

Table SI. Total open-chromatin region number, average length, standard deviation of the length and percentage of total genomic coverage of each cell line replicate of the DH data for humans and mice.

Tissue	Replicate	Assembly	Open-chromatin regions	Average length	SD	Genome coverage (%)
AG04449	1	hg38	327,756	258.0	248.4	2.7
AG04449	2	hg38	365,130	235.5	231.0	2.8
AG04450	1	hg38	291,529	266.9	265.5	2.5
AG04450	2	hg38	342,353	265.1	272.9	2.9
AG09309	1	hg38	249,524	361.5	323.7	2.9
AG09309	2	hg38	259,544	304.6	382.9	2.6
AG09319	1	hg38	192,157	343.6	322.5	2.1
AG09319	2	hg38	212,655	329.9	319.2	2.3
AG10803	1	hg38	215,259	361.0	316.7	2.5
AG10803	2	hg38	219,193	365.9	303.6	2.6
BJ	1	hg38	199,008	426.1	354.4	2.7
BJ	2	hg38	246,452	350.6	413.2	2.8
Caco-2	1	hg38	190,793	406.5	424.3	2.5
Caco-2	2	hg38	220,115	346.1	499.3	2.5
CMK	1	hg38	243,004	347.6	462.7	2.7
GM06990	1	hg38	180,473	397.0	486.4	2.3
GM06990	2	hg38	232,959	301.5	406.8	2.3
GM12865	1	hg38	243,414	371.8	466.5	2.9
GM12865	2	hg38	241,608	359.6	452.6	2.8
GM12878	1	hg38	280,250	316.9	510.7	2.9
GM12878	2	hg38	279,749	299.7	387.2	2.7
H1-hESC	1	hg38	418,068	242.6	295.9	3.3
H7-hESC	1	hg38	409,006	323.8	346.8	4.3
HAepiC	1	hg38	243,857	378.5	330.6	3.0
HAepiC	2	hg38	246,716	353.9	299.0	2.8
HCF	1	hg38	230,937	383.0	371.3	2.9
HCF	2	hg38	238,070	358.5	345.7	2.8
HCM	1	hg38	240,273	413.1	404.1	3.2
HCM	2	hg38	317,830	284.2	296.9	2.9
HCPEpiC	1	hg38	266,100	370.9	349.5	3.2
ECPEpiC	2	hg38	272,677	339.9	335.7	3.0
HEEpiC	1	hg38	287,557	336.8	318.7	3.1
HEEpiC	2	hg38	295,776	272.6	242.7	2.6
HeLa-S3	1	hg38	225,113	437.7	518.7	3.2
HeLa-S3	2	hg38	224,026	345.2	339.6	2.5
HepG2	1	hg38	144,133	360.6	399.8	1.7
HepG2	2	hg38	181,681	374.8	444.7	2.2
HGF	1	hg38	255,233	301.3	279.8	2.5
HGF	2	hg38	272,583	264.9	256.7	2.3
HL-60	1	hg38	236,648	457.7	633.2	3.5
HL-60	2	hg38	217,240	495.9	691.9	3.5
HMEC	1	hg38	313,242	296.3	393.0	3.0
HNPCEpiC	1	hg38	311,838	324.1	306.9	3.3
NCPCEpiC	2	hg38	344,514	255.9	255.5	2.8
HRCPEpiC	1	hg38	256,927	344.7	295.9	2.9
HRCPEpiC	2	hg38	284,171	310.5	277.7	2.8
HRE	1	hg38	313,368	284.1	360.3	2.9
HRE	2	hg38	340,026	258.7	262.6	2.8
HRPEpiC	1	hg38	293,652	365.1	332.8	3.5
HRPEpiC	2	hg38	281,023	343.6	316.0	3.1
HUVEC	1	hg38	255,563	343.6	442.4	2.8
K562	1	hg38	267,583	378.0	435.2	3.3
K562	2	hg38	270,176	383.5	449.3	3.3
MCF-7	1	hg38	291,780	252.9	256.5	2.4

Table S1. Continued.

Tissue	Replicate	Assembly	Open-chromatin regions	Average length	SD	Genome coverage (%)
MCF-7	2	hg38	316,287	322.4	419.6	3.3
NB4	1	hg38	224,877	402.7	492.4	2.9
NB4	2	hg38	232,810	385.3	500.2	2.9
NHDF-neo	1	hg38	241,089	393.8	337.2	3.1
NHDF-neo	2	hg38	227,444	386.3	337.8	2.8
NHEK	1	hg38	327,532	261.7	354.2	2.8
NHLF	1	hg38	259,706	401.6	344.7	3.4
NHLF	2	hg38	310,212	302.0	288.2	3.0
PANC-1	1	hg38	296,187	315.6	457.5	3.0
PANC-1	2	hg38	339,084	291.7	490.7	3.2
SAEC	1	hg38	278,012	326.3	307.5	2.9
SAEC	2	hg38	328,713	274.5	281.2	2.9
SkMC	1	hg38	263,450	341.4	272.3	2.9
SkMC	2	hg38	260,738	361.5	295.5	3.0
SK-N-SH (Retinoic Acid)	1	hg38	131,518	398.1	428.8	1.7
SK-N-SH (Retinoic Acid)	2	hg38	276,724	332.9	445.1	3.0
Th1	1	hg38	132,050	500.8	594.1	2.1
Th2	1	hg38	201,609	370.8	503.9	2.4
A549	1	hg38	276,601	266.3	323.5	2.4
A549	2	hg38	350,594	276.4	344.1	3.1
AoAF	1	hg38	212,505	432.6	418.5	3.0
AoAF	2	hg38	215,700	397.9	382.4	2.8
BE(2)-C	1	hg38	227,501	435.4	447.6	3.2
BE(2)-C	2	hg38	249,267	459.7	487.1	3.7
B-cells CD20+ (RO01778)	1	hg38	154,556	599.1	6276.4	3.0
B-cells CD20+ (RO01778)	2	hg38	201,243	514.5	690.6	3.3
CD34+ Mobilized	1	hg38	186,665	610.4	716.8	3.7
CD4+_Naive_ Wb11970640	1	hg38	230,625	276.6	374.4	2.1
CD4+_Naive_ Wb78495824	1	hg38	299,817	276.6	393.0	2.7
GM04503	1	hg38	254,552	478.7	468.2	3.9
GM04503	2	hg38	236,474	481.4	485.2	3.7
GM04504	1	hg38	223,293	442.0	444.4	3.2
GM04504	2	hg38	221,388	452.3	467.5	3.2
GM12864	1	hg38	313,606	270.6	355.2	2.7
H7-hESC	2	hg38	371,443	301.7	338.5	3.6
H7-hESCDiffa14d	1	hg38	358,151	237.2	358.7	2.7
H7-hESCDiffa14d	2	hg38	369,057	224.6	343.7	2.7
H7-hESCDiffa2d	1	hg38	351,624	292.6	462.4	3.3
H7-hESCDiffa5d	1	hg38	452,535	316.0	380.0	4.6
H7-hESCDiffa5d	2	hg38	382,576	251.3	271.4	3.1
H7-hESCDiffa9d	1	hg38	377,852	348.9	454.7	4.3
HAc	1	hg38	342,026	302.6	311.2	3.3
HAc	2	hg38	342,783	262.9	359.3	2.9
HA-h	1	hg38	360,293	375.4	449.7	4.4
HA-h	2	hg38	396,721	299.5	433.4	3.8
HA-sp	1	hg38	447,346	357.5	464.2	5.2
HA-sp	2	hg38	388,588	355.0	462.1	4.5
HBMEC	1	hg38	262,943	448.5	445.3	3.8
HBMEC	2	hg38	308,798	328.9	352.1	3.3

Table S1. Continued.

Tissue	Replicate	Assembly	Open-chromatin regions	Average length	SD	Genome coverage (%)
HBVP	1	hg38	547,523	274.3	346.7	4.9
HBVSMC	1	hg38	340,645	335.8	440.7	3.7
HBVSMC	2	hg38	332,379	325.3	462.3	3.5
HCFAa	1	hg38	283,275	412.7	426.8	3.8
HCFAa	2	hg38	260,748	391.3	378.4	3.3
HConf	1	hg38	274,909	318.9	337.8	2.8
HConf	2	hg38	290,614	325.1	312.7	3.1
HCT-116	1	hg38	234,854	307.6	394.6	2.3
HCT-116	2	hg38	247,187	296.2	381.6	2.4
HFF	1	hg38	266,378	418.9	444.0	3.6
HFF	2	hg38	287,823	323.2	339.1	3.0
HFF-Myc	1	hg38	347,249	345.6	375.3	3.9
HFF-Myc	2	hg38	321,472	259.9	299.0	2.7
HIPEpiC	1	hg38	315,578	335.3	323.8	3.4
HIPEpiC	2	hg38	323,737	354.5	324.0	3.7
HMEC	2	hg38	268,221	294.2	323.5	2.5
HMF	1	hg38	220,461	368.8	338.9	2.6
HMF	2	hg38	225,357	374.0	327.6	2.7
HMVEC-dAd	1	hg38	340,303	259.0	391.3	2.8
HMVEC-dAd	2	hg38	468,965	195.5	214.2	3.0
HMVEC-dBl-Ad	1	hg38	177,618	504.0	504.1	2.9
HMVEC-dBl-Ad	2	hg38	183,224	515.3	534.3	3.0
HMVEC-dBl-Neo	1	hg38	208,708	542.8	586.8	3.7
HMVEC-dBl-Neo	2	hg38	213,099	491.7	495.6	3.4
HMVEC-dLy-Ad	1	hg38	163,483	422.4	436.1	2.2
HMVEC-dLy-Ad	2	hg38	171,988	461.2	498.0	2.6
HMVEC-dLy-Neo	1	hg38	203,190	443.8	464.0	2.9
HMVEC-dLy-Neo	2	hg38	199,915	447.0	454.7	2.9
HMVEC-dNeo	1	hg38	193,833	424.1	474.8	2.7
HMVEC-dNeo	2	hg38	314,992	331.1	389.4	3.4
HMVEC-LBl	1	hg38	227,694	440.0	446.9	3.2
HMVEC-LBl	2	hg38	230,784	388.3	491.2	2.9
HMVEC-LLy	1	hg38	189,787	469.2	523.5	2.9
HMVEC-LLy	2	hg38	183,616	407.8	443.8	2.4
HPAEC	1	hg38	409,836	229.9	265.4	3.0
HPAF	1	hg38	218,520	445.1	443.0	3.1
HPAF	2	hg38	214,456	384.3	382.3	2.7
HPdLF	1	hg38	239,843	401.1	402.2	3.1
HPdLF	2	hg38	235,664	351.9	363.1	2.7
HPF	1	hg38	203,311	399.5	493.7	2.6
HPF	2	hg38	213,915	415.0	378.5	2.9
HRGEC	1	hg38	286,900	262.7	274.1	2.4
HRGEC	2	hg38	304,827	329.0	426.5	3.2
Bone Marrow HS27a	1	hg38	353,071	387.1	527.9	4.4
Bone Marrow HS5	1	hg38	291,393	462.5	523.2	4.4
HSMC	1	hg38	293,953	390.2	326.5	3.7
HSMC	2	hg38	309,782	366.5	319.4	3.7
HSMCtube	1	hg38	379,673	405.1	463.9	5.0
HSMCtube	2	hg38	337,727	355.0	365.3	3.9
HUVEC	2	hg38	332,792	296.1	386.8	3.2
HVMF	1	hg38	263,226	360.6	361.5	3.1
HVMF	2	hg38	265,083	386.4	412.0	3.3
Jurkat	1	hg38	228,956	441.5	595.8	3.3
Jurkat	2	hg38	288,980	315.6	455.3	2.9

Table S1. Continued.

Tissue	Replicate	Assembly	Open-chromatin regions	Average length	SD	Genome coverage (%)
LHCN-M2	1	hg38	239,960	407.6	408.8	3.2
LHCN-M2	2	hg38	251,807	419.3	385.6	3.4
LHCN-M2Diff4d	1	hg38	263,877	414.8	430.2	3.5
LHCN-M2Diff4d	2	hg38	273,651	472.8	591.2	4.2
LNCaP	1	hg38	258,097	341.3	303.3	2.8
LNCaP	2	hg38	271,782	397.7	390.1	3.5
M059J	1	hg38	259,996	465.9	464.9	3.9
M059J	2	hg38	254,450	476.5	478.7	3.9
MCF-7Est100nm1h	1	hg38	295,482	369.6	368.5	3.5
MCF-Est100nm1h	2	hg38	332,367	409.0	453.6	4.4
MCF-Estctrl0h	1	hg38	279,241	352.0	351.1	3.2
MCF-7Estctrl0h	2	hg38	338,213	404.2	440.6	4.4
Monocytes CD14+ RO01746	2	hg38	180,748	524.1	623.6	3.1
Bone Marrow MSC	1	hg38	262,739	412.7	404.9	3.5
Bone Marrow MSC	2	hg38	226,727	353.5	312.7	2.6
NH-A	1	hg38	264,672	382.9	338.8	3.3
NH-A	2	hg38	295,903	300.3	307.1	2.9
NHBE_RA	1	hg38	348,350	268.6	339.4	3.0
NHBE_RA	2	hg38	367,241	240.3	358.3	2.8
NHDF-Ad	1	hg38	267,739	404.9	369.5	3.5
NHDF-Ad	2	hg38	261,286	399.8	376.8	3.4
NHEK	2	hg38	364,028	259.8	337.4	3.1
NT2-D1	1	hg38	402,036	296.4	440.9	3.8
NT2-D1	2	hg38	338,750	229.4	344.5	2.5
PrEC	1	hg38	394,970	221.7	308.6	2.8
PrEC	2	hg38	392,970	220.4	223.4	2.8
RPMI-7951	1	hg38	208,047	407.2	367.4	2.7
RPMI-7951	2	hg38	209,097	420.9	478.9	2.8
RPTEC	1	hg38	290,692	336.9	364.6	3.2
RPTEC	2	hg38	304,682	361.9	400.8	3.6
SK-N-MC	1	hg38	353,337	265.9	324.5	3.0
SK-N-MC	2	hg38	363,847	280.8	414.3	3.3
T-47D	1	hg38	231,809	369.4	485.9	2.8
T-47D	2	hg38	247,653	323.1	450.1	2.6
Th1	2	hg38	423,717	287.9	321.7	3.9
Th17	1	hg38	253,068	184.0	209.8	1.5
Th1_Wb33676984	1	hg38	408,039	245.4	354.9	3.2
Th1_Wb54553204	1	hg38	449,760	266.2	422.6	3.9
Th1_Wb54553204	2	hg38	254,459	222.1	291.6	1.8
Th2	2	hg38	366,623	359.1	502.8	4.3
Th2_Wb33676984	1	hg38	324,062	241.3	409.5	2.5
Th2_Wb54553204	1	hg38	137,455	459.0	602.2	2.0
Treg_Wb78495824	1	hg38	186,283	483.5	5706.2	2.9
Treg_Wb83319432	1	hg38	434,716	416.5	3761.7	5.8
WERI-Rb-1	1	hg38	297,122	380.8	384.7	3.7
WERI-Rb-1	2	hg38	373,334	325.6	335.4	3.9
WI-38	1	hg38	220,400	378.2	354.7	2.7
WI-38	2	hg38	231,191	353.2	356.1	2.6
WI-38Ohtam	1	hg38	300,936	414.6	485.3	4.0
WI-38Ohtam	2	hg38	277,977	365.4	371.6	3.3
3134	1	mm10	119,182	530.6	560.9	2.3
3134	2	mm10	333,869	189.8	257.8	2.3
416B	1	mm10	185,403	511.8	574.9	3.5

Table S1. Continued.

Tissue	Replicate	Assembly	Open-chromatin regions	Average length	SD	Genome coverage (%)
416B	2	mm10	190,775	373.4	443.9	2.6
A20	1	mm10	226,589	452.4	712.4	3.8
A20	2	mm10	301,661	423.0	680.8	4.7
B-cell (CD19+)	1	mm10	190,877	503.6	676.3	3.5
B-cell (CD19+)	2	mm10	145,441	463.8	547.6	2.5
B-cell (CD43-)	1	mm10	153,814	451.1	535.1	2.5
B-cell (CD43-)	2	mm10	148,589	413.3	523.6	2.2
B-cell (CD43-)	3	mm10	229,601	412.5	566.2	3.5
B-cell (CD43-)	4	mm10	137,468	549.6	677.1	2.8
Cerebellum	2	mm10	240,894	292.1	411.7	2.6
Cerebellum	3	mm10	189,161	464.2	560.8	3.2
Cerebellum	1	mm10	244,687	304.8	407.9	2.7
Cerebrum	1	mm10	370,585	434.5	529.6	5.9
Cerebrum	2	mm10	405,317	316.9	414.2	4.7
Cerebrum	3	mm10	396,575	317.9	362.1	4.6
CH12	1	mm10	214,612	580.3	875.4	4.6
CH12	2	mm10	230,316	371.9	509.6	3.1
EPC (CD117- CD71 + TER119+)	1	mm10	179,543	451.2	755.8	3.0
EPC (CD117+ CD71 - TER119-)	1	mm10	273,682	432.6	567.4	4.3
EPC (CD117+ CD71 + TER119-)	1	mm10	196,824	526.8	775.5	3.8
EPC (CD117+ CD71 + TER119+)	1	mm10	192,638	579.6	851.1	4.1
ES-CJ7	1	mm10	352,556	322.8	395.7	4.2
ES-CJ7	2	mm10	373,218	311.7	385.7	4.3
ES-E14	1	mm10	270,472	465.0	573.5	4.6
ES-E14	2	mm10	319,157	337.2	450.3	3.9
ES-WW6_FIKO	1	mm10	258,802	460.3	542.8	4.4
ES-WW6_FIKO	2	mm10	298,856	367.4	467.8	4.0
ES-WW6	1	mm10	299,338	380.1	494.7	4.2
ES-WW6	2	mm10	316,611	319.0	416.6	3.7
Fat Pad	1	mm10	317,759	279.8	319.5	3.3
Fat Pad	2	mm10	306,100	313.1	353.9	3.5
Fibroblast	1	mm10	219,041	534.1	574.3	4.3
Fibroblast	2	mm10	213,254	439.5	443.6	3.4
Fore Limb Bud	1	mm10	302,649	293.0	354.5	3.2
Fore Limb Bud	2	mm10	394,477	419.2	538.7	6.1
Genital Fat Pad	1	mm10	290,565	446.7	695.4	4.8
Genital Fat Pad	2	mm10	433,625	483.1	599.8	7.7
Heart	1	mm10	244,143	425.8	506.6	3.8
Heart	2	mm10	243,244	531.9	585.9	4.7
Hind Limb Bud	1	mm10	354,420	290.9	382.1	3.8
Hind Limb Bud	2	mm10	416,082	298.8	439.6	4.6
Headless Embryo	1	mm10	347,843	343.8	481.5	4.4
Headless Embryo	2	mm10	308,678	349.4	515.3	3.9
Kidney	1	mm10	253,937	477.1	509.4	4.4
Kidney	2	mm10	294,647	275.9	302.2	3.0
Large Intestine	1	mm10	239,934	385.7	471.4	3.4
Large Intestine	2	mm10	279,719	469.4	676.2	4.8
Liver1	1	mm10	301,357	271.4	375.1	3.0
Liver1	2	mm10	277,265	308.0	480.9	3.1
Liver2	1	mm10	198,897	342.6	417.1	2.5
Liver2	2	mm10	182,638	450.8	536.4	3.0

Table S1. Continued.

Tissue	Replicate	Assembly	Open-chromatin regions	Average length	SD	Genome coverage (%)
Liver2	3	mm10	196,976	391.2	465.0	2.8
Liver2	4	mm10	216,831	353.2	453.0	2.8
Liver2	5	mm10	145,639	497.0	538.6	2.7
Liver2	6	mm10	142,294	514.9	559.8	2.7
Liver2	7	mm10	141,067	617.9	712.0	3.2
Liver2	8	mm10	155,058	476.1	529.5	2.7
Liver2	9	mm10	154,131	464.0	514.3	2.6
Liver2	10	mm10	183,017	510.2	656.3	3.4
Liver2	11	mm10	130,337	509.8	559.3	2.4
Liver2	12	mm10	152,388	537.7	618.8	3.0
Liver2	13	mm10	319,068	266.3	342.7	3.1
Liver2	14	mm10	165,080	434.9	480.6	2.6
Liver3	1	mm10	218,543	417.3	756.9	3.3
Liver4	1	mm10	295,213	270.5	381.6	2.9
Lung	1	mm10	281,022	331.1	356.5	3.4
Lung	2	mm10	294,607	361.0	587.7	3.9
Lung	3	mm10	332,528	292.0	506.6	3.6
MEL	1	mm10	193,797	535.2	727.4	3.8
MEL	2	mm10	209,259	638.7	856.4	4.9
MEL	3	mm10	217,555	430.1	571.2	3.4
Mesoderm	1	mm10	336,780	500.5	596.1	6.2
Mesoderm	2	mm10	308,899	379.1	377.1	4.3
mG/ER	1	mm10	199,413	413.3	552.0	3.0
mG/ER	2	mm10	169,648	582.7	842.5	3.6
mG/ERDiffc24h	1	mm10	223,288	391.9	579.9	3.2
mG/ERDiffc24h	2	mm10	175,002	492.5	709.5	3.2
mG/ERDiffc48h	1	mm10	141,260	474.9	564.9	2.5
mG/ERDiffc48h	2	mm10	211,133	335.4	445.5	2.6
NIH-3T3	1	mm10	218,174	378.1	447.9	3.0
NIH-3T3	2	mm10	296,391	256.4	269.5	2.8
Patski	1	mm10	283,584	357.1	450.0	3.7
Patski	2	mm10	305,255	342.9	445.8	3.8
Retina1	1	mm10	250,163	341.0	455.4	3.1
Retina2	1	mm10	278,879	301.5	443.4	3.1
Retina3	1	mm10	242,410	433.3	509.7	3.8
Skeletal Muscle	1	mm10	314,311	517.8	616.4	6.0
Skeletal Muscle	2	mm10	263,054	350.1	453.8	3.4
Spleen	1	mm10	134,630	438.6	513.6	2.2
Spleen	2	mm10	193,019	360.7	451.4	2.5
THelper-Activated	1	mm10	135,821	496.9	623.5	2.5
THelper-Activated	2	mm10	193,989	423.9	633.1	3.0
Thymus	1	mm10	170,852	571.7	756.3	3.6
Thymus	2	mm10	182,858	519.7	855.4	3.5
T-Naive	1	mm10	188,042	582.8	775.6	4.0
T-Naive	2	mm10	131,309	461.0	533.4	2.2
T-Naive	3	mm10	143,545	619.2	776.1	3.3
T-Naive	4	mm10	160,760	593.4	762.9	3.5
TReg-Activated	1	mm10	141,368	711.9	968.8	3.7
TReg-Activated	2	mm10	179,103	548.3	801.7	3.6
TReg	1	mm10	134,120	520.9	627.2	2.6
TReg	2	mm10	188,714	392.2	523.0	2.7
TReg	3	mm10	201,137	446.5	635.2	3.3
Whole Brain1	1	mm10	301,636	401.3	408.6	4.4
Whole Brain1	2	mm10	335,641	358.8	400.2	4.4
Whole Brain1	3	mm10	334,773	355.6	325.1	4.4

Table S1. Continued.

Tissue	Replicate	Assembly	Open-chromatin regions	Average length	SD	Genome coverage (%)
Whole Brain1	4	mm10	330,154	334.1	304.5	4.0
Whole Brain1	5	mm10	430,078	354.5	460.6	5.6
Whole Brain1	6	mm10	365,005	323.0	399.6	4.3
Whole Brain1	7	mm10	396,457	348.5	432.2	5.1
Whole Brain2	1	mm10	291,311	378.0	523.8	4.0
Whole Brain2	2	mm10	296,674	331.7	415.3	3.6
Whole Brain3	1	mm10	297,246	312.1	492.3	3.4
Whole Brain3	2	mm10	314,691	268.2	328.7	3.1
ZhBTc4	1	mm10	249,206	409.4	455.7	3.7
ZhBTc4	2	mm10	310,111	318.9	358.4	3.6
ZhBTc4Diffb24h	1	mm10	280,629	421.2	522.0	4.3
ZhBTc4Diffb24h	2	mm10	341,964	284.6	331.0	3.6
ZhBTc4Diffb6h	1	mm10	304,521	444.4	578.3	5.0
ZhBTc4Diffb6h	2	mm10	214,653	422.7	748.6	3.3

Table SII. Total conserved region number, average length, standard deviation of the length and percentage of total genomic coverage, of the pairwise alignment data for humans and mice.

Assembly	Conserved regions	Average length	SD	Genomic coverage (%)
hg38	1,507,742	674.6	697.6	32.8
mm10	1,507,742	645.4	665.3	35.6



Table III. TFBS prediction results of TFBIND, using FGA FASTA formatted sequence as input.

AC	ID	Score	Location	Strand	Consensus sequence	Signal sequence
M00253	V\$CAP_01	0.908329	1	(+)	NCANNNNN	CCACTCCT
M00057	V\$COMP1_01	0.775689	2	(-)	NNTNWKGATTGR CNRSRANMRRNN	CACTCCTAGTCCC ATCCTATTTA
M00183	V\$MYB_Q6	0.836515	6	(-)	NNNAACKGNC	CCTAGTCCC
M00281	V\$RFX1_02	0.790402	7	(-)	NNGTNRCNATRG YAACNNN	CTAGTCCCATCC TATTTA
M00087	V\$IK2_01	0.883181	8	(-)	NNNYGGGAWNNN	TAGTCCCATC
M00280	V\$RFX1_01	0.811872	8	(-)	NNGTNRCNWRG YAACNN	CTAGTCCCATCC TATTT
M00007	V\$ELK1_01	0.796259	10	(-)	NNNACMGGGAAGTN CNN	GTTCCCATCCTA TTTA
M00084	V\$MZF1_02	0.845789	10	(-)	KNNNKAGGGGNA	GTTCCCATCCTAT
M00223	V\$STAT_01	0.79758	11	(+)	TTCCCRKAA	TTCCCATCC
M00008	V\$SP1_01	0.780011	12	(-)	GRGGCRGGGW	TCCCATCCTA
M00059	V\$YY1_01	0.791284	12	(+)	NNNNCCATNTWNN NWN	TCCCATCCTATT TAAAT
M00075	V\$GATA1_01	0.838598	12	(-)	SNGATNNNN	TCCCATCCTA
M00076	V\$GATA2_01	0.89355	12	(-)	NNGATRNNN	TCCCATCCTA
M00077	V\$GATA3_01	0.848914	12	(-)	NGATARNG	TCCCATCCT
M00082	V\$EVI1_05	0.786735	14	(-)	AGATAAGATAN	CCATCCTATTT
M00138	V\$OCT1_04	0.786909	14	(-)	NNNNNNWATGC AAATNNNWNW	CCATCCTATTTAAA TCTGCAAGA
M00231	V\$MEF2_02	0.812238	14	(-)	NNNNNKCTAWAA ATAGMNNNN	CCATCCTATTT AAATCTGCAAG
M00232	V\$MEF2_03	0.781806	14	(-)	NNNNWKCTAWAA ATAGMNNNN	CCATCCTATTT AAATCTGCAAG
M00099	V\$S8_01	0.776485	16	(-)	WNNANYAAT TANYNN	ATCCTATTT AAATCTG
M00162	V\$OCT1_06	0.804687	18	(+)	CWNAWTKW SATRYN	CCTATTTAAAT CTG
M00162	V\$OCT1_06	0.860937	18	(-)	CWNAWTK WSATRYN	CCTATTTA AATCTG
M00216	V\$TATA_C	0.80169	18	(+)	NCTATAAAAR	CCTATTTAAA
M00252	V\$TATA_01	0.839635	19	(+)	STATAAARWNN NNN	CTATTTAAATC TGCA
M00200	V\$CAAT_C	0.715485	20	(-)	ACCAATCANCNGC YYSNCNCWNT	TATTTAAATCTGCA AGAGGTTTGGT
M00100	V\$CDXA_01	0.937224	21	(+)	MTTTATR	ATTTAAA
M00222	V\$TH1E47_01	0.810817	21	(+)	NNNGNRCTG GMWTT	ATTTAAATCTGCA AGA
M00252	V\$TATA_01	0.831261	21	(+)	STATAAWR NNNNN	ATTTAAATCTGCA AG
M00100	V\$CDXA_01	0.937224	22	(-)	MTTTATR	TTTAAAT
M00075	V\$GATA1_01	0.797631	23	(-)	SNGATNNNN	TTAAATCTGC
M00076	V\$GATA2_01	0.782589	23	(-)	NNGATRNNN	TTAAATCTGC
M00189	V\$AP2_Q6	0.803079	26	(+)	MKCCSCNGGCG	AATCTGCAAGAG
M00200	V\$CAAT_C	0.730118	27	(-)	ACCAATCANCN GCYYSNCNCWNT	ATCTGCAAGAGGT GGTAAATCAT
M00055	V\$NMYC_01	0.743005	29	(-)	NNNCACGTGNNN	CTGCAAGAGGTT
M00212	V\$POLY_C	0.778054	29	(-)	CAATAAAACCY YYYKCTN	CTGCAAGAGGTT TGGTTA
M00255	V\$GC_01	0.836355	33	(+)	NRGGGCGGGGC NK	AAGAGGTTTGGT TA
M00008	V\$SP1_01	0.871461	35	(+)	GRGGCRGGGW	GAGGTTTGGT
M00063	V\$IRF2_01	0.716799	37	(-)	GAAAAGYGAAASY	GGTTTGGTTAATC
M00116	V\$CEBPA_01	0.858037	37	(+)	NNATTRCNNAANN	GGTTTGGTTAATCA
M00116	V\$CEBPA_01	0.840047	37	(-)	NNATTRCNNAANN	GGTTTGGTTAATCA

Table SIII. Continued.

AC	ID	Score	Location	Strand	Consensus sequence	Signal sequence
M00117	V\$CEBPB_02	0.851013	37	(+)	NKNTTGCN YAAYNN	GGTTTGGTTAA TCA
M00159	V\$CEBP_01	0.950729	37	(+)	NNTKTGGW NANNN	GGTTTGGTTA ATC
M00190	V\$CEBP_Q2	0.8318	37	(+)	NNNTTGCN NAANNN	GGTTTGGTTAA TCA
M00254	V\$CAAT_01	0.847501	37	(-)	NNRRCCAATSA	GGTTTGGTTAAT
M00099	V\$S8_01	0.780531	39	(+)	WNNANYYAA TTANYNN	TTTGGTTAATC ATTGG
M00271	V\$AML1_01	0.853077	39	(+)	TGTGGT	TTTGGT
M00206	V\$HNF1_C	0.96145	40	(-)	NGTTAATKAW TNACCAM	TTGGTTAATCAT TGGCT
M00099	V\$S8_01	0.804298	41	(-)	WNNANYYAA TTANYNN	TGGTTAATCAT TGGCT
M00137	V\$OCT1_03	0.841565	41	(+)	NNNRTAAT NANNN	TGGTTAATCA TTG
M00132	V\$HNF1_01	0.914677	42	(+)	GGTTAATN WTTAMMN	GGTTAATCATT GGCT
M00173	V\$AP1_Q2	0.807613	42	(-)	RSTGACTNMNW	GGTTAATCATT
M00174	V\$AP1_Q6	0.843174	42	(-)	NNTGACTCANN	GGTTAATCATT
M00188	V\$AP1_Q4	0.863373	42	(-)	RSTGACTMANN	GGTTAATCATT
M00206	V\$HNF1_C	0.8563	42	(+)	NGTTAATKAWT NACCAM	GGTTAATCATTG GCTTT
M00095	V\$CDP_01	0.809203	43	(-)	CCAATAATCGAT	GTTAATCATTGG
M00199	V\$AP1_C	0.874636	43	(+)	NTGASTCAG	GTTAATCAT
M00199	V\$AP1_C	0.78484	43	(-)	NTGASTCAG	GTTAATCAT
M00099	V\$S8_01	0.771681	44	(-)	WNNANYYAA TTANYNN	TTAATCATTGGC TTTG
M00160	V\$SRY_02	0.785379	44	(+)	NWWAACAAWANN	TTAATCATTGGC
M00104	V\$CDPCR1_01	0.799088	46	(+)	NATCGATCGS	AATCATTGGC
M00131	V\$HNF3B_01	0.85586	46	(+)	NNNTRITTRYTY	AATCATTGGCTT
M00185	V\$NFY_Q6	0.916752	47	(-)	TRRCCAATSRN	ATCATTGGCTT
M00191	V\$ER_Q6	0.73289	47	(+)	NNARGNNANN NTGACCYNN	ATCATTGGCTTT GTCCTGT
M00192	V\$GR_Q6	0.773717	47	(+)	NNNNNNCNNT NTGTNCTNN	ATCATTGGCTTT GTCCTGT
M00253	V\$CAP_01	0.915722	48	(+)	NCANNNNN	TCATTGGC
M00254	V\$CAAT_01	0.939	48	(-)	NNRRCCAATSA	TCATTGGCTTGT
M00008	V\$SP1_01	0.830408	51	(+)	GRGGCRGGGW	TTGGCTTGT
M00203	V\$GATA_C	0.867661	52	(-)	NGATAAGNMNN	TGGCTTTGTCC
M00272	V\$P53_02	0.800703	53	(+)	NGRCWTGYCY	GGCTTTGTCC
M00032	V\$CETS1 P54_01	0.870722	56	(-)	NCMGG AWGYN	TTTGCCTGT
M00011	V\$EVI1_06	0.775619	57	(-)	ACAAGATAA	TTGTCTGT
M00079	V\$EVI1_02	0.77747	57	(-)	AGAYAAGATAA	TTGTCTGTGT
M00187	V\$USF_Q6	0.844003	59	(-)	GYCACGTGNC	GTCCTGTGTA
M00217	V\$USF_C	0.843006	60	(+)	NCACGTGN	TCCTGTGT
M00268	V\$XFD2_01	0.834	63	(+)	WNWATAAA CAWNNR	TGTGTAGACAG TCA
M00269	V\$XFD3_01	0.823921	63	(+)	WNWGTMAA CAWWMW	TGTGTAGACAG TCA
M00237	V\$AHRA RNT_02	0.760183	64	(-)	GRGKATYGCG TGMSWNSCC	GTGTAGACAGT CAACCCTC
M00280	V\$RFX1_01	0.79335	64	(+)	NNGTNRCN WRGYAACNN	GTGTAGACAGT CAACCC
M00209	V\$NFY_C	0.794123	65	(-)	NCTGATTG GYTASY	TGTAGACAGTC AAC

Table III. Continued.

AC	ID	Score	Location	Strand	Consensus sequence	Signal sequence
M00254	V\$CAAT_01	0.821519	65	(+)	NNNRCCAATSA	TGTAGACAGTCA
M00114	V\$TAXCREB_01	0.735152	68	(-)	GGGGGTTGA CGYANA	AGACAGTCAACC CTC
M00174	V\$AP1_Q6	0.771719	68	(-)	NNTGACTCANN	AGACAGTCAAC
M00200	V\$CAAT_C	0.734317	69	(+)	ACCAATCANCNNG CYYSNCNCWNNT	GACAGTCAACCC CCCTCTACGTCC
M00144	V\$PAX5_02	0.74151	70	(-)	RRMSWGANW YCTNRAGCGKRA CSRYNSM	ACAGTCAACCC CCTCTACGTCTT TTG
M00004	V\$CMYB_01	0.807501	71	(-)	NCNRNNGRCN GTTGGKGG	CAGTCAACCCTC CCTCTA
M00212	V\$POLY_C	0.860624	71	(+)	CAATAAAACCY YYYKCTN	CAGTCAACCCTC CCTCTA
M00008	V\$SP1_01	0.793035	72	(-)	GRGGCRGGW	AGTCAACCCT
M00008	V\$SP1_01	0.807191	73	(-)	GRGGCRGGW	GTCAACCCTC
M00084	V\$MZF1_02	0.853537	74	(-)	KNNNKAGGGGNA	TCAACCCTCCCTC
M00253	V\$CAP_01	0.889108	74	(+)	NCANNNNN	TCAACCCT
M00255	V\$GC_01	0.873836	74	(-)	NRGGGGCGG GGCNK	TCAACCCTCCC TCT
M00196	V\$SP1_Q6	0.848501	75	(-)	NGGGGGCGGGYN	CAACCCTCCCTCT
M00255	V\$GC_01	0.82876	75	(-)	NRGGGGCG GGCNK	CAACCCTCCCT CTA
M00008	V\$SP1_01	0.795583	76	(-)	GRGGCRGGW	AACCCTCCCT
M00008	V\$SP1_01	0.923839	77	(-)	GRGGCRGGW	ACCCTCCCTC
M00108	V\$NRF2_01	0.782461	78	(-)	ACCGAAGNS	CCCTCCCTCT
M00085	V\$ZID_01	0.764991	81	(+)	NGGCTCYATCAYC	TCCCTCTACGTCC
M00039	V\$CREB_01	0.816136	86	(-)	TGACGTMA	CTACGTCC
M00040	V\$CREBP1_01	0.747464	86	(+)	TTACGTAA	CTACGTCC
M00098	V\$PAX2_01	0.765405	86	(+)	NNNNGTCANGN RTKANNNN	CTACGTCTTTGT TCCTCC
M00134	V\$HNF4_01	0.807169	86	(-)	NNNRGGNCAAA GKTCANNN	CTACGTCTTTGT TCCTCC
M00032	V\$CETS1P54_01	0.879957	87	(-)	NCMGGAWGYN	TACGTCTTTT
M00003	V\$VMYB_01	0.804137	90	(-)	AAYAACGGNN	GTCCTTTGTT
M00160	V\$SRY_02	0.841163	91	(-)	NWWAACAAWANN	TCCTTTGTTCTC
M00024	V\$E2F_01	0.749307	92	(-)	TWSGCGCG AAAAYKR	CCTTTGTTCTC CCTA
M00255	V\$GC_01	0.848114	95	(-)	NRGGGGCGG GGCNK	TTGTTCTCCT ATG
M00205	V\$GRE_C	0.795573	96	(+)	GGTACAANNT GTYCTK	TGTTCTCCTAT GCTG
M00084	V\$MZF1_02	0.820045	98	(-)	KNNNKAGGGGNA	TTCCTCCTATGCT
M00107	V\$E2_01	0.746398	100	(-)	NNACCRNA NCGTRN	CCTCCTATGCTG TTGG
M00127	V\$GATA1_03	0.804018	100	(-)	RNSNNGATAA NNGN	CCTCCTATGCTG TT
M00243	V\$EGR1_01	0.780277	100	(-)	WTGCGTGGGCGK	CCTCCTATGCTG
M00244	V\$NGFIC_01	0.737512	100	(-)	WTGCGTGGGYGG	CCTCCTATGCTG
M00245	V\$EGR3_01	0.792083	100	(-)	NTGCGTGGGCGK	CCTCCTATGCTG
M00246	V\$EGR2_01	0.755209	100	(-)	NTGCGTRGGCGK	CCTCCTATGCTG
M00076	V\$GATA2_01	0.823184	102	(-)	NNNGATRNNN	TCCTATGCTG
M00217	V\$USF_C	0.80946	102	(+)	NCACGTGN	TCCTATGC
M00003	V\$VMYB_01	0.819974	107	(-)	AAYAACGGNN	TGCTGTTGGT
M00129	V\$HFH1_01	0.782838	107	(+)	NAWTGTTTATWT	TGCTGTTGGTAT
M00075	V\$GATA1_01	0.780849	108	(+)	SNNGATNNNN	GCTGTTGGTA

Table SIII. Continued.

AC	ID	Score	Location	Strand	Consensus sequence	Signal sequence
M00227	V\$VMYB_02	0.823706	108	(-)	NSYAACGGN	GCTGTTGGT
M00203	V\$GATA_C	0.834731	110	(-)	NGATAAGNMNN	TGTTGGTATCC
M00225	V\$STAT3_01	0.772484	111	(+)	NGNNATTTCCS GGAARTGNNN	GTTGGTATCCCAGA AATTCTT
M00225	V\$STAT3_01	0.732802	111	(-)	NGNNATTTCCSG GAARTGNNN	GTTGGTATCCCAGAA ATTCTT
M00023	V\$HOX13_01	0.788379	113	(+)	TGCNNNNWYCCYCAT TAKTNNNNNMNNYCN	TGGTATCCCAGAAAT TCTTGCTCAATTCCC
M00075	V\$GATA1_01	0.82922	113	(-)	SNGATNNNN	TGGTATCCCA
M00076	V\$GATA2_01	0.917456	113	(-)	NNNGATRNNN	TGGTATCCCA
M00086	V\$IK1_01	0.773237	113	(-)	NNNTGGGAATRCC	TGGTATCCCAGAA
M00053	V\$CREL_01	0.822303	114	(-)	SGGRNWTTC	GGTATCCCAG
M00087	V\$IK2_01	0.91034	114	(-)	NNNYGGGAWNNN	GGTATCCCAGAA
M00088	V\$IK3_01	0.790552	114	(-)	TNYTGGGAATACC	GGTATCCCAGAAA
M00162	V\$OCT1_06	0.869922	114	(-)	CWNAWTKWSATRYN	GGTATCCCAGAAAT
M00262	V\$STAF_01	0.725578	115	(+)	NTTWCCCANMATGC AAYRCGY	GTATCCCAGAAATTC TTGCTCA
M00141	V\$LYF1_01	0.928188	116	(-)	TTTGGGAGR	TATCCCAGA
M00214	V\$SEF1_C	0.709933	116	(-)	AACACGGATATCT GTGGTY	TATCCCAGAAATTC TTGCT
M00222	V\$TH1E47_01	0.809149	116	(-)	NNNGNRTCTGGMWTT	TATCCCAGAAATTCTT
M00223	V\$STAT_01	0.866398	117	(+)	TTCCCRKAA	ATCCCAGAA
M00223	V\$STAT_01	0.803126	117	(-)	TTCCCRKAA	ATCCCAGAA
M00088	V\$IK3_01	0.825839	118	(+)	TNYTGGGAATACC	TCCCAGAAATTCT
M00100	V\$CDXA_01	0.938695	121	(-)	MTTATR	CAGAAAT
M00109	V\$CEBPB_01	0.926201	127	(-)	RNRTKNNGMAAKNN	TTCTTGCTCAATTC
M00116	V\$CEBPA_01	0.86273	127	(+)	NNATRCNNAANNN	TTCTTGCTCAATTC
M00116	V\$CEBPA_01	0.82675	127	(-)	NNATRCNNAANNN	TTCTTGCTCAATTC
M00117	V\$CEBPB_02	0.963148	127	(+)	NKNTTGCNYYAAYNN	TTCTTGCTCAATTC
M00190	V\$CEBP_Q2	0.882959	127	(+)	NNNTTGCNNAANNN	TTCTTGCTCAATTC
M00190	V\$CEBP_Q2	0.849834	127	(-)	NNNTTGCNNAANNN	TTCTTGCTCAATTC
M00099	V\$S8_01	0.782048	129	(+)	WNNANYYAATTANYNN	CTTGCTCAATTCCCCT
M00199	V\$AP1_C	0.773178	129	(-)	NTGASTCAG	CTTGCTCAA
M00007	V\$ELK1_01	0.786907	132	(-)	NNNACMGGGAAGTNCNN	GCTCAATTCCCCTCAG
M00241	V\$NKX25_02	0.839809	133	(+)	CWTAATTG	CTCAATTC
M00253	V\$CAP_01	0.884672	134	(+)	NCANNNNN	TCAATTC
M00056	V\$MYOGNF 1_01	0.740865	136	(+)	CRSCTGTNNNNNTTGG CACNSNGCCARNN	AATCCCCTCAGCTT GTTTGCTTCCGATA
M00084	V\$MZF1_02	0.846538	137	(-)	KNNNKAGGGGNA	ATTCCCCTCAGCT
M00084	V\$MZF1_02	0.832792	138	(-)	KNNNKAGGGGNA	TTCCCCTCAGCTT
M00223	V\$STAT_01	0.897404	138	(+)	TTCCCRKAA	TTCCCCTCA
M00083	V\$MZF1_01	0.924821	139	(-)	NGNGGGGA	TCCCCTCA
M00141	V\$LYF1_01	0.842576	140	(-)	TTTGGGAGR	CCCCTCAGC
M00001	V\$MYOD_01	0.827165	142	(+)	SRACAGGTGKYG	CCTCAGCTTGTT
M00175	V\$AP4_Q5	0.883297	143	(+)	NNCAGCTGNN	CTCAGCTTGT
M00176	V\$AP4_Q6	0.889752	143	(+)	CWCAGCTGNN	CTCAGCTTGT
M00011	V\$EV1_06	0.777076	144	(-)	ACAAGATAA	TCAGCTTGT
M00253	V\$CAP_01	0.928043	144	(+)	NCANNNNN	TCAGCTTG
M00160	V\$SRY_02	0.800352	145	(-)	NWWAACA AWANN	CAGCTTGTTTGC
M00272	V\$P53_02	0.883939	145	(+)	NGRCWTGYCY	CAGCTTGTTT
M00272	V\$P53_02	0.819168	145	(-)	NGRCWTGYCY	CAGCTTGTTT
M00129	V\$HFH1_01	0.841872	147	(+)	NAWTGTTTATWT	GCTTGTTTGCTT
M00130	V\$HFH2_01	0.921168	147	(+)	NAWTGTTTRTTT	GCTTGTTTGCTT
M00131	V\$HNF3B_01	0.978889	147	(+)	NNNTRITTRYTY	GCTTGTTTGCTT
M00148	V\$SRY_01	0.934109	148	(-)	AAACWAM	CTTGTTT
M00007	V\$ELK1_01	0.791583	151	(-)	NNNACMGGGAAGTNCNN GTNCNN	GTTTGCTTCCGATA AG

Table III. Continued.

AC	ID	Score	Location	Strand	Consensus sequence	Signal sequence
M00225	V\$STAT3_01	0.721506	151	(+)	NGNNATTTCCS GGAARTGNNN	GTTTGCTTCCGATA AGCTGTT
M00025	V\$ELK1_02	0.850627	153	(-)	NNNNCCGGAARYNN	TTGCTTCCGATAAG
M00074	V\$CETS1P54_02	0.846531	153	(-)	NNAMMGGAWRWNN	TTGCTTCCGATAAs
M00032	V\$CETS1P54_01	0.868821	154	(-)	NCMGGAWGYN	TGCTTCCGAT
M00108	V\$NRF2_01	0.771802	154	(-)	ACCGGAAGNS	TGCTTCCGAT
M00126	V\$GATA1_02	0.81125	156	(+)	NNNNNGATANKGNN	CTTCCGATAAGCTG
M00128	V\$GATA1_04	0.852941	157	(+)	NNCWGATARNNNN	TCCGATAAGCTG
M00223	V\$STAT_01	0.939249	157	(+)	TTCCCRKAA	TCCGATAA
M00223	V\$STAT_01	0.912276	157	(-)	TTCCCRKAA	TCCGATAA
M00075	V\$GATA1_01	0.834156	158	(+)	SNNGATNNNN	TCCGATAAGC
M00076	V\$GATA2_01	0.887235	158	(+)	NNNGATRNNN	TCCGATAAGC
M00227	V\$VMYB_02	0.80355	158	(-)	NSYAACGGN	TCCGATAAG
M00077	V\$GATA3_01	0.852016	159	(+)	NNGATARNG	CCGATAAGC
M00278	V\$LMO2COM_02	0.960243	159	(+)	NMGATANS	CCGATAAGC
M00001	V\$MYOD_01	0.861417	161	(+)	SRACAGGTGKYG	GATAAGCTGTTG
M00175	V\$AP4_Q5	0.852557	162	(+)	NNCAGCTGNN	ATAAGCTGTT
M00175	V\$AP4_Q5	0.832699	162	(-)	NNCAGCTGNN	ATAAGCTGTT
M00176	V\$AP4_Q6	0.830619	162	(+)	CWCAGCTGGN	ATAAGCTGTT
M00109	V\$CEBPB_01	0.910847	165	(+)	RNRTKNNGMAAKNN	AGCTGTTGCAAAGG
M00116	V\$CEBPA_01	0.860383	165	(-)	NNATTRCNNAANN	AGCTGTTGCAAAGG
M00249	V\$CHOP_01	0.828106	165	(-)	NNRTGCAATMCCC	AGCTGTTGCAAAG
M00227	V\$VMYB_02	0.84988	166	(-)	NSYAACGGN	GCTGTTGCA
M00279	V\$MIF1_01	0.746669	166	(-)	NNGTTGCWWG GYAACNGS	GCTGTTGCAAA GGTAGCA
M00281	V\$RFX1_02	0.820314	166	(-)	NNGTNRCNATR GYAACNNN	GCTGTTGCAA AGGTAGCAT
M00116	V\$CEBPA_01	0.839656	167	(+)	NNATTRCNNAANN	CTGTTGCAAAGGTA
M00190	V\$CEBP_Q2	0.855355	167	(+)	NNNTTGCNNAANN	CTGTTGCAAAGGTA
M00280	V\$RFX1_01	0.811203	167	(-)	NNGTNRCNW RGYAACNN	CTGTTGCAA AGGTAGCA
M00281	V\$RFX1_02	0.819023	167	(+)	NNGTNRCNATR GYAACNNN	CTGTTGCAAAG GTAGCATT
M00035	V\$VMAF_01	0.762975	168	(-)	NNNTGCTGACT CAGCANN	TGTTGCAAAGG TAGCATT
M00227	V\$VMYB_02	0.838147	171	(+)	NSYAACGGN	TGCAAAGGT
M00058	V\$HEN1_02	0.741541	174	(+)	NNGGGNCGCAGC TGCGNCCCNN	AAAGGTAGCAT TTGATTCTCCA
M00058	V\$HEN1_02	0.738358	174	(-)	NNGGGNCGCAGCT GCGNCCCNN	AAAGGTAGCAT TTGATTCTCCA
M00068	V\$HEN1_01	0.754746	174	(+)	NNNGGNCNCAGC TGCGNCCCNN	AAAGGTAGCAT TTGATTCTCCA
M00068	V\$HEN1_01	0.780058	174	(-)	NNNGGNCNCAGC TGCGNCCCNN	AAAGGTAGCA TTGATTCTCCA
M00005	V\$AP4_01	0.759798	175	(-)	WGARYCAGCT GYGGNCNK	AAGGTAGCATTG ATTCT
M00122	V\$USF_02	0.792728	178	(+)	NNRNCACGTGNYNN	GTAGCATTGATTCT
M00122	V\$USF_02	0.792728	178	(-)	NNRNCACGTGNYNN	GTAGCATTGATTCT
M00123	V\$MYCMAX_02	0.781193	179	(-)	NANCACGTGNNW	TAGCATTGATT
M00162	V\$OCT1_06	0.842187	179	(+)	CWNAWTKWSATRYN	TAGCATTGATTCT
M00162	V\$OCT1_06	0.863281	180	(-)	CWNAWTKWSATRYN	AGCATTGATTCTC
M00184	V\$MYOD_Q6	0.851326	180	(+)	NNCANCTGNY	AGCATTGAT

Table III. Continued.

AC	ID	Score	Location	Strand	Consensus sequence	Signal sequence
M00160	V\$SR_Y_02	0.798004	181	(-)	NWAAACA AWANN	GCATTTGATTCT
M00253	V\$CAP_01	0.871858	181	(+)	NCANNNNN	GCATTTGA
M00240	V\$NKX25_01	0.852443	182	(-)	TYAAGTG	CATTTGA
M00075	V\$GATA1_01	0.786772	184	(+)	SNNGATNNNN	TTTGATTCTC
M00148	V\$SR_Y_01	0.962791	184	(-)	AAACWAM	TTTGATT
M00209	V\$NFY_C	0.794296	184	(+)	NCTGATTGGYTASY	TTTGATTCTCCAGT
M00254	V\$CAAT_01	0.813047	188	(+)	NNNRCCAATSA	ATTCTCCAGTCA
M00222	V\$TH1E47_01	0.810817	189	(-)	NNNNGNRTCTGGMWTT	TTCTCCAGTCAACAAT
M00023	V\$HOX13_01	0.753826	190	(+)	TGCNNNNWYCCYCAT TAKTNNNNNMNNYCN	TCTCCAGTCAACAAT TAGGAGATCTCACAT
M00185	V\$NFY_Q6	0.792909	190	(+)	TRRCCAATSRN	TCTCCAGTCAA
M00098	V\$PAX2_01	0.772599	192	(+)	NNNNGTCANGN RTKANNNN	TCCAGTCAACA ATTAGGAG
M00113	V\$CREB_02	0.775177	192	(-)	NNGNTGACGYNN	TCCAGTCAACAA
M00269	V\$XFD3_01	0.86987	193	(+)	WNWGTMAACA WWMW	CCAGTCAACAATTA
M00004	V\$CMYB_01	0.765445	194	(-)	NCNRNNGRCN GTTGGKGG	CAGTCAACAA TTAGGAGA
M00131	V\$HNF3B_01	0.892987	194	(-)	NNNTRITTRYTY	CAGTCAACAATT
M00099	V\$S8_01	0.814918	195	(+)	WNNANYYAATTANYNN	AGTCAACAATTAGGAG
M00160	V\$SR_Y_02	0.874046	196	(+)	NWAAACA AWANN	GTCAACAATTAG
M00042	V\$SOX5_01	0.939619	197	(+)	NNAACAATN	TCAACAATTA
M00099	V\$S8_01	0.789128	197	(-)	WNNANYYAATTANYNN	TCAACAATTAGGAGAT
M00137	V\$OCT1_03	0.84354	197	(+)	NNNRTAATNANN	TCAACAATTAGGA
M00185	V\$NFY_Q6	0.790853	197	(+)	TRRCCAATSRN	TCAACAATTAG
M00095	V\$CDP_01	0.744705	199	(-)	CCAATAATCGAT	AACAATTAGGAG
M00227	V\$VMYB_02	0.793622	200	(-)	NSYACGGN	ACAATTAGG
M00241	V\$NKX25_02	0.884009	201	(-)	CWTAATTG	CAATTAGG
M00056	V\$MYOGNF1_01	0.74029	202	(-)	CRSCTGTNNNNTTTG GCACNSNGCCARNN	AATTAGGAGATCTCA CATTCAGGAACAG
M00141	V\$LYF1_01	0.852543	203	(+)	TTTGGGAGR	ATTAGGAGA
M00223	V\$STAT_01	0.79884	204	(-)	TTCCCRKAA	TTAGGAGAT
M00115	V\$TAXCREB_02	0.659893	205	(-)	RTGACGCATAYCCCC	TAGGAGATCTCACAT
M00194	V\$NFKB_Q6	0.791045	205	(-)	NGGGGAMTTTCNN	TAGGAGATCTCACA
M00075	V\$GATA1_01	0.817374	207	(+)	SNNGATNNNN	GGAGATCTCA
M00075	V\$GATA1_01	0.781836	207	(-)	SNNGATNNNN	GGAGATCTCA
M00076	V\$GATA2_01	0.841678	207	(+)	NNNGATRNNN	GGAGATCTCA
M00076	V\$GATA2_01	0.853406	207	(-)	NNNGATRNNN	GGAGATCTCA
M00249	V\$CHOP_01	0.771943	207	(-)	NNRTGCAATMCCC	GGAGATCTCACAT
M00211	V\$PADS_C	0.852823	208	(-)	NGTGGTCTC	GAGATCTCA
M00115	V\$TAXCREB_02	0.611391	209	(+)	RTGACGCATAYCCCC	AGATCTCACATTCCA
M00123	V\$MYC MAX_02	0.812976	212	(+)	NANCACGTGNNW	TCTCACATTCCA
M00187	V\$USF_Q6	0.835337	213	(+)	GYCACGTGNC	CTCACATTCC
M00224	V\$STAT1_01	0.810143	213	(+)	NNNSANTTCCG GGAANTGNSN	CTCACATTCCAGGAA CAGGT
M00253	V\$CAP_01	0.921143	214	(+)	NCANNNNN	TCACATTC
M00162	V\$OCT1_06	0.864844	215	(-)	CWNAWKWSATRYN	CACATTCCAGGAAC
M00253	V\$CAP_01	0.874815	216	(+)	NCANNNNN	ACATTCCA
M00223	V\$STAT_01	0.894631	219	(+)	TTCCCRKAA	TTCCAGGAA
M00223	V\$STAT_01	0.97328	219	(-)	TTCCCRKAA	TTCCAGGAA
M00032	V\$CETS1P54_01	0.833514	221	(+)	NCMGGAWGYN	CCAGGAACAG
M00108	V\$NRF2_01	0.80814	221	(+)	ACCGGAAGNS	CCAGGAACAG
M00192	V\$GR_Q6	0.788504	222	(-)	NNNNNCNN TNTGTNCTNN	CAGGAACAGGGTGG CTTTG

Table SIII. Continued.

AC	ID	Score	Location	Strand	Consensus sequence	Signal sequence
M00056	V\$MYOGNF1_01	0.748058	226	(-)	CRSCTGTNNNNTTTG GCACNSNGCCARNN	AACAGGGTGGCTTTG AGAATGAAAAGAGG
M00212	V\$POLY_C	0.754152	226	(-)	CAATAAAACC YYYYKCTN	AACAGGGTGGCTTT GAGA
M00255	V\$GC_01	0.808917	227	(+)	NRGGGGCGGGGCK	ACAGGGTGGCTTTG
M00008	V\$SP1_01	0.830408	228	(+)	GRGGCRGGGW	CAGGGTGGCT
M00023	V\$HOX13_01	0.748087	229	(-)	TGCNNNNWYCCYCAT TAKTNNNNNMNNYCN	AGGGTGGCTTTGAGA ATGAAAAGAGGAGCA
M00057	V\$COMP1_01	0.773293	229	(-)	NNTNWKGATTGR CNRSRANMRRNN	AGGGTGGCTTTGAGA ATGAAAAGA
M00057	V\$COMP1_01	0.798443	230	(+)	NNTNWKGATTGRCN RSRANMRRNN	GGGTGGCTTTGAGAA TGAAAAGAG
M00201	V\$CEBP_C	0.812809	231	(-)	NGWNTKNKGY AAKNSAYA	GGTGGCTTTG AGAATGAA
M00008	V\$SP1_01	0.84145	232	(+)	GRGGCRGGGW	GTGGCTTTGA
M00059	V\$YY1_01	0.81979	236	(-)	NNNNNCCATN TWNWN	CTTTGAGAA TGAAAAGA
M00086	V\$IK1_01	0.782585	236	(+)	NNNTGGGAATRCC	CTTTGAGAATGAA
M00195	V\$OCT1_Q6	0.829421	240	(+)	NNNNATGCAAATNAN	GAGAATGAAAAGAGG
M00127	V\$GATA1_03	0.837335	241	(+)	RNSNNGATAANNGN	AGAATGAAAAGAGG
M00162	V\$OCT1_06	0.860547	241	(-)	CWNAWTKWSATRYN	AGAATGAAAAGAGG
M00216	V\$TATA_C	0.744389	241	(+)	NCTATAAAAR	AGAATGAAAA
M00210	V\$OCT_C	0.782714	242	(-)	CTNATTTGCATAY	GAATGAAAAGAGG
M00252	V\$TATA_01	0.782035	242	(+)	STATAAAWRNNNNNN	GAATGAAAAGAGGAG
M00148	V\$SR1_01	0.923256	243	(+)	AAACWAM	AATGAAA
M00063	V\$IRF2_01	0.702656	246	(+)	GAAAAGYGAAASY	GAAAAGAGGAGCA
M00255	V\$GC_01	0.784909	246	(+)	NRGGGGCGGGGCK	GAAAAGAGGAGCAT
M00144	V\$PAX5_02	0.742658	247	(+)	RRMSWGANWYCTNR AGCGKRACSRYSM	AAAAGAGGAGCATA GGAGGGTATATCCA
M00127	V\$GATA1_03	0.846644	252	(+)	RNSNNGATAANNGN	AGGAGCATAGGAGG
M00152	V\$SRF_01	0.725283	252	(-)	ATGCCATATA TGGWNNT	AGGAGCATAGG AGGGTAT
M00076	V\$GATA2_01	0.828597	254	(+)	NNNGATRNNN	GAGCATAGGA
M00243	V\$EGR1_01	0.780277	254	(+)	WTGCGTGGGCGK	GAGCATAGGAGG
M00244	V\$NGFIC_01	0.785504	254	(+)	WTGCGTGGGYGG	GAGCATAGGAGG
M00245	V\$EGR3_01	0.792083	254	(+)	NTGCGTGGGCGK	GAGCATAGGAGG
M00246	V\$EGR2_01	0.774995	254	(+)	NTGCGTRGGCGK	GAGCATAGGAGG
M00217	V\$USF_C	0.80946	256	(-)	NCACGTGN	GCATAGGA
M00255	V\$GC_01	0.802303	257	(+)	NRGGGGCGGGGCK	CATAGGAGGGTATA
M00084	V\$MZF1_02	0.832292	258	(+)	KNNKAGGGNAA	ATAGGAGGGTATA
M00088	V\$IK3_01	0.811421	260	(+)	TNYTGGAATACC	AGGAGGGTATATC
M00138	V\$OCT1_04	0.788373	261	(-)	NNNNNNWATGCA AATNNNWNW	GGAGGGTATATCCAT ATTTCTAA
M00255	V\$GC_01	0.832925	261	(+)	NRGGGGCGGGGCK	GGAGGGTATATCCA
M00127	V\$GATA1_03	0.783195	262	(-)	RNSNNGATAANNGN	GAGGGTATATCCAT
M00138	V\$OCT1_04	0.823296	262	(+)	NNNNNNWATGCA AATNNNWNW	GAGGGTATATCCATA TTTCTAAA
M00023	V\$HOX13_01	0.724773	263	(+)	TGCNNNNWYCCYCAT AKTNNNNNMNNYCN	AGGGTATATCCATATT TCTAAACGTGAAAG
M00133	V\$TST1_01	0.870616	263	(+)	NNKGAWTANANTNN	AGGGTATATCCATAT
M00135	V\$OCT1_01	0.798169	263	(-)	NNNNWATGCA AATNTNNN	AGGGTATATCCA TATTTCT
M00194	V\$NFKB_Q6	0.810738	263	(-)	NRGGGGAMTTTCCNN	AGGGTATATCCATA
M00203	V\$GATA_C	0.871078	263	(-)	NGATAAGNMNN	AGGGTATATCC
M00208	V\$NFKB_C	0.779289	263	(+)	NRGGACTTTCCA	AGGGTATATCCA
M00255	V\$GC_01	0.784909	263	(-)	NRGGGGCGGGGCK	AGGGTATATCCATA

Table III. Continued.

AC	ID	Score	Location	Strand	Consensus sequence	Signal sequence
M00051	V\$NFKAPPAB50_01	0.765882	264	(+)	GGGGATYCCC	GGGTATATCC
M00052	V\$NFKAPPAB65_01	0.790419	264	(+)	GGGRATTTCC	GGGTATATCC
M00053	V\$CREL_01	0.886819	264	(+)	SGRNWTTC	GGGTATATCC
M00054	V\$NFKAPPAB_01	0.813733	264	(+)	GGGAMTTYCC	GGGTATATCC
M00115	V\$TAXCREB_02	0.651439	264	(-)	RTGACGCATAYCCCC	GGGTATATCCATATT
M00135	V\$OCT1_01	0.775658	264	(+)	NNNNWTATGCA AATNTNNN	GGGTATATCCATATTT CTA
M00136	V\$OCT1_02	0.819978	264	(+)	NNGAATATKCANNNN	GGGTATATCCATATT
M00052	V\$NFKAPPAB65_01	0.787545	265	(-)	GGGRATTTCC	GGTATATCCA
M00053	V\$CREL_01	0.873471	265	(-)	SGRNWTTC	GGTATATCCA
M00074	V\$CETS1P54_02	0.869437	266	(-)	NNAMMGGAWRWNN	GTATATCCATATT
M00159	V\$CEBP_01	0.876823	266	(-)	NNTKTGGWNANNN	GTATATCCATATT
M00032	V\$CETS1P54_01	0.816404	267	(-)	NCMGGAWGYN	TATATCCATA
M00059	V\$YY1_01	0.88827	267	(+)	NNNNNCCATNTWNNNWN	TATATCCATATTTCTAA
M00103	V\$CLOX_01	0.768541	267	(+)	NNTATCGATTANYNW	TATATCCATATTTCT
M00136	V\$OCT1_02	0.806172	267	(-)	NNGAATATKCANNNN	TATATCCATATTTCT
M00162	V\$OCT1_06	0.839453	267	(-)	CWNAWTKWSATRYN	TATATCCATATTTCT
M00262	V\$STAF_01	0.720954	267	(+)	NTTWCCCANMAT GCAYYRCGNY	TATATCCATATT TCTAAACGTG
M00264	V\$STAF_02	0.751581	267	(+)	MNTTCCCAKMAT KCMWNGCRN	TATATCCATATT TTCTAAACGT
M00133	V\$TST1_01	0.874903	268	(-)	NNKGAWTWANANTNN	ATATCCATATTTCTA
M00152	V\$SRF_01	0.711327	268	(+)	ATGCCATATATGGWNNT	ATATCCATATTTCTAAAC
M00215	V\$SRF_C	0.754392	268	(-)	NCCWTATATGGNCWN	ATATCCATATTTCTA
M00222	V\$TH1E47_01	0.812485	268	(-)	NNNNGNRTCTGGMWTT	ATATCCATATTTCTAA
M00123	V\$MYCMAX_02	0.789598	270	(+)	NANACGTGNNW	ATCCATATTTCT
M00098	V\$PAX2_01	0.761026	271	(-)	NNNNGTCANGN RTKANNNN	TCCATATTTCT TAAACGTGA
M00215	V\$SRF_C	0.750878	271	(+)	NCCWTATATGGNCWN	TCCATATTTCTAAAC
M00268	V\$XFD2_01	0.8552	271	(-)	WNWATAAACAWNNR	TCCATATTTCTAAA
M00253	V\$CAP_01	0.878758	272	(+)	NCANNNNN	CCATATTT
M00162	V\$OCT1_06	0.813672	273	(-)	CWNAWTKWSATRYN	CATATTTCTAAACG
M00109	V\$CEBPB_01	0.945022	274	(-)	RNRTKNNNGMAAKNN	ATATTTCTAAACGT
M00116	V\$CEBPA_01	0.854517	274	(+)	NNATTRCNNAANNN	ATATTTCTAAACGT
M00117	V\$CEBPB_02	0.852856	274	(+)	NKNTTGCNYAAYNN	ATATTTCTAAACGT
M00190	V\$CEBP_Q2	0.831064	274	(+)	NNNTTGCNNAANNN	ATATTTCTAAACGT
M00057	V\$COMP1_01	0.826946	275	(-)	NNTNWKGATTGR CNRSRANMRRNN	TATTTCTAAACGT GAAAGAATATA
M00100	V\$CDXA_01	0.919568	276	(+)	MTTATR	ATTTCTA
M00101	V\$CDXA_02	0.981893	276	(+)	WWTWMTR	ATTTCTA
M00199	V\$AP1_C	0.77172	276	(+)	NTGASTCAG	ATTTCTAAA
M00055	V\$NMYC_01	0.772202	280	(+)	NNNCACGTGNNN	CTAAACGTGAAA
M00055	V\$NMYC_01	0.792579	280	(-)	NNNCACGTGNNN	CTAAACGTGAAA
M00062	V\$IRF1_01	0.811338	281	(+)	SAAAAGYGAAACC	TAAACGTGAAAGA
M00063	V\$IRF2_01	0.770611	281	(+)	GAAAAGYGAAASY	TAAACGTGAAAGA
M00073	V\$DELTAEF1_01	0.838856	281	(-)	NNNCACCTNAN	TAAACGTGAAA
M00041	V\$CREBP1CJUN_01	0.795	282	(-)	TGACGTYA	AAACGTGA
M00217	V\$USF_C	0.801744	282	(+)	NCACGTGN	AAACGTGA
M00217	V\$USF_C	0.817175	282	(-)	NCACGTGN	AAACGTGA
M00050	V\$E2F_02	0.750903	284	(-)	TTTSGCGC	ACGTGAAA
M00136	V\$OCT1_02	0.78235	287	(-)	NNGAATATKCANNNN	TGAAAGAATATAGAA
M00160	V\$SRY_02	0.774516	287	(+)	NWWAACA AWANN	TGAAAGAATATA



Table III. Continued.

AC	ID	Score	Location	Strand	Consensus sequence	Signal sequence
M00042	V\$SOX5_01	0.803681	288	(+)	NNAACAATNN	GAAAGAATAT
M00127	V\$GATA1_03	0.798628	290	(+)	RNSNNGATAANNGN	AAGAATATAGAAGG
M00252	V\$TATA_01	0.805887	292	(+)	STATAAAWRNNNNNN	GAATATAGAAGGTGC
M00216	V\$TATA_C	0.757856	293	(+)	NCTATAAAAR	AATATAGAAG
M00252	V\$TATA_01	0.774423	294	(+)	STATAAAWRNNNNNN	ATATAGAAGGTGCTT
M00071	V\$E47_02	0.800225	295	(+)	NNNMRCAGGTGTTMNN	TATAGAAGGTGCTTAG
M00255	V\$GC_01	0.846889	295	(+)	NRGGGGCGGGGCK	TATAGAAGGTGCTT
M00122	V\$USF_02	0.756681	296	(+)	NNRNCACGTGNYYN	ATAGAAGGTGCTTA
M00122	V\$USF_02	0.756681	296	(-)	NNRNCACGTGNYYN	ATAGAAGGTGCTTA
M00073	V\$DELTAEF1_01	0.855101	298	(-)	NNNCACCTNAN	AGAAGGTGCTT
M00146	V\$HSF1_01	0.886963	298	(+)	RGAANRTTCN	AGAAGGTGCT
M00147	V\$HSF2_01	0.896118	298	(+)	NGAANNWTCK	AGAAGGTGCT
M00147	V\$HSF2_01	0.857671	298	(-)	NGAANNWTCK	AGAAGGTGCT
M00184	V\$MYOD_Q6	0.827576	298	(-)	NNCANCTGNY	AGAAGGTGCT
M00261	V\$OLF1_01	0.766902	298	(+)	NNCNANTCCCYN	AGAAGGTGCTT
					GRGARNKGN	AGGTAAGCTAG
M00281	V\$RFX1_02	0.758554	299	(-)	NGGTNRCNATR	GAAGGTGCTTAGGTA
					GAAACNNN	AGCT
M00159	V\$CEBP_01	0.876823	300	(+)	NNTKTGGWNANNN	AAGGTGCTTAGGT
M00281	V\$RFX1_02	0.783516	300	(+)	NGGTNRCNATR	AAGGTGCTTAGGTAA
					GAAACNNN	GCTA
M00113	V\$CREB_02	0.792006	303	(+)	NGNTGACGYNN	GTGCTTAGGTAA
M00201	V\$CEBP_C	0.80327	303	(+)	NGWNTKNKGYA	GTGCTTAGGTAAAGCT
					AKNSAYA	AGC
M00037	V\$NFE2_01	0.794245	304	(+)	TGCTGASTCAY	TGCTTAGGTAA
M00080	V\$EV11_03	0.712757	304	(+)	AGATAAGATAA	TGCTTAGGTAA
M00109	V\$CEBPB_01	0.892273	304	(+)	RNRTKNNGMAAKNN	TGCTTAGGTAAAGCT
M00116	V\$CEBPA_01	0.803285	304	(+)	NNATTRCNNAANNN	TGCTTAGGTAAAGCT
M00116	V\$CEBPA_01	0.892061	304	(-)	NNATTRCNNAANNN	TGCTTAGGTAAAGCT
M00117	V\$CEBPB_02	0.853119	304	(-)	NKNTTGCNYAAYNN	TGCTTAGGTAAAGCT
M00045	V\$E4BP4_01	0.822939	305	(+)	NRTTAYGTAAYN	GCTTAGGTAAGC
M00045	V\$E4BP4_01	0.801134	305	(-)	NRTTAYGTAAYN	GCTTAGGTAAGC
M00159	V\$CEBP_01	0.881037	305	(+)	NNTKTGGWNANNN	GCTTAGGTAAGCT
M00177	V\$CREB_Q2	0.765644	305	(+)	NSTGACGTAANN	GCTTAGGTAAGC
M00177	V\$CREB_Q2	0.767335	305	(-)	NSTGACGTAANN	GCTTAGGTAAGC
M00178	V\$CREB_Q4	0.755679	305	(+)	NSTGACGTMANN	GCTTAGGTAAGC
M00178	V\$CREB_Q4	0.756941	305	(-)	NSTGACGTMANN	GCTTAGGTAAGC
M00179	V\$CREBP1_Q2	0.775143	305	(+)	NSTGACGTMASN	GCTTAGGTAAGC
M00179	V\$CREBP1_Q2	0.775143	305	(-)	NSTGACGTMASN	GCTTAGGTAAGC
M00073	V\$DELTAEF1_01	0.891488	306	(-)	NNNCACCTNAN	CTTAGGTAAGC
M00228	V\$VBP_01	0.878526	306	(+)	GTTACRTMAK	CTTAGGTAAG
M00228	V\$VBP_01	0.838882	306	(-)	GTTACRTMAK	CTTAGGTAAG
M00039	V\$CREB_01	0.811166	307	(-)	TGACGTMA	TTAGGTAA
M00040	V\$CREBP1_01	0.873321	307	(+)	TTACGTAA	TTAGGTAA
M00040	V\$CREBP1_01	0.875788	307	(-)	TTACGTAA	TTAGGTAA
M00079	V\$EV11_02	0.775976	309	(+)	AGAYAAGATAA	AGGTAAGCTAG
M00080	V\$EV11_03	0.779012	309	(+)	AGATAAGATAA	AGGTAAGCTAG
M00082	V\$EV11_05	0.801877	309	(+)	AGATAAGATAN	AGGTAAGCTAG
M00139	V\$AHR_01	0.722853	309	(-)	CYYCNRRTSTN	AGGTAAGCTAGC
					GCGTGASW	TGTAGC
M00272	V\$P53_02	0.799531	309	(+)	NGRCWTGYCY	AGGTAAGCTA
M00005	V\$AP4_01	0.818156	312	(+)	WGARYCAGCT	TAAGCTAGCTGTAG
					GYGGNCNK	CCCC
M00272	V\$P53_02	0.793962	313	(+)	NGRCWTGYCY	AAGCTAGCTG

Table III. Continued.

AC	ID	Score	Location	Strand	Consensus sequence	Signal sequence
M00272	V\$P53_02	0.835873	313	(-)	NGRCWTGYCY	AAGCTAGCTG
M00277	V\$LMO2COM_01	0.795424	314	(+)	SNNCAGGTGNNN	AGCTAGCTGTAG
M00176	V\$AP4_Q6	0.769732	315	(-)	CWCAGCTGGN	GCTAGCTGTA
M00184	V\$MYOD_Q6	0.777606	315	(-)	NNCANCTGNY	GCTAGCTGTA
M00227	V\$VM YB_02	0.785499	315	(+)	NSYAACGGN	GCTAGCTGT
M00072	V\$CP2_01	0.796312	316	(-)	GCMNAMCMAG	CTAGCTGTAGC
M00249	V\$CHOP_01	0.77559	318	(+)	NNRTGCAATMCCC	AGCTGTAGCCCC
M00273	V\$R_01	0.727636	322	(+)	NNGKCCNSNR NYGTGGTGYN	GTAGCCCCCAGTAG TAGTGAT
M00084	V\$MZF1_02	0.820545	323	(-)	KNNNKAGGGGNAA	TAGCCCCCAGTAG
M00189	V\$AP2_Q6	0.859145	324	(+)	MKCCCSCNGGCG	AGCCCCCAGTAG
M00083	V\$MZF1_01	0.835663	326	(-)	NGNGGGGA	CCCCCAGT
M00253	V\$CAP_01	0.896994	329	(+)	NCANNNNN	CCAGTAGT
M00255	V\$GC_01	0.789564	331	(+)	NRGGGGCGGGCNK	AGTAGTAGTGATTT