Table S7: Motifs enriched at functionally distinct classes of sites bound by exogenously introduced PU.1: effects of chromatin states and chromatin developmental dynamics

A. Motif analysis of Group 5,6 and 7 peaks defined in Fig. 4C. The top five motifs defined by Homer De Novo motif search are shown for each site category. **B.** Motif analysis of exogenous PU1WTHA-occupied non-promoter (distal) peaks in CD25$^+$ cells, as detected by αHA ChIP. Sites with quality scores above or below PWM score median are compared for co-enriched motifs, depending on whether they lie in normally inaccessible (PWM median score=9.74) or accessible (PWM median score=8.97) regions in DN3 cells. Note strongly similar pattern of motif preference for endogenous PU.1 at its natural sites (Fig. 1G, Supplementary Fig. S1D). The top five motifs defined by Homer De Novo motif search are shown for each site category. C. Top five motifs enriched at PU1WTHA αHA peaks in regions that change dynamically from DN1 to DN3.

Table 7: TOP MOTIFS AT SITES OCCUPIED BY EXOGENOUS PU.1 IN PRO-T CELLS

A

Fig 4C group 5

Motif	Best match	% of Targets	% of Bg	P-value
	*SpiB(ETS)*	80.9	7.9	1e-20016
	*Cebpa*	2.4	0.01	1e-1476
	*Klf5*	2.6	0.06	1e-955
	*Runx2*	26.0	11.9	1e-942
	*Zic*	2.9	0.12	1e-844

Fig 4C group 6

Motif	Best match	% of Targets	% of Bg	P-value
	*SpiB(ETS)*	63.2	3.1	1e-8735
	*Nr2f2*	9.6	0.3	1e-1381
	*Dlx2*	8.7	0.2	1e-1365
	*SD0003.1 at AC acceptor*	9.2	0.3	1e-1348
	*Mecom*	10.3	0.4	1e-1342

Fig 4C group 7

Motif	Best match	% of Targets	% of Bg	P-value
	*PU.1(ETS)*	65.1	16.3	1e-6469
	*Runx1*	12.5	4.8	1e-498
	*Sp1*	15.2	9.0	1e-217
	*SPI1*	1.3	0.1	1e-213
	*BORIS*	1.1	0.3	1e-89

B

PU1WTHA closed above PWM median score

Motif	Best match	% of Targets	% of Bg	P-value
	*SpiB(ETS)*	86.5	1.7	1e-24217
	*Scrt2*	9.6	0.2	1e-2204
	*Sox4*	8.2	0.2	1e-1772
	*Six6*	7.3	0.2	1e-1592
	*Oct*	6.3	0.1	1e-1548

PU1WTHA closed below PWM median score

Motif	Best match	% of Targets	% of Bg	P-value
	*Sfpi1*	84.0	15.3	1e-9022
	*Runx2*	36.5	20.8	1e-506
	*IRC900814*	13.3	5.5	1e-335
	*Cphx*	1.0	0.11	1e-111
	*Foxo1*	0.4	0.01	1e-91

PU1WTHA open above PWM median score

Motif	Best match	% of Targets	% of Bg	P-value
	*PU.1(ETS)*	42.6	3.0	1e-2123
	*Runx1*	17.7	6.8	1e-169
	*Ptf1a*	23.8	15.1	1e-67
	*Runx2*	22.8	15.1	1e-53
	*Ctcf*	1.8	0.3	1e-48

PU1WTHA open below PWM median score

Motif	Best match	% of Targets	% of Bg	P-value
	*Sfpi1*	52.7	22.7	1e-538
	*Runx1*	31.1	12.2	1e-315
	*Ctcf*	2.5	0.4	1e-69
	*E2A*	23.1	15.9	1e-45
	*Prdm1*	0.4	0.01	1e-39

C

PU1WTHA in closing regions

Motif	Best match	% of Targets	% of Bg	P-value
	*SpiB(ETS)*	64.6	2.8	1e-4969
	*Runx1*	26.5	8.9	1e-394
	PU.*1-IRF*	12.8	2.9	1e-291
	*Cebpa*	0.7	0.01	1e-67
	PU.*1(ETS)*	2.4	0.5	1e-59

PU1WTHA in opening regions

Motif	Best match	% of Targets	% of Bg	P-value
	PU.*1(ETS)*	64.3	5.9	1e-2208
	*Runx2*	20.7	9.2	1e-112
	*Tcf3*	30.1	17.0	1e-98
	*Tcf3(HMG)**	13.0	5.3	1e-81
	GATA	0.6	0.01	1e-32

**Tcf3(HMG) = Tcf7l1*