

Motif	Group Specificity	Group Specificity Rank	Site Specificity	Site Specificity Rank	Testset Sites	Average Testset Sites	SDev Testset Sites	TRANSFAC Correlation	TRANSFAC ID	Motif Finders	Sets	Repeats	Logo
1	1.40e-017	1	8.60e-017	1	8	0.89	0.78			AA	3	PAL	A _xG _CA_ _A e cA_x_ x A_CxG
2	5.60e-017	2	3.70e-015	2	9	1.00	0.50			AA	1, 3, 4, 5	TR	A_A CAGR_x A AG
3	9.30e-016	3	1.50e-014	3	9	1.00	0.71			AA	1, 2, 3, 4, 5	PAL,TR	x_A xCI xTGGG_x xG
4	6.00e-015	4	9.60e-014	5	9	1.00	0.71			AA	1, 2, 3, 4, 5	PAL,TR	I xG cAG_x I_ CTGG
5	2.10e-014	6	3.30e-013	8	10	1.10	0.93			AA	1, 2, 4, 5		x_xxA A I _cAGG _ A AG A
6	3.20e-014	7	1.90e-012	15	9	1.00	0.50			AA	1, 2, 3, 4, 5		A_ _xCTGGIRcAAR
7	4.50e-014	8	1.30e-013	6	5	0.56	0.53			AA, MD, ME	1, 2, 3, 4, 5	PAL	_A _GAA _TTcA AGG_ _ A
8	5.00e-014	9	2.90e-013	7	7	0.78	0.67			AA	1, 2, 3, 4, 5		T_x_xxAAGGT_xc_G
9	6.40e-014	10	3.70e-013	9	6	0.67	0.50			BP	5	PAL	x_x_xGxT_xT_xA_x
10	1.50e-013	11	9.00e-013	10	6	0.67	0.50			AA	3		A_xGcCAAG_ _AG_ _ xxA
11	2.80e-013	12	1.60e-012	14	9	1.00	1.00			AA, BP, ME	1, 4	PAL	x I xT _cGAG_xT_ x TG
12	3.20e-013	13	1.80e-011	19	9	1.00	0.50	0.69	TAL1BE	AA, ME	1, 3, 4, 5		CAGx xGx_ _cA
13	3.90e-013	14	2.30e-012	16	7	0.78	0.67			AA	1, 2, 4, 5	TR	_x xTc_xTGG_xA_x
14	5.90e-013	16	3.40e-011	20	9	1.00	0.50			AA	1, 2, 3, 4, 5	PAL,TR	_AG_ _ _AG_ _TcTG
15	6.10e-013	17	1.00e-012	11	4	0.44	0.53			AA	1, 2, 3, 4, 5		Ax_xAAAxTAT_ _xTGG
16	6.10e-013	17	1.00e-012	11	5	0.56	0.73			AA	2	PAL	A TxA_ _xT_ A AxGcTGG
17	1.10e-012	19	3.10e-012	17	7	0.78	0.97			AA	1, 3, 4, 5	TR	xGcG_ xGGA_x_ _ A xR_ x
18	9.10e-012	21	1.50e-011	18	6	0.67	0.87			AA	1, 2, 3, 4, 5		Ac_xG_GAGcTGGT_xG
19	2.20e-011	22	1.20e-010	23	7	0.78	0.67	0.60	SREBP	BP	1, 4	PAL	x_x_xTGG_xT_xA_x
20	2.20e-011	22	1.20e-010	23	6	0.67	0.50			BP	1, 4		TcGA_AAcT_xR_xT_
21	2.90e-011	24	8.00e-011	21	9	1.00	1.10	0.66	SP1	AA, BP	1, 4, 5	TR	_x _TGGG_xG_ x Tc
22	5.10e-011	26	1.40e-010	25	6	0.67	0.71	0.66	HEB	AA, BP	1, 2, 4, 5		xG_xRcCA_xTGGcA
23	1.40e-010	27	7.90e-010	29	8	0.89	0.78			AA	1, 2, 3, 5		G AA G _cAcGcC
24	1.60e-010	28	8.90e-010	30	7	0.78	0.67	0.67	LYF1	AA	2, 3, 5		Ax_xTcT_xCTGGc_
25	1.60e-010	28	2.30e-009	34	10	1.10	0.78	0.73	HEB	AA, BP	1, 4, 5		cAcG_cTcT_x_ x
26	2.70e-010	30	7.20e-010	28	6	0.67	0.71			BP, MD	1, 4, 5		xAA_x_xAxGcAcC
27	2.90e-010	31	4.00e-009	38	10	1.10	0.93			AA	2		I GcG_xR_x_xRcGA
28	3.50e-010	32	9.60e-008	53	12	1.30	0.50			AA, BP, MD, ME	1, 2, 3, 4, 5		_G_x_cTGG_xG_ G
29	4.30e-010	33	7.10e-010	27	5	0.56	0.73			AA	1, 2, 4, 5		G_xTAcCTcG_A_AxRcA
30	4.80e-010	34	1.30e-009	32	7	0.78	0.83	0.62	SRF_Q5	AA	2, 3		_TcT_xTGG_xG_x
31	5.60e-010	35	7.40e-009	40	7	0.78	0.44			AA, MD, ME	1, 4, 5		A_CTGGcAcA
32	8.30e-010	36	2.30e-009	34	7	0.78	0.83			AA	2, 3	PAL	AA G_TT A TcA_xGcI
33	1.00e-009	39	2.80e-009	36	9	1.00	1.60			AA	1, 4, 5	TR	CTGG_ _GcR_xTcTcG
34	1.80e-009	41	4.70e-009	39	6	0.67	0.71	0.61	AP2REP	BP	1, 4	PAL,TR	xGcAxGcAcTcG_ _
35	4.40e-009	43	5.70e-008	46	17	1.90	1.80			AA	1, 4, 5		x_xG_xR_ G_ _TAcRAG
36	6.30e-009	45	3.30e-008	44	7	0.78	0.67	0.67	NERF	BP, ME	1, 4, 5	TR	xGAcGAGc_cGcG_
37	8.50e-009	46	1.00e-008	41	6	0.67	1.10			AA	1, 3, 4, 5		Ax_xTAc_xG_TcAGcR
38	1.10e-008	47	6.00e-008	47	10	1.10	1.10			AA	3	PAL,TR	GAAR_xTAc_xcA_ AxCA
39	1.20e-008	48	2.30e-006	71	12	1.30	0.50			BP, ME	4, 5	TR	_GG_TcTcGcGc
40	1.80e-008	49	4.80e-008	45	9	1.00	1.10			AA	1, 3, 4, 5	PAL	A_xTc_ cCAxTcTGA
41	3.20e-008	50	8.40e-008	49	7	0.78	0.97			AA, BP, ME	1, 4, 5	PAL	AGcT_xxA_AxAAAAG
42	3.90e-008	51	6.40e-008	48	5	0.56	0.73	0.64	HNF4_0	BP, ME	1, 4, 5		xG_TcRcAcAcGcT_
43	4.00e-008	52	2.00e-007	57	8	0.89	0.93	0.80	VDR	AA	3, 4, 5	TR	GcGcAcAcGcGcA
44	4.10e-008	53	4.80e-007	64	12	1.30	1.00			AA	2		xAc_xAGcT_ _G_A
45	5.40e-008	55	8.80e-008	52	6	0.67	0.87			AA	3	TR	xT_GGT_xRcR_xG
46	6.20e-008	56	3.00e-007	62	7	0.78	0.67	0.60	RREB1	BP, ME	1, 4, 5	TR	xGcGc_cGcTcGcG_
47	7.10e-008	57	8.50e-008	51	7	0.78	1.20			AA	1, 4, 5		x_x_A_xR_xTcTcG_A_ _Ax_A
48	7.10e-008	57	8.40e-008	49	5	0.56	0.88			AA	2, 3, 5	PAL	C_GGcAcAcCCAcG_cGcG
49	8.60e-008	60	2.20e-007	58	7	0.78	0.97			BP	4, 5		_xTcAAcAc_xTcTcG
50	9.80e-008	63	3.10e-006	73	13	1.40	1.40	0.73	sp1	AA, BP, ME	1, 4		GcGcTcG_cTcR_ _Tc_
51	1.00e-007	64	2.80e-007	61	9	1.00	1.10			AA	1, 4, 5		A_xTcAc_ _AGcTcTcR
52	1.00e-007	64	1.20e-007	54	6	0.67	1.10	0.66	HFH3	AA	2, 3	TR	xGcRcTcGcTcTcTcT
53	1.40e-007	66	2.20e-007	58	6	0.67	0.87			AA	2, 3	PAL	cTAcAc_A_xR_xTcTcR
54	2.00e-007	68	3.20e-007	63	6	0.67	0.87	0.66	MEIS1	BP, MD	1, 3, 4, 5	PAL	G_xR_GcAcG_xG_c
55	2.70e-007	69	1.20e-006	66	9	1.00	0.87	0.76	MZF1	BP, ME	1, 4, 5	PAL	_TcTcTcGcGcGc
56	6.80e-007	71	1.70e-006	68	6	0.67	0.71			AA	1, 2, 3, 4, 5		T_ _AxAcA_AG
57	7.00e-007	72	1.80e-006	69	7	0.78	0.83	0.68	HNF4_0	AA	1, 2, 3, 4, 5	PAL	xTcAcTcTcAcAAcRc
58	1.10e-006	73	2.80e-006	72	8	0.89	1.10	0.75	HSF2	AA, BP, MD, ME	1, 3, 4, 5	PAL	_TcGAcTcTcTcAc_
59	1.40e-006	74	6.10e-006	76	10	1.10	1.10			AA	3		cAcTcAc_A_AAc
60	1.60e-006	75	7.30e-006	78	15	1.70	1.60			AA	3, 4		cAcAcTcTcAcGc_ _AcA