

Supplementary tables

Nuclear poly(A) tail size is regulated by Cnot1 during the serum response

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Supplementary Table 1.1

	Immediate decay model best fit parameters					
	alpha	lambda	epsilon	RSS	Transcript	lifetime
Arc STC1	1.291023	0.035008	6.695178	7945.3278	5525.837	28.56508
Arc STC2	1.207656	0.039539	6.695178	8635.1449	4132.223	25.29126
Btg2 STC1	0.450648	0.049465	0.191004	7027764.4	3544.749	20.21625
Btg2 STC2	0.588605	0.06568	0.191004	7850049.1	5246.837	15.2253
Ccrn4l STC	39.93553	0.020187	86.27389	246897.12	374040.5	49.53792
Ccrn4l STC	33.82768	0.018689	86.27389	570373.06	310707.6	53.50787
Csrnp1 STC	4.957353	0.067725	32.6063	6284.622	23064.42	14.76549
Csrnp1 STC	5.899285	0.086629	32.6063	2516.4594	22820.85	11.54345
Ctgf STC1	0.677385	0.012761	99.99997	34127.931	71809.33	78.36162
Ctgf STC2	0.43727	0.009608	99.99997	15653.275	49614.86	104.0766
Cyr61 STC	2.92945	0.045395	1.341972	297858215	165227.2	22.02877
Cyr61 STC	1.986544	0.039344	1.341972	195030933	118972.3	25.4169
Dusp1 STC	12.26347	0.110618	19.97353	19663384	1338433	9.040152
Dusp1 STC	12.1942	0.118817	19.97353	50476493	1680406	8.416305
Dusp6 STC	0.2731	0.04036	1.558522	12956.691	2804.539	24.77691
Dusp6 STC	0.192991	0.035295	1.558522	28632.653	2428.145	28.33272
Egr1 STC1	9.813667	0.074994	57.01007	624857.05	407813.3	13.33448
Egr1 STC2	8.08185	0.066611	57.01007	318911.52	326773.9	15.01252
Egr2 STC1	1.226405	0.056423	0.2222	29859538	5513.549	17.72332
Egr2 STC2	1.273512	0.056352	0.2222	13001435	5242.975	17.74568
Ereg STC1	28.33946	0.005556	86.62286	394599.47	272265.1	180
Ereg STC2	23.98453	0.005556	86.62286	394310.45	254071.2	180
Fos STC1	2.786748	0.057162	12.17582	1422915.4	83302.44	17.49415
Fos STC2	2.731225	0.066141	12.17582	1009602	84679.06	15.11922
Fosb STC1	0.434245	0.027029	0.406141	4372420.9	2912.299	36.99762
Fosb STC2	0.412392	0.028489	0.406141	2286283.6	2387.782	35.10184
Gadd45g S	0.243612	0.096474	0.502496	188640.89	2686.624	10.36547
Gadd45g S	0.126163	0.059156	0.502496	179604.92	1272.5	16.90446
Hbegf STC	10.98122	0.020424	50.74438	23093.273	48507.47	48.96095
Hbegf STC	14.48234	0.042198	50.74438	20116.35	51679.23	23.69789
Id1 STC1	0.404496	0.052013	3.835974	25660.398	6673.699	19.22592
Id1 STC2	0.359024	0.060429	3.835974	16666.046	7926.846	16.54825
Id2 STC1	0.547999	0.029846	1.102898	271145.89	5617.094	33.50549
Id2 STC2	0.583095	0.039514	1.102898	588926.91	7617.002	25.30748
Id3 STC1	0.262372	0.045065	0.31131	426846.27	2028.452	22.19039
Id3 STC2	0.266819	0.058987	0.31131	513415.72	2702.12	16.95296
Klf9 STC1	1.132767	0.020435	99.99997	2694.2717	38583.78	48.93446
Klf9 STC2	1.092296	0.018229	99.99997	5754.781	38824.75	54.85713
Myc STC1	0.33852	0.054606	1.227544	264941.74	11931.56	18.31317
Myc STC2	0.291501	0.047774	1.227544	425794.17	9493.379	20.93192
Npas4 STC	0.49522	0.016452	12.84932	3420.5901	2185.504	60.78251
Npas4 STC	0.372192	0.014533	12.84932	3590.6037	1950.45	68.80891
Ptgs2 STC	1.243045	0.017506	1.369972	134173532	123936.1	57.12403
Ptgs2 STC	1.731986	0.019929	1.369972	240604541	115264.9	50.17788
Rgs16 STC	0.814378	0.036062	6.433388	2418.4377	2217.03	27.72987
Rgs16 STC	0.343283	0.00871	6.433388	2596.1935	1186.365	114.8152
Serpine1 S	0.516	0.008119	0.682282	142388439	56288.92	123.1687
Serpine1 S	0.505808	0.008752	0.682282	295202088	50808.9	114.2648
Trib1 STC1	1.524029	0.053825	10.64782	46150.278	28528.81	18.57875
Trib1 STC2	1.299357	0.053923	10.64782	54683.056	26616.02	18.54486

Supplementary Table 1.2

	Delayed decay model best fit parameters						
	alpha	lambda	tau	epsilon	RSS	Transcript lifetime	
Arc STC1	1.071444	0.036918	6.930377	6.695178	7868.1199	4586.074	34.01734
Arc STC2	1.177338	0.04024	0.99519	6.695178	8639.1782	4028.494	25.84596
Btg2 STC1	0.261711	0.249117	27.67087	0.191004	953760.43	2065.998	31.68506
Btg2 STC2	0.291891	1.848072	28.22594	0.191004	5443509.1	2610.12	28.76704
Ccrn4l STC	39.59162	0.020121	0.327516	86.27389	246867.14	370819.7	50.02704
Ccrn4l STC	23.8529	11.55803	55.25475	86.27389	191006.16	219101.6	55.34127
Csrnp1 STC	3.03744	0.10104	13.05546	32.6063	6191.6347	14137.31	22.95253
Csrnp1 STC	2.842481	1.288798	21.42198	32.6063	1873.8482	11004.2	22.1979
Ctgf STC1	0.539671	0.034123	40.76378	99.99997	27343.073	57350.69	70.06924
Ctgf STC2	0.365666	0.038087	51.15572	99.99997	9659.9071	41613.42	77.41125
Cyr61 STC	1.788504	0.088894	23.35512	1.341972	121274928	100933.9	34.60452
Cyr61 STC	1.153555	0.090365	30.10443	1.341972	133924361	69156.48	41.17064
Dusp1 STC	6.166082	0.480805	16.20483	19.97353	8252397.4	672982.3	18.28468
Dusp1 STC	7.009078	0.209647	10.10748	19.97353	37676792	965856.6	14.87741
Dusp6 STC	0.195396	0.049732	14.21079	1.558522	11749.516	2022.884	34.31843
Dusp6 STC	0.1287	0.052641	22.0441	1.558522	24341.747	1643.174	41.04055
Egr1 STC1	5.399557	0.176167	17.5154	57.01007	436001.11	224384.9	23.19183
Egr1 STC2	4.849104	0.116123	15.38886	57.01007	252751.27	196064.6	24.00045
Egr2 STC1	0.741493	0.095975	18.07403	0.2222	20808722	3336.299	28.49344
Egr2 STC2	0.666864	0.553199	29.95134	0.2222	10674873	2748.809	31.75901
Ereg STC1	23.63229	0.091373	102.7256	86.62286	204207.81	227051.5	113.6698
Ereg STC2	19.75986	0.005582	498.5138	86.62286	242543.23	209327.8	677.6659
Fos STC1	1.87799	0.081617	12.53039	12.17582	627537.73	56142.66	24.78268
Fos STC2	1.666496	0.106448	14.33286	12.17582	683272.28	51674.67	23.72708
Fosb STC1	0.297017	0.053814	30.10023	0.406141	1446070.3	1993.833	48.6826
Fosb STC2	0.266607	0.058457	32.30647	0.406141	977486.22	1545.514	49.41301
Gadd45g S	0.144572	0.135438	9.852819	0.502496	195375.56	1604.129	17.23629
Gadd45g S	0.082512	0.069085	9.338697	0.502496	187296.19	840.6818	23.81364
Hbegf STC	9.296456	0.022779	11.93035	50.74438	22999.799	41069	55.82997
Hbegf STC	8.667402	0.728009	34.83298	50.74438	15397.265	30937.03	36.20659
Id1 STC1	0.246944	0.095076	19.54376	3.835974	13697.949	4103.987	30.06162
Id1 STC2	0.351985	0.06054	0.369018	3.835974	16671.43	7772.852	16.88691
Id2 STC1	0.543634	0.029841	0.264209	1.102898	271155.76	5572.64	33.77558
Id2 STC2	0.339197	0.11631	29.89068	1.102898	500536.65	4447.402	38.48842
Id3 STC1	0.15334	0.10537	24.69535	0.31131	237226.09	1197.025	34.18576
Id3 STC2	0.14482	0.15029	21.95593	0.31131	445114.69	1480.394	28.60972
Klf9 STC1	0.811019	0.044625	33.93791	99.99997	1793.6885	27653.26	56.34689
Klf9 STC2	0.826066	0.043481	36.66825	99.99997	4441.0184	29375.75	59.66666
Myc STC1	0.26722	0.057444	5.812246	1.227544	262368.09	9435.904	23.22052
Myc STC2	0.246316	0.048916	4.178563	1.227544	426314.95	8034.089	24.62157
Npas4 STC	0.418539	0.017709	13.73052	12.84932	3467.4986	1849.467	70.2003
Npas4 STC	0.291585	0.021791	28.99501	12.84932	3401.4195	1531.27	74.88643
Ptgs2 STC	1.001012	0.021314	19.8984	1.369972	121053158	99880.54	66.81669
Ptgs2 STC	1.287678	0.028608	26.86158	1.369972	199277370	85759.31	61.81624
Rgs16 STC	0.578865	0.43436	32.82203	6.433388	2266.2743	1588.113	35.12427
Rgs16 STC	0.31479	0.011171	18.97945	6.433388	2593.1203	1092.718	108.4945
Serpine1 S	0.502031	0.008138	3.577027	0.682282	142477494	54778.95	126.453
Serpine1 S	0.415976	0.051016	58.0937	0.682282	239083564	41850.38	77.69537
Trib1 STC1	0.860776	0.281353	27.67168	10.64782	41194.894	16140.1	31.22593
Trib1 STC2	0.650475	846.7088	34.11696	10.64782	45312.992	13361.69	34.11814

Supplementary Table 2. Parameters derived for the deadenylation models. Highlighted in yellow: Egr1 model timecourse 1 is an outlier for several parameters.

	Egr1		Egr2		Fos		Fosb		Ptgs2
	Time course 1	Time course 2	Time course 1	Time course 2	Time course 1	Time course 2	Time course 1	Time course 2	Time course 1
Max decay rate k^C (min^{-1})	1.30	0.72	0.95	1.31	1.08	0.77	1.18	2.90	0.33
Max deadenylation rate, k^A , (min^{-1})	18.30	11.86	9.14	7.73	10.48	7.84	4.79	3.78	7.32
Mean decay enzyme binding length, μ^C (bases)	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	14.33
Standard deviation of decay enzyme binding length, σ^C (bases)	40.30	18.26	16.51	11.11	23.56	18.34	15.06	13.45	26.73
Mean deadenylation enzyme release length, μ^A (bases)	82.17	0.03	12.60	0.00	0.00	0.00	4.94	13.68	0.00
Standard deviation of deadenylation enzyme release length, σ^A (bases)	99.71	24.74	27.21	57.86	24.55	19.42	5.42	4.45	8.28
Mean input length, μ (bases)	183.55	185.18	201.71	187.61	142.65	155.88	173.29	153.79	220.47
Standard deviation of input length distribution, σ (bases)	49.94	67.25	44.98	28.67	78.83	43.23	53.40	38.17	69.13

Supplementary Table 3. qPCR primer sequences

Primer	Sequence	Amplicon size (bp)
Unspliced Fos F	TGACCGGAATGCTTCTCTCT	165
Unspliced Fos R	TGTCACCGTGGGGATAAAGT	
Spliced Fos F	GGGACAGCCTTTCTACTACC	87
Spliced Fos R	GATCTGCGCAAAAGTCCTGT	
Unspliced Fosb F	GGGGTCGGTGTGTGTTATGT	164
Unspliced Fosb R	GATCCTGGCTGGTTGTGATT	
Spliced Fosb F	ACCCTCCGCCGAGTCTCAGT	128
Spliced Fosb R	TTGCGGTGACCGTTGGCACG	
Unspliced Egr1 F	GGGTCTCATCGTCCAGTGAT	166
Unspliced Egr1 R	GAAGCGGCCAGTATAGGTGA	
Spliced Egr1 F	AGTGATGAACGCAAGAGGCA	121
Spliced Egr1 R	TAGCCACTGGGGATGGGTAA	
Spliced Egr2 F	GTAGCGAGGGAGTTGGGTCT	219
Spliced Egr2 R	ATCATGCCATCTCCCGCCAC	
Unspliced Actb F	AAGATCTGGCACCCACACCTT	155
Unspliced Actb R	TGAGAAGCTGGCCAAAGAGA	
Spliced Actb F	CTAAGGCCAACCGTAAAAAG	104
Spliced Actb R	ACCAGAGGCATACAGGGACA	
Unspliced Rpl28 F	CATCGTGACACCTATTCCC	88
Unspliced Rpl28 R	ACGGTCTTGCGGTGAATTAG	
Spliced Rpl28 F	TACAGCACGGAGCCAAATAA	74
Spliced Rpl28 R	ACGGTCTTGCGGTGAATTAG	
Unspliced Sqstm1 F	GCCTCTGCTGCATTTTAGCCT	137
Unspliced Sqstm1 R	GAAAAGGCAACCAAGTCCCA	
Spliced Sqstm1 F	CCTCTAGGCATTGAGGTTGA	120
Spliced Sqstm1 R	GCTTGGCTGAGTGTTACTCT	
Cnot1 F	AGCATAGCAGCATGTCTTCC	147
Cnot1 R	GCAGAACCCCTGGTCTATC	
Malat1 F	GTGGGTGGGGGTGTTAGGTA	176
Malat1 R	CAACCTTCCTTAGCTGCCCG	
Gapdh F	AAGAAGGTGGTGAAGCAGGC	114
Gapdh R	ATCGAAGGTGGAAGAGTGGG	

Table 5. RL2-PAT primer sequences

Supplementary Table 5. Sequences of PAT primers		
Name	Sequence (5'→3')	Expected size of deadenylated product
Fos 3F1	CAGCGTCAATGTTTCATTGTCA	280
Fos 3F2 ('Fos PAT')	CTGACATTAACAGTTTTCCATG	221
Fosb	ATTGACTCCATAGCCCTCAC	184
Egr1	AGCTGAGCTTTCGGTCTCCA	314
Egr2	GTGCTTCAATGTCAGTCCCG	187
Id1	CAGCCTCCAGAGACTTTGGG	246
Ptgs2	CCTGCTGATTGAACCTGGGA	205
Actinb1 3f1	AAACTTCCGCCTTAATACTTC	219
Actinb1 3f2	GGAGGATGGTCGCGTCCAT	308
Actg1 3f1	ACCACCATCGGTTGTTAGTTG	222
Actg1 3f2	GTTGGGAACGTTGCATCGA	195
Sqstm1 3f1	AAGAGGGGACTGTCCATAGT	255
Sqstm1 3f2	TTGCACCAGCAGTCCAGAAT	358
Rpl28 3f1	GCCACTTCTTATGTGAGGAC	254
Rpl28 3f2	TCGTGGTAGTTATGAAACGCA	295
Rps4x of1	TTATTGGCAAGGGTAACAAC	221
Rps4x of2	CCGGCTCTTTTGATGTGGTT	296
PAT Anchor sequence	5'-rApp GGT CAC CTT GAT CTG AAG ddC- 3'	
PAT reverse primer (PATR1)	5'-GCT TCA GAT CAA GGT GAC CTT TTT- 3'	