*** Top 10 motifs enriched in known motif scanning analysis on *de novo* DMRs of ETV6-ALL

	Known Motif	Motif information	P-value	% of Targets	% of Background
1		REST-NRSF(Zf)/Jurkat-NRSF-ChIP-Seq/Homer	1e-203	0.12%	0.02%
2		EWS:ERG-fusion(ETS)/CADO_ES1-EWS:ERG-ChIP-Seq/Homer	1e-203	1.16%	0.72%
3		Ets1-distal(ETS)/CD4+-PolII-ChIP-Seq/Homer	1e-115	0.51%	0.29%
4		Hoxc9/Ainv15-Hoxc9-ChIP-Seq/Homer	1e-108	0.53%	0.31%
5		PU.1(ETS)/ThioMac-PU.1-ChIP-Seq(GSE21512)/Homer	1e-91	0.76%	0.52%
6		HOXA9/HSC-Hoxa9-ChIP-Seq(GSE33509)/Homer	1e-80	0.65%	0.44%
7		Hoxb4/ES-Hoxb4-ChIP-Seq(GSE34014)/Homer	1e-66	0.23%	0.12%
8		Gata4(Zf)/Heart-Gata4-ChIP-Seq(GSE35151)/Homer	1e-51	1.03%	0.81%
9		Gata1(Zf)/K562-GATA1-ChIP-Seq/Homer	1e-51	0.60%	0.43%
10		Gata2(Zf)/K562-GATA2-ChIP-Seq/Homer	1e-51	0.66%	0.48%

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*** Top 10 motifs enriched in known motif scanning analysis on *de novo* DMRs of HD-ALL

	Known Motif	Motif information	P-value	% of Targets	% of Background
1		EWS:ERG-fusion(ETS)/CADO_ES1-EWS:ERG-ChIP-Seq/Homer	1e-93	1.05%	0.69%
2		REST-NRSF(Zf)/Jurkat-NRSF-ChIP-Seq/Homer	1e-90	0.10%	0.02%
3		HOXA9/HSC-Hoxa9-ChIP-Seq(GSE33509)/Homer	1e-49	0.62%	0.42%
4		Hoxc9/Ainv15-Hoxc9-ChIP-Seq/Homer	1e-48	0.46%	0.30%
5		Ets1-distal(ETS)/CD4+-PolII-ChIP-Seq/Homer	1e-47	0.45%	0.28%
6		Pitx1(Homeobox)/Chicken-Pitx1-ChIP-Seq(GSE38910)/Homer	1e-32	6.11%	5.57%
7		Gata1(Zf)/K562-GATA1-ChIP-Seq/Homer	1e-30	0.57%	0.42%
8		PU.1(ETS)/ThioMac-PU.1-ChIP-Seq(GSE21512)/Homer	1e-30	0.67%	0.50%
9		Pdx1(Homeobox)/Islet-Pdx1-ChIP-Seq/Homer	1e-27	0.79%	0.62%
10		Gata2(Zf)/K562-GATA2-ChIP-Seq/Homer	1e-27	0.61%	0.46%

Supplementary Table S8

*** Top 10 motifs enriched in *de novo* motif finding analysis on *de novo* DMRs of ETV6-ALL

	Motif	P-value	% of Targets	% of Background	Closest Motif (Match score > 0.7)	Match Score
1	CGCGGCTTTTTGCCCC	1e-972	0.27%	0.01%	None	-
2	CGCGTA	1e-542	23.49%	20.24%	PB0199.1_Zfp161_2/Jaspar	0.78
3	AACGTTTT	1e-457	3.43%	2.27%	MA0004.1_Arnt/Jaspar	0.73
4	GACGTGAACGACAACGCGCC	1e-417	0.04%	0.00%	None	-
5	CAGGAAAT	1e-322	4.16%	3.05%	MA0156.1_FEV/Jaspar	0.96
6	GGGCTAAT	1e-307	15.93%	13.82%	None	-
7	CATTTA	1e-215	57.54%	55.07%	MA0038.1_Gfi/Jaspar	0.75
8	TCAGCACCACGGACAG	1e-199	0.10%	0.01%	MA0138.1_REST/Jaspar	0.91
9	CCCCGG	1e-177	41.35%	39.14%	None	-
10	TCAACGAC	1e-159	8.07%	6.96%	PB0179.1_Sp100_2/Jaspar	0.82

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*** Top 10 motifs enriched in *de novo* motif finding analysis on *de novo* DMRs of HD-ALL

	Motif	P-value	% of Targets	% of Background	Closest Motif (Match score > 0.7)	Match Score
1	CGCGGCTTTTTGCCCC	1e-523	0.27%	0.02%	None	-
2	ACCGCGGAGA	1e-461	22.80%	19.19%	PB0199.1_Zfp161_2/Jaspar	0.72
3	GACGTGAACGACAACGCGCC	1e-340	0.05%	0.00%	None	-
4	ACAACGTG	1e-195	3.86%	2.84%	MA0004.1_Arnt/Jaspar	0.78
5	TTAACCGG	1e-184	9.92%	8.32%	None	-
6	AAATCCCC	1e-170	19.99%	17.87%	NFkB-p65(RHD)/GM12787-p65-ChIP-Seq/Homer	0.80
7	CGCGCTCTGCGCGC	1e-153	4.54%	3.55%	PB0199.1_Zfp161_2/Jaspar	0.74
8	CCCGTTCCGCGTGGGGCT	1e-137	0.02%	0.00%	None	-
9	AATTTTCTGTCACGCTCC	1e-132	0.02%	0.00%	None	-
10	ACGCGGACGCGCAGGAGAAC	1e-126	0.02%	0.00%	None	-

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*** Top 10 motifs enriched in known motif scanning analysis on de-DMRs of ETV6-ALL

	Known Motif	Motif information	P-value	% of Targets	% of Background
1		ERG(ETS)/VCaP-ERG-ChIP-Seq/Homer	1e-752	4.69%	3.04%
2		EWS:ERG-fusion(ETS)/CADO_ES1-EWS:ERG-ChIP-Seq/Homer	1e-453	1.79%	1.02%
3		ETS1(ETS)/Jurkat-ETS1-ChIP-Seq/Homer	1e-433	2.83%	1.85%
4		EWS:FLI1-fusion(ETS)/SK_N_MC-EWS:FLI1-ChIP-Seq/Homer	1e-425	1.74%	1.00%
5		ETV1(ETS)/GIST48-ETV1-ChIP-Seq/Homer	1e-372	3.96%	2.86%
6		Ets1-distal(ETS)/CD4+-PolII-ChIP-Seq/Homer	1e-286	0.74%	0.36%
7		n-Myc(HLH)/mES-nMyc-ChIP-Seq/Homer	1e-268	3.71%	2.79%
8		Ptf1a(HLH)/Panc1-Ptf1a-ChIP-Seq(GSE47459)/Homer	1e-263	11.18%	9.60%
9		EBF(EBF)/proBcell-EBF-ChIP-Seq/Homer	1e-257	0.79%	0.41%
10		GABPA(ETS)/Jurkat-GABPa-ChIP-Seq/Homer	1e-248	2.47%	1.75%

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*** Top 10 motifs enriched in known motif scanning analysis on de-DMRs of HD-ALL

	Known Motif	Motif information	P-value	% of Targets	% of Background
1		ERG(ETS)/VCaP-ERG-ChIP-Seq/Homer	1e-1372	4.54%	2.99%
2		ETV1(ETS)/GIST48-ETV1-ChIP-Seq/Homer	1e-653	3.84%	2.82%
3		n-Myc(HLH)/mES-nMyc-ChIP-Seq/Homer	1e-561	3.69%	2.76%
4		Ets1-distal(ETS)/CD4+-PolII-ChIP-Seq/Homer	1e-467	0.68%	0.35%
5		c-Myc(HLH)/LNCAP-cMyc-ChIP-Seq/Homer	1e-461	2.99%	2.23%
6		Max(HLH)/K562-Max-ChIP-Seq/Homer	1e-452	3.16%	2.38%
7		SPDEF(ETS)/VCaP-SPDEF-ChIP-Seq/Homer	1e-434	2.66%	1.97%
8		USF1(HLH)/GM12878-Usf1-ChIP-Seq/Homer	1e-424	2.52%	1.85%
9		EBF1(EBF)/Near-E2A-ChIP-Seq/Homer	1e-334	3.50%	2.79%
10		Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-333	3.29%	2.60%

Supplementary Table S8

*** Top 10 motifs enriched in *de novo* motif finding analysis on de-DMRs of ETV6-ALL

	Motif	P-value	% of Targets	% of Background	Closest Motif (Match score > 0.7)	Match Score
1		1e-2789	23.43%	16.72%	c-Myc(HLH)/LNCAP-cMyc-ChIP-Seq/Homer	0.86
2		1e-1046	11.87%	8.76%	ERG(ETS)/VCaP-ERG-ChIP-Seq/Homer	0.94
3		1e-817	11.11%	8.42%	PB0136.1_IRC900814_2/Jaspar	0.77
4		1e-489	4.11%	2.84%	PB0143.1_Klf7_2/Jaspar	0.70
5		1e-482	16.66%	14.12%	None	-
6		1e-480	22.92%	20.03%	EBF1(EBF)/Near-E2A-ChIP-Seq/Homer	0.87
7		1e-439	25.94%	23.04%	PB0203.1_Zfp691_2/Jaspar	0.70
8		1e-358	11.02%	9.20%	None	-
9		1e-351	6.65%	5.24%	PH0044.1_Homez/Jaspar	0.75
10		1e-254	53.66%	51.08%	None	-

Supplementary Table S8

*** Top 10 motifs enriched in *de novo* motif finding analysis on de-DMRs of HD-ALL

	Motif	P-value	% of Targets	% of Background	Closest Motif (Match score > 0.7)	Match Score
1		1e-4780	20.18%	14.37%	c-Myc(HLH)/LNCAP-cMyc-ChIP-Seq/Homer	0.88
2		1e-1959	9.12%	6.49%	ERG(ETS)/VCaP-ERG-ChIP-Seq/Homer	0.96
3		1e-1479	47.40%	43.05%	None	-
4		1e-1456	33.62%	29.60%	EBF1(EBF)/Near-E2A-ChIP-Seq/Homer	0.74
5		1e-1190	13.24%	10.73%	PB0136.1_IRC900814_2/Jaspar	0.74
6		1e-779	32.80%	29.86%	None	-
7		1e-676	4.11%	3.04%	None	-
8		1e-586	24.42%	22.10%	None	-
9		1e-455	4.79%	3.82%	PB0180.1_Sp4_2/Jaspar	0.71
10		1e-422	11.52%	10.08%	PB0143.1_Klf7_2/Jaspar	0.72

Supplementary Table S8