

Motif	Group Specificity	Group Specificity Rank	Site Specificity	Site Specificity Rank	Testset Sites	Average Testset Sites	StDev Testset Sites	TRANSFAC Correlation	TRANSFAC ID	Motif Finders	Sets	Repeats	Logo
1	4.40e-012	1	8.40e-011	1	9	0.38	0.49	0.63	SP1	AA, ME	1, 2, 3, 4, 5		
2	2.80e-010	2	9.70e-008	7	27	1.10	1.40			AA, BP, ME	1, 2, 3, 4, 5	TR	
3	2.00e-009	3	5.50e-008	2	11	0.46	0.59	0.66	CACBIN	AA, BP, MD, ME	2, 3, 4, 5		
4	2.60e-009	4	2.60e-005	25	204	8.50	12.00	0.82	PR	ME	1, 2, 3, 4, 5		
5	6.90e-009	7	1.10e-007	8	12	0.50	0.72	0.71	OSF2	AA, ME	1, 2, 3, 4, 5	PAL	
6	7.20e-009	8	7.30e-008	5	10	0.42	0.65			BP, ME	1, 2, 3, 4, 5		
7	1.10e-008	10	1.70e-007	9	14	0.58	0.97	0.68	PU1	AA, ME	1, 2, 3, 4, 5	PAL	
8	1.30e-008	11	8.70e-008	6	8	0.33	0.56			ME	1, 2, 3, 4, 5		
9	2.50e-008	14	6.70e-008	3	9	0.38	1.10			AA, MD, ME	1, 2, 4, 5	TR	
10	2.90e-008	15	2.90e-007	10	9	0.38	0.58			ME	1, 2, 3, 4, 5		
11	7.70e-008	16	1.60e-005	22	26	1.10	1.40	0.75	HMX1	MD, ME	1, 2, 3, 4, 5		
12	8.10e-008	17	5.10e-007	12	10	0.42	0.78	0.81	DBP	ME	1, 2, 3, 4, 5		
13	2.70e-007	21	3.50e-006	16	12	0.50	0.72	0.64	EGR3	ME	1, 2, 3, 4, 5		
14	2.80e-007	22	1.80e-006	14	10	0.42	0.72	0.64	TAL1AL	ME	1, 2, 3, 4, 5		
15	1.00e-006	25	8.40e-006	19	11	0.46	0.88	0.63	SMAD	AA, ME	1, 2, 3, 5		
16	1.10e-006	26	4.90e-006	17	8	0.33	0.64	0.65	HAND1E	ME	1, 2, 3, 4, 5		
17	1.10e-006	26	7.00e-006	18	14	0.58	1.30	0.66	IRF	AA, MD, ME	1, 2, 3, 4, 5	TR	
18	2.50e-006	30	1.00e-005	20	13	0.54	1.00			MD	1, 2, 3, 4, 5	PAL,TR	
19	2.60e-006	32	1.50e-005	21	12	0.50	0.88	0.93	tef	AA, MD, ME	1, 2, 3, 4, 5		
20	5.50e-006	33	2.30e-005	24	8	0.33	0.56			ME	1, 2, 3, 4, 5		
21	6.10e-006	34	3.30e-005	27	9	0.38	0.65	0.67	PADS	ME	1, 2, 3, 4, 5	TR	
22	7.40e-006	35	3.70e-005	30	18	0.75	1.80			AA	1, 3	PAL,TR	
23	8.20e-006	36	1.60e-004	42	25	1.00	2.00			AA, ME	1, 2, 3, 4, 5		
24	8.30e-006	37	1.30e-004	39	53	2.20	3.10			BP, ME	1, 2, 3, 4, 5	PAL	
25	8.70e-006	38	3.50e-005	29	10	0.42	0.83	0.63	MSX1	AA, BP, MD, ME	1, 2, 3, 4, 5		
26	8.80e-006	39	8.60e-005	36	17	0.71	1.10	0.75	AP2GAM	AA, ME	1, 2, 3, 4, 5	PAL	
27	9.70e-006	40	2.50e-003	78	144	6.00	6.20	0.69	ZID	BP, ME	2, 4, 5		
28	1.10e-005	41	3.30e-005	27	8	0.33	0.76			ME	1, 2, 3, 4, 5	PAL,TR	
29	1.20e-005	42	3.70e-005	30	12	0.50	1.30	0.66	TEF	AA, MD, ME	1, 2, 3, 4, 5	PAL	
30	1.30e-005	43	5.50e-005	33	14	0.58	1.50			AA	1, 4	PAL,TR	
31	1.30e-005	43	1.40e-004	40	21	0.88	1.90			AA	2, 3, 5	TR	
32	2.10e-005	45	8.00e-005	35	8	0.33	0.64	0.64	NFKB_Q	ME	1, 2, 3, 4, 5		
33	3.50e-005	47	2.40e-004	48	16	0.67	1.40			AA	1, 2, 3, 4, 5		
34	3.60e-005	48	1.40e-004	40	8	0.33	0.70			ME	1, 2, 3, 4, 5		
35	3.60e-005	48	1.70e-004	43	10	0.42	0.88	0.70	NFKB	AA, ME	1, 2, 3, 4, 5		
36	4.40e-005	51	3.10e-004	51	18	0.75	1.70			AA	4	TR	
37	4.60e-005	52	1.70e-004	43	8	0.33	0.64	0.61	AHR	ME	1, 2, 4, 5		
38	4.70e-005	53	1.80e-004	45	7	0.29	0.55			ME	1, 2, 3, 4, 5	PAL	
39	4.90e-005	54	3.20e-004	52	19	0.79	1.80			AA	2, 3, 4	PAL	
40	6.40e-005	55	2.30e-004	47	16	0.67	1.80			AA	3	PAL	
41	8.00e-005	56	5.00e-004	55	10	0.42	0.65			ME	1, 2, 3, 4, 5	PAL	
42	9.10e-005	57	1.20e-003	68	24	1.00	1.80	0.63	CACBIN	AA, BP, ME	1, 2, 3, 4, 5		
43	1.00e-004	58	7.30e-004	59	9	0.38	0.49	0.68	LYF1	AA, ME	1, 2, 3, 4, 5		
44	1.40e-004	59	9.70e-004	65	20	0.83	2.00	0.61	HNF3	AA, ME	2, 3	TR	
45	1.60e-004	62	6.10e-004	56	15	0.62	1.60			AA	1, 2, 3, 5	TR	
46	1.70e-004	63	3.70e-003	84	21	0.88	0.95	0.63	SMAD	BP, ME	2, 3, 4, 5		
47	1.90e-004	64	8.20e-004	64	9	0.38	0.65	0.68	MYOGEN	ME	1, 3, 4, 5	PAL	
48	2.30e-004	66	8.10e-004	63	13	0.54	1.40	0.68	STAT5B	AA	2, 3	PAL	
49	2.50e-004	68	7.80e-004	61	39	1.60	2.70	0.69	NFMUE1	ME	1, 2, 3, 4, 5	PAL	
50	2.90e-004	69	1.20e-003	68	11	0.46	0.72			ME	1, 2, 3, 4, 5		
51	4.50e-004	72	1.70e-003	73	10	0.42	0.78	0.67	IK2	ME	1, 2, 3, 5		
52	5.00e-004	73	9.90e-004	66	12	0.50	1.60			AA	4	PAL,TR	
53	5.50e-004	75	2.10e-003	75	8	0.33	0.56	0.73	P300	BP, ME	1, 2, 3, 4, 5		
54	5.50e-004	75	2.40e-003	77	18	0.75	1.90			AA	1, 3, 4		
55	5.80e-004	78	2.60e-003	80	30	1.20	3.60			AA	1, 2, 4		
56	6.40e-004	79	1.60e-003	71	8	0.33	0.64	0.70	SMAD3	ME	1, 2, 3, 4, 5		
57	7.10e-004	80	2.20e-003	76	9	0.38	0.88	0.81	LPOLYA	MD, ME	1, 2, 3, 4, 5	TR	
58	8.60e-004	81	2.60e-003	80	7	0.29	0.55	0.71	DBP	MD, ME	2, 3, 4, 5		
59	8.70e-004	82	1.60e-003	71	34	1.40	3.20	0.61	LHX3	ME	1, 2, 3, 4, 5		
60	1.00e-003	83	2.70e-003	82	19	0.79	2.10			AA	3, 4, 5		