

Supplemental Materials

Genome-wide Analysis of mRNA Decay in Resting and Activated Primary Human T Lymphocytes

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Supplemental Table 1. Transcripts induced after three hours of α CD3 or α CD3+ α CD28 stimulation.

The transcripts shown were induced by α CD3+ α CD28 stimulation ($p \leq 0.05$) with a fold change of > 5.0 .

β_0 represents the initial hybridization intensity at the time of actinomycin D addition.

If the Affymetrix software determined a transcript to be absent in at least three of four experiments, the β_0 value is not shown.

These β_0 values, however, were used to calculate the fold changes for these transcripts.

Probe	Accession No.	MEDIA		α CD3			α CD3+ α CD28			Description
		β_0	95% C.I.	β_0	95% C.I.	Fold Change	β_0	95% C.I.	Fold Change	
1538_s_at	X00695	Absent		2517	[439, 4998]	271.2	4969	[1079, 9243]	535.5	interleukin-2 (IL-2)
1400_at	M13207	Absent		7334	[2049, 12860]	191.3	11232	[3892, 18848]	292.9	GM-CSF
1401_g_at	M13207	Absent		6759	[1804, 12125]	165.9	10737	[3786, 17801]	263.5	GM-CSF
34021_at	S82692	Absent		3193	[436, 6566]	58.5	6244	[1218, 11848]	114.5	interleukin-2
547_s_at	S77154	Absent		2021	[469, 3691]	89.1	2036	[584, 3642]	89.8	NGFI-B/nur77 transcrip. factor homolog
280_g_at	L13740	Absent		5689	[1035, 10973]	84.5	5730	[1317, 10430]	85.1	TR3 orphan receptor
35000_at	U03398	Absent		2926	[648, 5465]	69.9	3189	[631, 6109]	76.2	4-1BB ligand
39652_at	AL031736	Absent		3620	[436, 8026]	60.2	4081	[426, 9435]	67.8	lymphotactin
40659_at	U12767	Absent		5292	[1527, 9324]	56.6	5731	[1718, 9957]	61.3	mitogen induced nuclear orphan receptor
37279_at	U10550	Absent		Absent			761	[286, 1235]	59.4	Gem GTPase (gem)
37623_at	X75918	Absent		3510	[1138, 5929]	55.5	3711	[1174, 6265]	58.6	NOT (nuclear receptor)
33012_at	L09753	Absent		445	[210, 731]	36.6	591	[106, 1154]	48.6	CD30 ligand
37863_at	J04076	Absent		5163	[1888, 8467]	44.0	5590	[2195, 9132]	47.6	early growth response 2 protein (EGR2)
40661_at	D78579	Absent		2098	[700, 3507]	40.6	2227	[604, 3894]	43.1	neuron derived orphan receptor
37743_at	U60060	Absent		491	[91, 941]	31.9	630	[203, 1101]	40.9	zygin 1, isoform 1
40662_g_at	D78579	Absent		2673	[912, 4485]	36.7	2791	[711, 5189]	38.3	neuron derived orphan receptor
34916_s_at	S76792	Absent		846	[243, 1453]	13.8	2214	[549, 3886]	36.1	tax-transcrip. act. glycoprotein 1 receptor
190_at	U12767	Absent		5216	[1921, 8541]	28.8	5697	[2100, 9558]	31.5	mitogen induced nuclear orphan receptor
545_g_at	S76638	Absent		662	[301, 1034]	19.9	965	[335, 1645]	29.0	p50-NF-kappa B homolog
544_at	S76638	Absent		994	[458, 1574]	17.4	1645	[592, 2732]	28.7	p50-NF-kappa B homolog
1611_s_at	J00219	Absent		12279	[2708, 23189]	22.1	14448	[3472, 26178]	26.0	interferon (IFN-gamma)
31540_at	U03397	Absent		2339	[583, 4002]	19.1	3140	[695, 5462]	25.6	receptor protein 4-1BB
40375_at	X63741	Absent		7182	[3306, 11140]	25.1	7292	[2203, 12938]	25.4	pilot (early growth response 3)
529_at	U15932	Absent		1233	[559, 1906]	11.9	2356	[1250, 3504]	22.8	dual-specificity protein phosphatase 5
36296_at	D12614	Absent		1310	[201, 2628]	7.1	4143	[1416, 6881]	22.5	lymphotoxin (TNF-beta)
1237_at	S81914	366	[299, 452]	3835	[1225, 6486]	10.5	7366	[3254, 11410]	20.1	IEX-1, radiation-ind. Imm.-early gene
431_at	X02530	Absent		308	[216, 410]	15.9	376	[240, 537]	19.4	IFN- γ inducible early response gene
37627_g_at	D78261	Absent		312	[85, 563]	14.5	396	[71, 777]	18.4	ICSAT transcription factor
1852_at	X02910	1066	[96, 2593]	15881	[5745, 26224]	14.9	18640	[6363, 30772]	17.5	TNF-alpha
37625_at	U52682	652	[36, 1877]	7870	[4213, 11655]	12.1	11122	[5443, 17168]	17.1	LSIRF/IRF4
32441_at	X52142	Absent		308	[80, 554]	13.9	360	[99, 638]	16.2	CTP synthetase
39528_at	L24564	Absent		Absent			936	[291, 1594]	15.5	Ras-related associated with diabetes
41779_at	U70426	Absent		3866	[1206, 6724]	9.8	5901	[2277, 9473]	15.0	regulator of G-protein signalling 16
38505_at	AL050151	Absent		1166	[516, 1827]	11.6	1467	[574, 2375]	14.5	
37716_at	X05323	Absent		2874	[551, 5658]	11.7	3461	[1386, 5602]	14.0	OX-2 membrane glycoprotein precursor
36103_at	D90144	1757	[92, 5329]	21860	[7347, 36636]	12.4	24652	[8669, 40834]	14.0	LD78 alpha precursor
40702_at	X13274	Absent		19768	[7054, 33110]	11.2	23911	[13348, 35260]	13.6	interferon-gamma
36389_at	AF001622	244	[16, 657]	3219	[936, 5587]	13.2	3277	[893, 5855]	13.4	MHC I-restricted T cell assoc. molecule
33112_at	AF060981	Absent		3061	[353, 5944]	14.1	2914	[195, 6713]	13.4	NK-cell BY55 precursor
1021_at	J00219	Absent		24450	[8929, 40579]	10.4	30071	[19172, 42832]	12.7	interferon (IFN-gamma)
1368_at	M27492	Absent		217	[38, 434]	8.6	318	[102, 557]	12.6	interleukin 1 receptor
31742_at	AF064090	712	[134, 1386]	7854	[2240, 13703]	11.0	8773	[2981, 14752]	12.3	ligand for herpesvirus entry mediator
279_at	L13740	Absent		4030	[694, 7995]	12.0	4122	[869, 7844]	12.3	TR3 orphan receptor
41475_at	U91512	Absent		Absent			1117	[468, 1787]	11.8	adhesion molecule ninjurin 1
40405_at	X70991	Absent		1779	[289, 3641]	11.3	1854	[392, 3528]	11.8	NGFI-A binding protein 2
32609_at	AI885852	Absent		2141	[336, 4187]	7.9	3055	[513, 5837]	11.3	H2A histone family, member O
1851_s_at	U11821	Absent		2076	[878, 3289]	12.2	1910	[611, 3295]	11.2	Fas ligand (FasL)
33849_at	U020206	202	[23, 449]	1858	[638, 3080]	9.2	2259	[780, 3760]	11.2	pre-B cell enhancing factor (PBEF)
1292_at	L11329	771	[132, 1558]	7228	[1852, 13155]	9.4	7966	[2804, 13205]	10.3	protein tyrosine phosphatase (PAC-1)
36239_at	Z49194	Absent		698	[246, 1185]	10.5	672	[286, 1062]	10.2	oct-binding factor
1263_at	M20137	Absent		2073	[286, 4230]	6.6	3064	[583, 5996]	9.8	interleukin 3 (IL-3)
39858_s_at	AF071504	Absent		196	[55, 343]	5.8	324	[137, 518]	9.7	syntaxin 11
41048_at	D90070	Absent		1158	[444, 1912]	7.9	1416	[473, 2416]	9.6	ATL-derived PMA-responsive peptide
31495_at	D63789	Absent		32271	[17793, 47614]	8.6	35706	[23386, 50521]	9.5	SCM-1beta precursor
41778_at	U53347	Absent		3978	[1152, 7062]	7.9	4743	[2086, 7537]	9.4	neutral amino acid transporter B
40385_at	U64197	550	[199, 938]	2052	[635, 3541]	3.7	5148	[1797, 8970]	9.4	chemokine exodus-1

39857_at	AF044309	Absent	379	[163, 590]	5.5	627	[171, 1101]	9.1	syntaxin 11	
AFFX-HUMT	M11507	Absent	163	[54, 273]	6.5	227	[28, 484]	9.0	transferrin receptor (p90, CD71)	
38272_at	AF038844	Absent	590	[204, 990]	6.9	744	[311, 1196]	8.6	MKP-1 like protein tyrosine phosphatase	
258_at	M16441	Absent	951	[154, 1899]	3.0	2709	[963, 4478]	8.6	TNF and lymphotoxin genes	
39799_at	M94856	216	[45, 408]	1580	[990, 2283]	7.3	1846	[1015, 2793]	8.5	PA-FABP
40074_at	X16396	735	[284, 1219]	4779	[1753, 7792]	6.5	6008	[2603, 9425]	8.2	methylene THFD cyclohydrolase
35943_s_at	D13317	Absent	224	[64, 399]	5.1	354	[104, 623]	8.1	GA-binding protein transcription factor, β 1	
259_s_at	M16441	Absent	5526	[1838, 9487]	5.7	7712	[2803, 12946]	7.9	TNF and lymphotoxin genes	
1891_at	D14497	Absent	496	[125, 898]	4.8	815	[290, 1367]	7.8	MKKK 8	
39143_at	U08015	Absent	5392	[1991, 8969]	8.7	4779	[1081, 9031]	7.7	NF-ATc	
40982_at	AA926957	Absent	454	[132, 789]	6.1	546	[241, 857]	7.3	hypothetical protein FLJ10534	
287_at	L19871	Absent	265	[67, 488]	6.7	291	[87, 506]	7.3	activating transcription factor 3 (ATF3)	
32640_at	M24283	Absent	184	[69, 303]	4.0	334	[84, 594]	7.3	major group rhinovirus receptor (HRV)	
33755_at	AB014604	Absent	524	[153, 932]	6.1	619	[198, 1061]	7.2	oxysterol-binding protein-like protein 3	
41592_at	AB000734	Absent	382	[107, 685]	4.1	674	[351, 996]	7.2	TIP3 (JAK binding protein)	
36520_at	AB014590	Absent	276	[41, 562]	4.4	451	[141, 783]	7.2	KIAA0690 protein	
31496_g_at	D63789	5299	[189, 19049]	34706	[24869, 47263]	6.5	37814	[27320, 51154]	7.1	SCM-1beta precursor
1858_at	D38122	673	[155, 1242]	4632	[1973, 7226]	6.9	4756	[1847, 7607]	7.1	Fas ligand(FasL)
1521_at	X17620	328	[73, 615]	2029	[1314, 2910]	6.2	2300	[1776, 2963]	7.0	Nm23(homolog to <i>Dros . Awd</i> protein)
40362_at	X61498	Absent	753	[351, 1181]	4.6	1126	[450, 1823]	7.0	NF-kB (p49/p100) subunit	
1985_s_at	X73066	477	[94, 922]	2890	[2155, 3856]	6.1	3243	[2358, 4438]	6.8	non-metastatic cells 1 protein
36674_at	J04130	4576	[201, 15139]	28221	[21677, 35528]	6.2	30915	[24682, 38115]	6.8	Act-2(small inducible cytokine A4)
1856_at	X75042	518	[216, 841]	2291	[1044, 3614]	4.4	3482	[1754, 5482]	6.7	rel proto-oncogene
2042_s_at	M15024	212	[73, 351]	1149	[300, 2067]	5.4	1411	[241, 2821]	6.7	c-myb viral oncogene homolog (avian)
2002_s_at	U27467	471	[180, 783]	2431	[646, 4307]	5.2	3002	[989, 5041]	6.4	Bcl-2 related (Bfl-1)
37645_at	Z22576	1305	[298, 2420]	7887	[4431, 11375]	6.0	8244	[3227, 13399]	6.3	CD69 antigen (p60)
31615_i_at	U94902	Absent	260	[35, 553]	4.7	346	[60, 708]	6.3	soluble CD44	
1473_s_at	U22376	Absent	152	[42, 270]	5.0	182	[22, 408]	6.0	c-myb	
41193_at	AB013382	96	[64, 136]	397	[117, 691]	4.2	566	[200, 944]	5.9	dual specificity phosphatase 6, isoform b
33891_at	AL080061	Absent	241	[119, 369]	4.3	329	[194, 472]	5.9		
33342_at	AF039029	Absent	534	[196, 893]	6.3	485	[161, 830]	5.7	snurportin1	
37536_at	Z11697	579	[195, 1001]	1586	[609, 2597]	2.7	3291	[1799, 4806]	5.7	CD83 antigen
2049_s_at	M29039	251	[24, 93]	1073	[449, 1689]	4.3	1426	[549, 2299]	5.7	jun B proto-oncogene
34770_at	Z14138	Absent	Absent	Absent			257	[85, 429]	5.4	MKKK 8
40365_at	M63904	Absent	360	[159, 568]	3.6	533	[199, 881]	5.3	G protein, alpha 15 (Gq class)	
32186_at	M80244	2220	[632, 4003]	11041	[4164, 18141]	5.0	11720	[4570, 19039]	5.3	solute carrier family 7, member 5
37275_at	U13045	Absent	446	[118, 795]	4.7	496	[121, 907]	5.2	nuclear respiratory factor-2 subunit β 1	
1378_g_at	M58603	1495	[916, 2206]	5512	[2078, 8961]	3.7	7708	[4380, 11773]	5.2	nuclear factor κ -B(NF κ B)
973_at	Y10032	Absent	483	[177, 809]	2.5	994	[521, 1477]	5.1	serum/glucocorticoid regulated kinase	
34140_at	AL109679	Absent	Absent	Absent			55	[20, 91]	5.1	chromosome 15 open reading frame 5
33720_at	L48692	222	[103, 345]	944	[259, 1718]	4.2	1133	[412, 1859]	5.1	clone p5-23-3
41447_at	AB023207	488	[218, 756]	2198	[1007, 3421]	4.5	2477	[972, 3991]	5.1	carbohydrate (chondroitin) synthase 1

Supplemental Table 2. Transcripts repressed after three hours of α CD3 or α CD3+ α CD28 stimulation.

The transcripts shown were repressed by α CD3+ α CD28 stimulation ($p \leq 0.05$) with a fold change of > 5.0 .

β_0 represents the initial hybridization intensity at the time of actinomycin D addition.

Probe	Accession No.	MEDIA		α CD3		α CD3+ α CD28		Description	
		β_0	95% C.I.	β_0	95% C.I.	Fold Change	β_0		95% C.I.
34619_at	X72925	560	[66, 1227]	Absent		2.9	Absent	26.5	desmocollin type 1
1108_s_at	M18391	703	[381, 1063]	Absent		6.2	Absent	21.8	tyrosine kinase receptor (EphA1)
37764_at	D87328	163	[24, 334]	Absent		3.5	Absent	18.6	holocarboxylase synthetase
33766_at	X77777	1020	[318, 1772]	Absent		3.3	57 [2, 190]	17.9	
40472_at	AF007155	294	[31, 692]	Absent		2.3	Absent	14.9	
356_at	AB017430	355	[25, 918]	Absent		3.9	Absent	12.7	kinesin-like DNA binding protein
38546_at	AB006537	179	[14, 446]	Absent		6.4	Absent	12.0	interleukin 1 receptor accessory protein
38799_at	AF068706	972	[91, 1925]	Absent		2.6	Absent	11.3	gamma2-adaptin (G2AD)
936_s_at		454	[64, 900]	Absent		3.1	Absent	10.3	Protein Phosphatase Inhibitor Homolog
37590_g_at	AL109698	1237	[1040, 1442]	239	[132, 209]	5.2	125 [19, 250]	9.9	
38639_at	AF040963	541	[371, 754]	Absent		3.2	Absent	9.7	Mad4 homolog
1919_at	X16316	570	[163, 1025]	Absent		3.3	Absent	9.4	vav oncogene
38859_at	AL080141	383	[41, 719]	37	[2, 283]	3.6	42 [2, 132]	9.0	secretory pathway component Sec31B-1
38531_at	AA428150	474	[184, 809]	118	[55, 538]	3.6	Absent	8.9	hypothetical protein FLJ22709
32565_at	U66619	444	[58, 811]	Absent		2.4	Absent	8.8	SWI/SNF complex 60 KDa subunit
35662_at	U20536	316	[63, 601]	Absent		3.1	Absent	8.3	cysteine protease Mch2 isoform alpha
36724_s_at	U95626	606	[171, 1056]	100	[26, 446]	3.9	77 [19, 142]	7.9	ccr2a,2b,5,6 genes and lactoferrin
1606_at	L36645	1051	[695, 1473]	124	[52, 103]	5.4	Absent	7.8	receptor protein-tyrosine kinase (EphA4)
36200_at	X69838	1176	[263, 2095]	106	[64, 505]	2.6	151 [15, 333]	7.8	ankyrin repeat-containing protein
36941_at	U16954	611	[404, 828]	Absent		3.5	Absent	7.8	AF1Q protein
37199_at	AI760932	218	[53, 393]	Absent		4.0	Absent	7.7	CGI-60 protein
40976_at	AF052432	973	[393, 1563]	Absent		6.0	Absent	7.6	katanin p80 subunit
269_at	L40387	1560	[846, 2309]	270	[159, 479]	2.6	Absent	7.4	thyroid receptor interactor (TRIP14)
34858_at	D79998	858	[496, 1231]	209	[113, 393]	3.4	119 [21, 233]	7.2	
36626_at	X87176	246	[61, 457]	32	[2, 553]	3.3	Absent	7.1	hydroxysteroid (17- β) dehydrogenase 4
33914_r_at	D00726	77	[35, 118]	Absent		3.7	Absent	7.0	ferrochelatase
364_s_at	Z16411	85	[32, 136]	Absent		2.9	Absent	7.0	phospholipase C, beta 3
35283_at	H05692	337	[84, 604]	Absent		2.6	Absent	7.0	hypothetical protein FLJ10738
40599_at	AL109669	856	[477, 1235]	143	[61, 355]	3.2	123 [42, 210]	7.0	
38318_at	AL050128	2317	[1694, 2992]	361	[266, 1443]	5.0	334 [103, 574]	6.9	
943_at	D43968	487	[93, 972]	Absent		4.2	70 [2, 275]	6.9	AML1b protein (alt. spliced product)
34498_at	D89974	1031	[753, 1338]	Absent		2.9	Absent	6.8	vanin 2, isoform 1
35234_at	D50406	422	[146, 733]	57	[38, 231]	4.3	62 [10, 122]	6.8	RECK protein precursor
31869_at	AB014540	184	[81, 288]	Absent		4.0	Absent	6.7	
34914_at	U94778	697	[178, 1262]	Absent		3.0	Absent	6.6	Pro-Ser-Thr phosphatase interact. protein 1
36732_at	AI004207	1390	[998, 1933]	274	[76, 240]	3.1	211 [18, 499]	6.6	
35532_i_at	AJ001683	200	[48, 362]	Absent		2.9	Absent	6.6	NKG2F
35198_at	AF070596	409	[282, 571]	Absent		2.5	63 [8, 136]	6.5	
1202_g_at	D14889	2432	[1540, 3327]	437	[82, 491]	4.5	375 [44, 817]	6.5	RAB33A, member RAS oncogene family
41656_at	AF043325	2151	[1788, 2502]	323	[239, 6026]	2.7	332 [188, 491]	6.5	Gly-peptide N-tetradecanoyltransferase 2
35346_at	AB007856	207	[25, 462]	54	[7, 65]	6.3	33 [2, 93]	6.3	FEM-1-like death receptor binding protein
31927_s_at	D86062	508	[156, 889]	Absent		3.8	Absent	6.3	chromosome 21 ORF 33
37098_at	D38537	824	[630, 1078]	Absent		4.2	Absent	6.3	protoporphyrinogen oxidase
38888_at	AF055636	86	[12, 179]	Absent		4.1	Absent	6.2	Leu-rich glioma-inact. protein precursor
41446_f_at	H68340	3570	[2445, 4919]	448	[44, 787]	2.5	575 [33, 1603]	6.2	RNA helicase-related protein
35659_at	U00672	3599	[1915, 5270]	707	[301, 670]	5.6	581 [67, 1262]	6.2	interleukin-10 receptor
743_at	D50370	309	[157, 461]	Absent		2.9	50 [5, 109]	6.2	nucleosome assembly protein
41107_at	AB002372	706	[510, 921]	Absent		2.6	Absent	6.2	syntaphilin
37616_at	X79888	841	[667, 1033]	Absent		2.5	137 [59, 222]	6.2	enoyl-Coenzyme A hydratase precursor
32332_at	X694331	1377	[818, 1928]	220	[105, 960]	3.5	226 [107, 347]	6.1	isocitrate dehydrogenase 2
41700_at	M62424	887	[513, 1336]	154	[91, 3996]	2.5	146 [55, 247]	6.1	coagulation factor II receptor precursor
40041_at	AF017790	256	[79, 454]	73	[42, 22]	4.9	Absent	6.0	retinoblastoma-associated protein HEC
318_at	D64142	763	[131, 1522]	Absent		2.7	Absent	6.0	histone H1x
37363_at	AB007889	804	[376, 1283]	156	[106, 758]	2.5	135 [53, 228]	6.0	KIAA0429 gene product
40684_at	U78190	2948	[2370, 3704]	528	[386, 845]	2.6	498 [375, 651]	5.9	GTP cyclohydrolase1 feedback reg. protein
40497_at	AF040707	1309	[956, 1763]	331	[181, 1218]	2.7	222 [45, 426]	5.9	candidate tumor suppressor gene 21
33113_at	U65093	2139	[1146, 3112]	456	[286, 154]	3.1	368 [123, 635]	5.8	Cbp/p300-interacting transactivator
36792_at	Z24727	643	[518, 783]	112	[78, 538]	3.6	111 [23, 213]	5.8	tropomyosin 1 (alpha)

41120_at	D14686	781	[216, 1233]	Absent	3.6	Absent	5.8	glycine cleavage system T-protein		
589_at	M32313	258	[178, 363]	30	[3, 1772]	3.1	Absent	steroid 5-alpha-reductase		
36790_at	M19267	635	[454, 871]	86	[58, 795]	3.1	111	[38, 186]	5.7	tropomyosin 1 (alpha)
41266_at	X53586	2646	[1716, 3669]	462	[305, 263]	2.1	463	[268, 685]	5.7	integrin alpha 6
40102_at	AB018315	334	[208, 470]	Absent		3.2	Absent		5.7	oxysterol-binding protein-like protein 2
40296_at	AL023653	3874	[3102, 4653]	685	[451, 153]	3.8	679	[198, 1205]	5.7	
36843_at	AB005666	1504	[1192, 1825]	333	[157, 2377]	2.7	264	[72, 473]	5.7	signal-induced prolifer.-assoc. gene 1
34194_at	AL049313	434	[267, 634]	95	[49, 903]	3.8	76	[32, 123]	5.7	
35409_r_at	X16281	292	[127, 457]	Absent		3.8	Absent		5.7	zinc finger protein (clone 431)
31732_at	X00948	791	[431, 1151]	144	[61, 62]	0.8	140	[15, 315]	5.7	prepro-relaxin H2
37827_r_at	AJ237839	223	[124, 330]	Absent		5.0	Absent		5.6	chromosome 21 ORF 5
35575_f_at	AI698340	256	[40, 532]	Absent		3.3	Absent		5.6	DNA-binding protein
32181_at	M60922	2495	[1721, 3429]	536	[419, 634]	2.8	449	[71, 881]	5.6	flotillin 2
35288_at	AB007884	218	[85, 355]	Absent		3.2	Absent		5.5	Cdc42 guanine exchange factor 9
35958_at	AL050379	680	[216, 1201]	Absent		2.6	Absent		5.5	
33759_at	X04327	737	[502, 985]	152	[115, 718]	3.4	135	[34, 242]	5.5	2,3-bisphosphoglycerate mutase
1127_at	L07597	1647	[1313, 2007]	346	[173, 437]	4.1	301	[36, 648]	5.5	ribosomal protein S6 kinase 1
35775_at	AF070592	401	[132, 704]	Absent		3.5	Absent		5.5	
1347_at	S78187	7426	[6305, 8881]	1184	[909, 552]	4.1	1370	[753, 2041]	5.4	cdc25+ homolog
41409_at	AF044896	1514	[1130, 1918]	341	[208, 68]	3.4	281	[41, 585]	5.4	ICB-1 (basement membrane-induced gene)
1068_g_at	U03858	2185	[620, 3988]	343	[164, 636]	4.2	406	[32, 1024]	5.4	fms-related tyrosine kinase 3 ligand
37242_at	U79260	1469	[605, 2368]	359	[121, 554]	3.8	274	[27, 625]	5.4	
38065_at	X62534	5098	[3224, 7181]	1011	[599, 126]	3.8	956	[517, 1,451]	5.3	HMG-2
34530_at	W73822	2952	[1751, 4104]	650	[339, 1080]	3.3	555	[68, 1219]	5.3	
34632_r_at	Z23091	132	[63, 204]	Absent		3.7	Absent		5.3	platelet glycoprotein V precursor
32314_g_at	M12125	519	[81, 1006]	Absent		4.3	98	[14, 193]	5.3	tropomyosin 2 (beta)
41018_at	AL050015	1432	[1116, 1765]	Absent		4.3	Absent		5.3	DKFZP564O243 protein
1061_at	U00672	3763	[2164, 5352]	823	[433, 315]	4.0	718	[212, 1240]	5.2	interleukin-10 receptor
32630_f_at	Y07827	343	[251, 472]	Absent		7.9	Absent		5.2	butyrophilin, subfamily 3, member A1
40607_at	U97105	1187	[847, 1550]	258	[136, 554]	3.7	230	[136, 338]	5.2	dihydropyrimidinase-like 2
32672_at	AL049387	1065	[706, 1549]	199	[153, 59]	3.7	207	[85, 333]	5.1	
35756_at	AF089816	2262	[863, 3729]	470	[235, 220]	3.2	448	[83, 875]	5.1	RGS-GAIP interacting protein GIPC
35922_at	Y08982	108	[42, 178]	Absent		2.2	Absent		5.0	synaptonemal complex protein 2
39382_at	AB011089	243	[124, 381]	Absent		4.7	48	[10, 87]	5.0	tripartite motif protein TRIM2
39865_at	AI890903	2249	[1650, 3005]	433	[314, 303]	2.4	450	[256, 671]	5.0	
34292_at	X92475	878	[563, 1202]	214	[110, 337]	4.2	177	[25, 369]	5.0	chromosome X ORF 12
34198_at	U12128	253	[68, 458]	50	[13, 36]	5.0	Absent		5.0	protein tyrosine phosphatase 1E (PTP1E)

Supplemental Table 3. Activation-induced transcripts exhibiting rapid decay.

The transcripts shown were induced (p<.05) with a fold change of greater than 2.5 and had half-lives of less than or equal to 60 minutes under the α CD3+ α CD28 condition.

Probe	Accession Number	α CD3		α CD3+ α CD28		DESCRIPTION
		Half-life in minutes	[95% C.I.]	Half-life in minutes	[95% C.I.]	
1292_at	L11329	8	[1, 15]	8	[1, 15]	protein tyrosine phosphatase (PAC-1)
529_at	U15932	8	[1, 20]	8	[1, >360]	dual-specificity protein phosphatase 5
2049_s_at	M29039	20	[1, 35]	11	[1, 28]	jun B proto-oncogene
32640_at	M24283	10	[1, >360]	15	[1, >360]	major group rhinovirus receptor (HRV)
41690_at	AL049471	17	[1, 32]	16	[1, 28]	
41779_at	U70426	17	[1, 28]	17	[1, 30]	regulator of G-protein signalling 16
35000_at	U03398	16	[1, 22]	18	[10, 22]	4-1BB ligand
41592_at	AB000734	8	[1, 15]	18	[12, 29]	TIP3 (JAK binding protein)
40405_at	X70991	25	[22, 35]	18	[1, 41]	NGFI-A binding protein 2
38767_at	AF041037	43	[21, 88]	18	[2, 53]	antagonist of FGF signaling (sprouty-1)
37724_at	V00568	8	[1, 20]	18	[2, 28]	c-myc oncogene
1237_at	S81914	25	[7, 37]	20	[2, 32]	IEX-1, radiation-inducible imm.-early gene
1916_s_at	V01512	10	[1, 26]	20	[2, 35]	oncogene c-fos
39857_at	AF044309	31	[17, 54]	21	[15, >360]	syntaxin 11
36718_s_at	L42452	Absent		22	[1, >360]	pyruvate dehydrogenase kinase 3 (PDK3)
1851_s_at	U11821	24	[8, 29]	24	[5, 33]	Fas ligand (FasL)
39528_at	L24564	Absent		25	[16, 29]	Ras-related associated with diabetes
280_g_at	L13740	25	[22, 29]	25	[22, 31]	TR3 orphan receptor
37536_at	Z11697	37	[27, 46]	25	[22, 29]	CD83 antigen
279_at	L13740	25	[22, 32]	25	[15, 43]	TR3 orphan receptor
37623_at	X75918	25	[22, 29]	25	[22, 29]	NOT (nuclear receptor)
1461_at	M69043	25	[21, 34]	25	[21, 33]	MAD-3 (I κ B-like activity)
37279_at	U10550	Absent		25	[1, 45]	Gem GTPase (gem)
1858_at	D38122	25	[15, 34]	26	[18, 35]	Fas ligand (FasL)
37544_at	X64318	36	[14, 47]	26	[3, 51]	E4BP4 gene
32855_at	L00352	18	[1, 51]	27	[18, 40]	low density lipoprotein receptor
287_at	L19871	25	[15, 33]	28	[12, 38]	activating transcription factor 3 (ATF3)
41259_at	AI553745:	24	[1, 59]	29	[17, 45]	
37310_at	X02419	38	[24, 73]	29	[20, 47]	uPA
224_at	S81439	25	[14, 34]	29	[15, 35]	early growth response gene alpha
1337_s_at	X06614	Absent		29	[15, 35]	receptor of retinoic acid
38374_at	AF050110	32	[24, 36]	30	[20, 36]	early growth response protein alpha
34258_at	W28205	39	[11, >360]	30	[1, 85]	
39858_s_at	AF071504	35	[8, >360]	30	[22, 47]	syntaxin 11
1852_at	X02910	25	[15, 31]	31	[17, 42]	TNF alpha (cachectin)
37627_g_at	D78261	38	[23, 43]	32	[26, 40]	ICSAT transcription factor
38640_at	AI582831	25	[9, 143]	32	[19, 55]	
37028_at	U83981	29	[15, >360]	32	[15, 59]	apoptosis associated protein (GADD34)
41193_at	AB013382	32	[23, 48]	34	[22, 56]	dual specificity phosphatase 6, isoform b
35943_s_at	D13317	42	[29, 68]	34	[20, 60]	GA-binding protein transcription factor, β 1
1911_s_at	M60974	33	[29, 42]	34	[25, 42]	DNA-damage-inducible protein (gadd45)

40659_at	U12767	31	[16, 48]	34	[29, 48]	mitogen induced nuclear orphan receptor
33342_at	AF039029	20	[2, >360]	34	[22, >360]	snurportin1
34770_at	Z14138	Absent		36	[16, 53]	MKKK 8
259_s_at	M16441	29	[8, 36]	36	[22, 47]	TNF and lymphotoxin genes
35714_at	U89606	63	[2, >360]	37	[15, >360]	pyridoxal kinase
973_at	Y10032	59	[22, >360]	37	[9, 54]	serum/glucocorticoid regulated kinase
37863_at	J04076	36	[16, 47]	37	[22, 54]	early growth response 2 protein (EGR2)
40516_at	L19872	46	[43, 49]	38	[23, 61]	AH-receptor
33085_at	U64863	32	[29, 36]	38	[23, 50]	hPD-1
31821_at	AB011167	32	[24, 42]	38	[26, 72]	KIAA0595 protein
253_g_at	L42324	32	[29, 36]	38	[23, 45]	G protein-linked receptor gene, 5
31742_at	AF064090	32	[29, 42]	38	[29, 47]	ligand for herpesvirus entry mediator
41447_at	AB023207	32	[29, 39]	38	[29, 43]	carbohydrate (chondroitin) synthase 1
40661_at	D78579	38	[29, 48]	39	[30, 44]	neuron derived orphan receptor
40365_at	M63904	33	[29, 50]	39	[29, 47]	G protein, alpha 15 (Gq class)
37275_at	U13045	26	[18, 41]	39	[36, 43]	nuclear respiratory factor-2 subunit beta 1
1401_g_at	M13207	18	[10, 22]	39	[33, 43]	GM-CSF
37917_at	AC004982	50	[43, 61]	39	[32, 55]	
252_at	L42324	38	[29, 49]	39	[36, 43]	G protein-linked receptor gene, 5
38272_at	AF038844	29	[2, 47]	39	[36, 48]	MKP-1 like protein tyrosine phosphatase
41778_at	U53347	39	[33, 53]	40	[33, 49]	neutral amino acid transporter B
2031_s_at	U03106	34	[22, 56]	40	[30, 58]	wild-type p53 activated fragment-1 (WAF1)
32441_at	X52142	27	[1, >360]	41	[31, >360]	CTP synthetase
36389_at	AF001622	45	[29, >360]	41	[26, 86]	MHC I-restricted T cell associated molecule
36711_at	AL021977	27	[9, 56]	42	[25, 92]	v-maf like protein
34782_at	AL021938	47	[38, 58]	42	[36, 56]	JUMONJI
33513_at	U33017	33	[29, 56]	42	[29, 63]	signaling lymphocytic activ. molecule (SLAM)
2002_s_at	U27467	39	[31, 49]	42	[28, 60]	Bcl-2 related (Bfl-1)
849_g_at	U19261	57	[30, 64]	43	[31, 56]	Epstein-Barr virus-induced protein
31616_r_at	U94902	78	[64, 90]	43	[31, 90]	soluble CD44
1519_at	J04102	37	[8, 49]	44	[18, 53]	ets-2
2042_s_at	M15024	52	[35, 61]	44	[35, 56]	c-myb viral oncogene homolog (avian)
38692_at	AF045451	42	[36, 59]	45	[36, 57]	transcriptional regulatory protein p54 mRNA
37318_at	X81625	44	[35, 55]	45	[36, 56]	Cl1 protein
190_at	U12767	40	[29, 53]	45	[36, 51]	mitogen induced nuclear orphan receptor
1400_at	M13207	24	[15, 33]	45	[16, 74]	GM-CSF
1891_at	D14497	46	[37, 50]	46	[38, 50]	MKKK 8
39172_at	AL049319	48	[23, 159]	46	[24, 71]	
1265_g_at	M25393	40	[35, 66]	46	[41, 88]	protein tyrosine phosphatase
41475_at	U91512	Absent		46	[37, >360]	adhesion molecule ninjurin 1
40662_g_at	D78579	44	[33, 55]	47	[43, 56]	neuron derived orphan receptor
37645_at	Z22576	45	[36, 49]	47	[39, 56]	CD69 antigen (p60)
848_at	U19261	65	[39, 129]	47	[25, >360]	Epstein-Barr virus-induced protein
40074_at	X16396	40	[33, 49]	49	[36, 62]	MTD cyclohydrolase
547_s_at	S77154	44	[36, 51]	50	[36, 57]	NGFI-B/nur77 β -type homolog
37625_at	U52682	53	[43, 77]	50	[39, 88]	LSIRF/IRF4
37218_at	D64110	57	[36, 97]	51	[43, 69]	ANA
35008_at	AB002345	45	[36, 54]	51	[36., 56]	
34948_at	AI820065	84	[28, >360]	51	[39, 77]	

33338_at	M97936	73	[52, 97]	51	[43, 61]	transcription factor ISGF-3
36520_at	AB014590	53	[23, >360]	51	[9, >360]	KIAA0690 protein
39882_at	U66035	Absent		53	[43, >360]	X-linked deafness dystonia protein (DDP)
570_at	M83221	80	[61, >360]	54	[50, 98]	I-Rel
37377_i_at	M13452	70	[50, >360]	54	[45, >360]	lamin A
38994_at	AF037989	72	[44, 119]	55	[36, 91]	STAT-induced STAT inhibitor-2 mRNA
37716_at	X05323	41	[24, 80]	58	[35, >360]	OX-2 membrane glycoprotein precursor
514_at	U26710	60	[57, 63]	60	[51, 76]	cbl-b
31882_at	AJ001340	159	[36, >360]	60	[51, 164]	U3 snoRNP associated 55 kDa protein
32186_at	M80244	59	[47, 77]	60	[47, 73]	solute carrier family 7, member 5

Supplemental Table 4. Activation-repressed transcripts that exhibited rapid decay in the resting state.

The transcripts shown were repressed ($p < 0.05$) by greater than 2.5 fold three hours following α CD3+ α CD28 stimulation and had half-lives of less than or equal to 60 minutes under the media condition.

Probe	Accession No.	Media		Description
		Half-life (min)	95% C.I.	
507_s_at	U43189	17	[1, >360]	NERF-1a and NERF-1b
943_at	D43968	18	[1, >360]	AML1 oncogene
38045_at	U96136	23	[1, 55]	catenin, delta 2
1202_g_at	D14889	24	[9, 33]	RAB33A, member RAS oncogene family
1857_at	AF010193	25	[18, 47]	MAD 7 (Drosophila)
35659_at	U00672	25	[22, >360]	interleukin 10 receptor, alpha
36402_at	AL096747	25	[15, 57]	
39421_at	D43969	26	[16, >360]	aml1 oncogene
39013_at	Y11588	27	[10, 44]	APG5 autophagy 5-like (S. cerevisiae)
39411_at	AL080156	29	[14, 57]	
40852_at	AB025254	29	[2, >360]	
32587_at	U07802	30	[22, 49]	Tis11d
35346_at	AB007856	31	[1, >360]	FEM-1-like death receptor binding protein
1061_at	U00672	32	[29, >360]	interleukin 10 receptor, alpha
1201_at	D14889	33	[24, 42]	RAB33A, member RAS oncogene family
33113_at	U65093	33	[29, 48]	Cbp/p300-interacting transactivator
37694_at	D87685	33	[29, 43]	KIAA0244 protein
41329_at	AI458463	33	[28, 156]	hypothetical protein LOC57147
35233_r_at	AI056696	34	[10, >360]	alpha integrin binding protein 63
35588_at	AB011414	34	[13, 61]	Kruppel-type zinc finger (C2H2)
32034_at	AF041259	35	[22, 64]	zinc finger protein 217
34491_at	AJ225089	36	[29, 84]	2'-5'-oligoadenylate synthetase-like
38823_s_at	AI961743	36	[29, >360]	Ser/Thr kinase 17a (apoptosis-inducing)
40727_at	AL080090	36	[22, 102]	anaphase-promoting complex subunit 10
1062_g_at	U00672	37	[29, 48]	interleukin 10 receptor, alpha
33741_at	AI741756	37	[22, 81]	CGI-11 protein
269_at	L40387	39	[36, 47]	thyroid receptor interactor (TRIP14)
32588_s_at	X78992	39	[29, 54]	butyrate response factor 2
33123_at	L10379	39	[36, 48]	
34530_at	W73822	39	[36, 47]	
36741_at	D63482	39	[36, 53]	GPCR kinase-interactor 2
37256_at	AI829890	39	[30, 76]	
38342_at	D87076	39	[31, 61]	KIAA0239 protein
39753_at	X06256	39	[31, 51]	integrin alpha 5 subunit
41457_at	AB007883	39	[24, >360]	
32777_at	Y12478	40	[22, >360]	tryptophan rich basic protein
36009_at	AF091092	41	[30, 126]	weakly similar to glutathione peroxidase 2
36896_s_at	AF044288	41	[23, >360]	AH receptor nuclear translocator-like
1056_s_at	M90391	42	[36, >360]	interleukin 16
40290_f_at	L13972	42	[30, 99]	sialyltransferase 4A
32541_at	S46622	43	[29, 224]	calcineurin A catalytic subunit
32833_at	M59287	43	[7, >360]	
36190_at	M63256	43	[32, >360]	

649_s_at	L06797	43	[36, 50]	chemokine (C-X-C motif), receptor 4
37242_at	U79260	44	[30, >360]	
33249_at	M16801	45	[32, 56]	mineralocorticoid receptor mRNA (hMR)
33889_s_at	D79985	45	[30, 99]	integral membrane protein DGCR2
34299_at	AL096880	45	[32, >360]	zinc finger protein 278
36696_at	AB000359	45	[25, >360]	
34957_at	Y18504	46	[34, >360]	
37617_at	U90912	46	[43, 49]	
38669_at	D86959	46	[32, >360]	Ste20-related serine/threonine kinase
38822_at	AB011420	46	[43, 49]	Ser/Thr kinase 17a (apoptosis-inducing)
587_at	M31210	46	[37, 54]	endothelial differentiation protein (edg-1)
38719_at	U03985	47	[39, 56]	N-ethylmaleimide-sensitive factor
39932_at	AI655015	47	[36, >360]	
40084_at	U03494	47	[37, >360]	transcription factor CP2
31732_at	X00948	48	[29, >360]	prepro-relaxin H2
40570_at	AF032885	48	[40, 58]	forkhead box O1A
41796_at	AB029015	48	[41, 63]	
40567_at	X01703	49	[43, 67]	alpha-tubulin
40646_at	U20350	49	[43, >360]	chemokine (C-X3-C) receptor 1
34433_at	AF035299	50	[36, >360]	docking protein 1
32669_at	AB014571	51	[16, >360]	KIAA0671 gene product
34268_at	X91809	51	[34, >360]	G protein signalling regulator 19
38526_at	U02882	52	[36, 187]	phosphodiesterase 4D
32087_at	M65217	53	[36, >360]	heat shock transcription factor 2
33220_at	Z11773	53	[50, >360]	
34871_at	W30677	53	[43, 162]	
35848_at	AL049432	53	[50, 57]	
40320_at	AF000367	53	[50, 95]	CDC14 homolog A
39038_at	AF093118	54	[36, >360]	fibulin 5
41352_at	X62822	54	[44, 79]	sialyltransferase 1
31869_at	AB014540	55	[43, >360]	
37180_at	X14034	55	[38, 139]	phospholipase C, gamma 2
37907_at	M34677	55	[43, >360]	coagulation factor VIII-associated protein
40654_at	U88871	55	[13, >360]	peroxisomal biogenesis factor 7
1052_s_at	M83667	56	[37, >360]	NF-IL6-beta protein
319_g_at	D64142	56	[50, 65]	H1 histone family, member X
35203_at	AB002381	57	[43, 75]	histone acetyltransferase
40876_at	U31525	57	[43, 63]	glycogenin
32332_at	X69433	58	[39, >360]	mitochondrial isocitrate dehydrogenase
35815_at	AL049470	58	[44, >360]	
37399_at	D17793	58	[30, >360]	aldo-keto reductase family 1, member C3
38984_at	AB007896	58	[37, >360]	
752_s_at	D85429	58	[49, 69]	DnaJ homolog, subfam. B, memb. 1
33881_at	AA977580	59	[36, 92]	long-chain fatty-acid-Coenzyme A ligase 3
35937_at	U65416	59	[43, >360]	
36724_s_at	U95626	59	[39, >360]	ccr2a,2b,5,6 genes and lactoferrin
37980_at	U03644	59	[44, >360]	CBF1 interacting corepressor
41672_at	AF007128	59	[51, 64]	
600_at	M28215	59	[36, >360]	RAB5A, member RAS oncogene family
743_at	D50370	59	[39, >360]	nucleosome assembly protein 1-like 3

761_g_at	Y09216	59	[44, 63]	dual-specificity kinase 2 isoform 1
33602_at	AJ000479	60	[52, 91]	GPCR (EDG6)
35319_at	U25435	60	[45, 83]	CCCTC-binding factor (zinc finger protein)
35944_at	AL031228	60	[50, 80]	
39924_at	AB020660	60	[50, 120]	KIAA0853 protein
40098_at	AF001434	60	[57, 63]	EH domain containing 1
40656_at	D85730	60	[50, 139]	heat shock 70kD protein 1-like

Supplemental Table 5. Transcripts that were repressed by activation and exhibited activation-dependent mRNA destabilization.

The transcripts shown in the top section had half-lives of greater than 2 hours in the media condition and less than 2 hours in the α CD3+ α CD28 condition, were repressed greater than 2.5-fold by α CD3+ α CD28 stimulation, and exhibited transcript destabilization in the α CD3+ α CD28 condition ($p < .05$).

The transcripts shown in the bottom section had half-lives of greater than 2 hours in the media condition, were repressed greater than 2.5 fold by α CD3 or α CD3+ α CD28 activation, and went from Present to Absent upon stimulation (according to Affymetrix software).

PROBE_ID	Accession No.	MEDIA		α CD3		α CD3+ α CD28		Description
		Half-life in minutes	[95% C.I.]	Half-life in minutes	[95% C.I.]	Half-life in minutes	[95% C.I.]	
34283_at	AL050125	>360	[40, >360]	32	[27, 44]	25	[6, 75]	
34979_at	AB018323	>360	[51, >360]	66	[10, >360]	39	[29, 64]	
41611_at	L40371	>360	[77, >360]	97	[44, >360]	39	[29, 278]	activating signal cointegrator 1
41462_at	AF065482	>360	[93, >360]	53	[37, >360]	44	[23, >360]	sorting nexin 2
32668_at	AL080076	154	[63, >360]	40	[22, 63]	45	[36, 50]	single-stranded DNA binding protein 2
35790_at	AF054179	131	[68, >360]	41	[32, 56]	47	[43, 56]	vacuolar protein sorting 26 (yeast)
38470_i_at	D86981	137	[91, >360]	53	[50, 61]	47	[32, 76]	amyloid beta precursor protein-binding protein 2
38774_at	U77942	>360	[92, >360]	161	[102, >360]	52	[25, 165]	syntaxin 7
34269_at	AL050102	>360	[262, >360]	59	[37, 92]	53	[45, >360]	
36012_at	Y09631	>360	[66, >360]	46	[43, 50]	54	[36, 77]	progesterone-induced blocking factor 1
39000_at	AF043324	>360	[142, >360]	59	[29, >360]	55	[37, 82]	N-myristoyltransferase 1
38010_at	AF002697	125	[93, >360]	50	[36, >360]	56	[50, 95]	BCL2/adenovirus E1B 19kD-interacting protein 3
32212_at	AL049703	>360	[343, >360]	46	[36, 63]	57	[23, 348]	programmed cell death 8 (apoptosis-inducing factor)
35140_at	R59697	>360	[88, >360]	74	[60, 106]	59	[43, >360]	cyclin-dependent kinase 8
34733_at	X85237	180	[134, >360]	74	[63, 101]	60	[57, 77]	splicing factor 3a, subunit 1, 120kD
35642_at	AF053551	203	[58, >360]	124	[91, >360]	60	[50, 108]	metaxin 2
38281_at	U67319	128	[67, >360]	89	[54, >360]	61	[52, 87]	caspase 7, isoform delta precursor
36913_at	U75679	>360	[94, >360]	75	[52, >360]	67	[32, 165]	stem-loop (histone) binding protein
1189_at	X85753	>360	[177, >360]	232	[94, >360]	68	[54, 110]	cyclin-dependent kinase 8
35199_at	AB023199	190	[80, >360]	70	[51, >360]	68	[51, 96]	KIAA0982 protein
38670_at	AL031685	144	[83, >360]	69	[58, >360]	68	[59, 84]	
32125_at	AA928996	>360	[222, >360]	100	[72, >360]	69	[51, >360]	
36629_at	AI635895	>360	[87, >360]	60	[53, 68]	69	[61, 221]	delta sleep inducing peptide, immunoreactor
38802_at	Y12711	>360	[116, >360]	57	[43, >360]	69	[54, 121]	progesterone binding protein
41288_at	AL036744	217	[79, >360]	87	[58, >360]	71	[64, 121]	
33893_r_at	AB007939	>360	[97, >360]	53	[44, >360]	72	[51, >360]	KARP-1-binding protein
36032_at	AL031427	312	[138, >360]	60	[57, 68]	72	[59, 113]	
38398_at	AB002356	127	[103, 204]	134	[73, >360]	73	[64, 137]	MAP-kinase activating death domain
40805_at	AB007900	255	[78, >360]	18	[1, >360]	73	[60, 92]	KIAA0440 protein
32042_at	S72904	>360	[157, >360]	>360	[154, >360]	74	[64, >360]	cytosolic ovarian carcinoma antigen 1
32804_at	AF091263	235	[107, >360]	63	[44, >360]	74	[50, >360]	RNA binding motif protein 5
33835_at	AB018264	134	[78, >360]	61	[50, 86]	74	[70, 82]	KIAA0721 protein
34039_at	AJ001383	>360	[193, >360]	187	[50, >360]	74	[58, 91]	lymphocyte antigen 94 (mouse) homolog (NK-p46)
34779_at	R90942	>360	[>360]	>360	[>360, >360]	76	[64, >360]	NeuAc-alpha-2,3-Gal-beta-1,3-GalNAc-alpha-2, 6-sialyltransferase
33886_at	AF006516	170	[76, >360]	67	[57, 84]	77	[50, 91]	spectrin SH3 domain binding protein 1
36473_at	AB023220	>360	[290, >360]	128	[104, >360]	77	[64, >360]	ubiquitin specific protease 20

37729_at	Y08614	>360	[185, >360]	92	[59, >360]	80	[71, 94]	exportin 1
34825_at	AL031775	>360	[129, >360]	81	[57, >360]	81	[50, 208]	
37962_r_at	D63506	162	[115, 214]	81	[65, >360]	81	[61, >360]	syntaxin 4 binding protein
40961_at	X72889	324	[136, >360]	88	[70, >360]	81	[67, 97]	SWI/SNF related, subf
36013_at	AF006621	>360	[141, >360]	81	[70, >360]	83	[57, >360]	chromosome 4 open reading frame 1
35847_at	AB028980	>360	[117, >360]	88	[84, >360]	84	[58, >360]	
39442_at	AL080115	>360	[165, >360]	79	[61, 102]	84	[62, >360]	DKFZP564G0222 protein
33305_at	M93056	>360	[129, >360]	53	[50, >360]	85	[52, >360]	
37619_at	D42084	213	[159, >360]	82	[60, >360]	86	[71, 128]	
40868_at	AA442799	331	[138, >360]	74	[59, 133]	86	[56, >360]	hypothetical protein FLJ20274
1496_at	M34668	>360	[176, >360]	99	[77, 112]	87	[79, 91]	protein tyrosine phosphatase, receptor type, A
176_at	U37352	162	[118, 192]	86	[55, >360]	87	[72, 100]	protein phosphatase 2, regulatory subunit B (B56), gamma isoform
33228_g_at	AI984234	>360	[101, >360]	102	[74, >360]	87	[70, 117]	interleukin 10 receptor, beta
38831_f_at	AF053356	178	[144, 181]	82	[59, >360]	87	[70, 105]	
879_at	M30818	149	[101, >360]	130	[85, >360]	87	[72, 102]	myxovirus (influenza virus) resistance 2 (mouse)
32569_at	L13385	>360	[101, >360]	77	[59, >360]	88	[65, 140]	PAF acetylhydrolase, isoform lb, alpha subunit
33748_at	D86976	>360	[107, >360]	115	[99, 281]	88	[84, 104]	
38119_at	X12496	277	[198, >360]	>360	[107, >360]	88	[84, 107]	glycophorin C, isoform 1 NM_016815 glycophorin C, isoform 2
39897_at	N36997	188	[96, >360]	81	[71, >360]	88	[76, 298]	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16
39117_at	AB014562	>360	[144, >360]	109	[80, >360]	90	[74, 222]	
40786_at	U37352	123	[101, >360]	73	[55, >360]	90	[53, >360]	protein phosphatase 2, regulatory subunit B (B56), gamma isoform
32038_s_at	AI739308	199	[175, 296]	108	[78, >360]	91	[81, 125]	46kD arginine/serine-rich splicing factor
36102_at	AF038962	>360	[196, >360]	74	[58, >360]	91	[78, >360]	voltage-dependent anion channel 3
36633_at	AA114830	241	[187, >360]	84	[61, 118]	92	[59, >360]	A kinase (PRKA) anchor protein 10
41699_f_at	AL080149	>360	[155, >360]	105	[86, 253]	93	[85, >360]	bromodomain-containing protein 1
1873_at	D21089	156	[140, 170]	81	[61, >360]	94	[85, 249]	xeroderma pigmentosum, complementation group C
32674_at	D83032	132	[99, >360]	88	[72, 171]	94	[74, 101]	nuclear protein
33258_g_at	D26535	>360	[>360]	82	[71, 114]	94	[66, 135]	dihydrolipoamide S-succinyltransferase
38290_at	AF037195	>360	[99, >360]	>360	[119, >360]	94	[68, 145]	regulator of G-protein signalling 14
38075_at	X68194	>360	[108, >360]	>360	[69, >360]	95	[74, >360]	synaptophysin-like protein
38113_at	AB018339	170	[99, >360]	147	[57, >360]	95	[89, 102]	
38695_at	AA203303	>360	[>360]	79	[64, 101]	95	[73, >360]	NADH dehydrogenase (ubiquinone)
39377_at	D87453	>360	[>360]	182	[128, >360]	95	[76, 176]	mitochondrial ribosomal protein S27
33444_at	D30756	>360	[115, >360]	125	[87, >360]	96	[87, >360]	membrane component, chromosome 17, surface marker 2
36322_at	AB012668	>360	[120, >360]	>360	[>360] >360]	96	[86, 112]	fucosyltransferase 7 (alpha (1,3) fucosyltransferase)
38303_at	AB001523	>360	[217, >360]	94	[73, 115]	96	[71, >360]	transmembrane protein 1
41758_at	AL096879	>360	[117, >360]	86	[66, >360]	96	[75, 131]	chromosome 22 open reading frame 5
746_at	D50640	>360	[326, >360]	73	[59, >360]	96	[78, >360]	
1794_at	M92287	213	[121, >360]	>360	[148, >360]	100	[74, 176]	cyclin D3
41474_at	Y08319	253	[115, >360]	75	[67, >360]	100	[61, >360]	kinesin heavy chain member 2
172_at	U57650	>360	[202, >360]	116	[98, >360]	101	[91, >360]	inositol polyphosphate-5-phosphatase, 145kD
39993_at	D11466	341	[110, >360]	109	[88, >360]	101	[72, >360]	phosphatidylinositol glycan, class A isoform 1
41177_at	AW024285	>360	[144, >360]	114	[100, 129]	101	[88, 133]	hypothetical protein FLJ12443
35221_at	X91648	>360	[108, >360]	108	[77, >360]	103	[98, 347]	
40070_at	D50912	144	[112, 157]	>360	[71, >360]	103	[60, 151]	RNA binding motif protein 10
34830_at	W25986	>360	[>360]	158	[95, >360]	104	[84, >360]	hypothetical protein DKFZp564K0822
38662_at	AL047596	>360	[327, >360]	116	[93, >360]	106	[80, >360]	capicua (Drosophila) homolog

32085_at	AB023198	>360	[153, >360]	106	[74, >360]	108	[65, >360]	
32119_at	AL049423	>360	[>360]	96	[84, >360]	108	[102, 114]	
35187_at	AL080216	>360	[124, >360]	128	[93, >360]	108	[92, 158]	
39137_at	X80878	227	[189, >360]	127	[66, >360]	108	[89, >360]	nuclear factor related to kappa B binding protein
37438_at	AB007879	>360	[236, >360]	>360	[172, >360]	109	[92, >360]	KIAA0419 gene product
37532_at	M91432	297	[150, >360]	95	[78, 205]	109	[105, 118]	
39147_g_at	U72936	>360	[>360]	120	[99, >360]	109	[102, 146]	transcriptional regulator ATRX
1361_at	U40705	141	[119, >360]	139	[120, 313]	110	[99, 132]	telomeric repeat binding factor 1, isoform 1
31638_at	AC005329	>360	[247, >360]	135	[77, >360]	111	[66, >360]	NADH dehydrogenase (ubiquinone)
35872_at	D50640	>360	[>360]	94	[78, 108]	112	[92, >360]	
33238_at	U23852	>360	[176, >360]	>360	[105, >360]	115	[94, 157]	
37266_at	U69645	>360	[131, >360]	203	[95, >360]	116	[74, >360]	
38768_at	X96752	>360	[>360]	130	[109, 151]	118	[106, >360]	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain
32655_s_at	X87613	>360	[>360]	150	[107, >360]	119	[112, 127]	thyroid hormone receptor coactivating protein
1012_at	U57317	>360	[209, >360]	Absent		Absent		p300/CBP-associated factor
1108_s_at	M18391	283	[87, >360]	Absent		Absent		EphA1
1220_g_at	X15949	>360	[>360]	Absent		Absent		interferon regulatory factor 2
1255_g_at	L36861	>360	[111, >360]	Absent		Absent		guanylate cyclase activator 1A (retina)
1300_at	Y08837	>360	[180, >360]	Absent		Absent		X-ray repair cross complementing protein 2
1339_s_at	X14675	137	[94, >360]	Absent		Absent		
1464_at	S73149	170	[136, >360]	Absent		Absent		
1488_at	L77886	302	[131, >360]	Absent		Absent		protein tyrosine phosphatase, receptor type, K
1919_at	X16316	>360	[>360]	Absent		Absent		vav 1 oncogene
1954_at	AF035121	225	[155, >360]	Absent		Absent		kinase insert domain receptor (a type III receptor tyrosine kinase)
1997_s_at	U19599	>360	[325, >360]	Absent		Absent		BCL2-associated X protein
2004_at	U29671	141	[74, >360]	Absent		Absent		
210_at	M95678	>360	[>360]	Absent		Absent		phospholipase C, beta 2
303_at	HG960-HT960	>360	[158, >360]	Absent		Absent		
31392_r_at	U88965	>360	[183, >360]	Absent		Absent		chromosome 1 open reading frame 1
31517_f_at	M90355	174	[123, >360]	Absent		Absent		
31528_f_at	Z83738	>360	[>360]	Absent		Absent		H2B histone family, member E
31776_at	AI446234	>360	[233, >360]	Absent		Absent		
318_at	Y14155	>360	[16, >360]	Absent		Absent		
31881_at	D64142	>360	[30, >360]	Absent		Absent		H1 histone family, member X
31927_s_at	D86062	223	[52, >360]	Absent		Absent		chromosome 21 open reading frame 33
32158_at	U53174	>360	[>360]	Absent		Absent		RAD9 homolog (S. pombe)
32184_at	X61118	>360	[128, >360]	Absent		Absent		LIM domain only 2
32202_at	U67322	>360	[>360]	Absent		Absent		HBV associated factor, isoform 1
32207_at	M64925	229	[157, >360]	Absent		Absent		palmitoylated membrane protein 1
32246_g_at	AF014837	>360	[334, >360]	Absent		Absent		putative methyltransferase
32267_at	X78933	>360	[134, >360]	Absent		Absent		zinc finger protein HZF10
32538_at	S95936	228	[89, >360]	Absent		Absent		transferrin precursor
32565_at	U66619	>360	[>360]	Absent		Absent		SWI/SNF related, subf
32596_at	W25828	>360	[188, >360]	Absent		Absent		retinoblastoma-like 2 (p130)
32630_f_at	Y07827	>360	[273, >360]	Absent		Absent		butyrophilin, subfamily 3, member A1
32676_at	M93405	>360	[>360]	Absent		Absent		aldehyde dehydrogenase 6 family, member A1

33185_at	AB018304	>360	[138, >360]	Absent	Absent	KIAA0761 protein
33256_at	Y14494	274	[108, >360]	Absent	Absent	solute carrier family 25 (mitochondrial carrier, Aralar), member 12
33278_at	AC004381	>360	[108, >360]	Absent	Absent	
33410_at	S66213	>360	[92, >360]	Absent	Absent	integrin alpha chain, alpha 6
33427_s_at	AF106861	>360	[179, >360]	Absent	Absent	attractin
33469_r_at	X68679	>360	[117, >360]	Absent	Absent	complement factor H related 3
336_at	X16576	262	[74, >360]	Absent	Absent	zinc finger protein 46 (KUP)
33616_at	D38081	>360	[>360]	Absent	Absent	thromboxane A2 receptor
33707_at	AF058921	>360	[>360]	Absent	Absent	phospholipase A2, group IVC (cytosolic, calcium-independent)
33736_at	Y16522	273	[42, >360]	Absent	Absent	stomatin (EBP72)-like 1
33749_at	AB007455	>360	[>360]	Absent	Absent	TP53 target gene 1
33850_at	W28892	272	[118, >360]	Absent	Absent	putative translation initiation factor
33914_r_at	D00726	141	[81, >360]	Absent	Absent	ferrochelatase
33922_at	U17838	>360	[286, >360]	Absent	Absent	PR domain containing 2, with ZNF domain
34001_at	AF033199	>360	[158, >360]	Absent	Absent	
34028_at	U55312	>360	[190, >360]	Absent	Absent	
34217_at	AB015132	>360	[200, >360]	Absent	Absent	Kruppel-like factor 7 (ubiquitous)
34249_at	AF084535	>360	[106, >360]	Absent	Absent	epilepsy, progressive myoclonus type 2, Lafora disease (laforin)
34416_at	X57110	>360	[121, >360]	Absent	Absent	Cas-Br-M (murine) ecotropic retroviral transforming sequence
34498_at	D89974	>360	[299, >360]	Absent	Absent	vanin 2, isoform 1 precursor
34560_at	Z18954	>360	[302, >360]	Absent	Absent	S100 calcium-binding protein A5
34568_at	X82634	>360	[196, >360]	Absent	Absent	type I hair keratin 3B
34619_at	X72925	>360	[131, >360]	Absent	Absent	
34689_at	AJ243797	>360	[129, >360]	Absent	Absent	three prime repair exonuclease 1
34732_at	X65873	>360	[1, >360]	Absent	Absent	kinesin family member 5B
34738_at	L11931	195	[107, >360]	Absent	Absent	serine hydroxymethyltransferase 1 (soluble)
34790_at	S70154	>360	[54, >360]	Absent	Absent	acetyl-Coenzyme A acetyltransferase 2
34914_at	U94778	>360	[>360]	Absent	Absent	proline-serine-threonine phosphatase interacting protein 1
34956_at	T77051	250	[166, >360]	Absent	Absent	
35019_at	AF054180	>360	[53, >360]	Absent	Absent	zinc finger protein 254
35283_at	H05692	>360	[28, >360]	Absent	Absent	hypothetical protein FLJ10738
35288_at	AB007884	>360	[78, >360]	Absent	Absent	Cdc42 guanine exchange factor 9
35409_r_at	X16281	151	[121, >360]	Absent	Absent	
35454_at	AB007919	201	[92, >360]	Absent	Absent	KIAA0450 gene product
35492_at	AC004523	>360	[212, >360]	Absent	Absent	cytochrome P450 isoform 4F12
35532_i_at	AJ001683	>360	[121, >360]	Absent	Absent	killer cell lectin-like receptor subfamily C, member 4
35575_f_at	AI698340	>360	[>360]	Absent	Absent	DNA-binding protein
356_at	D21089	314	[132, >360]	Absent	Absent	xeroderma pigmentosum, complementation group C
35647_at	U20536	>360	[52, >360]	Absent	Absent	caspase 6, isoform beta
35662_at	AB017430	>360	[>360]	Absent	Absent	kinesin-like 4
35710_s_at	U95006	>360	[>360]	Absent	Absent	
35763_at	AB011112	>360	[>360]	Absent	Absent	
35775_at	AF070592	>360	[>360]	Absent	Absent	
35913_at	U88047	>360	[98, >360]	Absent	Absent	dead ringer-like 1
35922_at	Y08982	139	[51, >360]	Absent	Absent	synaptonemal complex protein 2
35958_at	AL050379	>360	[310, >360]	Absent	Absent	
35978_at	AF009242	267	[127, >360]	Absent	Absent	proline-rich Gla (G-carboxyglutamic acid) polypeptide 1

35980_at	AB011153	>360	[45, >360]	Absent	Absent	phospholipase C, beta 1(phosphoinositide-specific)
36330_at	Y17448	>360	[82, >360]	Absent	Absent	cytoplasmic cysteine conjugate-beta lyase
36345_g_at	U34038	>360	[62, >360]	Absent	Absent	coagulation factor II (thrombin) receptor-like 1 precursor
364_s_at	AB011542	>360	[300, >360]	Absent	Absent	
36488_at	D87469	347	[86, >360]	Absent	Absent	cadherin EGF LAG seven-pass G-type receptor 2
36499_at	Z16411	126	[104, >360]	Absent	Absent	phospholipase C, beta 3 (phosphatidylinositol-specific)
36598_s_at	L36818	>360	[275, >360]	Absent	Absent	inositol polyphosphate phosphatase-like 1
36630_at	Z50781	>360	[>360]	Absent	Absent	delta sleep inducing peptide, immunoreactor
36713_at	AL080170	245	[106, >360]	Absent	Absent	
36737_at	U59057	>360	[290, >360]	Absent	Absent	crystallin, beta A4
36794_at	X16282	>360	[159, >360]	Absent	Absent	
36820_r_at	S75313	157	[64, >360]	Absent	Absent	ataxin 3, isoform 1
36941_at	U16954	189	[59,v 195]	Absent	Absent	AF1Q protein
37098_at	D38537	>360	[>360]	Absent	Absent	protoporphyrinogen oxidase
37157_at	X56667	>360	[137, >360]	Absent	Absent	calbindin 2, full length protein isoform
37199_at	AI760932	>360	[>360]	Absent	Absent	CGI-60 protein
372_f_at	X90392	>360	[192, >360]	Absent	Absent	deoxyribonuclease I-like 1
37214_g_at	Z84718	>360	[>360]	Absent	Absent	
37437_at	AB011162	>360	[212, >360]	Absent	Absent	KIAA0590 gene product
37443_at	AL031588	246	[50, >360]	Absent	Absent	G-2 and S-phase expressed 1
37468_at	AF058925	124	[57, >360]	Absent	Absent	Janus kinase 2
37472_at	U60337	>360	[285, >360]	Absent	Absent	mannosidase, beta A, lysosomal
37476_at	AA650210	>360	[209, >360]	Absent	Absent	TRIAD3 protein
37556_at	M81637	>360	[58, >360]	Absent	Absent	grancalcin, EF-hand calcium binding protein
37584_at	AJ007669	>360	[>360]	Absent	Absent	X-ray repair complementing defective repair in Chinese hamster cells 9
37764_at	D87328	>360	[68, >360]	Absent	Absent	holocarboxylase synthetase
37788_at	AF052115	>360	[296, >360]	Absent	Absent	
37825_at	M84443	>360	[61, >360]	Absent	Absent	galactokinase 2
37827_r_at	AJ237839	>360	[43, >360]	Absent	Absent	chromosome 21 open reading frame 5
37857_at	AL080188	>360	[251, >360]	Absent	Absent	
38020_at	AB014552	155	[65, >360]	Absent	Absent	KIAA0652 gene product
38034_at	M16505	126	[42, >360]	Absent	Absent	steroid sulfatase (microsomal), arylsulfatase C, isozyme S
38162_at	AF007156	353	[78, >360]	Absent	Absent	KIAA0751 gene product
38247_at	U67058	296	[34, >360]	Absent	Absent	
38406_f_at	AI207842	>360	[251, >360]	Absent	Absent	prostaglandin D2 synthase (21kD, brain)
38507_at	X16867	>360	[326, >360]	Absent	Absent	
38546_at	AB006537	122	[17, >360]	Absent	Absent	interleukin 1 receptor accessory protein
38637_at	L16895	>360	[118, >360]	Absent	Absent	lysyl oxidase
38639_at	AF040963	>360	[269, >360]	Absent	Absent	Mad4
38645_at	AL096748	>360	[>360]	Absent	Absent	DKFZP434A043 protein
38785_at	X52228	>360	[>360]	Absent	Absent	mucin 1, transmembrane
38799_at	AF068706	>360	[>360]	Absent	Absent	adaptor-related protein complex 1, gamma 2 subunit
38888_at	AF055636	>360	[173, >360]	Absent	Absent	leucine-rich, glioma inactivated 1 precursor
38948_at	Y18206	>360	[234, >360]	Absent	Absent	protein phosphatase 1, regulatory subunit 3D
39068_at	L76702	>360	[123, >360]	Absent	Absent	protein phosphatase 2, regulatory subunit B (B56), delta isoform
39249_at	AB001325	>360	[185, >360]	Absent	Absent	aquaporin 3
39350_at	U50410	151	[146, >360]	Absent	Absent	glypican 3

39361_f_at	AF043906	>360	[142, >360]	Absent	Absent	transmembrane 4 superfamily member 6
39408_at	Z80345	>360	[106, >360]	Absent	Absent	
39534_at	L77564	123	[51, >360]	Absent	Absent	
39845_at	AF020760	>360	[>360]	Absent	Absent	protease, serine, 25
39910_at	AA663800	>360	[255, >360]	Absent	Absent	hypothetical protein
39968_at	U50136	>360	[>360]	Absent	Absent	
39986_at	AL050100	282	[110, >360]	Absent	Absent	
40102_at	AB018315	122	[72, >360]	Absent	Absent	oxysterol-binding protein-like protein 2
40136_at	AB014576	>360	[>360]	Absent	Absent	KIAA0676 protein
40266_at	AB028959	>360	[>360]	Absent	Absent	KIAA1036 protein
40274_at	U48213	>360	[352, >360]	Absent	Absent	
40361_at	D78333	171	[102, >360]	Absent	Absent	chaperonin containing TCP1, subunit 6B (zeta 2)
40381_at	AB023189	>360	[114, >360]	Absent	Absent	KIAA0972 protein
40386_r_at	M96956	>360	[227, >360]	Absent	Absent	teratocarcinoma-derived growth factor 1
40415_at	X14813	>360	[341, >360]	Absent	Absent	acetyl-Coenzyme A acyltransferase 1
40434_at	U97519	196	[57, >360]	Absent	Absent	podocalyxin-like
40455_at	AB020637	126	[84, 144]	Absent	Absent	
40472_at	AF007155	>360	[260, >360]	Absent	Absent	
40575_at	AB011155	248	[197, >360]	Absent	Absent	discs, large (Drosophila) homolog 5
40672_at	U57721	297	[138, >360]	Absent	Absent	kynureninase (L-kynurenine hydrolase)
40817_at	M96824	>360	[>360]	Absent	Absent	nucleobindin 1
40976_at	AF052432	>360	[257, >360]	Absent	Absent	katanin p80 subunit B 1
41002_at	U59299	>360	[>360]	Absent	Absent	solute carrier family 16 (monocarboxylic acid transporters), member 5
41018_at	AL050015	189	[85, >360]	Absent	Absent	DKFZP564O243 protein
41083_at	AC006276	>360	[>360]	Absent	Absent	
41106_at	AF022797	>360	[>360]	Absent	Absent	K ⁺ conductance calcium-activated channel, subfamily N,
41107_at	AB002372	>360	[165, >360]	Absent	Absent	syntaphilin
41120_at	D14686	>360	[>360]	Absent	Absent	
41209_at	M15856	>360	[>360]	Absent	Absent	lipoprotein lipase precursor
41227_at	AL022162	>360	[293, >360]	Absent	Absent	phosphatidylinositol polyphosphate 5-phosphatase, isoform a
41282_s_at	AA194159	>360	[226, >360]	Absent	Absent	peroxisome biogenesis factor 10
41306_at	AA004795	160	[104, >360]	Absent	Absent	amyloid beta (A4) precursor protein-binding, family A, member 2, isoform 1
41378_at	AF010236	220	[84, >360]	Absent	Absent	
41396_at	AB006629	>360	[311, >360]	Absent	Absent	cytoplasmic linker 2, isoform 1
41590_at	AI652660	>360	[226, >360]	Absent	Absent	CGI-87 protein
41871_at	AI660929	150	[120, >360]	Absent	Absent	lung type-I cell membrane-associated glycoprotein, isoform 2 precursor
732_f_at	HG2148-HT2218	>360	[76, >360]	Absent	Absent	
748_s_at	D63940	196	[106, >360]	Absent	Absent	MAX interacting protein 1
936_s_at	HG3570-HT3773	>360	[>360]	Absent	Absent	

Supplemental Table 6. Short half-life transcripts that contain ARE-like sequence elements.

The transcripts shown had half-lives less than 60 min in either the Media condition, CD3 or CD3+ CD28 condition, and were identified through the overlap of Accession numbers between our dataset and the ARE database.

Probe	Accession No.	MEDIA	α CD3	α CD3+ α CD28	Description
		Half-life [95% C.I.] (in min)	Half-life [95% C.I.] (in min)	Half-life [95% C.I.] (in min)	
32669_at	U07563	51 [16,>360]	Absent	11 [1,49]	homolog of Yeast RRP4 (ribosomal RNA processing 4), 3'-5'-exoribonuclease
35659_at	L76259	25 [22,>360]	12 [1,>360]	12 [1,>360]	6-pyruvoyltetrahydropterin synthase
33705_at	AB007939	18 [9,82]	15 [1,27]	17 [1,22]	KIAA0470 gene product
41779_at	AB014569	Absent	17 [1,28]	17 [1,30]	KIAA0669 gene product
1237_at	S81914	>360 [211,>360]	25 [7,37]	20 [2,32]	immediate early response 3
37312_at	L04510	43 [29,111]	31 [20,43]	24 [2,42]	ADP-ribosylation factor domain protein 1, 64kD
1461_at	M69043	32 [29,49]	25 [21,34]	25 [21,33]	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
279_at	L13740	Absent	25 [22,32]	25 [15,43]	nuclear receptor subfamily 4, group A, member 1
280_g_at	L13740	Absent	25 [22,29]	25 [22,31]	nuclear receptor subfamily 4, group A, member 1
1635_at	U07563	108 [73,>360]	46 [26,>360]	26 [22,53]	v-abl Abelson murine leukemia viral oncogene homolog 1
40448_at	S78234	42 [35,>360]	27 [17,36]	26 [17,46]	cell division cycle 27
36402_at	AB018254	25 [15,57]	18 [1,50]	28 [2,43]	KIAA0711 gene product
37310_at	U80017	336 [76,>360]	38 [24,73]	29 [20,47]	survival of motor neuron 1, telomeric
1061_at	U00672	32 [29,>360]	37 [15,>360]	31 [17,53]	interleukin 10 receptor, alpha
1852_at	X02910	>360 [68,>360]	25 [15,31]	31 [17,42]	tumor necrosis factor (TNF superfamily, member 2)
39695_at	AB014528	36 [29,55]	32 [23,52]	32 [25,48]	KIAA0628 gene product
41789_r_at	D50487	>360 [30,>360]	39 [33,47]	33 [9,53]	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA helicase)
1062_g_at	U00672	37 [29,48]	41 [29,53]	34 [29,48]	interleukin 10 receptor, alpha
40659_at	X77922	Absent	31 [16,48]	34 [29,48]	sialyltransferase 8A
237_s_at	M60483	39 [29,103]	52 [37,64]	35 [29,42]	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
259_s_at	M16441	Absent	29 [8,36]	36 [22,47]	tumor necrosis factor (TNF superfamily, member 2)
39703_at	X16396	34 [22,>360]	44 [16,64]	37 [2,50]	methylene THF dehydrogenase (NAD+ dependent)
40516_at	U12767	40 [34,73]	46 [43,49]	38 [23,61]	nuclear receptor subfamily 4, group A, member 3
41447_at	AB014569	46 [31,>360]	32 [29,39]	38 [29,43]	KIAA0669 gene product
1401_g_at	M13207	Absent	18 [10,22]	39 [33,43]	colony stimulating factor 2 (granulocyte-macrophage)
35681_r_at	AB020700	Absent	33 [22,71]	39 [13,>360]	KIAA0893 protein
38822_at	AB023188	46 [43,49]	44 [31,56]	39 [30,43]	KIAA0971 protein
40099_at	M92843	87 [71,137]	41 [36,60]	39 [29,75]	zinc finger protein 36, C3H type, homolog (mouse)
40661_at	U51166	Absent	38 [29,48]	39 [30,44]	thymine-DNA glycosylase
41215_s_at	AB023207	>360 [57,>360]	39 [36,46]	39 [31,49]	carbohydrate (chondroitin) synthase 1
806_at	U56998	68 [45,>360]	46 [43,56]	39 [36,49]	putative serine/threonine protein kinase PRK
38526_at	AF045451	52 [36,187]	112 [57,>360]	40 [30,72]	NGFI-A binding protein 1 (EGR1 binding protein 1)
41384_at	AI452442	Absent	10 [1,>360]	40 [1,>360]	KIAA0669 gene product
35074_at	AB011141	38 [29,>360]	Absent	44 [23,50]	zinc finger homeobox 1b
1400_at	M13207	Absent	24 [15,33]	45 [16,74]	colony stimulating factor 2 (granulocyte-macrophage)

190_at	U12767	Absent	40	[29,53]	45	[36,51]	nuclear receptor subfamily 4, group A, member 3	
32541_at	X97544	43	[29,224]	33	[23,43]	45	[36,50]	translocase of inner mitochondrial membrane 17 homolog A (yeast)
38692_at	X59739	>360	[85,>360]	42	[36,59]	45	[36,57]	zinc finger protein, X-linked
40570_at	D78579	48	[40,58]	45	[35,53]	45	[34,51]	nuclear receptor subfamily 4, group A, member 3
33439_at	U47741	81	[43,>360]	55	[32,>360]	46	[8,>360]	CREB binding protein (Rubinstein-Taybi syndrome)
37537_at	X63717	44	[28,>360]	35	[29,53]	46	[43,53]	tumor necrosis factor receptor superfamily, member 6
38218_at	U02882	Absent	Absent	[1,69]	46	[8,53]	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	
40101_g_at	L19872	>360	[128,>360]	66	[51,77]	46	[37,>360]	aryl hydrocarbon receptor
40678_at	X95525	>360	[41,>360]	167	[85,>360]	46	[31,356]	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100 kD
40865_at	D13891	48	[38,251]	38	[29,74]	46	[37,76]	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
33421_s_at	L20971	Absent	Absent	34	[4,>360]	47	[31,98]	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)
40662_g_at	U41816	Absent	Absent	44	[33,55]	47	[43,56]	prefoldin 4
143_s_at	U75309	67	[37,>360]	29	[2,>360]	48	[23,>360]	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100 kD
39604_at	AF000982	43	[26,>360]	47	[36,61]	48	[29,63]	asparagine synthetase
40074_at	AF000367	>360	[34,>360]	40	[33,49]	49	[36,62]	CDC14 cell division cycle 14 homolog A (<i>S. cerevisiae</i>)
744_at	D50487	>360	[63,>360]	80	[54,>360]	49	[30,>360]	RNA helicase (HRH1)
36926_at	M20681	39	[35,>360]	41	[24,60]	50	[30,63]	solute carrier family 2 (facilitated glucose transporter), member 3
37643_at	AF002697	>360	[52,>360]	54	[39,>360]	50	[41,56]	BCL2/adenovirus E1B 19kD interacting protein 3
41788_i_at	L06797	105	[22,>360]	43	[22,55]	50	[26,88]	chemokine (C-X-C motif), receptor 4 (fusin)
649_s_at	U50553	43	[36,50]	45	[36,49]	50	[36,56]	asparagine synthetase
1102_s_at	M10901	49	[43,130]	50	[37,65]	51	[30,69]	nuclear receptor subfamily 3, group C, member 1
32111_at	M80244	113	[37,>360]	54	[50,63]	51	[43,60]	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
37272_at	D50917	59	[50,>360]	51	[36,75]	51	[36,73]	transcriptional regulator interacting with the PHS-bromodomain 2
36453_at	M10901	>360	[184,>360]	66	[44,>360]	52	[31,>360]	nuclear receptor subfamily 3, group C, member 1
37313_at	X95263	42	[33,>360]	35	[29,82]	52	[43,74]	PWP2 periodic tryptophan protein homolog (yeast)
39744_at	AB014551	83	[55,>360]	55	[40,>360]	52	[44,56]	rho/rac guanine nucleotide exchange factor (GEF) 2
1479_g_at	L10717	48	[43,>360]	57	[45,81]	53	[42,66]	IL2-inducible T-cell kinase
32026_s_at	AF048732	>360	[76,>360]	53	[38,75]	53	[46,62]	cyclin T2
34370_at	AI970189	89	[62,>360]	45	[34,73]	53	[43,62]	Homo sapiens cDNA FLJ31348 fis, clone MESAN2000026
35720_at	AB020651	115	[43,>360]	50	[37,63]	53	[37,68]	KIAA0844 protein
36690_at	X80692	59	[50,128]	47	[40,81]	53	[40,74]	mitogen-activated protein kinase 6
41050_at	AF117829	64	[45,100]	66	[44,97]	53	[27,76]	receptor-interacting serine-threonine kinase 2
39299_at	AF000993	>360	[175,>360]	74	[36,>360]	55	[34,>360]	ubiquitously transcribed tetratricopeptide repeat gene, X chromosome
31854_at	AF035582	106	[56,>360]	66	[40,>360]	56	[38,79]	calcium/calmodulin-dependent serine protein kinase (MAGUK family)
31854_at	AB002311	106	[56,>360]	66	[40,>360]	56	[38,79]	PDZ domain containing guanine nucleotide exchange factor(GEF)1
38010_at	AF042378	125	[93,>360]	50	[36,>360]	56	[50,95]	spindle pole body protein
38669_at	AB011420	46	[32,>360]	32	[29,95]	57	[50,70]	serine/threonine kinase 17a (apoptosis-inducing)
34446_at	D84145	163	[67,>360]	67	[36,>360]	59	[36,>360]	novel RGD-containing protein
36198_at	AL096747	72	[57,91]	60	[50,>360]	59	[42,84]	hypothetical gene DKFZp570I0164
37555_at	AB002303	110	[85,>360]	54	[50,70]	59	[47,91]	endosome-associated FYVE-domain protein
38931_at	AF068836	37	[29,>360]	51	[18,>360]	59	[50,63]	pleckstrin homology, Sec7 and coiled/coil domains, binding protein
38931_at	M31516	37	[29,>360]	51	[18,>360]	59	[50,63]	decay accelerating factor for complement (CD55, Cromer blood group system)
595_at	U56998	>360	[79,>360]	60	[32,90]	59	[36,161]	cytokine-inducible kinase

32186_at	AB026118	41	[29,>360]	59	[47,77]	60	[47,73]	60	[47,73]	mucosa associated lymphoid tissue lymphoma translocation gene 1
33831_at	D31797	74	[51,>360]	53	[44,83]	60	[45,79]	60	[45,79]	tumor necrosis factor (ligand) superfamily, member 5 (hyper-IgM syndrome)
35697_at	X16983	Absent		25	[17,44]	60	[37,>360]	60	[37,>360]	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)
826_at	U50553	249	[79,>360]	54	[44,>360]	61	[43,82]	61	[43,82]	helicase-like protein 2 (DDX14)
40320_at	AF032885	53	[50,95]	49	[32,>360]	65	[48,223]	65	[48,223]	forkhead box O1A (rhabdomyosarcoma)
32350_at	S46622	>360	[>360]	46	[36,59]	66	[41,104]	66	[41,104]	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma)
32350_at	AB014571	>360	[>360]	46	[36,59]	66	[41,104]	66	[41,104]	likely ortholog of mouse suppressors of cytokine signalling 5
1478_at	L10717	>360	[58,>360]	58	[50,70]	67	[59,76]	67	[59,76]	IL2-inducible T-cell kinase
34751_at	L39060	>360	[213,>360]	54	[44,63]	68	[51,223]	68	[51,223]	TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kD
37914_at	M97347	>360	[98,>360]	52	[31,>360]	68	[51,>360]	68	[51,>360]	glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransferase)
32055_g_at	AL050164	Absent		Absent		69	[51,>360]	69	[51,>360]	chromodomain protein, Y chromosome-like
35959_at	U82328	Absent		Absent		69	[42,>360]	69	[42,>360]	Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein
36296_at	AF032119	Absent		41	[32,>360]	69	[37,>360]	69	[37,>360]	calcium/calmodulin-dependent serine protein kinase (MAGUK family)
1779_s_at	M16750	68	[52,>360]	60	[40,>360]	71	[37,>360]	71	[37,>360]	pim-1 oncogene
41003_at	Y16521	56	[43,>360]	44	[31,76]	71	[43,83]	71	[43,83]	CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 2
1562_g_at	U27193	204	[36,>360]	39	[22,54]	72	[18,>360]	72	[18,>360]	dual specificity phosphatase 8
31847_at	X59131	112	[66,>360]	53	[40,70]	72	[34,>360]	72	[34,>360]	highly charged protein
33893_r_at	S82692	>360	[97,>360]	53	[44,>360]	72	[51,>360]	72	[51,>360]	interleukin 2
33249_at	AB016247	45	[32,56]	68	[42,>360]	74	[59,91]	74	[59,91]	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like
34781_at	AF004715	203	[106,>360]	53	[43,>360]	78	[57,>360]	78	[57,>360]	jerky homolog-like (mouse)
36103_at	D13641	>360	[167,>360]	60	[37,70]	80	[26,118]	80	[26,118]	translocase of outer mitochondrial membrane 20 (yeast) homolog
36164_at	D12614	>360	[54,>360]	54	[41,154]	80	[58,86]	80	[58,86]	lymphotoxin alpha (TNF superfamily, member 1)
38353_at	D86959	345	[84,>360]	60	[37,152]	82	[43,>360]	82	[43,>360]	Ste20-related serine/threonine kinase
36979_at	X02419	60	[50,95]	61	[57,70]	88	[50,>360]	88	[50,>360]	plasminogen activator, urokinase
36414_s_at	J04130	>360	[48,>360]	Absent		97	[58,>360]	97	[58,>360]	small inducible cytokine A4
33316_at	D15050	27	[22,>360]	80	[63,>360]	104	[54,>360]	104	[54,>360]	transcription factor 8 (represses interleukin 2 expression)
32829_at	M16801	86	[72,>360]	60	[50,126]	106	[51,>360]	106	[51,>360]	nuclear receptor subfamily 3, group C, member 2
41787_at	M59465	Absent		53	[43,69]	106	[56,>360]	106	[56,>360]	tumor necrosis factor, alpha-induced protein 3
41343_at	U70426	>360	[167,>360]	60	[57,>360]	123	[84,>360]	123	[84,>360]	regulator of G-protein signalling 16
34021_at	X81198	Absent		46	[36,71]	142	[78,>360]	142	[78,>360]	archain 1
1538_s_at	X00695	Absent		34	[28,57]	150	[79,>360]	150	[79,>360]	interleukin 2
160025_at	X70340	>360	[130,>360]	40	[22,>360]	157	[73,>360]	157	[73,>360]	transforming growth factor, alpha
39954_r_at	U72206	>360	[72,>360]	Absent		248	[72,>360]	248	[72,>360]	rho/rac guanine nucleotide exchange factor (GEF) 2
36674_at	U46024	40	[36,>360]	198	[163,>360]	264	[142,>360]	264	[142,>360]	myotubular myopathy 1
33945_at	D84454	Absent		187	[80,>360]	327	[64,>360]	327	[64,>360]	solute carrier family 35 (UDP-galactose transporter), member 2
35731_at	D90144	>360	[205,>360]	52	[30,>360]	344	[159,>360]	344	[159,>360]	small inducible cytokine A3
32975_g_at	AB018351	Absent		Absent		>360	[94,>360]	>360	[94,>360]	KIAA0808 gene product
35006_at	U00672	89	[60,>360]	Absent		>360	[82,>360]	>360	[82,>360]	interleukin 10 receptor, alpha
36920_at	U16954	>360	[>360]	39	[36,43]	>360	[61,>360]	>360	[61,>360]	ALL1-fused gene from chromosome 1q
34230_r_at	AL049701	>360	[26,>360]	Absent		Absent		Absent		KIAA0471 gene product
36941_at	X57206	189	[59,195]	Absent		Absent		Absent		inositol 1,4,5-trisphosphate 3-kinase B
40591_at	D78579	104	[50,>360]	Absent		Absent		Absent		nuclear receptor subfamily 4, group A, member 3

Supplemental Statistical Methods

We used a first order decay model to compute the half-lives of transcripts expressed in T cells. Affymetrix software was used to assign hybridization intensities represented by the average difference between the positive match and mismatch probes (the AD) for each time point under each stimulation condition. These AD values were scaled equally across points and normalized to the AD value of GAPDH at time 0 for each experiment. Let y_{ijkl} = the normalized, scaled AD values at time t_{ik} for gene j on experiment k under the l^{th} stimulation condition, where $i = 1, \dots, I_k$ (the number of points in a given experiment), $j = 1, \dots, 12,625$ (the number of genes on each microarray), $k = 1, 2, 3, 4$ and $l = 1, 2, 3$. It is customary to model the intensity at a feature on a microarray as a signal that is corrupted by multiplicative error (e.g., Newton, et al. (2001)). The AD values reported by the Affymetrix software are linear combinations of these variables (which are corrupted by multiplicative error), hence the AD is subject to additive error. This additive error becomes clearest when we find (like many others using version 4.0 of the Affymetrix software) that some of these AD values are negative. Moreover, since these AD values are averages the central limit theorem implies the distribution of these quantities is approximately Gaussian. For these reasons, we propose the following model for y_{ijkl}

$$y_{ijkl} = \beta_{0jkl} e^{-\beta_{1j} t_{ik}} + \epsilon_{ijkl}.$$

To use this decay model, 12 observations are used to estimate 6 parameters (the 4 experiment specific intercepts the decay rate and the variance of the errors) for each of the 37,875 separate nonlinear regressions. We here treat each gene as independent of the other genes given the normalization, as is commonly done in the analysis of microarrays (e.g. Dudoit et al. (2002) and Efron (2001)).

Since the sample size is small the usual approximations for the standard errors (based on Gaussian errors and maximum likelihood) of these estimates are not reliable. In addition, estimates based on resampling would be inaccurate since the justification of resampling schemes relies on asymptotic arguments (see, e.g., van der Vaart). Thus, we suppose the parameters are random variables and use Bayesian methods to compute probability intervals (see for example, Box and Tiao 1973, Section 8.2.6). An essential ingredient in the Bayesian approach is a prior distribution for each model parameter. For the standard deviation, we use the usual uniform distribution over the natural parameter space (see for example, Berger (1980)). We use priors that are uniform over the real line for the intercepts as is commonly done in regression models (Berger (1980)), and we use a prior for the half-lives that supposes they are uniform over the range from 1 minute to

10 hours. Since we are primarily interested in inference for the half-lives, we used a vague prior for this parameter, but we could have instead used a vague prior for the decay rate. Since these 2 priors are both reasonable *a priori*, we used both to assess sensitivity of the results to the prior distribution, although the results presented in the manuscript use the vague prior on the half-life scale (since this is the parameter of interest, as discussed in Berger (1980)). The results are not unduly sensitive to the specification of the prior (the correlation of the posterior probabilities of differences in half-lives across conditions from the 2 models exceeds 0.7 for all comparisons).

We find the marginal posterior distribution of the regression parameters (under the assumption of Gaussian error after analytically integrating the error variance out of the posterior distribution) is

$$p(\beta_{0jM}, \beta_{1jM} | y_{ijM} \quad i = 1, \dots, k_I \quad k = 1, \dots, 4) \propto \left(\sum_{k=1}^4 \sum_{i=1}^{I_k} (y_{ijM} - \beta_{0jM} e^{-\beta_{1jM} t_{ik}})^2 \right)^{-0.5}$$

We can then use the posterior distribution of the parameters to construct credible intervals and answer questions we may have about the parameters, such as the marginal probability that different stimulation conditions are associated with different half-lives (these marginal probabilities are what is reported in the body of the manuscript). We can also use the simulations to find the largest possible set of genes so that the joint posterior probability that this set of genes have half-lives that differ across experimental conditions exceeds some value, such as 0.95. This is the usual Bayesian approach to multiple comparisons, see e.g., Meng and Dempster (1987). The latter computation indicates that there are 29 genes that have a half-life that differs across at least one condition. We can also compute these quantities for specific comparisons, such as media compared to stimulation with anti-CD3 antibodies (24 genes), media compared to stimulation with anti-CD28 antibodies (18 genes) and anti-CD3 compared to anti-CD28 (16 genes). Since the posterior probabilities computed by this method are asymptotically equivalent to *p*-values (see Rubin (1984)) we refer to the results as *p*-values and confidence intervals in the manuscript to use terms more familiar to the audience (although strictly speaking we are reporting posterior probabilities and credible intervals).

We use a sequential rejection sampling algorithm to draw simulations from the posterior distribution in a quick and reliable fashion (Gelman et al. (1995)). By independence across genes and stimulation conditions, we can fit each non-linear regression independently of the rest. Let y_k denote the measurements from the k^{th}

experiment. To sample from the posterior, we use the recursion,

$$p(\beta_{1jl}|y_1, \dots, y_k) \propto \int p(y_k|\beta_{1j}, \beta_{0jkl})p(\beta_{1j}|y_1, \dots, y_{k-1})p(\beta_{0k}) d\beta_{0k},$$

that is seen to be true by an application of Bayes theorem and the structure of the model. Here, the integrand is the posterior from the non-linear regression for one experiment with a non-informative prior on the intercept and prior for the decay rate given by the posterior from the previous experiment (in practice it makes sense to start the recursion with an experiment with 4 time points). We used rejection sampling with a histogram based proposal density to simulate from this bivariate distribution. We then numerically integrate the intercept out of the distribution (by summing over this dimension in the samples). From the rates it is easy to get the half-lives (since half-life = $\log 2 / |\lambda|$), so we can draw simulations from the distribution of half-lives. We drew 10,000 samples for each half-life and used these to construct the credible intervals. To compute the y-intercept (β_{0jkl}) for each transcript under each stimulation condition, we fit a model identical to the model described above with the exception that we supposed there is a common intercept for all experiments.

An essential component of fitting parametric models is checking the assumptions used for parameter estimation. Although we expect the AD values to be approximately normal by the central limit theorem, we examined the residuals from the model as a check on the normality assumption. To make our simulation algorithm as fast as possible, we numerically integrated the experiment specific intercepts out of the posterior, yet these intercepts are clearly necessary to construct sets of residuals. Hence we fit the decay model to a subset of 1,155 genes (chosen to include all of the genes with significant differences) for one of the experiments with 4 time points (we further restricted these diagnostics to the media condition). In this fashion we obtain estimates (the posterior medians) of the intercept and decay rate, and this allows us to define residuals. If we then standardize these residuals by their gene specific standard deviation we should obtain a set of independent, standard normal deviates (4 such deviates for each gene). As a check on normality at the level of the gene, we computed the correlation between the ordered residuals and the corresponding quantiles of the normal distribution. Using the parametric bootstrap, the critical value for this correlation is 0.87 (i.e. 95% of the time we expect that this correlation should exceed 0.87 if the residuals are truly standard normal deviates). For the 1155 genes we used for diagnostic purposes, 42 (about 4%) had correlations less than this value. Hence this check gives no reason to doubt the normality of the errors.

References

- Berger, J. (1980), *Statistical Decision Theory and Bayesian Analysis*, Springer, New York.
- Box, G., Tiao, G. (1973), *Bayesian Inference in Statistical Analysis*, Wiley.
- Dudoit, S., Yang, Y., Callow, M., Speed, T. (2002), ``Statistical methods for identifying differentially expressed gene in replicated cDNA microarray experiment'', *Statistica Sinica*, 12 111-139.
- Efron, B., Tibshirani, R., Storey, J., Tusher, V. (2001), ``Empirical Bayes analysis of a microarray experiment'', *Journal of the American Statistical Association*, 96, 1151-1160.
- Meng, C., Dempster, A. (1987), ``A Bayesian approach to the multiplicity problem for significance testing with binomial data'', *Biometrics*, 43, 301-311.
- Newton, M., Kendziorski, C., Richmond, C., Blattner, F., Tsui, K. (2001), ``On Differential variability of expression ratios: improving statistical inference about gene expression changes from microarray data'', *Journal of Computational Biology*, 8:37-52.
- Rubin, D. (1984) ``Bayesianly justifiable and relevant frequency calculations for the applied statistician'', *Annals of Statistics*, 12, 1151-1172.
- van der Vaart, A. (1998), *Asymptotic Statistics*, Cambridge University Press, Cambridge.