

Table S1. 39 Acetylation Island Sequences Conserved Between Human and Pufferfish and their Relative Enhancer Activities in Jurkat Cells.

Name	Chromosome	Begin	End	Length (bp)	% Identity	Normalized acetylation count	Name of nearest gene	Distance to the nearest TSS (bp)	Fold luciferase expression	p-value
1	chr10	23733713	23733831	119	72.3	0.36	<i>C10orf67</i>	-95935	1.1	
2	chr22	24176234	24176337	104	74.0	1.00	<i>LRP5L</i>	-93156	<u>5.5</u>	2.7E-09
3	chr7	50103100	50103211	112	78.6	2.00	<i>ZNFN1A1</i>	-82767	<u>3.2</u>	2.2E-10
4	chr11	33569190	33569358	169	81.7	0.50	<i>C11orf69</i>	-88927	0.7	
7	chr8	1636821	1636979	159	83.6	4.00	<i>CLN8</i>	-62368	<u>2.7</u>	9.9E-09
9	chr13	22623866	22624000	135	75.6	10.00	<i>C1QTNF9</i>	-57715	<u>2.0</u>	2.2E-07
11	chr5	78617216	78617584	369	74.4	12.00	<i>JMY</i>	-40239	0.5	
12	chr5	78616547	78616697	151	74.8	4.17	<i>JMY</i>	-41126	0.4	
13	chr16	89903099	89903218	120	74.4	9.00	<i>PRDM7</i>	-32187	0.4	
15	chr9	126118330	126118461	132	80.3	12.00	<i>FAM102A</i>	-29292	<u>1.8</u>	1.5E-06
17	chr11	64402763	64402928	166	77.7	1.50	<i>CDC42BPG</i>	-15362	0.5	
19	chr2	27268753	27268870	118	82.2	8.50	<i>EMILIN1</i>	-7598	1.2	
22	chr1	6229617	6229750	134	71.6	10.00	<i>TNFRSF25</i>	6051	1.2	
25	chr1	8737285	8737388	104	71.2	2.75	<i>CA6</i>	21798	0.5	
27	chr5	156622099	156622215	117	69.2	3.25	<i>ITK</i>	33298	0.6	
28	chr15	40589598	40589731	134	72.6	1.50	<i>CEP27</i>	32490	1.2	
29	chr4	40142196	40142760	565	72.7	6.25	<i>RHOH</i>	46415	0.5	
30	chr1	910650	910764	115	75.7	3.00	<i>C1orf159</i>	46763	<u>3.8</u>	7.3E-11
32	chr12	123303818	123303931	114	78.1	6.25	<i>NCOR2</i>	52008	<u>2.6</u>	1.2E-09
34	chr2	86240990	86241120	131	77.1	1.50	<i>POLR1A</i>	66388	<u>1.5</u>	1.3E-05
C01	chr16	2414491	2414603	113	79.8	0.50	<i>CCNF</i>	-4747	<u>1.5</u>	2.3E-05
C02	chr17	80578170	80578285	116	72.4	0.33	<i>PYCR1</i>	-4387	0.5	
C03	chr15	87925608	87925884	277	72.6	0.18	<i>KIF7</i>	-4266	0.9	
C04	chr21	36423508	36423619	112	76.8	4.50	<i>CBR3</i>	-4039	0.8	
C06	chr3	52186980	52187146	167	69.4	0.33	<i>ALAS1</i>	-3438	0.9	
C07	chr7	100407710	100407825	116	78.4	0.50	<i>MOGAT3</i>	-3227	1.3	
C08	chr2	241821099	241821240	142	69.7	3.50	<i>ANKMY1</i>	-2954	<u>2.7</u>	4.8E-09
C09	chr19	50837301	50837424	124	71.8	3.75	<i>EML2</i>	-2792	0.5	
C10	chr17	7956030	7956209	180	80.6	2.00	<i>TMEM88</i>	-2740	1.0	
C11	chr11	65159652	65159777	126	73.8	2.50	<i>MAP3K11</i>	-2572	1.0	
C12	chr1	143223207	143223325	119	69.7	3.75	<i>LIX1L</i>	-2446	<u>2.4</u>	2.5E-08
C13	chr7	92076841	92076958	118	73.9	1.00	<i>CDK6</i>	-1600	1.0	
C14	chr19	19635087	19635188	102	70.6	2.00	<i>ATP13A1</i>	-1162	<u>4.7</u>	2.5E-10
C15	chr2	70290281	70290447	167	76.0	2.78	<i>PCBP1</i>	1047	<u>1.8</u>	6.1E-07
C16	chr7	5312252	5312688	437	88.8	1.92	<i>ACTB</i>	1871	0.7	
C17	chr6	109820712	109820828	117	71.8	3.00	<i>MICAL1</i>	1932	1.1	
C18	chr1	231827152	231827462	311	77.5	2.33	<i>IRF2BP2</i>	2078	1.2	
C19	chr3	32967043	32967143	101	70.3	1.50	<i>CCR4</i>	2210	0.7	
C20	chr1	44681921	44682055	135	74.8	1.83	<i>PLK3</i>	2592	1.4	

Length denotes the size of each conserved histone acetylation island sequence, which forms the center of the ~1.2kb sequence tested in the enhancer assays. The normalized acetylation count is the total acetylation tag count divided by the number of tag types in each region. Negative values denote regions upstream of a transcription start site (TSS) relative to the direction of transcription. Constructs with fold luciferase values of 1.5 or greater (underlined values) were regarded to have enhancer activity in our assays. The p-values for the constructs showing enhancer activity were obtained by performing Student t-tests on duplicate luciferase assays compared to those of nine randomly chosen non-acetylated regions (Table S3).

Table S2. 51 Human-Mouse Non-Conserved Acetylation Island Sequences and their Relative Enhancer Activities in Jurkat Cells.

Name	Chromosome	Begin	End	Length (bp)	Normalized acetylation count	Name of the nearest gene	Distance to the nearest TSS (bp)	Fold luciferase expression	p-value
41	chr9	42283555	42283784	229	5.44	<i>ZNF658</i>	-489624	0.6	
44	chr8	8239572	8240108	536	3.33	<i>CLDN23</i>	-356967	1.2	
45	chr10	6973863	6974282	419	1.50	<i>PRKCQ</i>	-347619	<u>3.2</u>	1.0E-10
46	chr3	18756848	18758504	1656	1.67	<i>SATB1</i>	-316504	0.6	
47	chr21	31478536	31479430	894	3.40	<i>TIAM1</i>	-304215	0.8	
48	chr11	11135671	11137049	1378	3.67	<i>MRV11</i>	-291748	1.1	
49	chr15	28634195	28634446	251	3.50	<i>CHRNA7</i>	-232275	<u>12.6</u>	6.2E-13
50	chr15	31098145	31099581	1436	1.38	<i>RYR3</i>	-219651	0.7	
51	chr10	470348	470863	515	1.60	<i>C10orf108</i>	-179024	<u>2.0</u>	6.2E-07
52	chr11	2685734	2686973	1239	2.40	<i>KCNQ1DN</i>	-168628	<u>1.8</u>	2.8E-05
54	chr1	9186483	9187191	708	1.80	<i>MGC4399</i>	-121912	0.6	
55	chr1	24705506	24706806	1300	1.50	<i>RUNX3</i>	-97970	0.9	
59	chr1	19264616	19265033	417	1.83	<i>CAPZB</i>	-48896	0.4	
60	chr6	29970069	29970470	401	4.75	<i>HLA-A</i>	-45700	<u>2.0</u>	3.9E-08
61	chr7	5606595	5607104	509	2.14	<i>TRIAD3</i>	-40965	<u>5.1</u>	9.7E-10
66	chr1	25702441	25703408	967	2.57	<i>SEPN1</i>	-27950	0.9	
67	chr1	9397102	9397566	464	3.50	<i>PIK3CD</i>	-23782	<u>1.6</u>	3.3E-06
68	chr10	22315316	22315749	433	2.25	<i>DNAJC1</i>	-18840	<u>1.9</u>	3.8E-07
71	chr6	2799060	2799800	740	3.50	<i>SERPINB1</i>	-11980	<u>2.7</u>	2.4E-08
72	chr17	8303820	8304309	489	2.20	<i>C17orf59</i>	-9864	<u>2.6</u>	2.0E-08
73	chr22	16074256	16074616	360	4.00	<i>CECR1</i>	-8923	<u>6.4</u>	1.3E-13
74	chr22	16638500	16639513	1013	2.00	<i>BID</i>	-6688	<u>1.9</u>	7.7E-07
76	chr19	1804025	1804986	961	3.00	<i>REXO1</i>	-4575	1.2	
77	chr3	15116062	15116620	558	4.17	<i>ZFYVE20</i>	-3431	0.5	
78	chr4	2227674	2228665	991	1.60	<i>MXD4</i>	-2296	0.8	
79	chr3	25682158	25682749	591	3.67	<i>TOP2B</i>	-1405	1.2	
80	chr1	3323158	3323874	716	3.33	<i>FAM79A</i>	-674	0.7	
81	chr14	22757668	22758458	790	3.00	<i>DHRS1</i>	336	<u>1.9</u>	1.6E-07
83	chr6	15357320	15358161	841	3.40	<i>JARID2</i>	2815	<u>1.5</u>	7.4E-06
84	chr11	35128292	35128862	570	1.00	<i>CD44</i>	3567	0.7	
85	chr17	3905376	3906763	1387	2.00	<i>ITGAE</i>	4364	<u>1.5</u>	6.4E-05
87	chr11	1843887	1844624	737	1.75	<i>LSP1</i>	5379	1.3	
90	chr1	25921192	25921573	381	2.00	<i>PAFAH2</i>	7763	0.8	
91	chr12	6941004	6941522	518	8.25	<i>PHB2</i>	8630	<u>2.3</u>	1.2E-08
92	chr22	20330598	20330960	362	2.50	<i>SDF2L1</i>	9503	0.7	
93	chr11	2373918	2374887	969	2.17	<i>CD81</i>	11063	<u>1.8</u>	5.1E-06
94	chr16	11741507	11741863	356	1.40	<i>SNN</i>	12759	<u>7.0</u>	8.1E-13
96	chr19	6741322	6742083	761	1.40	<i>VAV1</i>	17601	0.8	
99	chr19	6751820	6752244	424	4.00	<i>VAV1</i>	28099	0.7	
100	chr7	707149	707706	557	8.50	<i>CENTA1</i>	30899	<u>1.9</u>	1.4E-07
101	chr6	30038689	30038984	295	6.50	<i>HCG9</i>	-9729	<u>6.8</u>	3.9E-12
102	chr8	22421150	22421590	440	3.33	<i>SORBS3</i>	-9598	0.9	
104	chr23	15053936	15054439	503	5.33	<i>TMEM27</i>	-9356	<u>2.2</u>	2.7E-08
106	chr7	2291733	2292588	855	4.14	<i>LFNG</i>	-9246	<u>1.5</u>	6.8E-06
110	chr20	3787104	3788163	1059	3.50	<i>C20orf29</i>	-8039	<u>2.1</u>	1.5E-07
116	chr23	12347063	12347779	716	3.00	<i>TMSB4X</i>	-6873	1.1	
117	chr14	33005773	33006003	230	6.36	<i>C14orf11</i>	-6817	<u>2.2</u>	1.1E-07
122	chr16	1411039	1411441	402	3.75	<i>UNKL</i>	-6346	<u>2.2</u>	1.4E-07
125	chr4	2845016	2846100	1084	2.70	<i>SH3BP2</i>	-5853	<u>2.3</u>	8.1E-07
128	chr10	15005285	15006189	904	3.60	<i>DCLRE1C</i>	-5185	0.8	
129	chr17	7581127	7582722	1595	3.05	<i>ZBTB4</i>	5360	1.0	

Items shown in this table are as described in the Table S1 legend.

Table S3. 9 Randomly Chosen Non-Acetylated Sequences and their Relative Enhancer Activities in Jurkat Cells.

Name	Chromosome	Begin	End	Length (bp)	Fold luciferase expression
NC1	15	28,649,780	28,650,965	1185	0.9
NC2	6	29,976,105	29,977,348	1243	0.8
NC3	7	5,589,897	5,591,118	1221	1
NC4	10	22,306,865	22,308,034	1169	0.8
NC5	13	22,612,263	22,613,420	1157	0.9
NC6	5	78,627,889	78,629,129	1240	1
NC7	16	89,900,776	89,902,011	1235	0.9
NC8	9	126,131,232	126,132,433	1201	0.9
NC9	12	123,350,008	123,351,207	1199	1.1

Items shown in this table are as described in the Table S1 legend.

Table S4. 9 Non-Conserved Orthologous Mouse Sequences and their Relative Enhancer Activities in Human Jurkat and Mouse EL4 Cells.

Name	Chromosome	Begin	End	Length (bp)	Name of the nearest gene	Luciferase activity in Jurkat cells	Luciferase activity in EL4 cells
M45	chr2	10749536	10750530	995	<i>Prkcq</i>	1.4	<u>1.8</u>
M61	chr5	141957110	141957884	775	<i>Ubce7ip1</i>	<u>2.1</u>	<u>2.1</u>
M71	chr13	32764172	32766175	1687	<i>Serpinb1c</i>	<u>1.5</u>	<u>3.7</u>
M73	chr6	122267622	122268796	953	<i>Cecr5</i>	<u>3.2</u>	<u>1.9</u>
M74	chr6	122627111	122628570	1291	<i>Bid</i>	0.7	1.1
M81	chr14	46872614	46873296	659	<i>Dhrs1</i>	0.8	0.9
M83	chr13	44799911	44801020	1003	<i>Jarid2</i>	0.9	1.1
M93	chr7	135134467	135134898	415	<i>Cd81</i>	<u>2.2</u>	<u>9.5</u>
M94	chr16	10639198	10640489	1292	<i>Snn</i>	1.3	<u>3.3</u>

Items shown in this table are as described in the Table S1 legend.