

Supplemental Table 1 for TIRF-PBM

<u>Position</u>	<u>Sequence</u>	<u>Gene</u>	<u>TBP Annotation</u>
1	CTCAGGAATCCCATAAAGTAATGTGGAGCTCAGTTCAAGTCAATCGGTCC		Poor
2	CTCAGGAATTCCTATAGAGTAATGTGGAGCTCAGTTCAAGTCAATCGGTCC		Poor
3	TCCTGAAGGGGCACCCCTAGCTTGGTCTATCGTCGTCAGTCAATCGGTCC		
4	GAATTCCTATGAAGTAATGTGGAGCTCCGTTCTCAAGTCAATCGGTCC		
5	CTGCTCCGTCCGCCTTCGAGGAGAGGTCGGCATCTTCAAGTCAATCGGTCC		Poor
6	CTCAGGAATTCCTATAAAGTAATGTGGAGCTCAGTTCAAGTCAATCGGTCC		Good
7	CTCAGGAATTCCTATCAAGTAATGTGGAGCTCAGTTCAAGTCAATCGGTCC		Poor
8	TCCTGAAGGGGCGCCCTAGCTTGGTCTATCGTCGTCAGTCAATCGGTCC		Poor
9	TCTTTTCTTGCTTAAATCTATAACTACAAAAACATCAAGTCAATCGGTCC	TPI1	Good
10	CGCGCCTGCGCTCTATATATACAGCGCCCTGCCCTCAAGTCAATCGGTCC	HIST1HIC	
11	ATGTACACAGAAGCAAAGTACGAATCAGAATCAAAATCAAGTCAATCGGTCC	TAF5	Good
12	CAAATGTATGCACCATATCCATTCTAAACATAGTTTCAAGTCAATCGGTCC	UBI1	Good
13	TGGATCAATCGTATAAAGAGAATTCCTGGTATGGATCAAGTCAATCGGTCC		Good
14	TGGTATAAAGATCAATCGAGAATTCCTGGTATGGATCAAGTCAATCGGTCC		Good
15	GCCGGCCGGCCGGCCGGCCCGGGCCCGCGCTCAATTCAATCGGTCC		Poor
16	CTCAGGAATTCCTCTAAAGTAATGTGGAGCTCAGTTCAAGTCAATCGGTCC		Poor
17	CTCAGGAATTCCTAGAAAAGTAATGTGGAGCTCAGTTCAAGTCAATCGGTCC		Good
18	CTGAAGGGGGGCTATAAAAGGGGATGGGGCTCCTCAAGTCAATCGGTCC		Good
19	AAATCTTTTCTTTTCCATTCAATCAATTAATTTTCAATTCAATCGGTCC	CLN2	
20	GAATTCCTAAAAAGTAATGTGGAGCTCCGTTCTGCTCAAGTCAATCGGTCC		
21	CTCGCTCCATCTCCAGAACTACAAGTCCCAGAGTGTCAAGTCAATCGGTCC	HPIP	
22	TTCTTGAAGGGGGCTATAAAAGGGGTTGGGGCGTCAAGTCAATCGGTCC		Good
23	CTCAGGAATTCCTACAAAAGTAATGTGGAGCTCAGTTCAAGTCAATCGGTCC		Poor
24	TCCTGAAGGGGCACCTATAAAAGGTCCTATCGTCGTCAGTCAATCGGTCC		
25	CTGAAGGGGGGCTATAAAAGGGGTTGGGGCTCCTCAAGTCAATCGGTCC		Good
26	ATGACTGAATCAAGGCCGTTCTGCTAAGAAAGTCAAGTCAATCGGTCC	CYC1	Good
27	CTCAGGAATTCCTATACAGTAATGTGGAGCTCAGTTCAAGTCAATCGGTCC		Good
28	CTCAGGAATTCGATAAAGTAATGTGGAGCTCAGTTCAAGTCAATCGGTCC		Good
29	TCCTGAAGGGACGCCATAAAAGGTCCTATCGTCGTCAGTCAATCGGTCC		Good
30	TCCTGAAGGGGCGACTAGCTTGGTCTATCGTCGTCAGTCAATCGGTCC		Good
31	GAAAAACATCTAACATAAATATATAAACGAAACATCAAGTCAATCGGTCC	HHT1	
32	TGGATCAATCGAGAATTCGCGCAAGTGGTATGGATCAAGTCAATCGGTCC		
33	GATTTAATATTAACCTTATATATGTAACCTTATTTATCAATTCAATCGGTCC		
34	CTCAGGAATTCCTATAACGTAATGTGGAGCTCAGTTCAAGTCAATCGGTCC		Good
35	TCCTGAAGGGGCGACTATAAAAGGTCCTATCGTCGTCAGTCAATCGGTCC		Poor
36	AGCTAAAATTTGGACAGCTCTCATTACTAAATTAATCAATTCAATCGGTCC	GCY1	Good
37	TGATTTCTCGAAGAATATACTAAAAATGAGCAGTCAATTCAATCGGTCC	HIS3	
38	GAATTCCTGTAAAGTAATGTGGAGCTCCGTTCTGCTCAAGTCAATCGGTCC		Poor
39	ACCAGCCCATATAAATGTCACGTGCTCTAACTCTCAAGTCAATCGGTCC	CRYGS	
40	ATTCCAGTATGGCGTATAAATAAAGCGAGGAGAATCAAGTCAATCGGTCC	SFRS3	Poor
41	GTATAAAGTTCTGTAAGGGGGGCGGGTGGGGTCAAGTCAATCGGTCC		Good
42	GATCGATCGATCGATCGATCGATCGATCGATTCAATTCAATCGGTCC		Good
43	CTCAGGAATTCCTGTAAAGTAATGTGGAGCTCAGTTCAAGTCAATCGGTCC		Poor
44	TCCTGAAGGAGCGCCTATAAAAGGTCCTATCGTCGTCAGTCAATCGGTCC		Good
45	TCCTGAAGGGACGCCCTAGCTTGGTCTATCGTCGTCAGTCAATCGGTCC		
46	CTTGAAGGGGGCTATAAAAGGGGTTGGGGCGCGTCAAGTCAATCGGTCC		Good
47	CTCAGGAATTCCTATGAAGTAATGTGGAGCTCAGTTCAAGTCAATCGGTCC		Good
48	CTCAGGAATTCCTATAAAGTAATGTGGAGCTCAGTTCAAGTCAATCGGTCC		Poor

49	TCCTGAAGAGGCGCCCTAGCTTGGTCCTATCGTCGTCAAGTCAATCGGTCC		Poor
50	TCCTGAAGGGGAGCCCTAGCTTGGTCCTATCGTCGTCAAGTCAATCGGTCC		Good
51	TCCTGAAGGGGCGACCTAGCTTGGTCCTATCGTCGTCAAGTCAATCGGTCC		
52	CTGAAGGGGGGCTATAAAAAGTTTATGGGGCTCCTCAAGTCAATCGGTCC		Good
53	TACTTCAGTTGTGAAGTGTAAACAAGTCTTATAAATCAAGTCAATCGGTCC	UGA4	Good
54	CCCCCGCCTACGCAAGTTTCCGGATCCGTCCATCAAGTCAATCGGTCC		
55	TCGGCTGGGAGGGAGGTGTAGCCGGTCTTTGGGGTCAAGTCAATCGGTCC		
56	GATCGATCGATCGAATCTCGATCGATCGATCGATTCAATTCAATCGGTCC		
57	GTTCTGAAGGGGGGCTATAAACGGGGTGGGGTCAAGTCAATCGGTCC		
58	TCCTGAAGGAGCGCCCTAGCTTGGTCCTATCGTCGTCAAGTCAATCGGTCC		
59	CTGAAGGGGGGCTATAAAAAGAGGTGGGGCTCCTCAAGTCAATCGGTCC		
60	CCGTAGTGCCTCGCCTCCGTTGCCGGGAAACGACTCAAGTCAATCGGTCC	POL1	Poor
61	AAAAACAATAAATCCTATAACCAGTTCTCCCGTCAAGTCAATCGGTCC	MYO4	Poor
62	TACTTGAAGTTGACAATATTATTTAAGGACCTATTTCAAGTCAATCGGTCC	LEU2	Poor
63	CTCAATCAATTTGTGAAGGTATAACTGTAGCCGTGTCAAGTCAATCGGTCC	ATP16	Good
64	ACATTTTTTCGTTTGTAGATAAATCAAGAATCTCAATTCAATCGGTCC	ARG8	
65	CCCGCCCCGACTAGGACCCCTGCAGATGATCAGGTCAAGTCAATCGGTCC		Poor
66	ATGATGTCCTTTTCCAAAACGCCACTCCTAGAGCTCAAGTCAATCGGTCC	TAF2	
67	TGCATAAGATTTGGTCCAGTACTCGCAGGAAATGGTCAAGTCAATCGGTCC	HO	
68	TGGATCAATCGAGAATCCTGGTATGGTATAAAGATCAAGTCAATCGGTCC		
69	GTTCTGAAGGGGGGCTATAAACGGGGTGGGGTCAAGTCAATCGGTCC		Good
70	TCCTGAAGGGGAGCCTATAAAAAGTCTATCGTCGTCAAGTCAATCGGTCC		Good
71	TCCTGAAGGGGCGCATATAAAAAGTCTATCGTCGTCAAGTCAATCGGTCC		Good
72	ATGATTACTAATTTTAACTTCGAGTTCAATCTCTCAAGTCAATCGGTCC	ACT1	Good
73	ACAACGAGACACGAAGGTATAAAAAATAAATACATCAAGTCAATCGGTCC		
74	TATTATGGCACTTCTGTATAACTGGCTTTCATTCTCAAGTCAATCGGTCC	PPH22	
75	GAATTCCTATAAAGTAATGTGGAGCTCCGTTCTCAAGTCAATCGGTCC		Good
76	TTGTGCTACGGTCTCTCCACCCCTGCTGCTGTCAAGTCAATCGGTCC	RAB30	Good
77	GGTGAGGGTACTTATGCGGTTGTTACTTGGGTTGTCAAGTCAATCGGTCC	KIN28	
78	GTTCTGAATATAAAAAGGGGGGCGGGTGGGGTCAAGTCAATCGGTCC		
79	TCCTGAAGGGGCGCCTATAAAAAGTCTATCGTCGTCAAGTCAATCGGTCC		
80	CTGAAGGGGGGCTATAAAAAGTTAGTGGGGCTCCTCAAGTCAATCGGTCC		
81	CCAACCGGACTTTGGGCTAGCGTTTAGAAAAGTCTCAAGTCAATCGGTCC	PYK	
82	CGTCACTGGCGTGACCGTCCGCGCTACATACTGCGTCAAGTCAATCGGTCC	RPL5	
83	GAATTCCTATATATTAATGTGGAGCTCCGTTCTCAAGTCAATCGGTCC		Poor
84	GGGGGCTATAAAAAGGGGTGGGGGCGGTTCTCAAGTCAATCGGTCC		Poor
85	GAAGCGAGTACGGAGGTACCAGCTGGTCTCCGTAGTCAAGTCAATCGGTCC	ZNF513	
86	GTTCTGAAGGGGGGCGGGTGGGTATAAAAAGGTCAAGTCAATCGGTCC		Good
87	TCCTGAAGAGGCGCCTATAAAAAGTCTATCGTCGTCAAGTCAATCGGTCC		
88	TGGCACTCGGGAGGCAGCGGCACTTTGGGGAAAGTCAAGTCAATCGGTCC	PGK	
89	TAAATATTCTTTCTTATACATTAGGACCTTTGCATCAAGTCAATCGGTCC	CYC1	
90	TATCACAGAAAAAAGAAAATATAATAAATTAGTATCAAGTCAATCGGTCC	POX1	Poor
91	CTAATATACACGGATACAAAAGAAATACACATAAATCAATTCAATCGGTCC	ARG1	Poor
92	TTGCCTGAAAAGAGTATAAAAAGAAATTCAGCATGATCAAGTCAATCGGTCC	AFP	
93	GGAAGTGACGTACGTGTCACACGTGGTCCGGCGTCAAGTCAATCGGTCC	GNL2	Poor
94	CCGGGTTCTGTTTCCCGCCGCGGCACTCCAGATCAAGTCAATCGGTCC	MID1	Poor
95	AACAAGTACAACACTCTCAATAAATTATGCGCTTCAAGTCAATCGGTCC	POL2	Poor
96	ATTTTTTAGTCTATATATACTCGCTCTGCCTTGTCAAGTCAATCGGTCC		