein	10.02	2.46	12.42	1.83	4.64
SMc04010	3003664	3005650	-	3003684	3005501	hypothetical protein	3.8	5.91	2.96	2.17	8.73
SMc04043	3046813	3047832	-	3046833	3047714	conserved hypothetical protein	3	4.72	2.84	5.84	6.41
SMc04046	3051050	3051558	-	3051070	3051474	conserved hypothetical protein	3.11	8.17	0.35	4.29	1.17
SMc04053*	3056365	3056982	+	3056489	3056962	hypothetical protein	1.54	9.01	1.18	9.64	15.36
SMc04150	116592	117706	+	116646	117686	conserved hypothetical protein	0.8	38.52	1.92	0.8	2.31
SMc04152	114969	115574	+	114969	115574	hypothetical protein	1.56	26.58	0.9	1.5	1.22
SMc04161	2151304	2151794	-	2151324	2151794	conserved hypothetical protein	1.36	6.54	0.93	0.7	1.25
SMc04164	2153577	2153920	+	2153700	2153900	hypothetical protein	8.29	59.95	10.7	4.43	15.42

Table S3.- Cont.

CoIP-RNA[2]							Enrichment in CoIP-RNA				
Gene ID[1]	Start	Stop	S[3]	ORF start	ORF stop	Gene product	Hfq-log	Hfq-stat	Hfq-cold	Hfq-heat	Hfq-salt
SMc04177	2168048	2168544	-	2168068	2168529	hypothetical protein	1.75	1.99	8.55	3	5.63
SMc04188	2177171	2177570	+	2177209	2177550	conserved hypothetical protein	5.04	6.07	0.67	1	0.84
SMc04191	2178659	2179099	-	2178679	2179041	hypothetical protein	3.11	2.83	0.9	0.67	15.42
SMc04216	2044278	2044527	+	2044306	2044527	hypothetical protein	0.25	9.9	0.13	0.76	0.34
SMc04238*	2064679	2065059	+	2064803	2065039	conserved hypothetical protein	0.81	5.74	0.36	0.64	1.67
SMc04239	2065407	2065712	+	2065483	2065692	hypothetical protein	24.6	21.17	5.07	4.19	3.06
SMc04261	2090616	2091031	-	2090636	2091031	hypothetical protein	2.06	0.28	6.76	0.73	2.6
SMc04298*	2215328	2215596	+	2215382	2215576	hypothetical protein	1.1	78.79	0.5	11.19	5.93
SMc04299*	2215594	2217387	-	2215614	2217326	hypothetical protein	1.04	12.43	0.45	1.79	1.18
SMc04324	2227042	2227451	-	2227062	2227451	hypothetical protein	4.08	3.99	5.4	1.11	4.13
SMc04329	2138186	2138964	-	2138206	2138910	hypothetical protein	5.36	1.1	1.12	0.5	0.68
SMc05001	242774	243118	-	242774	243064	hypothetical protein	0.59	1.35	2.7	2	10.96
SMc05008	2312846	2313374	-	2312866	2313225	hypothetical signal peptide protein	4.75	28.79	4.98	5.59	21.82
VBISMc0802	662774	663307	+	662922	663287	hypothetical protein	5.01	0.72	9.93	1.33	2.91
VBISMc1000	815544	816023	+	815598	816023	hypothetical protein	1.06	0.46	5.1	0.43	4.35
VBISMc1492	1208828	1209144	-	1208848	1209090	hypothetical protein	35.6	5.51	7.4	11.33	22.72
VBISMc2174	1728061	1728376	-	1728081	1728221	hypothetical protein	1.05	1.12	1.06	1.27	6.01

[1]Genes belonging to the Hfq regulon (extracted from the literature) are shaded. Genes of the RpoE2 regulon are in red and the asterisk indicates those with RpoE2 promoter signatures. Genes depending on the Sin/ExpR quorum sensing system are in green. Genes belonging to both regulons are underlined.

[2] Coordinates of cDNA clusters acording to the MTU model and the annotation of the *S. meliloti* 1021 genome

[3]S, coding strand

PSBP, Periplasmic Solute-Binding Protein

Table S4. Bacterial strains and plasmids

Strain/Plasmid	Relevant characteristics	Reference
Bacteria		
S. meliloti		
Sm2B3001	*expR*$^+$ Sm2011 derivative; Nal^r Sm^r	76
SmpWsinI^{FLAG}	Sm2B3001 derivative expressing FLAG-tagged SinI	This work
Smhfq^{FLAG}	Sm2B3001 derivative expressing FLAG-tagged Hfq	This work
SmΔhfq	Sm2B3001 Δ*hfq* derivative	This work
1021ΔR1/2	AbcR1/2 double deletion mutant; Er^r, Sm^r	42
E. coli		
DH5α	F$^-$, ø80d*lacZ*ΔM15, Δ(*lacZYA-argF*)U169, *deo*R, *recA*1, *endA*1, *hsdR*17(rK$^-$, mK$^+$), *phoA*, *supE*44, λ–, *thi*-1, *gyrA*96, *relA*1	Bethesda Research Lab
HB101	*sup*E44, Δ(*mcrC-mrr*), *rec*A13, *ara*-14, *pro*A2, *lac*Y1, *gal*K2, *rps*L20, *xyl*-5, *mtl*- 1, *leu*B6, *thi*-1	Promega Corporation
Plasmids		
pSRKKm	pBBR1MCS-2 derivative with a P$_{lac}$ promoter, *lacIq*, *lacZa*+, Km^r	77
pSRKGm	pBBR1MCS-2 derivative with a P$_{lac}$ promoter, *lacIq*, *lacZa*+, Gm^r	77
pK18Hfq3xFlag	Suicide plasmid for Hfq tagging	29
pK18Δhfq	Suicide plasmid for *hfq* deletion	29
pSRK	Engineered pSRKKm lacking the LacIQ operator; Km^r	42
pSRK-R1	pSRK derivative constitutively expressing AbcR1	42
pSRK-R2	pSRK derivative constitutively expressing AbcR2	42
pR-EGFP	Reporter fusion plasmid for cloning of sRNA targets	42
pR*SMa0495::egfp*	pR-EGFP expressing the *SMa0495::egfp* translational fusion	This work
pR*prbA::egfp*	pR-EGFP expressing the *prbA::egfp* translational fusion	This work

Table S5. Oligonucleotide sequences

Name	Nucleotide sequence
sinI-NdeI-fwd	5'-CGCCATATGATCAGGATAGTGAACGGAAAC-3'
sinI-FX-rev*	5'-CGCTCTAGATCA<u>CTTGTCATCGTCATCCTTGTAATCGATATCGTGA TCCTTGTAATCACCATCGTGATCCTTGTAATC</u>GGCGGCGCGTGCCGTTTC-3'
TrueSeq_Sense_ primer	5'-AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCG ATCT-3'
TrueSeq Antisense NNNNNN primer Barcode	5'-CAAGCAGAAGACGGCATACGAGATNNNNNNGTGACTGGAGTTCAGACGTGTGC TCTTCCGATCTTTTTTTTTTTTTTTTTTTTTTTTT-3'
Smr7C probe	5'-GATGAGGCCTTTGTCCTCATCTGGT-3'
Smr9C probe	5'-CGCGTGATCTTTAATCCGTTTCCGG-3'
SmelC457 probe	5'-GAGCAGTTGAACTTCGGTTCCTCCG-3'
SmelB126 probe	5'-CCGCTAGTCGAAATTCTGAGGGAGA-3'
SmelB075 probe	5'-CGCGATCATTCCAACCGCAACGCAA-3'
SMc_Hfq_ncRNA_6 probe	5'-CCGAAAGTAGCGGAAAAGGGGAACA-3"
SMc_Hfq_asRNA_18 probe	5'-TGCCTATTACAAGGACCTCGCCGAC-3'
SMc01642_F	5'-GGATCCGAACAGCGCGGATAACGCGCAA-3'
SMc01642_R	5'-GCTAGCTTTGCCGAGCATGACCTGAC-3'
SMa0495_F	5'-GCTAGCCATTGCAACCGCCGACCCCA-3'
SMa0495_R	5'-GGATCCTAGAAGGCATCGAATTTCCA-3'

*The 3XFLAG sequence is underlined.

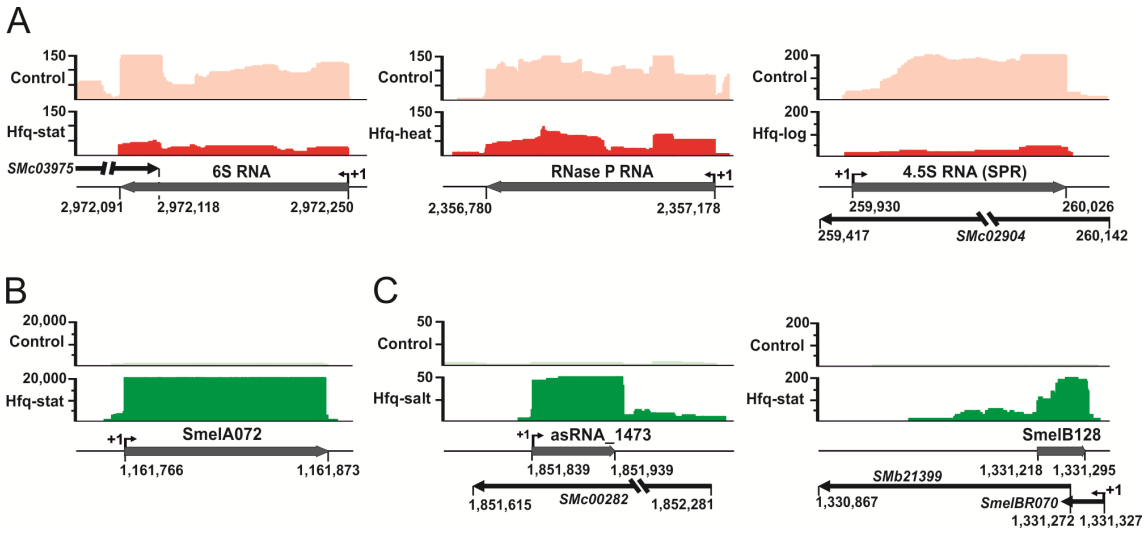

Figure S1. Additional examples of Hfq dependent and independent sRNAs. IGB plots and genomic information are as described in the legend to **Fig. 2**. (**A**) Housekeeping Hfq-independent sRNAs. (**B**) The Hfq-bound *trans*-sRNA SmelA072. (**C**) The Hfq-bound asRNAs SMc_Hfq_asRNA_1473 and SmelB128.

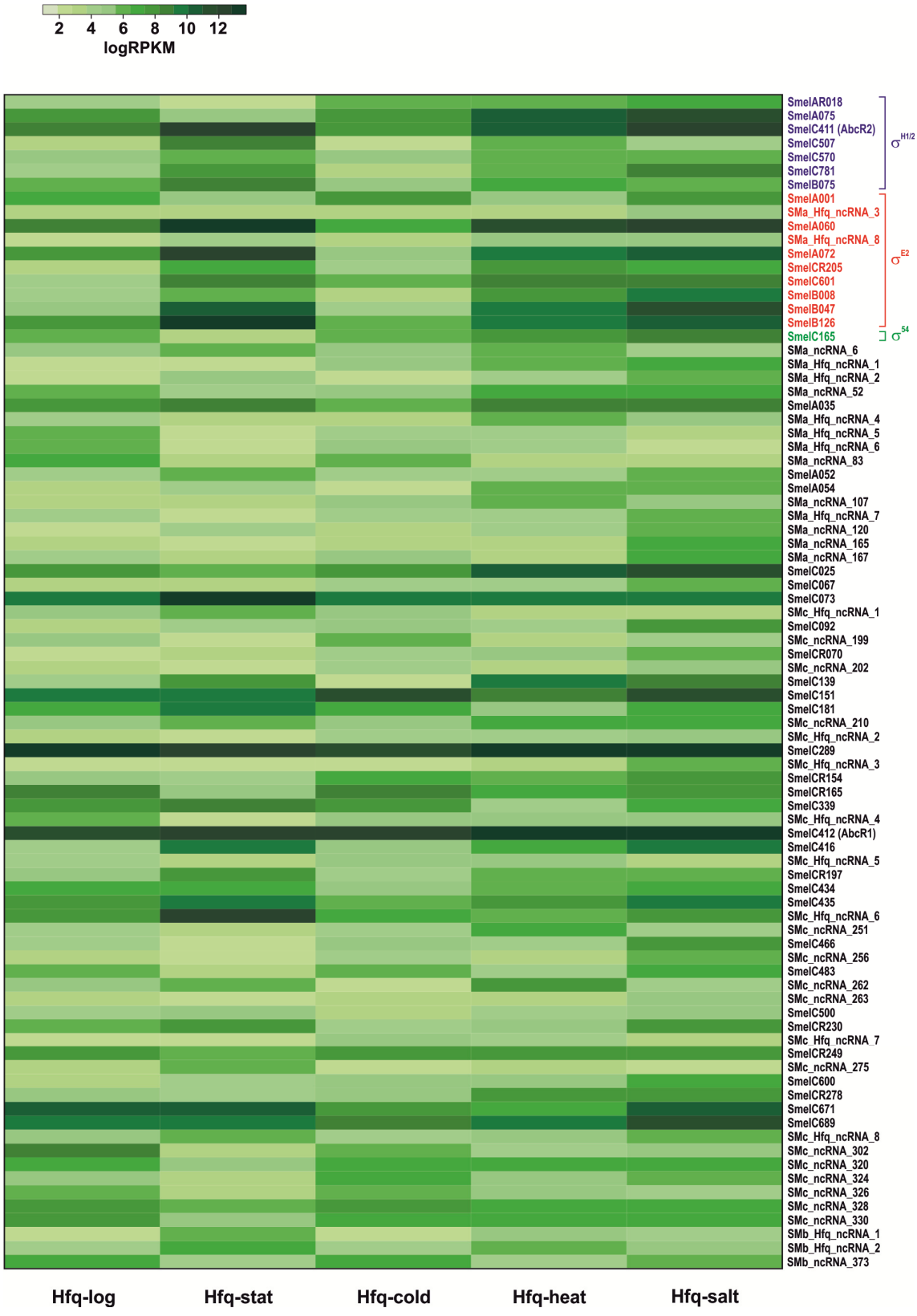

Figure S2. Recovery of the Hfq-bound *trans*-sRNAs in the five CoIP-RNA libraries. An RPKM value for each *trans*-sRNA was calculated from the raw read counts and plotted in a heat map according to the colour scale shown on top. sRNAs with predicted $\sigma^{H1/2}$, σ^{E2} and σ^{54} promoters are indicated.

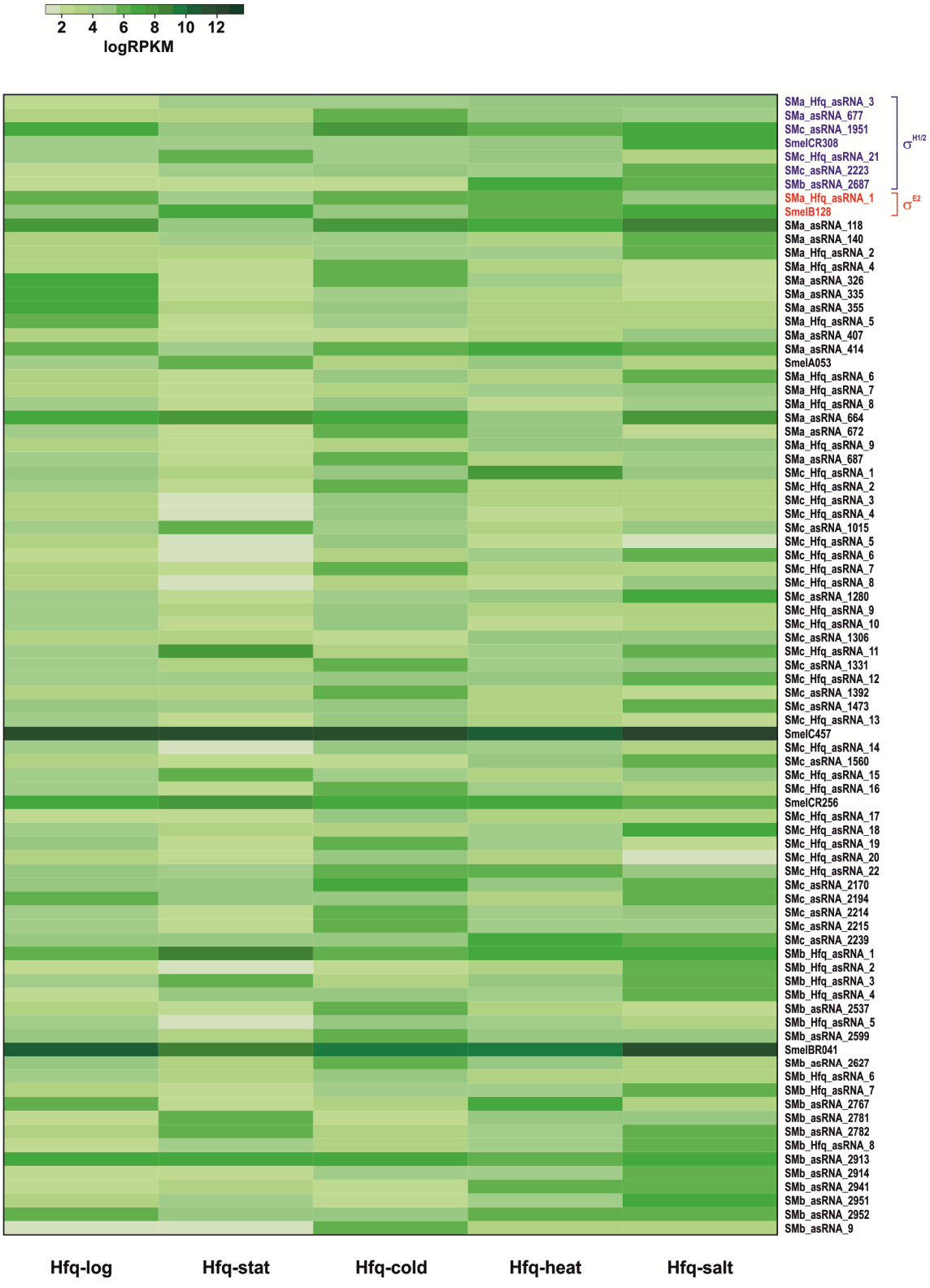

Figure S3. Recovery of the Hfq-bound asRNAs in the five CoIP-RNA libraries. An RPKM value for each asRNA was calculated from the raw read counts and plotted in a heat map according to the colour scale shown on top. sRNAs with predicted $\sigma^{H1/2}$, σ^{E2} and σ^{54} promoters are indicated.

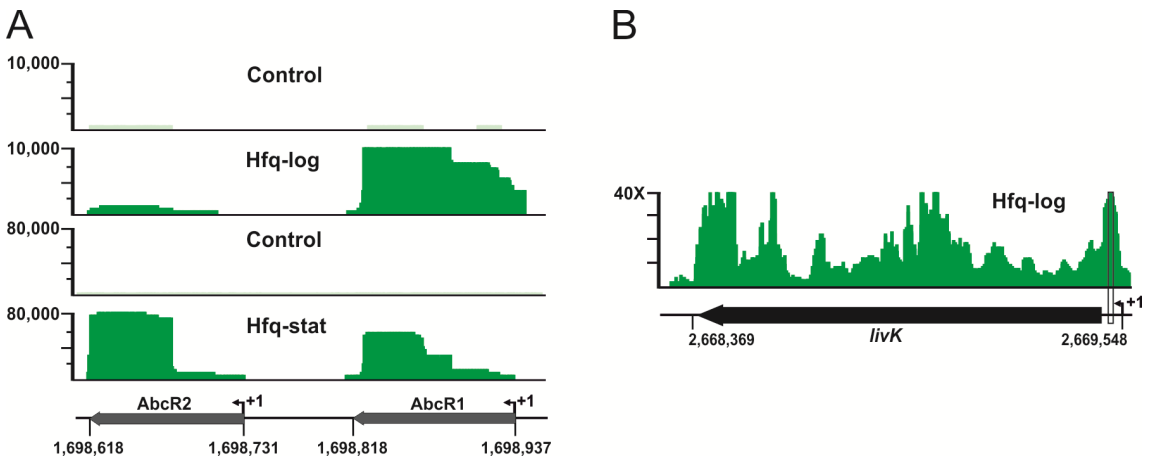

Figure S4. Enrichment of the AbcR1 and AbcR2 sRNAs (**A**) and the *livK* mRNA (**B**) in the indicated CoIP-RNA libraries. IGB plots and genomic information are as described in the legends to **Figs. 2** and **5**, respectively. The inset indicates the predicted interaction region of *livK* with AbcR1.