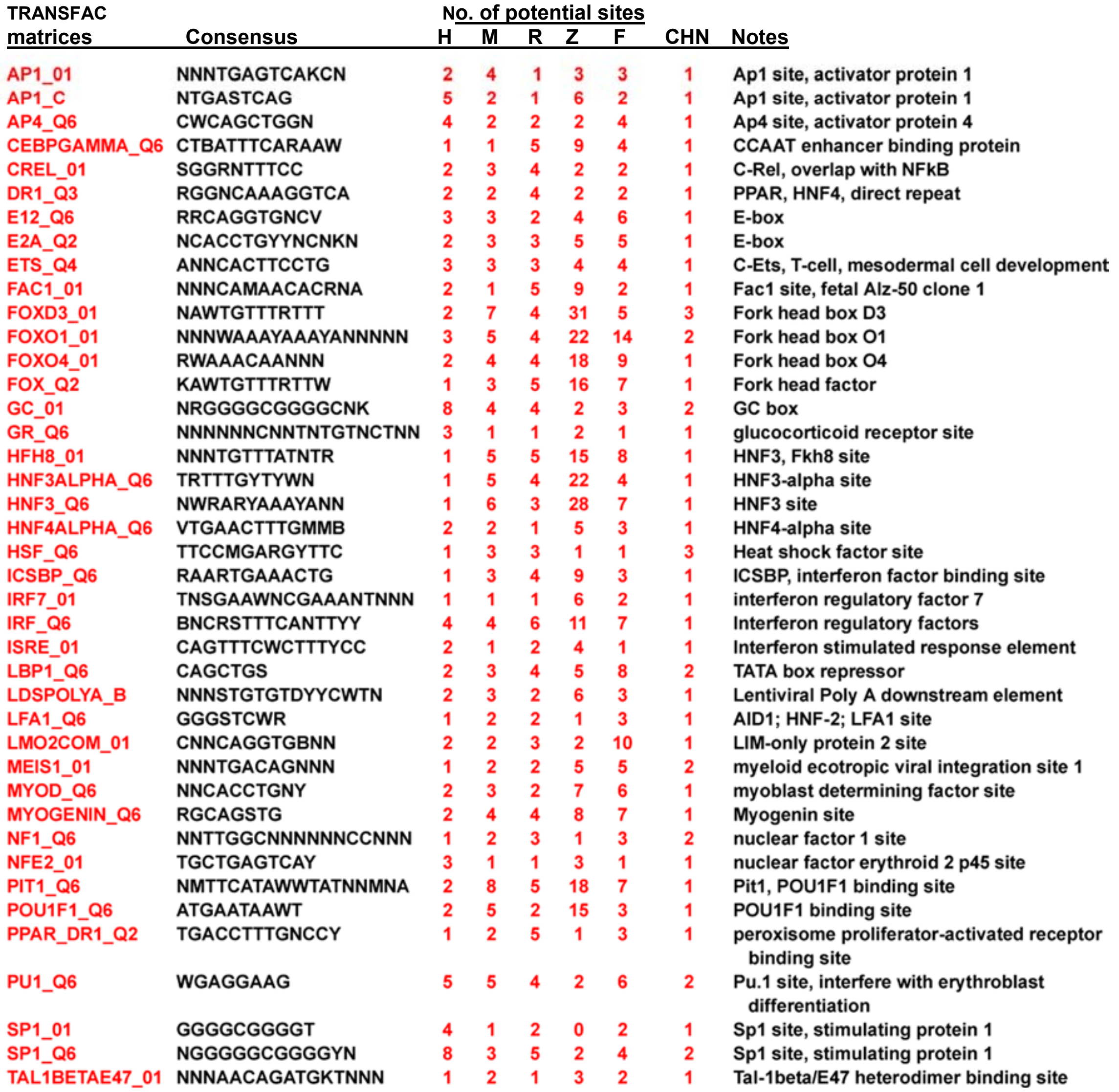
Table 4. Conserved transcription factor binding sites identified in orthologous *Fiaf* genes



TRANSFAC matrices	Consensus	No. of potential sites					CHN	Notes
		H	M	R	Z	F		
AP1_01	NNNTGAGTCAKCN	2	4	1	3	3	1	Ap1 site, activator protein 1
AP1_C	NTGASTCAG	5	2	1	6	2	1	Ap1 site, activator protein 1
AP4_Q6	CWCAGCTGGN	4	2	2	2	4	1	Ap4 site, activator protein 4
CEBPGAMMA_Q6	CTBATTTCARAAW	1	1	5	9	4	1	CCAAT enhancer binding protein
CREL_01	SGGRNTTTCC	2	3	4	2	2	1	C-Rel, overlap with NFkB
DR1_Q3	RGGNCAAAGGTCA	2	2	4	2	2	1	PPAR, HNF4, direct repeat
E12_Q6	RRCAGGTGNCV	3	3	2	4	6	1	E-box
E2A_Q2	NCACCTGYYNCNKN	2	3	3	5	5	1	E-box
ETS_Q4	ANNCACTTCCTG	3	3	3	4	4	1	C-Ets, T-cell, mesodermal cell development
FAC1_01	NNNCAMAACACRNA	2	1	5	9	2	1	Fac1 site, fetal Alz-50 clone 1
FOXD3_01	NAWTGTTTRTTT	2	7	4	31	5	3	Fork head box D3
FOXO1_01	NNNWAAAYAAAYANNNNN	3	5	4	22	14	2	Fork head box O1
FOXO4_01	RWAAACAANNN	2	4	4	18	9	1	Fork head box O4
FOX_Q2	KAWTGTTTRTTW	1	3	5	16	7	1	Fork head factor
GC_01	NRGGGGCGGGGCNK	8	4	4	2	3	2	GC box
GR_Q6	NNNNNNCNNTNTGTNCTNN	3	1	1	2	1	1	glucocorticoid receptor site
HFH8_01	NNNTGTTTATNTR	1	5	5	15	8	1	HNF3, Fkh8 site
HNF3ALPHA_Q6	TRTTTGYTYWN	1	5	4	22	4	1	HNF3-alpha site
HNF3_Q6	NWRARYAAAYANN	1	6	3	28	7	1	HNF3 site
HNF4ALPHA_Q6	VTGAACTTTGMMB	2	2	1	5	3	1	HNF4-alpha site
HSF_Q6	TTCCMGARGYTTC	1	3	3	1	1	3	Heat shock factor site
ICSBP_Q6	RAARTGAAACTG	1	3	4	9	3	1	ICSBP, interferon factor binding site
IRF7_01	TNSGAAWNCGAAANTNNN	1	1	1	6	2	1	interferon regulatory factor 7
IRF_Q6	BNCRSTTTCANTTYY	4	4	6	11	7	1	Interferon regulatory factors
ISRE_01	CAGTTTCWCTTTYCC	2	1	2	4	1	1	Interferon stimulated response element
LBP1_Q6	CAGCTGS	2	3	4	5	8	2	TATA box repressor
LDSPOLYA_B	NNNSTGTGTDYYCWTN	2	3	2	6	3	1	Lentiviral Poly A downstream element
LFA1_Q6	GGGSTCWR	1	2	2	1	3	1	AID1; HNF-2; LFA1 site
LMO2COM_01	CNNCAGGTGBNN	2	2	3	2	10	1	LIM-only protein 2 site
MEIS1_01	NNNTGACAGNNN	1	2	2	5	5	2	myeloid ecotropic viral integration site 1
MYOD_Q6	NNCACCTGNY	2	3	2	7	6	1	myoblast determining factor site
MYOGENIN_Q6	RGCAGSTG	2	4	4	8	7	1	Myogenin site
NF1_Q6	NNTTGGCNNNNNNCCNNN	1	2	3	1	3	2	nuclear factor 1 site
NFE2_01	TGCTGAGTCAY	3	1	1	3	1	1	nuclear factor erythroid 2 p45 site
PIT1_Q6	NMTTCATAWWTATNNMNA	2	8	5	18	7	1	Pit1, POU1F1 binding site
POU1F1_Q6	ATGAATAAWT	2	5	2	15	3	1	POU1F1 binding site
PPAR_DR1_Q2	TGACCTTTGNCCY	1	2	5	1	3	1	peroxisome proliferator-activated receptor binding site
PU1_Q6	WGAGGAAG	5	5	4	2	6	2	Pu.1 site, interfere with erythroblast differentiation
SP1_01	GGGGCGGGGT	4	1	2	0	2	1	Sp1 site, stimulating protein 1
SP1_Q6	NGGGGGCGGGGYN	8	3	5	2	4	2	Sp1 site, stimulating protein 1
TAL1BETAE47_01	NNNAACAGATGKTNNN	1	2	1	3	2	1	Tal-1beta/E47 heterodimer binding site

List of the TRANSFAC matrices that meet the selection criteria described above. Column 1, name of the TRANSFAC matrix. Column 2, consensus sequence of the matrix defined by using the International Union of Pure and Applied Chemistry (IUPAC) alphabet (M equals A or C; R, A or G; W, A or T; S, C or G; Y, C or T; K, G or T; V, A or C or G; H, A or C or T; D, A or G or T; B, C or G or T; and N, A or C or G or T). Column 3, number of high scoring sites in each sequence based on the results of applying the program PATSER to the selected genomic sequence. HMRZF each represents the species of the selected sequence (H-human, M-mouse, R-rat, Z-zebra fish, F-fugu). Column 4, CHN statistic (defined in ref. *1*), number of high scoring sites that appear in conserved blocks between human and mouse *Fiaf* genes. Column 5, a description of the matrix based on the TRANSFAC database annotation.

1. Hu, Y., Wang, T., Stormo, G. D. & Gordon, J. I. (2004) *Proc. Natl. Acad. Sci. USA* **101,** 5559-5564.