

Supplementary Information

Predicting Selective RNA Processing and Stabilization operons and their protein stoichiometry via genome sequence

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13 This file contains following materials:

14 1. Supplementary Figure.

15 2. Supplementary Tables.

Supplementary Figure

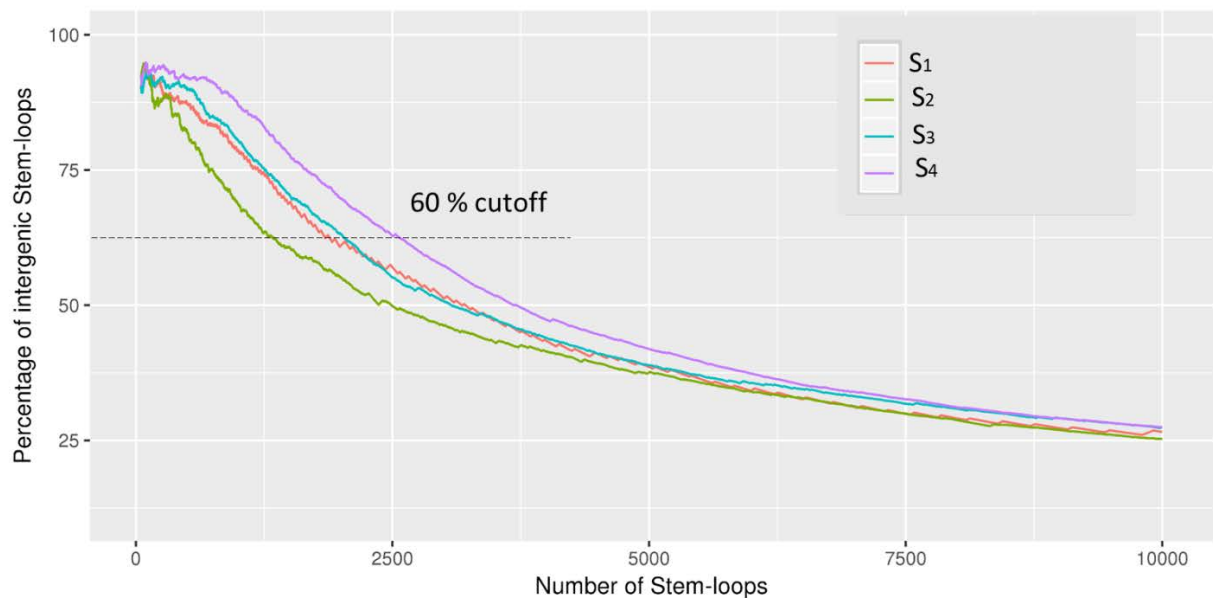


Figure S1: Selection of Stable stem-loops based on the four stability factors. Stable stem-loops were extracted from the millions of genome mapped stem-loops. Three stability factors for each stem-loop were calculated (**Materials and Methods**), and the stability factor which harbors the most number of intergenic stem-loops per 100 stem-loops was used with the 60% cutoff. Stability factor 4 (S₄) harbored the most number of intergenic stem-loops.

Supplementary Tables

Table S1. Bacterial genomes used in evaluating the SLOFE method.

Organism name	Genome size	RefSeq	Stable SLs	SRPS operons	Bi-cistronic operons
<i>Ruminiclostridium cellulolyticum</i> H10	4.07 mb	NC_011898.1	1441	53	11
<i>Clostridium acetobutylicum</i> ATCC 824	3.94 mb	NC_003030.1	2158	45	9
<i>Clostridium thermocellum</i> ATCC 27405	3.84 mb	NC_009012.1	1007	32	7
<i>Bacillus subtilis</i> Str. 168	4.22 mb	NC_000964.3	1829	42	11
<i>Escherichia coli</i> Str. K-12 substr. MG1655	4.64 mb	NC_000913.3	177	-	-


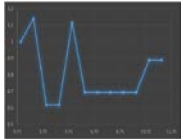
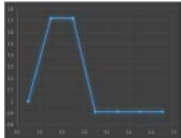


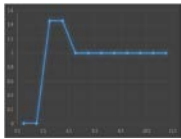
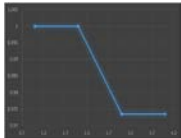
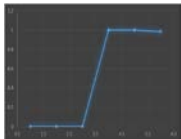
Table S2. Calculation of the normalized read-depth difference (NRD) for the predicted SRPS SLs in *Ccel*. The Normalized Read-depth Difference (NRD) data in cellulose, cellobiose and glucose carbon substrates from the dRNA-Seq study was used to calculate the difference in the read-depth of two neighboring genes flanked around the SLs. “Bi” denotes the bi-cistronic operon.

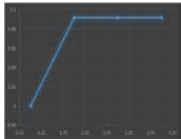
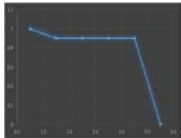
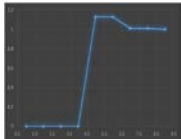
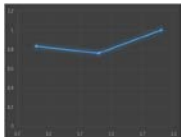
Stem-loop	Operon	ΔG	Cellulose			Cellobiose			Glucose			Max NRD	Remarks
			5' gene read-depth	3' gene read-depth	NRD	5' gene read-depth	3' gene read-depth	NRD	5' gene read-depth	3' gene read-depth	NRD		
SL_RS00005	1	-19.7	175	159	0.091429	2136	1695	0.206461	1429	874	0.388383	0.388383	non-SRPS
SL_RS00055	4-Bi	-18	221	183	0.171946	118	58	0.508475	94	57	0.393617	0.508475	SRPS
SL_RS00075	6	-14.1	17	49	-0.65306	140	84	0.4	181	100	0.447514	0.447514	non-SRPS
SL_RS00440	42	-18.4	656	17	0.974085	3094	74	0.976083	5422	268	0.950572	0.976083	SRPS
SL_RS00755	80	-23.2	795	90	0.886792	92	13	0.858696	130	43	0.669231	0.886792	SRPS
SL_RS01335	142	-25.2	967	132	0.863495	5526	1370	0.752081	6277	2499	0.60188	0.863495	SRPS
SL_RS01350	142	-14.7	430	168	0.609302	3505	1799	0.486733	8393	3972	0.526748	0.609302	SRPS
SL_RS01680	170-Bi	-16.2	147	1	0.993197	554	13	0.976534	850	19	0.977647	0.993197	SRPS
SL_RS01850	190	-15	34	59	-0.42372	205	307	-0.33224	197	446	-0.55829	-0.33224	non-SRPS
SL_RS02130	216	-24.4	-	-	-	-	-	-	-	-	-	0	-
SL_RS02230	228-Bi	-21.2	1858	1709	0.080194	16161	14943	0.075367	5538	5244	0.053088	0.080194	non-SRPS
SL_RS02395	237	-16.8	1326	1568	-0.15433	2192	1744	0.20438	4662	3320	0.287859	0.287859	non-SRPS
SL_RS02895	288	-19.9	-	-	-	-	-	-	-	-	-	0	-
SL_RS02990	295-Bi	-16.2	246	0	1	1043	8	0.99233	1393	13	0.990668	1	SRPS
SL_RS03180	314	-18.6	208	21	0.899038	733	41	0.944065	1036	226	0.781853	0.944065	SRPS
SL_RS03695	376	-23.5	24668	8503	0.655302	28656	14389	0.497871	3968	2052	0.482863	0.655302	SRPS
SL_RS03700	376	-26.8	85031	351	0.995872	14389	331	0.976996	2052	153	0.925439	0.995872	SRPS

SL_RS03710	376	-14.5	547	5705	-0.90411	550	4232	-0.8700	203	950	-0.78631	-0.78631	SRPS
SL_RS03715	376	-26.2	5705	50	0.991236	4232	100	0.976371	950	33	0.965263	0.991236	SRPS
SL_RS03740	376	-16.3	73	4	0.945205	133	6	0.954887	48	5	0.895833	0.954887	SRPS
SL_RS03930	391	-17.3	499	744	-0.32930	1296	1894	-0.31573	1652	2377	-0.30500	-0.30500	non-SRPS
SL_RS03960	391	-20.7	2725	130	0.952294	6440	578	0.910248	5536	993	0.820629	0.952294	SRPS
SL_RS04310	432-Bi	23.7	18	12	0.333333	116	42	0.637931	276	45	0.836957	0.836957	SRPS
SL_RS05015	495	-20	84	12	0.857143	26	8	0.692308	61	24	0.606557	0.857143	SRPS
SL_RS05150	511	-18.5	2721	133	0.951121	940	118	0.874468	122	32	0.737705	0.951121	SRPS
SL_RS05250	514	-26.1	880	394	0.552273	346	133	0.615607	77	54	0.298701	0.615607	SRPS
SL_RS05495	545	-22	260	3267	-0.92041	148	1093	-0.86459	67	1273	-0.94736	-0.86459	non-SRPS
SL_RS05655	566-Bi	-28.4	169	139	0.177515	814	503	0.382064	1194	681	0.429648	0.429648	non-SRPS
SL_RS05685	569	-17.9	2045	128	0.937408	94	3	0.968085	72	14	0.805556	0.968085	SRPS
SL_RS06165	617	-16.6	7	4	0.428571	39	11	0.717949	83	80	0.036145	0.717949	SRPS
SL_RS06175	617	-14.4	28	5	0.821429	48	42	0.125	84	80	0.047619	0.821429	SRPS
SL_RS06180	617	-18.4	5	3	0.4	42	15	0.642857	80	34	0.575	0.642857	SRPS
SL_RS06215	617	-24.7	7	3	0.571429	19	19	0	71	103	-0.31067	0.571429	SRPS
SL_RS06275	622	-18.2	62	7	0.887097	175	9	0.948571	147	16	0.891156	0.948571	SRPS
SL_RS06525	632	-16.8	-	-	-	-	-	-	-	-	-	0	-
SL_RS07065	693	-16.7	55	14	0.745455	421	261	0.380048	940	246	0.738298	0.745455	SRPS
SL_RS07075	693	-28.7	450	10	0.977778	4738	248	0.947657	878	111	0.873576	0.977778	SRPS
SL_RS07235	716	-19.6	93	10	0.892473	436	44	0.899083	870	131	0.849425	0.899083	SRPS
SL_RS07520	746	-24	3253	650	0.800184	1729	357	0.793522	2562	764	0.701795	0.800184	SRPS
SL_RS07530	746	-17.8	546	183	0.664835	247	100	0.595142	271	182	0.328413	0.664835	SRPS
SL_RS08285	813	-20.3	16	2	0.875	104	26	0.75	61	21	0.655738	0.875	SRPS
SL_RS08610	849-Bi	-28	279	105	0.623656	1481	636	0.57056	4551	1413	0.689519	0.689519	SRPS

SL_RS08720	863	-19.7	2136	36	0.983146	6982	197	0.971785	5963	226	0.9621	0.983146	SRPS
SL_RS09085	898	-15.5	1879	129	0.931346	41895	1795	0.957155	19769	759	0.961607	0.961607	SRPS
SL_RS09255	915	-16.2	41	3	0.926829	339	25	0.926254	417	51	0.877698	0.926829	SRPS
SL_RS10060	1000	-16.7	6219	223	0.964142	18300	2367	0.870656	24934	4374	0.824577	0.964142	SRPS
SL_RS10050	1000	-26.3	430	24	0.944186	2589	248	0.90421	4609	287	0.937731	0.944186	SRPS
SL_RS10295	1018	-15.4	139	214	-0.35046	440	649	-0.32203	580	786	-0.26208	-0.26208	non-SRPS
SL_RS10685	1052	-20	41638	1242	0.970171	79521	8757	0.889878	1191	54	0.95466	0.970171	SRPS
SL_RS10675	1052	-16.8	1599	2026	-0.21076	8982	17873	-0.49745	71	199	-0.64321	-0.21076	SRPS
SL_RS10860	1073	-16.2	-	-	-	-	-	-	-	-	-	0	-
SL_RS11420	1135-Bi	-17.9	1528	238	0.844241	5991	910	0.848105	4475	1483	0.668603	0.848105	SRPS
SL_RS12550	1247	-18	38	18	0.526316	77	7	0.909091	215	59	0.725581	0.909091	SRPS
SL_RS12610	1254-Bi	-27	304	293	0.036184	537	1081	-0.50323	955	615	0.356021	0.356021	non-SRPS
SL_RS13360	1341-Bi	-22.4	62	11	0.822581	73	6	0.917808	393	28	0.928753	0.928753	SRPS
SL_RS13485	1354	-35.4	230	147	0.36087	481	467	0.029106	446	952	-0.53151	0.36087	non-SRPS
SL_RS13510	1358-Bi	-16.2	3	0	1	5	1	0.8	16	6	0.625	1	SRPS
SL_RS13525	1359-Bi	-27.5	105	4	0.961905	178	6	0.966292	307	8	0.973941	0.973941	SRPS
SL_RS13720	1382	-23	-	-	-	13	29	-0.55172	24	43	-0.44186	-0.44186	non-SRPS
SL_RS14235	1435	-23.3	-	-	-	-	-	-	-	-	-	0	-
SL_RS14390	1445	-18.4	-	-	-	-	-	-	-	-	-	0	-
SL_RS14525	1466-Bi	-16.2	-	-	-	139	1	0.992806	259	2	0.992278	0.992806	SRPS
SL_RS14630	1477-Bi	-16.7	13	39	-0.66666	123	39	0.682927	105	26	0.752381	0.752381	SRPS
SL_RS15510	1560	-18.4	161	74	0.540373	669	389	0.418535	686	477	0.304665	0.540373	SRPS
SL_RS15870	1600	-25.9	-	-	-	-	-	-	-	-	-	0	-
SL_RS17245	1745	-18.6	889	1962	-0.54689	4635	5332	-0.13072	6528	8018	-0.18583	-0.13072	SRPS

Table S3. Correlation between SLOFE-predicted transcript ratio and those experimentally measured for selected operons from *Ccel*, *Cace*, *Cthe* and *Bsub*. These operons have skewed transcript ratios as predicted by SLOFE.

Operon ID	Organism	Predicted ratio	Correlation with transcript	Plot	Annotation
142	<i>Clostridium cellulolyticum</i>	1.00:1.00:0.58:0.58:0.58:0.62:0.62:0.62	0.698		ATP synthase
376	<i>Clostridium cellulolyticum</i>	1.00:1.14:0.62:0.62:1.11:0.69:0.69:0.69:0.69:0.69:0.88:0.88	0.751		Cellulosome
693	<i>Clostridium cellulolyticum</i>	1.00:1.72:1.72:0.91:0.91:0.91:0.91	0.556		ABC transporter
1000	<i>Clostridium cellulolyticum</i>	0:0:0:1.00:1.00:1.26	0.940		Two-component system
593	<i>Clostridium acetobutylicum</i>	1.00:1.00:0.53:0.53:0.53:0.53:0.53:0.53:0.53:0.53:0.82	0.701		Cellulosome
1068	<i>Clostridium acetobutylicum</i>	0:0:1.45:1.45:1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00	0.672		Cell division protein and lipoprotein
482	<i>Clostridium thermocellum</i>	1.00:1.00:0.97:0.97	0.672		Amino acid-binding protein
1135	<i>Clostridium thermocellum</i>	0:0:0:1.00:1.00:0.98	0.460		Restriction endonuclease Protein

531	<i>Clostridium thermocellum</i>	1.00:1.09:1.09:1.09	0.802		Magnesium chelata
679	<i>Bacillus subtilis</i>	1.00:0.90:0.90:0.90:0.90:0	0.773		ABC transporter
1491	<i>Bacillus subtilis</i>	0:0:0:0:1.12:1.12:1.01:1.0 1:1.00	0.762		Chaperone protein
1513	<i>Bacillus Subtilis</i>	0.8318:0.75:1.00	0.980		Mother cell lysis

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Table S4. SLOFE-predicted ratios of the SRPS operons from *Ccel* (A), *Cthe* (B), *Cace* (C) and *Bsub* (D). SLOFE predicted ratios for all the SRPS operons using ΔG of SLs.

(A) SLOFE-predicted ratios of the SRPS operons from *Ccel*.

# Operon	# of genes	Ratio
1	4	1.00:0:0:0
4	2	1.00:0.89
6	3	1.00:1.00:1.354
42	9	1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00:0
80	4	1.00:0.94:0.94:0.94
142	8	1.00:1.00:0.58:0.58:0.58:0.62:0.62:0.62
170	2	1.00:0.96
190	4	1.00:1.00:1.5:1.5
216	3	1.00:0:0
228	2	1.00:0.91
237	3	1.00: 1.00:0
288	5	1.00:0:0:0:0
295	2	1.00:0.85
314	3	1.00:0.989:0.989
376	12	1.00:1.14:0.62:0.62:1.11:0.69:0.69:0.69:0.69:0.69:0.88:0.88
391	24	1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.2:1.2:1.2:1.2:1.2:1.2:0:0
432	2	1.00: 1.00
495	3	1.00:0.805:0.805
511	9	1.00:0:0:0:0:0:0:0:0
514	11	1.00:1.00:1.00:1.00:1.00:1.00:1.00:0.74:0.74:0.74:0.74
545	3	1.00: 1.00:0.95
566	2	1.00:0:0
569	3	1.00:0:0
617	14	1.00:1.00:0.86:0.86:0.97:1.48:1.48:1.48:1.48:1.48:1.48:1.48:0:0
622	4	1.00:1.00:1.00:0
693	6	1.00:1.72:1.72:0.91:0.91:0.91:0.91
716	3	1.00:0:0
746	6	1.00:0.74:0.74:0.78:0.78:0.78
813	7	1.00:1.00:1.00:1.00:1.17:1.17:1.17

849	2	0:1.00
863	5	0.845:1.00:1.00:1.00:1.00
898	7	0:0:0:0:1.00:1.00:1.00
915	2	1.00:0:0
1000	6	0.8859:0.8859:0.8859:1.00:1.00:1.26
1018	13	0:0:0:0:0:0:0:1.00:1.00:1.00:1.00:1.00:1.00:1.00
1052	4	0.84:0.64: 1.00
1073	3	1.00: 1.00:0.96
1135	2	0:1.00
1247	3	1.00:0:0
1254	2	0:1.00
1341	2	1.60:1.00
1354	3	0.5649:0.5649:1.00
1358	2	1.00:0.96
1359	2	0.57:1.00
1382	7	0:0:1.00:1.00:1.00:1.00:1.00
1435	16	0:0:0:0:0:0:0:1.00: 1.00: 1.00: 1.00: 1.00: 1.00: 1.00: 1.00
1445	5	1.59:1.59: 1.00: 1.00: 1.00
1466	2	1.00:0.96
1477	2	1.00:0.76
1560	3	0.56: 1.00: 1.00
1600	5	0: 1.00: 1.00: 1.00: 1.00
1745	4	1.00:0.658:0.658:0.658

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39 **(B)** SLOFE-predicted ratios of the SRPS operons from *Cthe*.

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# operon	# of genes	Ratio
275	5	1:1:1:0.77:0.77
357	3	1:1:0.96
482	4	1:1:0.97:0.97
531	4	1:1.09:1.09:1.09
548	7	1:1:1:1:1:1:1.33
552	4	1:1:1:0.74
728	3	0:0:1
747	3	1:1:0.46
791	5	1:1:0.99:0.99:0.99

794	5	0:0:1:1:1
804	23	0:1:1:1:1:1:1:1:0.74:0.74:0.74:0.65:0.65:0.98:0.98:0.98:0.98:0.98:0.98:0.74:0.74:0.74
806	7	0:0:0:0:1:1:1
938	3	0:0:1
957	8	0:0:0:0:1:1:1:1
1135	6	0:0:0:1:1:0.98
1209	3	0:0:1
1228	5	1:1:1:0:0
1353	5	1:1:1:0:0
1359	4	1:1:1:0.82
1395	8	1:1:1:0.97:0.97:0.97:0.97:0.97
1465	3	1:1:0.65
1487	6	1:0.93:0.93:0.93:0.93:0.93
1522	3	1:1.52:1.52
1536	6	1:1:1:0:0:0

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42 (C) SLOFE-predicted ratios of the SRPS operons from *Cace*.

# operon	# of genes	Ratio
120	5	1.00:1.00:1.21:1.21:0
205	6	1.00:1.00:0:0:0:0
216	2	1.00:0.58
239	5	1.00:1.00:1.00:0.77:0.77
244	10	1.00:1.00:1.00:1.00:1.00:0.83:0.83:0.83:0.83:0.83
304	7	1.00:0.90:0.90:1.14:1.14:1.14:0
317	2	1.00:0.48
356	3	1.00:1.00:1.36
362	6	1.00:1.00:1.29:1.29:1.29:1.29
401	3	1.00:1.20:1.20
466	2	1.00:1.39
481	4	1.00:0.89:1.24:0
593	9	1.00:1.00:0.53:0.53:0.53:0.53:0.53:0.53:0.53:0.82
614	2	1.00:1.12
633	2	1.00:0:0
635	3	1.00:1.00:0.80

673	2	1.00:1.24
715	8	1.00:1.00:1.00:1.00:1.00:1.00:0:0
730	10	1.00:1.7:1.7:1.7:1.7:1.7:1.7:1.7:1.7
738	5	1.00:1.13:1.03:1.03:1.03
789	6	1.00:1.00:1.10:1.10:1.10:1.10
849	3	0:0:1.00
909	11	1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00:0:0
910	2	0:1.00
943	2	1.00:0:0
944	17	1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00: 1.20
949	9	1.00:1.00:1.00:1.00:1.02:1.02:1.20:1.20:0.89
965	11	1.00:0.74:0.74:0.74:0.74:0.74:0.74:0.84:0.84:0.84:0.84
967	7	1.00:1.00:1.00:1.00:0:0:0
981	2	1.00:0.57
986	4	0:1.00:1.00:1.00
1008	26	1.00:1.16:1.16:1.16:1.16:1.16:1.16:1.16:1.16:1.16:1.16:1.16:1.14:1.14:1.14: 1.14:1.14:1.14:1.14:1.14:1.14:1.14:1.14:1.14
1068	12	0:0:1.45:1.45:1.00:1.00:1.00:1.00:1.00:1.00:1.00:1.00
1090	6	0:1.02:1.21:1.21:1.38:1.00
1132	4	0:0:1.52:1.31
1248	9	0:0:1.00:1.00:1.00:1.00:1.00:1.00
1283	6	0:1.17:1.17:1.17:1.00:1.00
1336	3	1.00:1.00:1.08
1359	2	1.00:1.35
1362	2	1.00:1.01
1412	2	1.00:0:0
1454	5	1.00:1.09:1.09:0.82:0.82
1519	35	1.00:1.00:1.00:1.00:0.92:0.92:0.92:0.92:0.92:0.92:0.92:0.92:0.92:0.92:0.92: 0.92:0.92:0.92:0.92:0.92:0.92:0.92:0.92:0.92:0.92:0.92:0.92:1.03:1.03: 1.03:1.03:1.03
1522	4	0:0:1.00:1.00
1537	5	1.00:1.05:1.05:1.05:1.05
1553	9	0:0:0:0:0.66:0.78:0.78:0.78:1.00
1566	4	1.00:1.00:1.29:1.29
1684	3	1.00:1.00:0.75

1850	7	0:0.84:0.84:0.84:0.84:0.84:1.00
1894	5	0:0:0:0:1.00
1952	3	1.00:1.24:1.24
1956	4	0:0:0:1.00
1976	6	1.00:1.00:1.00:1.00:1.05:1.05
1990	13	1.00:1.00:1.00:1.00:1.00:0.80:0.80:0.80:0.80:0.92:0.92:0.92:0.92
2016	8	0:0:0:0:0:0:1.00:1.00
2030	3	1.00:2.11:2.11
2279	8	1.00:1.00:1.00:1.00:1.00:0.64
2358	3	0:1.00:1.00
2363	4	0:0:0:1.00

Table S5. Pearson correlation coefficients between predicted ratio and experimentally measured ratio for the SRPS operons of *Ccel*, for each of the six methods (CAI, RCA, RCBS, MELP, Gene-order and SLOFE). Correlations with the experimentally measured abundance of transcripts (A) and proteins (B) were both shown.

(A) Correlations with the experimentally measured abundance of transcripts.

#Operon	# of gene	CAI	MELP	RCBS	RCA	Gene-order	SLOFE
1	4	0.164	0.060	-0.221	0.441	0.726	0.488
6	3	0.863	-0.945	0.916	0.028	-0.341	0.914
42	9	0.121	-0.465	-0.547	0.042	0.496	0.676
80	4	0.901	0.546	0.930	0.845	0.892	0.975
142	8	0.817	-0.682	0.555	0.804	0.349	0.714
190	4	-0.261	-0.826	-0.274	0.768	0.387	0.166
237	3	0.168	-0.894	-0.711	-0.415	-0.360	0.423
376	12	0.667	0.472	0.508	0.565	0.820	0.752
391	24	0.159	0.226	-0.271	0.288	0.070	0.579
511	9	0.591	-0.439	0.519	0.533	0.813	0.901
514	11	-0.368	-0.522	-0.770	-0.132	0.342	0.412
545	3	0.953	0.826	-0.962	0.232	-0.091	-0.780
569	3	0.698	0.017	0.258	0.288	1.000	0.969
617	14	-0.184	-0.201	-0.321	-0.335	-0.513	0.036
622	4	0.768	0.312	0.510	0.620	-0.410	0.525
693	6	0.615	0.182	0.182	0.294	0.228	0.381
716	3	-0.264	0.672	-0.697	0.807	0.925	0.989
746	6	-0.157	-0.318	-0.449	-0.285	0.916	0.737
813	7	0.240	-0.297	0.151	0.583	0.045	0.232
863	5	-0.040	-0.421	-0.357	0.334	-0.166	0.547

898	7	0.806	-0.054	0.049	0.808	0.414	0.857
1000	6	0.973	0.539	0.884	0.931	0.926	0.972
1018	13	0.367	0.443	-0.165	0.128	0.375	0.400
1052	4	0.974	0.639	0.765	0.735	0.906	0.040
1247	3	0.998	0.159	0.652	0.977	-0.194	0.194
1354	3	-0.882	0.349	0.699	-0.829	0.612	0.784
1382	7	0.276	0.375	-0.929	0.750	0.670	0.886
1560	3	0.985	0.246	0.182	0.910	0.472	0.962
1745	4	0.249	-1.000	-0.924	-0.395	0.860	0.638
314	3	-0.915	-0.914	-0.991	-0.994	0.666	0.826
495	3	0.995	-0.388	0.967	0.999	0.992	0.993
Average		0.364	-0.074	0.004	0.333	0.414	0.587

(B) Correlations with the experimentally measured abundance of proteins. Dash (-) denotes no data available.

#	# of gene	CAI	MELP	RCBS	RCA	Gene-order	SLOFE
1	4	0.547	0.534	-0.659	-0.715	0.748	0.524
6	3	-	-	-	-	-	-
42	9	0.328	-0.361	-0.284	0.403	0.282	0.983
80	4	0.971	0.705	0.966	0.940	0.951	1.000
142	8	0.092	-0.439	-0.138	-0.115	0.178	0.060
190	4	0.531	0.420	0.242	-0.199	-0.903	0.507
237	3	-0.610	-0.278	0.035	0.388	0.442	0.953
363	3	0.734	-0.475	-0.515	0.987	0.971	1.000
376	12	0.584	0.771	0.419	0.322	0.576	0.283
391	24	-0.052	0.216	-0.168	0.146	0.236	0.076
511	9	-	-	-	-	-	-
514	11	-0.555	-0.352	-0.818	-0.138	0.405	0.822

545	3	0.444	0.683	-0.417	0.997	0.971	0.500
569	3	0.853	0.228	-0.012	0.515	0.971	1.000
617	14	-	-	-	-	-	-
622	4	-	-	-	-	-	-
693	6	0.292	0.634	0.624	-0.022	0.653	0.484
716	3	-0.118	-0.555	-0.583	0.885	0.971	1.000
746	6	0.185	-0.200	-0.516	-0.038	0.339	0.096
813	7	-0.189	-0.536	-0.214	0.170	0.743	1.000
863	5	0.306	-0.548	-0.514	0.505	-0.379	0.145
898	7	-0.008	-0.770	-0.659	0.482	0.475	0.626
1000	6	0.704	0.318	0.520	0.541	0.890	0.925
1018	13	0.382	0.392	0.401	-0.030	0.740	0.712
1052	4	0.957	0.391	0.568	0.528	0.791	0.333
1247	3	-	-	-	-	-	-
1354	3	-	-	-	-	-	-
1382	7	-	-	-	-	-	-
1560	3	0.995	0.500	-0.092	0.763	0.693	1.000
1745	4	0.764	-0.541	-0.162	0.529	-0.669	0.262
Average		0.354	0.032	-0.086	0.341	0.482	0.621

Table S6. Pearson correlation coefficients between predicted ratio and experimentally measured ratio for the SRPS operons of *Cthe*, for each of the six methods (CAI, RCA, RCBS, MELP, Gene-order and SLOFE). Correlations with the experimentally measured abundance of transcripts were shown.

#	#of genes	CAI	MELP	RCBS	RCA	Gene-order	SLOFE
357	3	-0.818	-0.157	-0.018	-0.684	0.682	0.037
531	4	-0.423	-0.764	0.073	0.522	-0.832	0.803
548	7	0.127	-0.192	0.248	0.360	0.727	0.601
552	4	0.787	0.418	0.392	-0.532	-0.312	0.467
728	3	-0.582	-0.986	-0.612	-0.301	0.167	-0.075
747	3	-0.855	-0.515	-0.250	0.394	-0.780	0.907
791	5	0.219	-0.367	-0.234	0.216	0.053	-0.094
794	5	0.210	-0.109	0.634	0.307	0.798	0.711
804	23	-0.087	0.281	0.051	0.406	-0.366	0.171
806	7	-0.293	-0.441	-0.330	-0.248	-0.343	-0.359
938	3	-0.783	0.197	0.921	0.788	1.000	0.977
957	8	-0.059	0.147	0.392	-0.467	0.050	0.408
1135	6	-0.702	-0.527	-0.364	0.177	0.186	0.461
1209	3	0.999	0.019	0.283	0.648	-0.739	-0.556
1228	5	0.255	-0.824	-0.053	0.505	0.070	-0.021
1359	4	0.630	0.987	0.467	-0.291	0.300	-0.527
1395	8	-0.007	0.311	-0.132	-0.307	-0.890	0.886
1465	3	0.859	-0.900	-0.941	0.900	0.104	0.789
1487	6	0.035	0.161	0.118	0.157	0.587	0.387
1536	6	-0.193	0.308	0.002	-0.422	0.424	0.873
Average		-0.034	-0.148	0.032	0.106	0.044	0.342

Table S7. Pearson correlation coefficients between predicted ratio and experimentally measured ratio for the SRPS operons of *Cace*, for each of the six methods (CAI, RCA, RCBS, MELP, Gene-order and SLOFE). Correlations with the experimentally measured abundance of transcripts were shown.

#	#of genes	CAI	MELP	RCBS	RCA	Gene-order	SLOFE
205	6	0.367	-0.377	-0.566	-0.555	0.658	0.742
239	5	-0.217	-0.793	-0.487	0.376	0.639	0.970
304	7	0.271	-0.508	-0.420	-0.496	-0.451	0.101
356	3	0.277	0.146	0.396	0.894	-0.982	0.816
362	6	0.777	-0.352	-0.077	-0.132	-0.749	0.740
401	3	0.457	-1.000	-0.489	-0.010	-0.692	0.498
481	4	0.687	0.739	0.791	0.381	-0.998	-0.459
593	9	0.190	-0.327	0.039	-0.300	0.484	0.702
635	3	-0.511	-0.923	-0.979	0.409	0.907	0.932
715	8	-0.202	-0.617	-0.216	-0.031	-0.405	0.153
730	10	0.090	0.080	-0.684	-0.393	-0.877	0.615
738	5	-0.579	-0.069	-0.311	-0.109	0.076	0.923
849	3	0.904	-1.000	0.595	0.594	0.916	0.793
909	11	0.281	-0.179	-0.272	-0.184	-0.490	0.214
965	11	0.700	0.543	0.324	-0.617	0.590	0.224
967	7	0.677	-0.417	-0.466	0.048	0.876	0.464
1008	26	-0.269	0.589	-0.194	0.312	0.197	-0.019
1090	6	0.406	0.045	0.412	0.694	-0.155	0.191
1132	4	0.058	0.970	0.459	-0.718	0.721	0.331
1248	9	-0.238	0.308	0.111	-0.690	-0.173	0.217
1283	6	0.372	0.411	0.314	0.090	-0.651	-0.545
1336	3	0.998	-0.931	0.073	0.961	0.083	0.320
1454	5	-0.119	-0.217	-0.309	-0.890	-0.228	0.046
1519	35	0.220	0.161	0.213	0.219	-0.098	-0.451

1522	4	0.116	-0.252	-0.656	0.687	-0.776	0.598
1537	5	-0.220	-0.518	0.030	0.439	-0.167	0.117
1553	9	0.431	0.497	0.304	-0.678	-0.553	-0.199
1566	4	0.396	-0.159	0.047	0.462	-0.678	-0.166
1684	3	0.774	0.308	0.453	-0.358	-0.833	-0.179
1793	5	-0.180	-0.238	-0.315	0.073	0.040	0.106
Average		0.23048	-0.136	-0.0627	0.01606	-0.1256	0.2931

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Table S8. Pearson correlation coefficients between predicted ratio and experimentally measured ratio for the SRPS operons of *Bsub*, for each of the six methods (CAI, RCA, RCBS, MELP, Gene-order and SLOFE). Correlations with the experimentally measured abundance of transcripts (A) and proteins (B) were both shown.

(A) Correlations with the experimentally measured abundance of transcripts.

#	#of genes	CAI	MELP	RCBS	RCA	Gene-order	SLOFE
40	6	0.524	-0.435	-0.299	0.283	-0.356	0.325
47	7	0.094	-0.459	0.007	0.320	-0.027	0.800
49	31	0.077	-0.447	-0.586	0.077	0.064	0.011
130	3	0.848	-0.870	0.997	0.999	0.998	0.985
200	4	-0.814	-0.331	-0.208	0.171	0.334	0.725
361	12	0.678	-0.779	-0.582	0.695	-0.289	0.157
394	4	-0.488	-0.411	-0.045	0.042	0.958	0.975
406	3	0.263	0.227	0.806	0.622	-0.791	0.636
460	3	-0.913	-0.900	-0.999	-0.723	0.614	0.786
679	6	0.014	0.061	0.697	0.037	0.865	0.773
744	10	0.239	-0.553	-0.251	0.095	0.430	0.538
836	5	0.657	0.969	0.467	0.715	-0.635	0.904
925	11	-0.129	0.046	0.318	0.117	-0.706	-0.114
934	6	0.887	0.182	0.060	0.244	-0.124	0.353
961	11	0.482	-0.450	0.022	-0.233	-0.608	-0.378
964	3	-0.346	0.475	0.154	0.110	0.758	0.892
1513	3	0.695	-0.901	-0.878	0.903	0.739	0.980
1672	4	-0.170	0.573	0.448	-0.485	0.511	0.991
1693	3	0.934	0.970	0.780	-0.737	0.953	0.998
1850	7	-0.403	-0.772	-0.484	0.209	0.083	0.392
1894	5	-0.211	-0.886	-0.685	-0.364	0.934	0.759
1952	3	-0.985	-1.000	-0.928	0.437	-0.884	-0.950

1956	4	0.840	-0.860	-0.613	0.502	0.947	0.934
1976	6	0.685	0.766	0.693	-0.522	-0.755	-0.389
1990	13	-0.411	-0.600	-0.632	-0.301	0.389	0.322
2363	4	-0.921	-0.992	-0.442	-0.738	-0.570	-0.349
Average		0.082	-0.284	-0.084	0.095	0.147	0.464

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72 **(B)** Correlations with the experimentally measured abundance of proteins.

#	#of genes	CAI	MELP	RCBS	RCA	Gene-order	SLOFE
40	6	0.643	-0.331	-0.170	0.402	-0.252	0.336
47	7	-0.900	0.061	0.516	-0.843	-0.567	0.933
49	31	0.177	0.230	0.405	0.057	0.009	0.450
130	3	0.804	-0.906	0.988	0.999	0.989	0.996
200	4	0.642	0.984	0.901	0.266	-0.346	0.353
361	12	-0.339	-0.172	0.554	-0.606	-0.140	0.140
394	4	-0.330	-0.630	-0.304	-0.373	0.630	0.833
406	3	0.983	-0.779	-0.184	0.975	0.208	-0.419
460	3	0.785	0.804	0.426	-0.276	0.414	0.183
679	6	-0.146	-0.267	0.485	-0.319	0.949	0.370
744	10	-0.169	0.166	-0.401	-0.468	-0.240	-0.074
836	5	0.866	0.181	0.980	-0.119	-0.478	0.659
925	11	0.716	-0.326	-0.257	-0.239	-0.127	0.320
934	6	0.857	0.312	0.237	0.422	-0.367	0.509
961	11	0.685	-0.412	-0.384	0.155	0.550	0.516
964	3	-0.270	0.544	0.232	-0.021	0.704	0.854
1513		-0.857	0.982	0.724	-0.983	-0.539	-0.896
1672	4	-0.280	0.780	0.723	-0.850	-0.105	0.757
1693	3	0.972	0.932	0.853	-0.647	0.983	0.998

1850	7	0.539	-0.966	0.577	-0.359	0.914	0.370
1894	5	-0.185	-0.822	-0.786	-0.512	0.949	0.851
1952	3	0.447	1.000	0.623	-0.987	-0.195	0.572
1956	4	0.794	-0.907	-0.980	-0.028	0.596	0.334
1976	6	0.719	0.766	0.934	-0.828	-0.251	0.241
1990	13	0.302	0.304	0.154	-0.210	-0.214	0.136
2363	4	0.287	-0.106	0.990	-0.179	0.957	0.996
Average		0.298	0.055	0.301	-0.214	0.194	0.435

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Table S9. Pearson correlation coefficients between predicted ratio and experimentally measured ratio for the bicistronic SRPS operons of *Ccel* (A), *Bsub* (B), *Cthe* (C), *Cace* (D) for each of the six methods (CAI, RCA, RCBS, MELP, Gene-order and SLOFE). Correlations with the experimentally measured abundance of transcripts and proteins were both shown for those SRPS operons where transcript and protein data are available, e.g., for *Ccel* and *Bsub*. Pearson correlation coefficients were calculated between the ratios predicted using these methods and the experimentally determined ratios at the transcript (or protein) level. NA denotes no data available.

#	# of genes	RCA		CAI		MELP		RCBS		Gene order		SLOFE	
		Gene	Protein	Gene	Protein	Gene	Protein	Gene	Protein	Gene	Protein	Gene	Protein
4	2	-	NA	-	NA	-	NA	-	NA	0.388225	NA	0.614764	NA
170	2	-0.051	-0.039	-0.010	-0.008	-0.096	-0.074	-0.050	-0.039	0.421	0.323	0.034	0.026
228	2	0.617	0.499	0.563	-0.459	0.106	-0.027	0.337	0.915	0.062	-0.016	0.308	-0.080
295	2	-0.078	-0.591	0.020	0.016	0.714	0.563	0.077	0.061	0.403	0.318	0.131	0.104
566	2	-0.067	-0.004	0.879	0.057	-0.463	-0.030	0.258	0.017	0.114	0.562	0.067	0.952
849	2	0.315	0.117	0.142	0.053	0.072	0.027	0.122	0.045	0.853	0.436	0.504	0.738
915	2	-0.093	NA	0.119	NA	0.731	NA	0.001	NA	0.533	NA	0.903	NA
1135	2	0.139	0.116	0.128	0.107	0.443	0.372	0.171	0.143	0.680	0.571	0.868	0.967
1254	2	-0.348	-0.070	-0.734	-0.033	0.101	0.242	0.255	0.096	0.033	0.728	0.020	0.810
1466	2	-0.063	NA	0.032	NA	-0.031	NA	0.009	NA	0.460	NA	0.037	NA
1477	2	0.198	NA	-0.021	NA	-0.472	NA	0.876	NA	-0.960	NA	0.531	NA
Average		0.052	0.004	0.102	-0.038	0.100	0.153	0.187	0.177	0.272	0.417	0.365	0.502

(A) Correlations with the experimentally measured abundance of transcripts and proteins for bi-cistronic operons in *Ccel*.

82 (B) Correlations with the experimentally measured abundance of transcripts and proteins for bi-cistronic operons in *Bsub*.

#	# of genes	RCA		CAI		MELP		RCBS		Gene order		SLOFE	
		Gene	Protein	Gene	Protein	Gene	Protein	Gene	Protein	Gene	Protein	Gene	Protein
1	2	-0.100	-0.039	-0.044	-0.017	0.753	0.516	0.212	0.083	-0.463	-0.839	-0.273	-0.703
280	2	0.104	0.025	-0.053	-0.013	0.195	0.816	0.588	0.141	-0.424	-0.565	-0.250	-0.957
620	2	-0.271	-0.704	-0.026	-0.066	-0.459	-0.177	-0.670	-0.575	0.463	0.178	0.844	0.456
893	2	-0.498	-0.111	0.006	0.001	-0.264	-0.843	-0.948	-0.235	0.412	0.541	0.921	0.205
1212	2	-0.374	-0.097	-0.246	-0.064	-0.220	-0.843	0.025	0.006	0.603	0.432	0.356	0.732
1411	2	-0.048	-0.108	-0.031	-0.070	-0.130	-0.289	-0.045	-0.099	0.955	0.472	0.454	0.993
1463	2	-0.083	-0.087	0.011	0.012	0.773	0.810	0.193	0.202	0.356	0.373	0.603	0.632
1635	2	-0.008	-0.004	-0.002	-0.001	0.203	0.097	0.151	0.072	0.891	0.538	0.526	0.911
1768	2	-0.026	-0.024	0.020	0.018	-0.053	-0.050	-0.095	-0.089	0.612	0.573	0.701	0.656
1934	2	-0.034	-0.036	0.035	0.037	-0.873	-0.821	-0.155	-0.165	0.513	0.546	0.869	0.924
2144	2	-0.190	0.240	-0.058	0.073	-0.964	0.762	-0.487	0.616	-0.755	0.597	0.227	-0.287
Average		-0.121	-0.071	-0.029	-0.004	-0.155	-0.055	-0.118	-0.023	0.297	0.280	0.472	0.370

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84 (C) Correlations with the experimentally measured abundance of transcripts for bi-cistronic operons in *Cthe*.

#	# of gene	RCA	CAI	RCBS	MELP	Gene-order	SLOFE
236	2	-0.012	-0.009	-0.018	-0.145	0.669	0.883
569	2	-0.567	0.373	0.042	0.010	-0.029	0.990
699	2	0.540	-0.148	-0.221	0.078	-0.153	-0.090
1265	2	0.052	0.243	0.417	0.755	-0.347	0.301
1289	2	0.181	-0.021	0.930	0.225	-0.527	-0.311
1380	2	-0.146	0.194	-0.770	0.227	-0.595	-0.351
1518	2	0.486	-0.055	0.868	0.176	0.125	0.074
Average		0.076	0.082	0.178	0.189	-0.122	0.214

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86 (D) Correlations with the experimentally measured abundance of transcripts for bi-cistronic operons in *Cace*.

# Operon	# of gene	Gene-order	MELP	RCA	CAI	RCBS	SLOFE
216	2	-0.104	0.069	0.418	0.817	0.318	-0.123
466	2	-0.758	0.356	-0.063	0.037	0.442	0.933
614	2	0.725	-0.829	-0.006	-0.079	-0.211	-0.200
633	2	0.877	0.381	-0.088	-0.160	0.067	0.518
943	2	0.061	-0.539	-0.321	0.101	0.313	0.036
981	2	-0.626	0.552	0.005	-0.051	0.098	0.721
1362	2	0.165	0.984	-0.144	0.553	-0.415	0.148
1412	2	-0.776	-0.355	0.025	-0.245	0.365	-0.458
1749	2	0.259	0.157	0.190	-0.353	0.963	0.330
Average		0.057	0.064	0.070	0.076	0.108	0.210

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