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## Epigenetic analysis of patients with T-ALL identifies poor outcomes and a hypomethylating agent-responsive subgroup

Aurore Touzart, Anand Mayakonda, Charlotte Smith, Joschka Hey, Reka Toth, Agata Cieslak, Guillaume Andrieu, Christine Tran Quang, Mehdi Latiri, Jacques Ghysdael, et al.

### ► To cite this version:

Aurore Touzart, Anand Mayakonda, Charlotte Smith, Joschka Hey, Reka Toth, et al.. Epigenetic analysis of patients with T-ALL identifies poor outcomes and a hypomethylating agent-responsive subgroup. *Science Translational Medicine*, 2021, 13 (595), pp.eabc4834. 10.1126/scitranslmed.abc4834 . hal-03282998

**HAL Id: hal-03282998**

**<https://amu.hal.science/hal-03282998>**

Submitted on 14 Feb 2022

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**Title: Epigenetic blueprint identifies poor outcome and hypomethylating agent-responsive T-ALL subgroup**

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**One Sentence Summary:** In-depth characterization of normal and adult T-ALL methylomes identify clinically aggressive hypermethylated subgroup sensitive to DNA hypomethylating agents.

**Abstract:** Adult T-cell acute lymphoblastic leukemia (T-ALL) is an aggressive hematological malignancy still associated with poor outcome calling for new therapeutic options. DNA methylation landscapes of adult T-ALL remain largely uncharacterized. Here, we systematically analyzed the DNA methylation profiles of normal thymic sorted T-cell subpopulations and 143 primary adult T-ALLs as part of French GRAALL 2003-2005 trial. Our results indicated that T-ALL is epigenetically distinct consisting of five major subtypes (C<sub>1</sub>-C<sub>5</sub>) which were either associating with co-occurring *DNMT3A/IDH2* mutations (C<sub>1</sub>), *TAL1* deregulation (C<sub>2</sub>), *TLX3* (C<sub>3</sub>), *TLX1/in cis-HOXA9* (C<sub>4</sub>) or in *trans-HOXA9* (C<sub>5</sub>) overexpression. **Integrative analysis of DNA methylation and Gene expression identified potential cluster-specific oncogenes and tumor suppressor genes.** Importantly, **in addition to an aggressive hypomethylated subgroup (C<sub>1</sub>), our data identified an unexpected subset of hypermethylated T-ALL (C<sub>5</sub>) associated with poor**

1 outcome and primary therapeutic response. Using mouse xenografts, we showed that  
2 hypermethylated T-ALL samples displayed therapeutic response to the DNA hypomethylating  
3 agent, 5-Azacytidine, which significantly delayed tumor progression suggesting epigenetic-based  
4 therapies as a novel treatment option in hypermethylated T-ALL

5 **[Main Text: ]**

## 6 **Introduction**

7 T-ALL (T-cell Acute Lymphoblastic Leukemia) is an aggressive hematological malignancy, most  
8 common among children (10-15% of ALL) and young adults (20-25% of ALL) (1, 2). Although  
9 intensive chemotherapy results in high cure rates, survival remains particularly poor in relapsing  
10 patients (3) calling for novel targeted therapeutic approaches. Both pediatric and adult T-ALLs  
11 harbor common oncogenic driver mutations leading to deregulation of specific transcription  
12 factors (TFs), including basic helix-loop-helix family members (*TAL1*, *TAL2*, *LYL1* and  
13 *BHLHB1*), LIM-only domain family members (*LMO1* and *LMO2*), homeobox genes (*TLX1*, *TLX3*,  
14 *HOXA*, *NKX2-1*, *NKX2-2*) as well as oncogenic TFs such as *MYB* and *MYC* (4). Investigation of  
15 transcriptional signatures identified molecular subgroups with specific driver oncogenes and  
16 maturation arrest stages including *TAL1/LMO* (mature or late cortical stage), *TLX1*, *TLX3* and  
17 *NKX2-1/NKX2-2* (early cortical stage), *LYL1*, *MEF2C* and *HOXA* (immature stage) (5). In addition  
18 to these oncogenic drivers, numerous additional recurrent genetic alterations have been described,  
19 including mutations in genes involved in the NOTCH1 pathway (*NOTCH1*, *FBXW7*) and deletion  
20 or epigenetic silencing of *CDKN2A*, both observed in more than 70% of T-ALLs (6). Past work  
21 has demonstrated that cancer-specific changes in DNA methylation (DNAm) include both global  
22 hypomethylation and focal hypermethylation changes at discrete loci, associated with distinct  
23 histone modification patterns and chromatin conformations, creating functional chromatin states  
24 (7). T-ALL is among a subset of cancers with the highest frequency of mutations in enzymes  
25 regulating epigenetic processes, suggesting that deregulation of the epigenetic landscape may play  
26 an important role in T-ALL leukemogenesis (8, 9). Notably, genes involved in establishing DNAm  
27 patterns are frequently mutated in adult T-ALL. *DNMT3A* mutations are found in about 18% of  
28 cases and are associated with an adverse outcome (10, 11). Mutations in TET family genes and  
29 *IDH1/2* are also frequent (12-14).

30 Several studies have utilized DNAm as a marker to characterize cancer samples in search of  
31 markers for relapse prediction, molecular classification or mechanisms involved in disease  
32 transformation (15-17). In pediatric T-ALL, DNAm analysis identified two distinct CpG island  
33 methylator phenotype (CIMP) groups, in which CIMP-negative patients displayed a significantly  
34 higher cumulative incidence of relapse as compared to CIMP-positive patients, suggesting  
35 prognostic relevance of aberrant DNAm profiles in T-ALL (18-20). Similar observations have also  
36 been made recently in adult T-ALL (21). Given the potential therapeutic impact of epigenetic  
37 anomalies, in particular their reversible nature by hypomethylating agents, we analyzed genome-  
38 wide DNAm patterns of primary adult T-ALL samples. Our results indicate that T-ALL is  
39 heterogeneous and consists of epigenetically distinct subgroups with characteristic clinical  
40 features. Of note, we identify an unexpected hypermethylated T-ALL subgroup of poor clinical  
41 outcome, which is likely to benefit from targeted therapy.

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## Results

### *DNA methylation blueprints identify distinct epigenetic subgroups of T-ALL*

To better understand the role of DNAm in T-ALL leukemogenesis, we performed genome-wide DNAm analysis using Illumina Infinium Methylation EPIC BeadChip (EPIC arrays) in a series of 143 primary adult T-ALL samples, as well as on sorted normal thymic T-cell subpopulations (see **Methods** section). Patient clinical, phenotypic, and oncogenetic characteristics are described in **Table 1**. Using unsupervised clustering, we classified T-ALL samples **within the cohort** into five distinct, robust and stable sub-clusters (**Figure 1A, B** and see **methods** and **Supplementary Figure S1**). These data-driven *de novo* clusters showed variable degrees of genome-wide DNAm levels compared to normal thymic populations (**Figure 1C**). Based on their genome-wide DNAm level, we named the clusters C<sub>1</sub>, C<sub>2</sub>, C<sub>3</sub>, C<sub>4</sub> and C<sub>5</sub>, with C<sub>1</sub> displaying the lowest level of DNAm and C<sub>5</sub> the highest.

Additional characterization of the clusters revealed a significant association with thymic maturation arrest stages and key oncogenetic alterations (**Figure 1D-G**). C<sub>1</sub> represented the smallest cluster ( $n = 14$  samples, 9.8%) and was characterized by an Early Thymic Precursor (ETP) phenotype (7/11;  $P < 0.01$ ), an immature maturation arrest stage (9/12;  $P < 0.01$ ) and under-representation of classical T-ALL oncogenic drivers (*HOXA*, *TALI*, *TLX1* and *TLX3*). C<sub>2</sub> was associated with a more mature  $\alpha\beta$ -lineage maturation arrest stage (28/31;  $P < 0.01$ ) and was mainly characterized by *TALI* deregulation (SIL-TAL1 or upstream-neoenhancer positive) (16/33;  $P < 0.01$ ). Of note, all but one of the *TALI* deregulated cases (16/17) clustered together, suggesting that they display similar DNAm signature regardless of the molecular mechanism leading to *TALI* deregulation. Importantly, overall genome-wide methylation levels of C<sub>1</sub> and C<sub>2</sub> showed no significant changes compared to normal thymic subpopulations despite the differences in maturation arrest stages or genetic alterations (**Figure 1C**). In contrast, clusters C<sub>3</sub>, C<sub>4</sub>, and C<sub>5</sub> displayed significant genome-wide hypermethylation compared to normal thymic subpopulations (t-test,  $P < 0.001$ ; **Figure 1C**) and were enriched for overexpression of HOX gene family members. Although *TLX1* and *TLX3* proteins are very similar, *TLX1* and *TLX3* deregulated leukemia clustered separately. C<sub>3</sub> contained samples enriched for overexpression of *TLX3* (14/22) and a TCR $\gamma\delta$  phenotype whereas C<sub>4</sub> contained samples displaying *TLX1* overexpression (25/38), and *cis*-activated (resulting from *cis*-deregulation by translocation into the TCR $\beta$  locus) *HOXA9* overexpression (7/37) along with IM $\beta$ /pre- $\alpha\beta$  ( $\alpha\beta$  lineage) maturation arrest stages. C<sub>5</sub> samples were most significantly hypermethylated compared to normal thymic subpopulations (**Figure 1C**; t-test,  $P < 0.001$ ) and were characterized by *trans*-activated (translocations involving MLL, MLLT10 rearrangements, SET-NUP214) *HOXA9* overexpression (16/30) and ETP and immature maturation arrest stages, as described (22). Importantly, ETP-ALLs clustered in C<sub>1</sub> and C<sub>5</sub>, which displayed distinct hypo-, and hyper- methylation profiles respectively, suggesting a high degree of heterogeneity within ETP-ALLs, and that an ETP phenotype alone cannot drive or result from methylation changes.

Besides the classical T-ALL driver events - CNVs and mutational alterations for a targeted panel of genes that are frequently altered in T-ALL were also studied (see **methods**; **Supplementary Figure S2A**) (22). Among genes involved in establishing DNA methylation patterns, *DNMT3A* was the most frequently mutated (14%) followed by *TET2* (5%), *IDH2* (4%), *TET3* (3%) and *IDH1* (1%). Comparison of mutational events within each cluster against all other

1 clusters identified thirteen genes, which were preferentially mutated in particular epigenetic  
2 clusters (**Figure 1H**; Fisher's exact test,  $FDR < 0.05$ ; **Supplementary Table S1**). Whereas  
3 *DNMT3A*, *TET2/3*, *IDH1* mutations alone did not seem to be significantly associated with any  
4 specific methylation cluster, all *IDH2* mutations co-occurred with *DNMT3A* mutations. A large  
5 fraction of these co-occurring *IDH2/DNMT3A* mutations (5/6) were found within the C<sub>1</sub> subgroup,  
6 suggesting their potential synergistic role for the underlying leukemogenesis (23) (**Figure 1H**). In  
7 the entire cohort, *DNMT3A* mutations were largely of loss-of-function/dominant-negative type,  
8 with 30% (6/20) involving the R882 hotspot, thereby affecting the methyltransferase domain  
9 (**Supplementary Figure S2B**). Mutations in *IDH2* occurred at the known oncogenic hotspot R140  
10 (**Supplementary Figure S2C**) (24).

11 *PTEN* alterations were enriched in C<sub>2</sub> (enriched in *TALI* deregulated cases). *PTEN*  
12 mutations were mostly loss-of-function INDELS thereby dysregulating the PI3K signaling  
13 pathway, in line with the higher frequency of *PTEN* alterations in *TALI* deregulated and mature  
14 T-ALL cases (25, 26). The C<sub>2</sub> subgroup was also characterized by a lower frequency of mutations  
15 affecting both epigenomic regulators in general and the JAK-STAT pathway. C<sub>3</sub> was particularly  
16 enriched for *WT1* and *STAT5B* mutations affecting the JAK-STAT pathway (25). C<sub>4</sub> demonstrated  
17 a significantly higher frequency of *BCL11B* mutations. Importantly, *SUZ12* and *EZH2* alterations,  
18 both critical components of the PRC2 complex, clustered in the C<sub>5</sub> subgroup. A large fraction of  
19 *NFI* alterations and a low frequency of *CDKN2A* deletions were also observed in this subgroup.

20 Altogether, based on methylation profiles we have identified five robust subgroups of T-  
21 ALL, and demonstrated that epigenetic clusters correlate with the driver oncogenes and are  
22 associated with distinct maturation arrest stages. In particular, we have identified a novel  
23 uncharacterized subgroup (C<sub>1</sub>) with co-occurring *DNMT3A/IDH2* mutations.  
24

#### 25 *T-ALL methylomes differ from thymic T-cell subpopulations but DNA methylation predicts* 26 *maturation arrest stages of epigenetic clusters*

27 We compared T-ALL samples with a series of sorted normal thymic subpopulations including  
28 thymic CD34+, 4ISP (Immature Simple positive CD4+), DP and TCR-/CD3- (Double Positive  
29 CD4+ CD8+ TCR- CD3-), DP and TCR+/CD3+ (Double Positive CD4+ CD8+ TCR+ CD3+),  
30 SP4 (Single positive CD4+) and SP8 (Single Positive CD8+) cells (see **Methods** section). We first  
31 analyzed the dynamics of DNAm changes during normal T-cell maturation; principal component  
32 analysis (PCA) robustly separated different subpopulations, suggesting significant heterogeneity  
33 in the T-cell precursor methylomes and thereby implicating epigenetic programming as an  
34 underlying part of T-cell development (**Figure 2A**). We next performed differential methylation  
35 analysis, which identified a set of differentially methylated probes (DMPs) for each thymic  
36 subpopulation (tDMPs) (**Supplementary Figure S3A**)(**Supplementary Table S2**). CD34+ cells  
37 contained the highest number of tDMPs ( $n = 7385$ ), followed by the more mature SP4/SP8 cells  
38 ( $n = 5148$  and  $n = 6145$  respectively) with varying degrees of overlap between the subpopulations  
39 (**Supplementary Figure S3B**). Genes associated with precursor CD34+ cell-specific tDMPs were  
40 affiliated with the gene ontology terms including chemotaxis or cell migration, in line with the  
41 process by which migratory hematopoietic precursors from the bone marrow respond to homing  
42 signals from thymic epithelial cells before restricting towards the thymic lineage (**Figure 2B**). In  
43 contrast, 4ISP cells were significantly enriched for terms associated with lymphocyte activation  
44 and differentiation, and immune system development, suggesting lineage commitment towards T-

1 cell development (**Figure 2C**). Similar terms were also enriched for the mature subpopulations  
2 (**Supplementary Figure S3C-F**).

3 To further characterize tDMPs, we identified eight sub-clusters (tDMP1-tDMP8) based on  
4 the kinetics of DNAm changes (**Figure 2D and 2E**) (**Supplementary Table S3**). tDMP1 and  
5 tDMP2 consisted of hypermethylated probes which became slightly hypomethylated in terminal  
6 stages, and were associated with processes such as cellular morphogenesis and cell development  
7 (**Supplementary Figure S4A, B**). Clusters tDMP3, tDMP4, and tDMP5 showed a continuous gain  
8 of DNAm, suggesting silencing of cellular pathways associated with cell adhesion, cell  
9 communication, regulation of GTP-ase activity and the PI3k pathway (**Figure 2E and**  
10 **Supplementary Figure S4C, D, E**). In contrast, clusters tDMP6, tDMP7 and tDMP8 contained  
11 genes associated with DMPs which showed progressive hypomethylation during differentiation.  
12 These clusters were exclusively associated with T-cell differentiation and activation and the  
13 adaptive immune system, implying the presence of a core set of CpGs whose hypomethylation is  
14 critical for T-cell maturation (**Supplementary Figure S4F-H**).

15 As a complementary to the DNAm analysis of thymopoiesis, we also analyzed the gene  
16 expression data from 6 distinct thymic cell types generated by Roels et al (CD34+CD1-,  
17 ISPCD28+, DPCD3-, DPCD3+, SPCD4+ and SPCD8+) (27). Gene expression profiles of well-  
18 known candidate genes involved in thymopoiesis showed an inverse correlation with their  
19 promoter DNAm levels (**Supplementary Figure S5A**). We further characterized the dynamics of  
20 gene expression and promoter DNAm profiles by comparing each mature thymic cell type to the  
21 CD34+ immature early thymic precursors. Both differential expression and differential promoter  
22 DNAm analysis revealed a linearly increasing number of differentially regulated genes along the  
23 maturation stages (**Supplementary Figure S5B**). Next we identified a common set of genes which  
24 were both differentially expressed and showed a differential promoter methylation - which further  
25 revealed a core subset of genes which are both transcriptionally and epigenetically regulated in  
26 thymic developmental processes ( $N = 942$ ) (**Supplementary Figure S5B-C, Supplementary**  
27 **Table S4**). In addition, expression of these genes showed significant inverse correlation with their  
28 promoter DNAm levels with high expressed genes showing least methylation and vice-versa  
29 (**Supplementary Figure S5D, E**). Large fraction of these genes also overlapped with the genes  
30 identified in recent single cell based assays thereby further validating the results (data not shown)  
31 (28).

32 Next, we sought to investigate whether tDMPs can recapitulate the known hierarchy of T-  
33 cell maturation stages. Using an unsupervised, distance-based neighbor joining approach, tDMPs  
34 robustly reconstructed T-cell developmental stages, with the phylogenetic tree leading to either  
35 mature SP4 or SP8 cells originating from precursor thymic CD34+ cells (**Figure 2F**). Phylogenetic  
36 trees constructed using random CpGs failed to infer the same, thereby hinting at a critical role of  
37 tDMP-associated genes in T-cell development (**Supplementary Figure S6A and S6B**). **Of note,**  
38 **similar to DNAm, DEGs involved in thymopoiesis were also able to reconstruct the thymic**  
39 **developmental trajectory (Figure 2F, inset plot) suggesting a possible coordinated regulation of**  
40 **DNAm and gene expression profiles.** We then hypothesized that T-ALL samples display distinct  
41 DNA methylomes compared to normal thymic subpopulations and that these DMPs are distinct  
42 from tDMPs associated with T-cell differentiation. To address this, we performed PCA on the  
43 entire sample cohort of primary T-ALL and normal T-cell subpopulations. This analysis showed  
44 clear separation of T-ALL samples from normal T-cell subpopulations, irrespective of their  
45 maturation stage, inferring that T-ALL are highly heterogeneous in their methylome (**Figure 2G**;

1 left panel). We repeated the PCA analysis by excluding tDMPs and did not observe any significant  
2 changes, suggesting that T-ALL differed in their DNA methylomes compared to thymic  
3 subpopulations (**Figure 2G**; right panel). Unsupervised hierarchical clustering showed similar  
4 results, suggesting that in addition to the DNAm signature obtained from the cell-of-origin, a  
5 significant number of DNAm changes in T-ALL are primarily related to leukemogenesis and are  
6 T-ALL specific. Interestingly, a subset of leukemic samples clustered close to normal  
7 subpopulations, implying a lower deviation of their methylome (**Supplementary Figure S6C, D**).

8 Finally, we asked how T-ALL clusters diverge from normal T-cell development. In order  
9 to investigate this in an unsupervised way, we first performed PCA on the entire cohort (thymic  
10 subpopulations and T-ALL) using only tDMPs as reference. This analysis recovered the known  
11 developmental trajectory of T-cell subpopulations, and the possible ordering of T-ALL clusters  
12 relative to the trajectory (**Figure 2H**). We next projected DNAm of T-ALL samples onto the  
13 normal thymic developmental tree, which highlighted the possible deviation of T-ALL samples  
14 from the normal developmental trajectory, thereby indicating potential maturation arrest stages  
15 (**Figure 2I**). We then calculated the average methylation of T-ALL samples belonging to the same  
16 one of earlier identified clusters  $C_1$  to  $C_5$ , and rebuilt the developmental trajectory. This display  
17 showed the hierarchical ordering of clusters along the normal T-cell developmental path, with  $C_5$ ,  
18 and  $C_1$  being derived from earlier T-cell maturation stages, followed by  $C_3$ ,  $C_4$ , and  $C_2$  - in line  
19 with the respective maturation arrest stages (**Figure 2I**; inlet plot). Of note, all five epigenetic  
20 clusters were positioned between ISP and DP TCR- stages of T-cell development suggesting an  
21 early epigenetic divergence occurring between the cortex to subcapsular thymic zones (29). Taken  
22 together, our results suggest the potential role of DNAm in predicting the normal T-cell  
23 developmental trajectory and the order of maturation arrest stages for the five epigenetic T-ALL  
24 subgroups.

### 25 *Methylation changes in normal and T-ALL-associated regulatory elements*

26 To further understand the heterogeneity among the epigenetic clusters, we compared each cluster  
27 with the normal thymic subpopulations to identify DMPs ( $FDR < 0.05$ ,  $|\text{meth change}| > 0.2$ )  
28 (**Supplementary Table S5**). This analysis revealed varying degrees of DMPs with  $C_1$  (34424  
29 hyper/21478 hypo) and  $C_2$  (48538 hyper/ 27757 hypo) displaying approximately equal proportion  
30 of hyper- and hypo- methylated probes. In contrast  $C_3$  (76873 hyper/ 22272 hypo),  $C_4$  (97297  
31 hyper/ 26728 hypo), and  $C_5$  (101198 hyper/ 14503 hypo) contained large number of  
32 hypermethylated probes (**Figure 3A**). Further genomic and CpG annotations of the DMPs showed  
33 no significant differences in their overall distribution within clusters however, hypermethylated  
34 DMPs were strongly enriched in promoters and CpG islands across all the clusters  
35 (**supplementary Figure S7A**). Recent evidence showed that DNAm changes in regulatory regions  
36 play a critical role in maintaining cellular identity, and malignant transformation in both solid and  
37 leukemic cancers (30, 31). Consequently, we generated the promoter (H3K4me3) and enhancer  
38 (H3K27ac/H3K4me1) landscape of normal thymic cell types at various developmental stages  
39 (Immature CD34+, EC (Early Cortical CD4+ CD8+ TCR/CD3-), LC (Late Cortical; CD4+ CD8+  
40 TCR/CD3+), SP4 (Single Positive; CD4+, TCR $\alpha\beta$ +), SP8 (Single Positive CD8+, TCR $\alpha\beta$ +)) using  
41 the data collected from the BLUEPRINT consortium (32). We defined three types of enhancers  
42 (active, poised and putative) based on the presence or absence of H3K27ac, and H3K4me1 histone  
43 marks (**Supplementary Figure S7B and S7C**). In addition, we also collected H3K27ac and  
44 H3K4me3 ChIP-seq profiles for 12 primary T-ALLs belonging to four distinct methylation  
45 clusters (7 to  $C_2$ , 2 to  $C_4$  and 3 to  $C_5$ ). PCA analysis based on the histone marks still retained the

1 DNAm-based clustering (**Figure 3B and 3C**). We next identified super-enhancers (SEs) and  
2 typical enhancers (TEs) for each normal T-cell and T-ALL methylation cluster. SE-associated  
3 genes from both normal and T-ALL contained genes known to be involved in T-cell maturation,  
4 and T-ALL leukemogenesis, respectively (**Supplementary Figure S7D**) (**Supplementary Table**  
5 **S6**). Interestingly, a number of SEs identified in T-cell subtypes increased with the developmental  
6 stages but, we observed significantly higher number of SEs in T-ALL compared to normal T-cells  
7 ( $P < 0.001$ ; t-test) (**Figure 3D**).

8 Next, we performed an enrichment analysis, which further revealed the dynamics of  
9 DNAm changes in T-ALL associated regulatory elements (**Figure 3E**). Hypermethylated DMPs  
10 across all five clusters were mainly enriched within known TSS ( $\pm 1000$  base pairs) and active  
11 promoters (H3K4me3 peaks) derived from normal T-cell developmental datasets. Of note, we also  
12 observed enrichment of hypermethylated DMPs within normal thymus derived poised enhancers  
13 (H3K4me1+/H3K27ac-), suggesting a potential shut-down of enhancers that could be primed for  
14 activation in later T-cell developmental stages (33). In contrast, hypomethylated DMPs were  
15 enriched within intergenic regions. T-ALL associated SEs and TEs were largely enriched for  
16 hypomethylated DMPs suggesting active downstream expression of SE associated genes. Given  
17 the role of SEs in disease progression, hypomethylation of T-ALL specific regulatory elements  
18 suggests a DNAm mediated activation of SEs and further cancer progression (34).

19 Several studies have reported the binding of core oncogenic or cell specific master TFs  
20 within enhancer elements (35, 36). We therefore checked for the enrichment of TF motifs within  
21 100 bps of hypomethylated DMPs located within T-ALL derived SEs and TEs. This revealed  
22 specific TF dynamics within each cluster (**Figure 3F**) (**Supplementary Table S7**). For example,  
23 C<sub>2</sub> was enriched for TAL1, RUNX1/2, GATA4/6, MYB TF motifs, which have been reported to  
24 form auto-regulatory loops in *TAL1* deregulated T-ALLs thereby driving oncogenesis (37). C<sub>1</sub> was  
25 primarily associated with bZIP and “myeloid like” motifs such as CEBP, CHOP, GATA1/2, PU1  
26 and AP1, in accordance with the samples being enriched for Immature/ETP geno/phenotypes  
27 (**Figure 1D**). Similarly, C<sub>5</sub> was enriched for HOXA cluster-specific homeobox TFs.

28 Altogether, our results show diverging roles of DNAm in chromatin regulation by which  
29 disease associated enhancers are frequently hypomethylated, leading to probable chromatin  
30 activation, whereas normal developmental associated promoters are possibly repressed by  
31 hypermethylation. In addition, enrichment of several key oncogenic TF motifs within disease  
32 associated enhancers highlights the active ongoing oncogenic transcriptional programs.

### 33 *Integrative analysis of DNAm and Gene expression among epigenetic subgroups*

34 To understand the influence of DNAm on gene expression in T-ALL clusters, we generated  
35 the expression profiles by means of RNA-sequencing for a total of 48 samples (C<sub>1</sub> = 4, C<sub>2</sub> = 13,  
36 C<sub>3</sub> = 6, C<sub>4</sub> = 7, C<sub>5</sub> = 14) including 4 normal total thymus control. In the PCA analysis of the RNA-  
37 seq data, although the samples tended to cluster according to their methylation cluster, the  
38 distinction between the different leukemia groups appeared much less clear than based on their  
39 methylation signature. Interestingly, total thymus samples were clustered with C<sub>2</sub> samples similar  
40 to DNAm results. (**Figure 4A**). In addition, clusters showed clear expression of their candidate  
41 driver transcription factors (**Figure 4B**). We performed differential gene expression (DGE)  
42 analysis by comparing each cluster against total thymus samples. This analysis revealed a varying  
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1 degrees of gene expression changes with C<sub>1</sub> displaying the lowest and C<sub>5</sub> the highest number of  
2 DE genes (DEGs) (**Supplementary Table S8**). Significant portion of these DE genes were up-  
3 regulated suggesting an activated gene expression profiles (**Figure 4C**). In order to measure the  
4 genome-wide influence of DNAm on gene expression, we performed correlation analysis between  
5 gene expression and the corresponding promoter DNAm levels of all protein coding genes ( $N =$   
6  $15,912$  genes) across all 44 T-ALL samples (**Figure 4D**). Only a fraction of genes ( $N = 235$ )  
7 significantly correlated with their promoter DNAm levels ( $FDR < 0.1$ ). The fact that DNA  
8 methylation levels at promoter regions do not necessarily correlate with gene expression levels has  
9 also been observed in multiple studies(38, 39). However, except for C<sub>1</sub> cluster, we globally found  
10 an expected inverse correlation between DE genes and their promoter DNAm levels - with up-  
11 regulated genes displaying lower methylation levels compared to down regulated genes (**Figure**  
12 **4E**). Therefore, in order to better depict DNAm clusters, we identified cluster-specific genes with  
13 significant inverse correlation between DNAm and gene expression in a robust manner. We used  
14 all the DMPs (from **Figure 3A**) within promoter regions and studied their corresponding gene  
15 expression (**Figure 4F**). Careful cataloging of these genes revealed several interesting cluster-  
16 specific genes, already involved in oncogenic processes, with an inverse correlation between  
17 DNAm and gene expression. In C<sub>1</sub> cluster - enriched in immature, ETP-ALL, co-occurring  
18 DNMT3A/IDH2 mutations and myeloid features - among genes hypomethylated and  
19 overexpressed, we identified the myeloid factors, *AZUI*, *CSF3*, the oncogenic genes *EGFL7*(40),  
20 *FES*(41), *SLC2A5*(42) involved in AML, *SI00A6* involved in several solid tumor types(43-45) and  
21 *JDP2*(46). Similarly, we also found several other cluster-specific candidate oncogenes such as  
22 *CD160*(47), *CD47*(48), *FOSL1*(49) in C<sub>2</sub>, *MAPK8*(50-53) and *MYEOV*(54, 55) in C<sub>3</sub>, and *CAPG*,  
23 *RGS17*(56, 57), *FAM83A*(58), *LGALS*(59), *NCR1*(60) and *EMPI*(61) in C<sub>5</sub>. On the other hand,  
24 DNA hypermethylation, a hallmark of cancer, has been extensively involved in tumor suppressor  
25 genes (TSG) inactivation. In line with this concept, we found among genes hypermethylated and  
26 down regulated several candidate TSGs, especially in cluster C<sub>5</sub>, which displayed the highest  
27 number of repressed DEGs: *NPTX1*(62) in C<sub>4</sub>, *ALS2CL*(63), *AMPH*(64), *CMTM8*(65),  
28 *DEPDC7*(66), *HOOK1*(67), *MITF*(68), *MPPED2*(69), *PCDH9*(70), *RARRES1*(71), *RASEF*(72),  
29 *RNF180*(73), *SI00A16*(74) and *SLFN5*(75) in C<sub>5</sub>. Despite the limited number of RNAseq data  
30 available in this series, our gene expression analysis reinforces the biological relevance of the  
31 methylation-based clustering and leads to the identification of potential cluster-specific oncogenes  
32 and tumor suppressor genes.

### 34 *Subgroup C<sub>5</sub> associates with poor outcome in GRAALL-treated patients*

35 CIMP-negative T-ALL patients have been shown to be significantly associated with higher  
36 cumulative incidences of relapse compared to CIMP-positive patients, suggesting a prognostic  
37 relevance of DNAm profiles in both pediatric and adult T-ALL (19, 21). Evaluation of the  
38 prognostic relevance of the five DNAm clusters revealed diverse levels of overall survival (OS)  
39 and event-free survival (EFS) ( $P = 0.08$  and  $P = 0.045$ , respectively) with C<sub>4</sub> and C<sub>1</sub> displaying the  
40 most favorable and most unfavorable outcomes respectively ( $P = 0.002$  OS and  $P = 0.01$  EFS)  
41 (**Supplementary Figure S8A and S8B**). Based on genome-wide DNAm levels (see **Figure 1C**),  
42 we classified five clusters into three groups with significantly different methylation levels, C<sub>(1+2)</sub>,  
43 C<sub>(3+4)</sub> and C<sub>(5)</sub> which displayed hypomethylation, intermediate-hypermethylation and high-  
44 hypermethylation respectively. In line with previous reports, patients in the hypomethylated C<sub>(1+2)</sub>  
45 subgroup demonstrated shorter OS (5-year OS probability; 50% [95% CI = 35% to 63%] vs 71.5%

1 [95% CI = 58% to 81%];  $P = 0.031$ ) and EFS (5-year EFS probability; 44% [95% CI = 30% to  
2 57%] vs 69% [95% CI = 55% to 79%];  $P = 0.015$ ) as compared to the intermediate-  
3 hypermethylated  $C_{(3+4)}$  subgroup. Interestingly, the high-hypermethylated  $C_{(5)}$  subgroup displayed  
4 distinct clinical outcome and had significantly poorer survival probability as compared to the  $C_{(3+4)}$   
5 subgroup (5-year OS probability; 53% [95% CI = 34% to 68%] vs 72% [95% CI = 58% to 81%];  
6  $P = 0.037$ ) and EFS (5-year EFS probability; 46% [95% CI = 28% to 62%] vs 69% [95% CI =  
7 55% to 79%];  $P = 0.045$ ). Patients in both  $C_5$  and  $C_{(1+2)}$  showed similar shorter OS and EFS (**Figure**  
8 **5A and 5B**). Importantly, the adverse prognosis associated with  $C_{(5)}$  and  $C_{(1+2)}$  did not seem to be  
9 related to the same clinical parameters.  $C_5$  patients demonstrated poor early response with  
10 significantly slower D8 prednisone and D15 bone marrow responses, and higher post-induction  
11 Minimal Residual Disease (MRD) levels (prednisone response; 28.1% vs 54.2%, Bone marrow  
12 response; 21.9% vs 66.7% and negative post-induction MRD; 38.1% vs 78.3% respectively) unlike  
13 to the  $C_{(1+2)}$  patients who relapsed despite a good initial response (**Table 2**). **In both EFS and OS**  
14 **multivariate analyses, the difference between  $C_{(1+2)}$  and  $C_{(3+4)}$  remained statistically significant as**  
15 **the difference between  $C_{(5)}$  and  $C_{(3+4)}$  lost this significance (Supplementary Table S9). Overall,**  
16 **these data identified a subset of hypermethylated T-ALL with poor primary therapeutic response,**  
17 **paving the way for specific targeted therapeutic schedules.**

#### 18 *In vivo responses to hypomethylating agents*

19 As we observed significant differences in the DNAm patterns and overall levels in the leukemic  
20 subgroups, we reasoned that epigenetic treatment with DNMT inhibitors (hypomethylating agents)  
21 could be of potential interest in the treatment of, particularly hypermethylated T-ALL. The *TLX1+*  
22 ALL-SIL cell line (belonging to  $C_4$ ) was transduced to stably express luciferase and transplanted  
23 in NSG mice. At day 2 post-transplantation, mice ( $n = 3-5$  per group) received a daily dose of  
24 5mg/kg intra-peritoneal 5-azacytidine for two courses of five days with an interval of two days,  
25 with bioluminescence measurement of bulk leukemic engraftment. This preventive 5-azacytidine  
26 *in vivo* treatment significantly delayed leukemic engraftment and increased the overall survival of  
27 the treated mice ( $P = 0.0067$  respectively) (**Figure 6A, B**). In order to test all cluster subtypes  
28 using more relevant models of human T-ALL, we established Patients Derived Xenografts (PDX)  
29 from five primary T-ALL samples (**Supplementary Figure S9**). Mice were treated *in-vivo* in a  
30 “curative-like” setting (two courses, starting when peripheral blood blast counts exceeded 1%).  
31 Leukemic blast expansion was regularly measured by flow cytometry analysis. For the PDX lines  
32 derived from three patients UPNT-M149, UPNT-670 and UPNT-529, belonging respectively to  
33 the hypermethylated  $C_3$ ,  $C_4$ , and  $C_5$  clusters, 5-azacytidine treatment significantly increased  
34 survival, delayed tumor expansion ( $P = 0.001$ ,  $P = 0.01$  and  $P = 0.02$  respectively) and led to  
35 drastic, albeit transient, decreases in leukemic burdens (**Figure 6C, 6D and 6E**). In contrast, for  
36 the two hypomethylated  $C_2$  patients UPNT-525 and UPNT-894 (**Figure 6F, 6G**), curative  
37 treatment had no significant effect and **in contrast** was associated with a rapid increase of  
38 peripheral blast counts and death of the recipient mice. **Of note, we observed increase in the tumor**  
39 **burden upon termination of the treatment which might be due to the short duration of the treatment**  
40 **(2 weeks) being insufficient in the complete clearance of blast cells thereby resulting in the**  
41 **recurrence of residual clones surviving the treatment.**

42 Altogether, these results, **although obtained in a limited number of mice**, indicate the  
43 efficacy of DNMT inhibitor treatment in T-ALLs with a hypermethylated profile, including those  
44 belonging to the poor prognosis  $C_5$  cluster. Aberrant hypermethylation could be a predictive factor

1 for therapeutic response and the use of hypomethylating agents for a subset of T-ALLs with  
2 unfavorable prognosis.

### 3 **Discussion**

4 Historically, epigenetic studies in T-ALL have focused on promoter regions (18, 19, 76, 77). We  
5 now provide extensive DNAm analysis in a large cohort of 143 primary adult T-ALL samples  
6 using Illumina Infinium Methylation EPIC arrays covering over 850,000 CpGs across promoters  
7 and regulatory regions. Using an unbiased approach, we identified five epigenetic clusters, four of  
8 which are associated with activation of distinct oncogenic TFs identified by expression-based  
9 studies (5, 25). In addition, we identified a novel and likely adult-specific subgroup of T-ALL with  
10 co-occurring *DNMT3A* and/or *IDH2* mutations (78), which showed hypomethylation, and an  
11 immature/ETP phenotype. Patients in this group were associated with poor prognosis. These  
12 results highlight the role of developmental stage specific oncogenic events, which remodel the  
13 underlying methylome to drive leukemogenesis. Importantly, features associated with these  
14 DNAm clusters complement the previously reported gene expression-based analyses (25). For  
15 example, expression-based studies have shown extensive overlap in expression signatures between  
16 *TLX1* and *TLX3* T-ALLs, whereas these two oncogenic subgroups are robustly separated in their  
17 DNAm patterns and methylation-based arrest stages, suggesting more profound differences in  
18 deregulated pathways. *HOXA9* deregulated samples showed large differences in their DNAm  
19 based on the mode of overexpression. Samples with *HOXA9* deregulation clustered in two distinct  
20 subgroups, those displaying deregulation in *cis* (under the influence of the TCR $\beta$  enhancer)  
21 clustered with *TLX1* deregulated samples (C<sub>4</sub>) displaying early cortical maturation arrest stages  
22 whereas, *HOXA9* samples in *trans* (under the influence of *SET-NUP214*, *MLLT10* or *MLL* fusions)  
23 formed a distinct hypermethylation cluster (C<sub>5</sub>), associated with a more immature maturation arrest  
24 stage (22). C<sub>5</sub> was also enriched in PRC2 alterations (*SUZ12* and *EZH2* mutation/deletion). Murine  
25 models of ETP-ALL driven by *Ezh2* and *Tp53* inactivation have also been characterized by  
26 hypermethylation of T-cell developmental genes, thereby promoting leukemic transformation  
27 (79). The loss of *Ezh2* in murine ETPs induced the pathogenic epigenetic switch from H3K27me<sub>3</sub>  
28 to DNA hypermethylation of pivotal T-cell development regulators, such as *Runx1*, but sustained  
29 the expression of stem cell signature genes and promoted the transformation of ETPs, supporting  
30 a pathogenic role for inactivating PRC2 mutations in ETP-ALL. It would be interesting to compare  
31 these observations with human primary T-ALLs. DNAm clearly separated immature/ETP ALLs  
32 into C<sub>1</sub> hypomethylated *DNMT3A/IDH2*-rich and C<sub>2</sub> hypermethylated *trans*-*HOXA/PRC2* groups,  
33 paving the way for distinct therapy. *TALI* deregulated samples, irrespective of the mechanism of  
34 deregulation (*SIL-TALI*, or upstream neo-enhancers (80)) clustered together, suggesting a  
35 disruption of common downstream pathways (81, 82). *TALI* is one of the most frequently  
36 deregulated driver oncogene in T-ALL (approximately 30% of cases) either through deletions  
37 (*SIL-TALI*; 10-20%), oncogenic neoenhancer (20%) (80) or rare V(D)J-mediated translocations  
38 [t(1;14); 1-2%]. In about 40% of *TALI*<sup>+</sup> cases, however, such lesions are absent, and *TALI* is  
39 overexpressed due to unknown mechanisms. In cluster C<sub>2</sub>, only 16/34 samples displayed either the  
40 *SIL-TALI* deletion or oncogenic neoenhancer suggesting that this cluster may also contain samples  
41 with *TALI* overexpression due to as yet unexplained/unidentified mechanisms of deregulation.

42 Cluster C<sub>1</sub>, enriched for co-occurring *DNMT3A/IDH2* mutants, was completely devoid of  
43 any previously recognized TF overexpression, but all *DNMT3A/IDH2* mutated cases also harbored  
44 *NOTCH1* mutations, in line with previous observations, highlighting the synergistic role of  
45 deregulated epigenome and *NOTCH1* signaling pathways in disease progression (83, 84). High  
46 variant allele frequency of *DNMT3A* mutations indicated a large fraction of homozygous or

1 compound heterozygous mutations (data not shown) suggesting a distinct *DNMT3A* mutation  
2 spectrum in T-ALL as compared to acute myeloid leukemia cases (83-86). In the context of disease  
3 progression, higher variant allele frequency combined with significantly older age group (**data not**  
4 **shown**) suggests that *DNMT3A* clones could have arisen early in hematopoiesis, prior to T-cell  
5 lineage restriction. This hypothesis is further corroborated by recent evidence for age related  
6 *DNMT3A* mutations in T-ALL (11). This early acquisition of *DNMT3A* in T-cell progenitors  
7 further could acquire secondary genetic hits (such as *NOTCH1/IDH2*) upon thymic entry, thereby  
8 deregulating the methylome during T-cell development. Interestingly, unlike co-occurring  
9 *IDH2/DNMT3A* mutations, single mutations in epigenetic factors (*DNMT3A*, *IDH1*, *TET2/3*)  
10 involved in DNAm were not associated with a specific methylome, raising the question of the role  
11 played by such genomic alterations in leukemogenesis. Cluster-specific methylome analysis  
12 revealed non-random and systematic distribution of DMPs, with significant hypermethylation of  
13 T-cell developmental associated active promoters and poised enhancers, whereas T-ALL  
14 associated enhancers showed significant hypomethylation. Our results echo similar observations  
15 of enhancer hypomethylation in solid tumors as well as in leukemia (30, 31). Moreover,  
16 identification of disease-associated TFs within the enhancer elements suggests an enhancer  
17 dependent active oncogenic transcriptional program mediated by hypomethylated chromatin (34,  
18 36). **Similar to cluster specific somatic and epigenetic alterations, our integrated gene expression**  
19 **and DNAm analysis further highlights the combined effects of DNAm and gene expression in T-**  
20 **ALL pathogenesis. For example, *SLC2A5* which is hypomethylated as well as overexpressed in**  
21 ***C*<sub>1</sub>, is also overexpressed in a subset of AML and in childhood Philadelphia chromosome positive**  
22 **ALL and associated with poor outcome. The encoded protein which is a fructose transporter**  
23 **responsible for fructose uptake by the small intestine and enhances fructose use of leukemic cells**  
24 **(42, 87). *JDP2* – a bZIP family transcription factor specific to *C*<sub>1</sub> - has been identified as a novel**  
25 **oncogene in ETP T-ALL and shown to be associated with poor prognosis (46). Importantly,**  
26 **enrichment of myeloid like genes and bZIP family transcription factors in *C*<sub>1</sub> is also corroborated**  
27 **by independent motif analysis results (Figure 3F). Another gene - *EMPI* specifically**  
28 **hypomethylated/overexpressed in *C*<sub>5</sub>, has been shown to be associated with poor outcome in**  
29 **pediatric ALL and to confer prednisolone resistance (61). Interestingly, our clinical study showed**  
30 **also an association of *C*<sub>5</sub> with a poor early prednisone response.**

31  
32 Another significant finding of this study is the recapitulation of the maturation arrest stages  
33 based on DNAm. Lymphopoiesis is a complex process mediated by expression of several TFs and  
34 cell surface markers in a stage specific manner (29). Our DNAm based phylogenetic trees robustly  
35 captured these developmental stages, thereby illustrating the prominent role of DNAm in  
36 regulating thymopoiesis. These results further highlight previous observations in mouse  
37 hematopoiesis, wherein DNAm dynamics orchestrate myelopoiesis and lymphopoiesis to form  
38 different terminal DNAm patterns (88). Similar observations have also been made in human  
39 lymphopoiesis, in which DNAm dynamics during B cell maturation display a continuum of  
40 changes (89). By combining T-ALL samples, these phylogenetic trees robustly recaptured the  
41 known clinically relevant subgroups, thereby reflecting developmental arrest at different stages of  
42 thymic maturation. **Similar results have also been observed in an independent analysis using open**  
43 **chromatin signals highlighting the conserved epigenetic marks at several layers (90). Overall, our**  
44 **results show an early occurrence of *C*<sub>5</sub>, and *C*<sub>1</sub> clusters, characterized by in *trans* overexpression**  
45 **of *HOXA* and mutations in myeloid-like genes such as *DNMT3A/IDH2* respectively, whereas *C*<sub>3</sub>**  
46 **(enriched in *TLX3* cases) and *C*<sub>4</sub> (enriched in *TLX1* and cis *HOXA* deregulated cases) showed**

1 intermediate arrest stages. Finally, C<sub>2</sub> enriched in *TALI* deregulated samples occurred latest, in  
2 keeping with the known late cortical maturation stage arrest of the *TALI* deregulated T-ALL  
3 subgroup (5). The combined observation of hypomethylated disease enhancers and maturation  
4 arrest stages further highlight the plasticity induced by DNAm in tumor progression.

5 Importantly, unlike previous transcriptional studies, we identified patient clusters with  
6 clinical relevance and an unexpected subgroup of highly hypermethylated patients (C<sub>5</sub>) associated  
7 with unfavorable outcome similar to hypomethylated patients and who could benefit from targeted  
8 therapy (91, 92). Epigenetic drugs such as (93)(94)(95). Our results from use of  
9 hypomethylating treatment of T-ALLs with known methylation status suggest that 5-azacytine  
10 could be a promising therapeutic option in hypermethylated T-ALL. In contrast, hypomethylated  
11 samples showed poor response to treatment, suggesting that a certain degree of aberrant  
12 hypermethylation is required to observe treatment efficacy. Follow-up studies are required to  
13 confirm the therapeutic potential of hypomethylating agents in T-ALL and it would be interesting  
14 to study their efficacy in combination with other compounds such as conventional chemotherapy  
15 or epigenetic therapy, such as an *EZH2* inhibitor.

## 16 **Materials and Methods**

17 *Study Design:* Blood or bone marrow from a total of 143 adult patients diagnosed with T-ALL  
18 (15-60 years old) from two successive French ALL cooperative groups ( $n = 22$  from GRAALL-  
19 2003 and  $n = 121$  from GRAALL-2005) were analyzed. The GRAALL-2003 protocol was a  
20 multicenter Phase II trial, which enrolled 76 adults with T-ALL between November 2003 and  
21 November 2005, of whom 50 had sufficient diagnostic tumor material available for NGS study but  
22 only 22 had enough high-quality DNA for EPIC array (96). The multicenter randomized  
23 GRAALL-2005 Phase III trial was very similar to the GRAALL-2003 trial, with the addition of a  
24 randomized evaluation of an intensified sequence of hyper-fractionated cyclophosphamide during  
25 induction and late intensification (97). Between May 2006 and May 2010, 261 adults with T-ALL  
26 were randomized in the GRAALL-2005, of which 185 had available diagnostic material for NGS  
27 study but only 121 had enough high-quality DNA for EPIC array. In this study, the main criterion  
28 for inclusion was the availability of high-quality DNA. Survival outcomes of the 143 patients did  
29 not differ from those of the remaining 194 T-ALL patients. As expected in retrospective studies,  
30 initial white blood cell count (WBC) was higher in the study cohort. A full comparison of the  
31 clinical features of each group is shown in **Supplementary Table S10**. All samples contained  
32 >80% blasts. Phenotypic and oncogenetic characteristics were obtained as described (22, 98, 99).  
33 Informed consent was obtained from all patients at enrolment. All trials were conducted in  
34 accordance with the declaration of Helsinki, approved by local and multicenter research ethical  
35 committees. The GRAALL-2003 and -2005 studies were registered at  
36 <http://www.clinicaltrials.gov> as #NCT00222027 and #NCT00327678, respectively.

37  
38 *Univariate and multivariate survival analysis for OS and EFS:* Since methylation subgroups were  
39 strongly associated with maturation arrest and tumor biology, we only considered age, log(WBC),  
40 CNS involvement, prednisone response, and D8 bone marrow response as covariates to avoid  
41 multicollinearity. Methylation clusters were reduced to a 3-class variable with intermediate  
42 methylation clusters (C<sub>(3+4)</sub>) considered as baseline. Covariates finally used in the multivariate cox  
43 model were those associated with outcome in univariate analyses ( $P < 0.1$ ). As shown in  
44 **Supplementary Table S9**, univariate analysis for EFS identified age, prednisone response, BM  
45 response, CNS involvement, and methylation clustering as covariates in the multivariate model.

1 **Univariate analysis for OS identified age, prednisone response, CNS involvement, and methylation**  
2 **clustering as covariates for multivariate analysis.**

3 *Thymic subpopulations sorting:* Human thymic subpopulations were obtained from children  
4 undergoing cardiac surgery. Informed consent was obtained from parents and the study was  
5 approved by the Ethics committee (CPP Ile de France II, project number 2012-03-04). Thymii  
6 were dissociated into single cell suspensions. Six specific subpopulations were purified by sorting  
7 using FACS ARIA III (BD Biosciences): thymic CD34+, 4ISP (Immature Simple positive CD4+),  
8 DP-TCR-/CD3- (Double Positive CD4+ CD8+ TCR- CD3-), DP-TCR+/CD3+ (Double Positive  
9 CD4+ CD8+ TCR+ CD3+), SP4 (**Single** positive CD4+) and SP8 (**Single** Positive CD8+). For the  
10 immature subpopulation, thymocytes were pre-purified by depletion of CD3 and CD8 positive  
11 fraction by magnetic activated cell sorting using CD3 MicroBeads (Miltenyi, Bergisch Gladbach,  
12 Germany, Cat #130-050-101) and CD8 MicroBeads (Miltenyi, Cat#130-045-201) respectively.  
13 Antibodies used for cell labelling of CD3-/CD8- thymic fraction: CD1a FITC, clone NA1/34  
14 (Dako, Glostrup, Denmark Cat#F7141), CD34 APC (BD Biosciences, Erembodegem, Belgium  
15 Cat#345804), CD8 PC7 (Beckman Coulter, Brea, CA, USA, Cat#737661), CD3 Alexa-700 (BD  
16 Biosciences, Cat#557943), CD4 V450, clone RPA-T4 (BD Biosciences, Cat#60345), CD45 V500,  
17 clone HI30 (BD Biosciences, Cat#560777). Final purity after sorting was over 95%. Total thymus  
18 DNA was used as control.

19 *Targeted Next-generation sequencing:* Nextera XT (Illumina, San Diego, CA, USA) DNA  
20 Libraries were prepared according to the manufacturer's instructions and sequenced using the  
21 Illumina MiSeq sequencing system. The custom NGS panel comprised genes coding for factors  
22 involved in molecular pathways known to be mutated in T-ALL, namely cytokine receptor and  
23 RAS signaling (*NRAS*, *KRAS*, *JAK1*, *JAK3*, *STAT3*, *STAT5B*, *IL7R*, *BRAF*, *NF1*, *SH2B3* and  
24 *PTPN11*), hematopoietic development (*RUNX1*, *ETV6*, *GATA3*, *IKZF1*, *EP300*), chemical  
25 modification of histones (*SUZ12*, *EED*, *EZH2*, *KMT2A*, *KMT2D* and *SETD2*) and DNAm  
26 (*DNMT3A*, *IDH1*, *IDH2*, *TET2*, *TET3*). This panel was originally inspired by the genes found to  
27 be preferentially altered in pediatric ETP-ALL (Zhang et al. 2012) and we have reported a subset  
28 of the results described in the current paper in previous clinic-biological and genetic analyses (*11*,  
29 *13*). Mutational data was later integrated with copy number and analyzed with maftools  
30 Bioconductor package.

31 *MLPA T-ALL panel:* CNV for a targeted panel of genes were studied using SALSA MLPA P383  
32 T-ALL probemix (MRC-Holland, Amsterdam, Netherland).

33 *PDX and 5-azacytidine treatment of xenografted mice:* 5-azacytidine was purchased from Sigma  
34 Aldrich (St. Louis, MO, USA) and was prepared in 0.9% NaCl and stored as recommended by the  
35 manufacturer. Treatment protocol: at Day 0 (D0),  $1 \times 10^6$  human leukemic cells were resuspended  
36 in 100  $\mu$ L of PBS buffer and injected retro-orbitary in NSG mice. For ALL-SIL cell line, at D2, a  
37 group of mice received as "preventive" treatment 5 mg/kg/day 5-Azacytidine intra-peritoneal (IP)  
38 for 5 days twice with 2 days break. Untreated mice received the same volume of NaCl IP. Primary  
39 PDX models were treated with the same 5-azacytidine courses but in a "curative-like" setting,  
40 starting when peripheral blood blast counts exceeded 1%. Leukemic engraftment in peripheral  
41 blood was studied by flow cytometry using mouse-CD45 and human-CD45 antibodies. Mice were  
42 sacrificed when the blast fraction was more than 80% or if mice presented clinical signs of disease  
43 (loss of weight >10%, neurological signs, tumor development). **During the treatment, mice were**  
44 **constantly supervised for weight loss, behavioral disorders such as hyperactivity, physiological**  
45 **disorders such as increased respiratory rate, hair loss, neurological signs which revealed no**

1 **obvious treatment induced side effects.** Mouse study was approved by national ethic committee:  
2 PROJET APAFIS # 8853 N° 2017020814103710.

### 3 **Data analysis:**

4 *EPIC arrays:* Intensity Data (IDAT) files from EPIC arrays were processed and normalized with  
5 RnBeads Bioconductor package (100). Probes with high SNP probability and bad detection P-  
6 values were filtered out. EPIC arrays were also used for copy number analysis using conumee  
7 Bioconductor package, and further processed with GISTIC2 to identify recurrent copy number  
8 aberrations. Probes located in regions with altered copy numbers were excluded from downstream  
9 analysis (**Supplementary Figure S1C**).

10 *Clustering and dimension reduction:* To identify epigenetic clusters, we used Non Negative  
11 Factorization (NMF) on the top 5% of most variable probes ( $n = 38,583$ ) (101). NMF decomposes  
12 a matrix into two smaller matrices whose product sufficiently recomposes the original matrix.  
13 Critical step in NMF is identifying the number of factors. We used the method described by Brunet  
14 et al where, NMF is run on a range of values and a cophenetic correlation coefficient (measure of  
15 goodness of fit) was determined (102). An optimal number of clusters was identified for which  
16 cophenetic correlation reaches its maximum value (**Supplementary Figure S1A**). Furthermore,  
17 to measure the fitness of identified clusters, we repeated the above clustering procedure for varying  
18 number of probes (5000 up to 38583). Clusters were stable and reached maximum cophenetic  
19 correlation coefficient at  $n = 5$ . **Finally, we used 5 clusters generated by using  $N = 38,583$  probes  
20 for all downstream analysis.** These 5 epigenetic clusters were also robust as measured by rand-  
21 index, and samples showed little to no changes in cluster assignments as the number of probes  
22 used for clustering increased (**Supplementary Figure S1B**). **Moreover we randomly sampled 80%  
23 of the initial cohort ( $N = 114$ ) and repeated the clustering. Rand Index - a similarity score between  
24 two clustering results - was measured between original clusters and new clusters generated on  
25 subsamples. We repeated the entire process 10 times and results showed high similarity (Rand  
26 index 0.85 – 0.99) to the original clustering (data not shown). Clusters were later visualized using  
27 Uniform Manifold Approximation and Projection (UMAP).**

28 *Statistical analysis:* DMPs ( $FDR < 0.1$  and  $|\text{methylation change}| > 20\%$ ) were identified for every  
29 cluster by comparing them to 12 normal thymic samples using Limma Bioconductor package  
30 (103). **Differential gene expression analysis was performed using DESeq2 Bioconductor package  
31 adjusting for batch covariates wherever required.** Survival analysis was performed with Surv R-  
32 package. For predicting T-cell developmental trajectory and T-ALL maturation arrest stages, we  
33 calculated Manhattan distance between samples with *dist* function in R. Phylogenetic trees were  
34 later constructed from distance matrix using neighbor joining method, and visualized in R with  
35 ape package. All data analysis, visualization, and test statistics were performed in R statistical  
36 environment (version 4.0), and complete source code used for data analysis is provided as  
37 **Supplementary Data S1.**

38 *ChIP-seq analysis:* BAM files for ChIP-seq datasets were obtained from the BLUEPRINT (32).  
39 Peak calling was performed using MACS2 with parameters `--bdg --SPMR --nomodel --extsize 200`  
40 `--q 0.05`. Peaks overlapping with UCSC blacklisted regions were excluded. ChIP-seq results were  
41 visualized using deepTools. SEs were identified and annotated for every T-ALL and normal  
42 thymic samples with Rose software. Consensus SEs for each T-ALL cluster (**Supplementary  
43 Figure S7D**) were generated by merging H3K27ac BAM files from samples belonging to same  
44 cluster. Enrichment analysis of DMPs within regulatory regions was performed with LOLA

1 Bioconductor package. Enrichment of all vertebrate motifs around 100 base-pairs of hypo-  
2 methylated CpG probes was done using findMotifsGenome.pl from homer tools. As a background  
3 we randomly selected a subset of ca. 850,000 EPIC probes ( $n = 183,896$ ; corresponding to total  
4 number of unique DMPs identified across all 5 clusters). Significant motifs were chosen based on  
5  $P < 1e-5$ . Since homer motif database lacked the motifs for *TALI* TF, we re-analyzed public  
6 datasets containing ChIP-seq for TAL1 (GSM935496) thereby defining de-novo motif. This was  
7 later included in the homer database for downstream analysis.

## 8 **Supplementary Materials**

### 9 **Supplementary Figures**

- 10 • Supplementary Figure-S1. Identification of epigenetic clusters.
- 11 • Supplementary Figure-S2: Genomic landscape of adult T-ALL.
- 12 • **Supplementary Figure-S3: Gene expression analysis of T-ALL clusters**
- 13 • Supplementary Figure-S4: Differentially Methylated Probes associated with T-cell  
14 maturation (tDMPs).
- 15 • Supplementary Figure-S5: Characterization of Differentially Methylated Probes associated  
16 with T-cell maturation (tDMPs) based on methylation dynamics.
- 17 • **Supplementary Figure-S6: Gene expression dynamics during Thymopoiesis**
- 18 • Supplementary Figure-S7: Influence of thymic maturation associated Differentially  
19 Methylated Probes (tDMPs)
- 20 • Supplementary Figure-S8: Defining normal and disease associated enhancers.
- 21 • Supplementary Figure-S9: Overall Survival (OS) and Event Free Survival (EFS) of  
22 methylation clusters. A and B.

### 23 **Supplementary Tables**

- 24 • **Supplementary Table S1:** Significantly mutated genes in every cluster compared to rest  
25 of the clusters (Related to Figure 1H). (XLSX)
- 26 • **Supplementary Table S2:** Differentially methylated probes identified in each of the  
27 normal thymic cell-types (Related to Figure-2). (XLSX)
- 28 • **Supplementary Table S3:** Differentially methylated probes identified in each of the  
29 normal thymic cell-types classified into 8 subgroups based on methylation dynamics  
30 (Related to Figure-2D, E, and Supplementary Figure S4). (XLSX)
- 31 • **Supplementary Table S4: Genes which are both differentially expressed and showing a  
32 differential promoter methylation in normal thymic cell types (Related to Supplementary  
33 Figure S5B). (XLSX)**
- 34 • **Supplementary Table S5:** Differentially methylated probes found in each cluster along  
35 with the genomic annotations (Related to Figure 3A). (XLSX)



- 1 • **Supplementary Table S6:** Super and Typical Enhancers identified in normal thymic cell-  
2 types, and in T-ALL clusters (Related to Figure 3D, and Supplementary Figure S7D).  
3 (XLSX)
- 4 • **Supplementary Table S7:** Significantly enriched TF motifs detected within 100 base pair  
5 vicinity of hypo-methylated probes located within the super or typical enhancer regions  
6 from T-ALL clusters (Related to Figure 3F). (XLSX)
- 7 • **Supplementary Table S8:** Differentially expressed genes in cluster compared to total  
8 thymus (Related to Figure 4C). (XLSX)
- 9 • **Supplementary Table S9:** Univariate and Multivariate analyses of EFS and Overall  
10 Survival.
- 11 • **Supplementary Table S10:** Clinical characteristics and outcome of the study cohort  
12 versus non-investigated patients (GRAALL-2003/05 trials).

13 **Supplementary Data S1:** Complete source used for data analysis.

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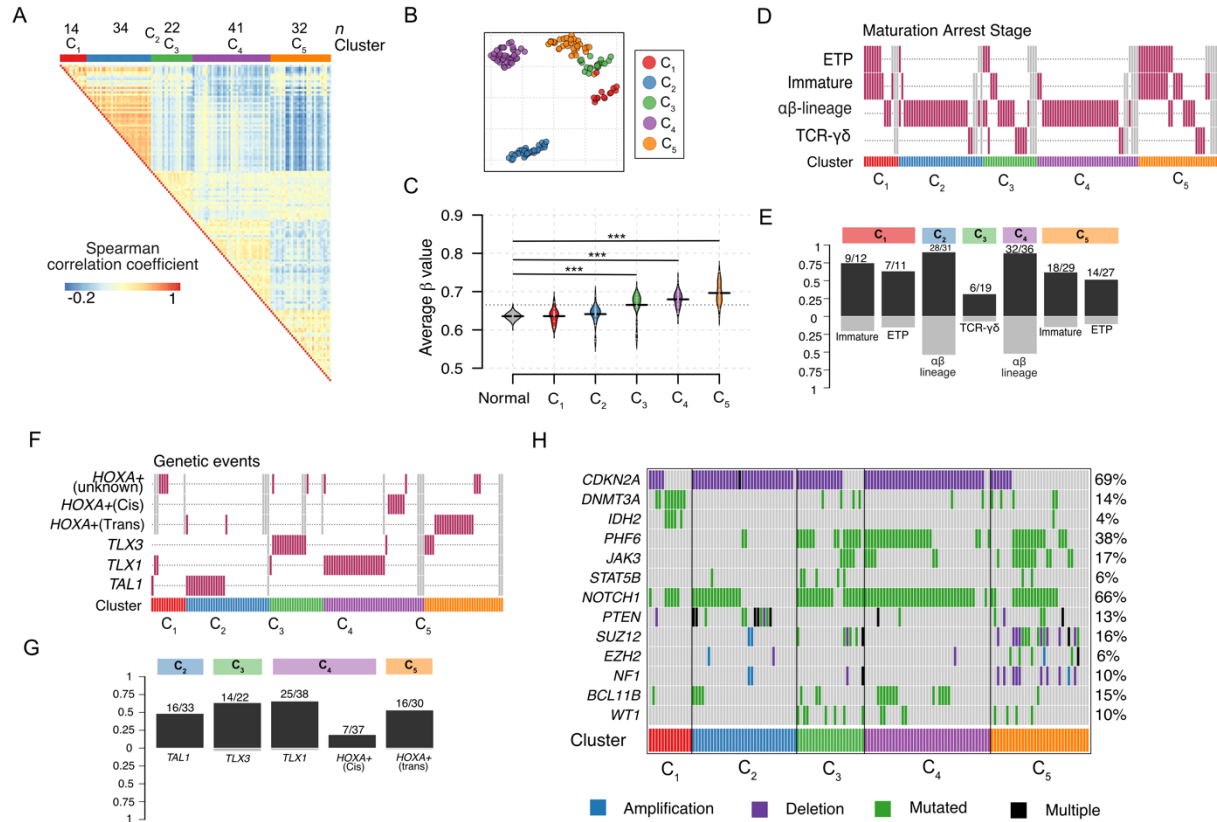
17

18 **Acknowledgments:** The authors would like to thank the Biomis core facility at Institute Pasteur,  
19 Paris and the Genomics and Proteomics Core facilities at DKFZ. **Funding:** The Study was  
20 supported in part by the Baden-Württemberg Stiftung to CP and the Helmholtz-Foundation. The  
21 GRAALL was supported by grants P0200701 and P030425/AOM03081 from Le Programme  
22 Hospitalier de Recherche Clinique, Ministère de l'Emploi et de la Solidarité, France and the Swiss  
23 Federal Government in Switzerland. AT was supported by a grant from the French CARPEM  
24 (CAncer Research for PErsonalized Medicine) SIRIC program and the DKFZ Postdoctoral  
25 fellowship. The Work in VA lab was supported by ARC-Labelisation and the associations "Force  
26 hémato" and "Laurette Fugain". This study was also supported in VA and SS lab by grants from  
27 INCA PLBIO18-031, **PLBIO 2018-00252** and ITMO Cancer Epig-2015. **Author contributions:**  
28 A.T, V.A, and C.P conceived and designed the study; A.T, and C.S performed the flow cytometry,  
29 library preparation for NGS, and mice experiments. A.M analysed the data and performed  
30 statistical analysis. All authors have critically reviewed the manuscript. **Competing interests:** The  
31 authors declare no potential conflicts of interest. **Data and materials availability:** All microarray  
32 raw IDAT files have been deposited to gene expression omnibus (GEO) under the accession  
33 number GSE147667. **A complete reproducible source code used for data analysis is provided as**  
34 **Supplementary Data S1.**

35

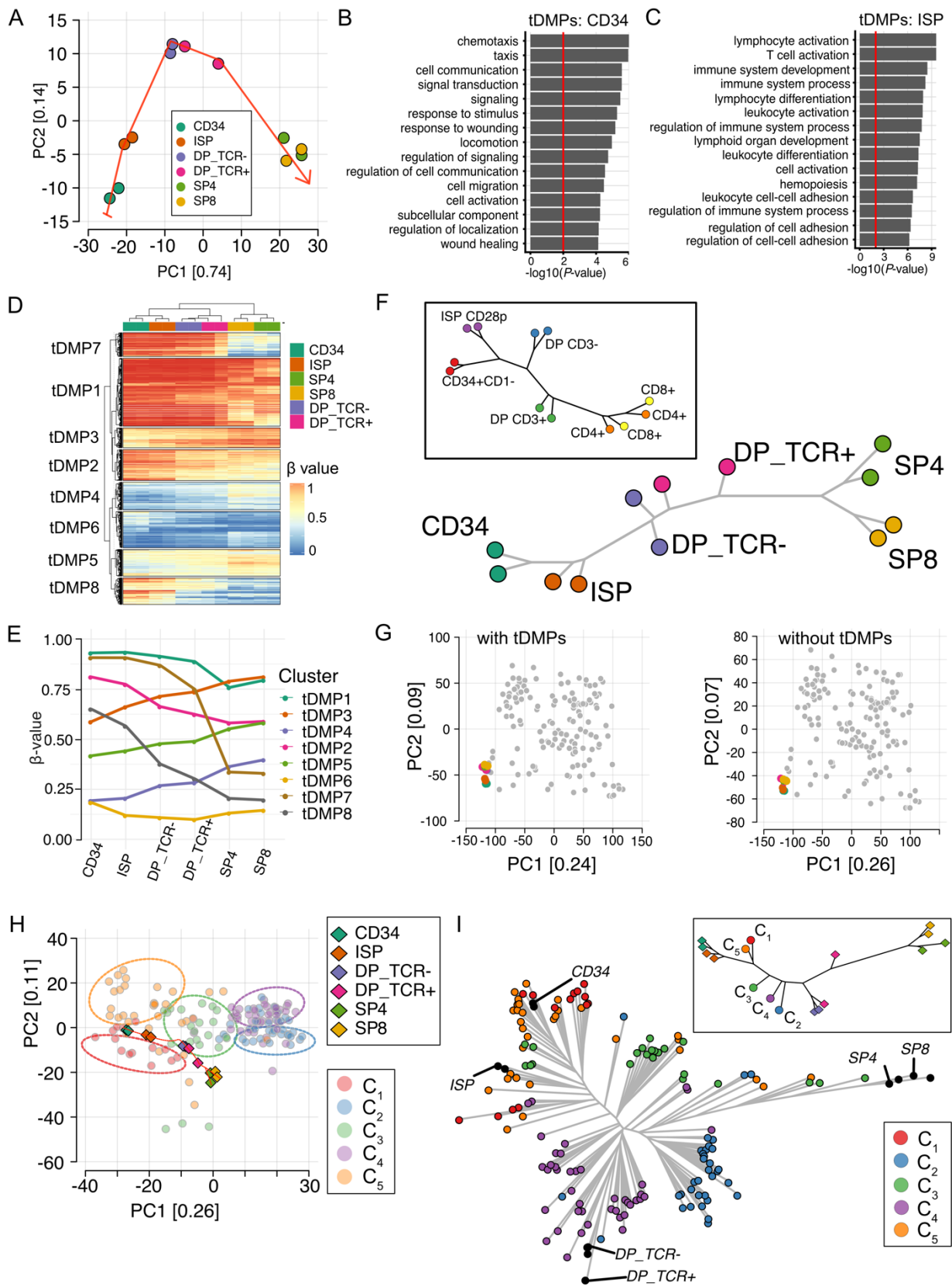
36 **Figures:**



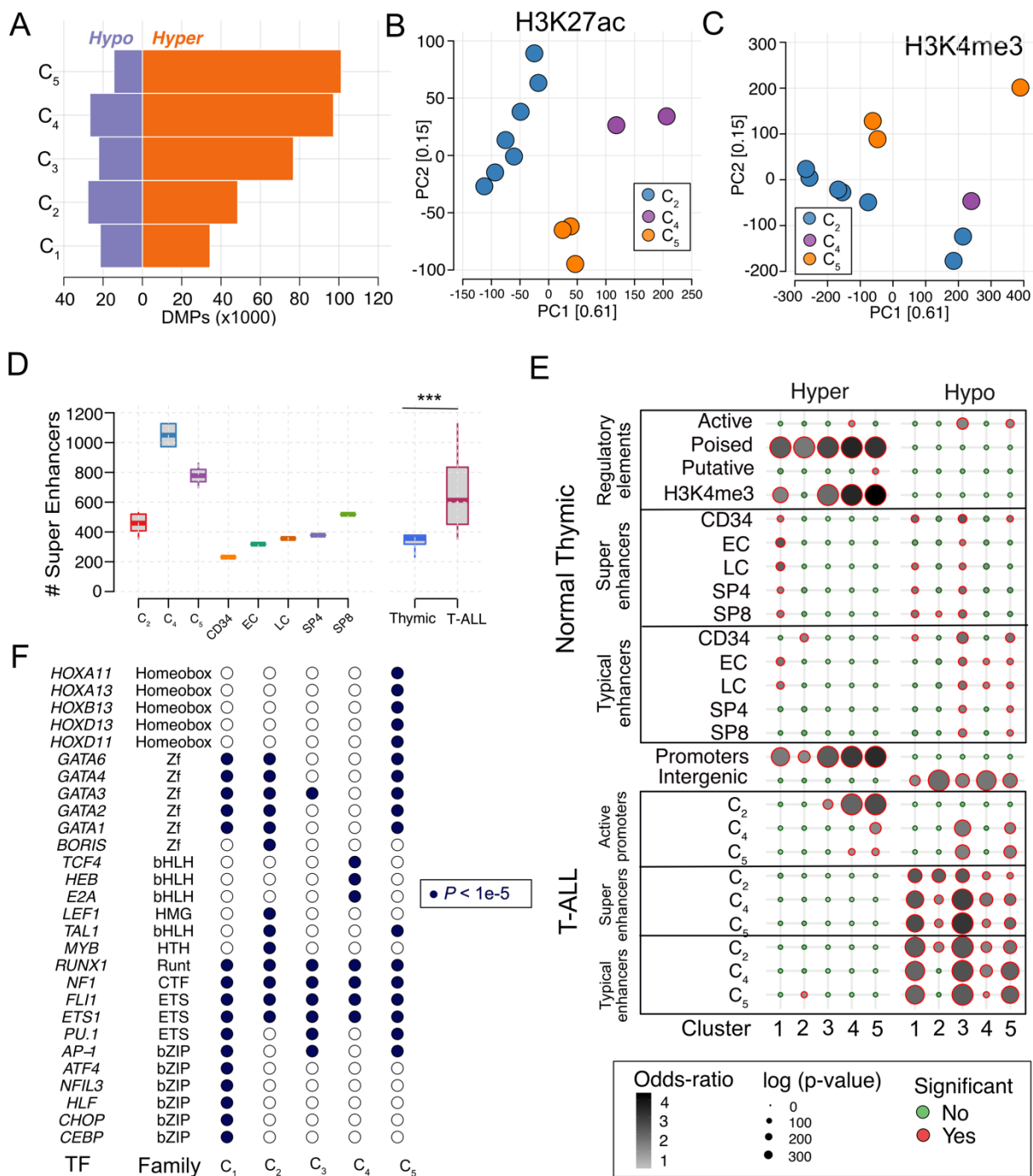


**Figure-1: Epigenetic clusters in T-ALL.** **A.** Heatmap of spearman correlation coefficient values between all leukemic samples. Top annotation bars indicate cluster sizes ( $n$ ) and titles respectively (top to bottom). **B.** Uniform Manifold Approximation and Projection (UMAP) plot of T-ALL samples color-coded according to the cluster. **C.** Violin plots depicting genome-wide DNAm values for every cluster. (\*\*\*)  $P < 0.001$  two tailed t-test for differences in mean). **D.** Heatmap showing association between maturation arrest stages (row) and T-ALL samples (columns). Each column represents a sample, and their corresponding cluster assignments are displayed as a colour coded bottom annotation bar. Rows are ordered according to T-cell maturation stages (from top most immature to bottom most mature). Gray bars indicate data not available. **E.** Bar plots displaying significant association between clusters and maturation arrest stages (Fisher's exact test;  $P < 0.01$ ). Bars are annotated with the ratio of samples belonging to a maturation arrest stage (as indicated by the bar title), and total number of samples within the clusters for which annotations are available, with the corresponding fraction on Y-axis. Bottom gray bars indicate number of samples in background with the highlighted maturation arrest stage. **F.** Heatmap showing association between genetic events (row) and T-ALL samples (columns). Each column represents a sample, and their corresponding cluster assignments are displayed as a color-coded bottom annotation bar. Rows are ordered according to genetic events (either somatic epigenetic mutations or deregulated TFs). Gray bars indicate data not available. **G.** Bar plots displaying significant association between clusters and genetic events (Fisher's exact test;  $P < 0.01$ ). Bars are annotated with the ratio of samples with the (as indicated by the bar title), and total number of samples within the clusters for which annotations are available, with the corresponding fraction on Y-axis. Bottom gray

- 1 bars indicate number of samples in background with the highlighted genetic event. **H.**
- 2 Cluster specific mutations found across the cohort (Fisher's exact test;  $FDR < 0.05$ ).



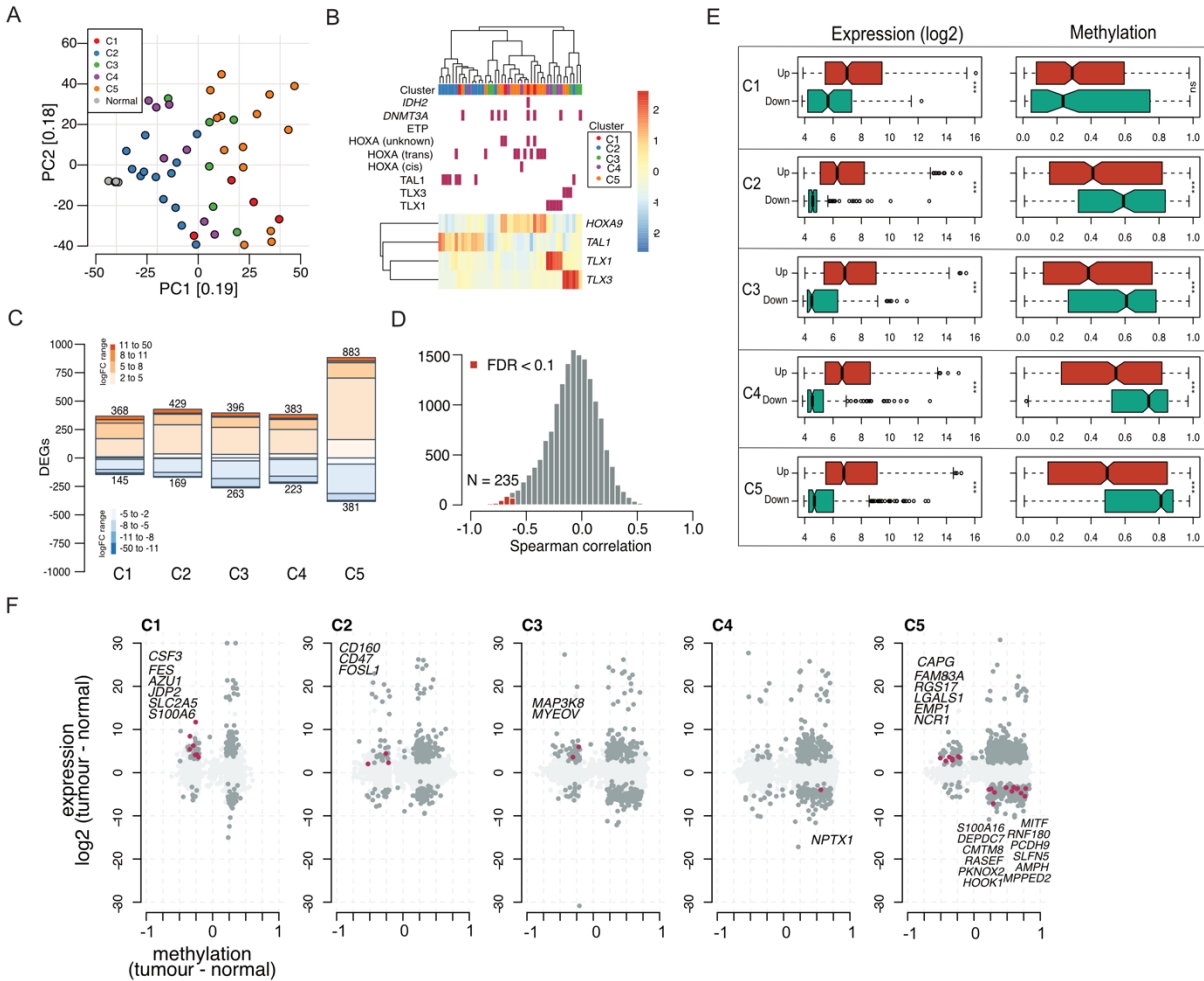
1 **Figure-2: DNA methylation predicts T-cell differentiation and maturation arrest stages of**  
2 **T-ALL clusters.** **A.** Principal Component Analysis (PCA) shows separation and ordering  
3 of T-cell subtypes according to different maturation stages (clockwise from bottom left to  
4 bottom right). The red curve indicates the direction of increasing T-cell maturation stages.  
5 **B and C.** Functional characterization of Differentially Methylated Probes (DMPs) from  
6 CD34 cells (B) and ISP cells (C), shows enrichment of cell-type specific biological  
7 processes. Vertical red bar indicates  $P = 0.001$  (Hypergeometric test). **D.** Heatmap of  
8 DMPs from T-cell maturation stages categorized into distinct subgroups (tDMP1-tDMP8)  
9 based on dynamics of changes in DNAm across cell-types. **E.** Average DNAm of tDMP  
10 subgroups across T-cell subtypes (x-axis). **F.** T-cell developmental phylogenetic tree  
11 inferred from tDMPs shows the ordering of T-cell subtypes. **Inset plot shows similar**  
12 **phylogenetic tree inferred from 1000 most differentially variably expressed genes.** **G.** PCA  
13 of normal (colored) and T-ALL samples (in gray) with (left) and without (right) tDMPs  
14 shows little to no changes in variance explained by first two principal components. **H.** PCA  
15 of normal T-cell and T-ALL methylomes using tDMPs. Normal T-cell subpopulations ( $n$   
16 = 12) are depicted in diamond shapes and T-ALLs ( $n = 143$ ) are circles - color coded  
17 according to the cluster ( $C_1 - C_5$ ). The known T-cell developmental trajectory starting from  
18 CD34 is shown as a red curve overlaid on top of normal T-cell population. **I.** Phylogenetic  
19 tree of the entire cohort ( $n = 143$  T-ALLs;  $n = 12$  normal T-cells) constructed using tDMPs  
20 shows ordering of T-ALL samples (color coded according to their corresponding clusters)  
21 along T-cell developmental pathway (left to right). Normal T-cell are in thick black circles  
22 labelled for cell-types. Inlet panel shows a simplified phylogenetic tree constructed with  
23 average DNAm levels of epigenetic clusters along with normal T-cell types (in diamond  
24 shapes) shows order of maturation arrest stages of T-ALL subtypes (in circles) along the  
25 T-cell developmental pathway (left to right).



1  
2 **Figure-3: Characterization of Differentially Methylated Probes (DMPs) associated with T-**  
3 **ALL clusters.** **A.** Numbers of hyper- and hypomethylated DMPs identified in each T-ALL  
4 cluster (C<sub>1</sub>- C<sub>5</sub>) as compared to normal pooled thymic subpopulations. **B and C.** Principal  
5 component analysis of primary T-ALL samples based on active H3K27ac peaks (peaks  
6 2500 bp away from known TSS) (B) and H3K4me3 peaks (C). Samples are color coded  
7 according to their corresponding cluster. **D.** Dot plot for enrichment of hyper- and  
8 hypomethylated DMPs across all 5 clusters (X-axis) in various regulatory regions (Y-axis)

1 as highlighted in the left side of the plot. Dots are color coded for significance and size of  
 2 the dots represents  $P$  values in log10 scale. **E.** Boxplot of number of super enhancers  
 3 identified in each T-ALL samples, clusters and thymic cell types (X-axis) (\*\*\*) t-test;  $P <$   
 4 0.01). **F.** Disease associated TF motifs detected among hypomethylated DMPs (+/- 100bp)  
 5 enriched within T-ALL associated super and typical enhancer regions.

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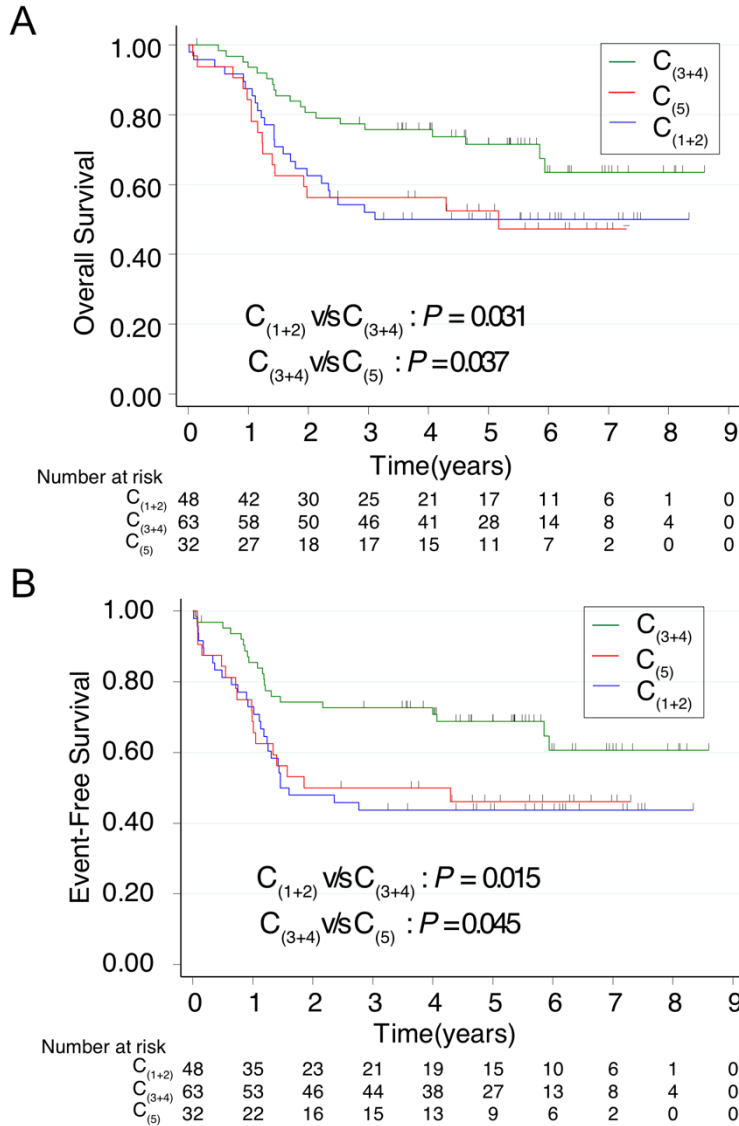


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 8 **Figure-4: Integrated analysis of DNA methylation and gene expression. A.** Principal  
 9 component analysis of gene expression data for 48 samples (44T-ALL + 4 total thymus). Samples  
 10 are color coded for their T-ALL cluster. **B.** Heatmap of known T-ALL oncogenes. Top annotation  
 11 bars depict validated genetic annotations. **C.** Barplot of number of differentially expressed genes  
 12 (DEGs) in each cluster compared to total thymus samples ( $FDR < 0.1$ ). Up and down regulated  
 13 genes are color coded for their fold change range. **D.** Histogram of Pearson correlation coefficient  
 14 between promoter\* DNAm and gene expressions of all protein coding genes ( $N = 15,912$  genes)  
 15 across all tumor samples ( $N = 44$ ). **E.** Distribution of gene expression (Up and Down regulated  
 16 genes from **panel C**) and their corresponding promoter\* DNAm for every cluster. Notches indicate  
 17 95% CI around the median. (\*\*\*)  $P < 0.001$ , t-test for differences in mean). **F.** Scatter plot of gene  
 18 expression and DNAm differences in DMPs between tumor and normal samples for all 5 clusters

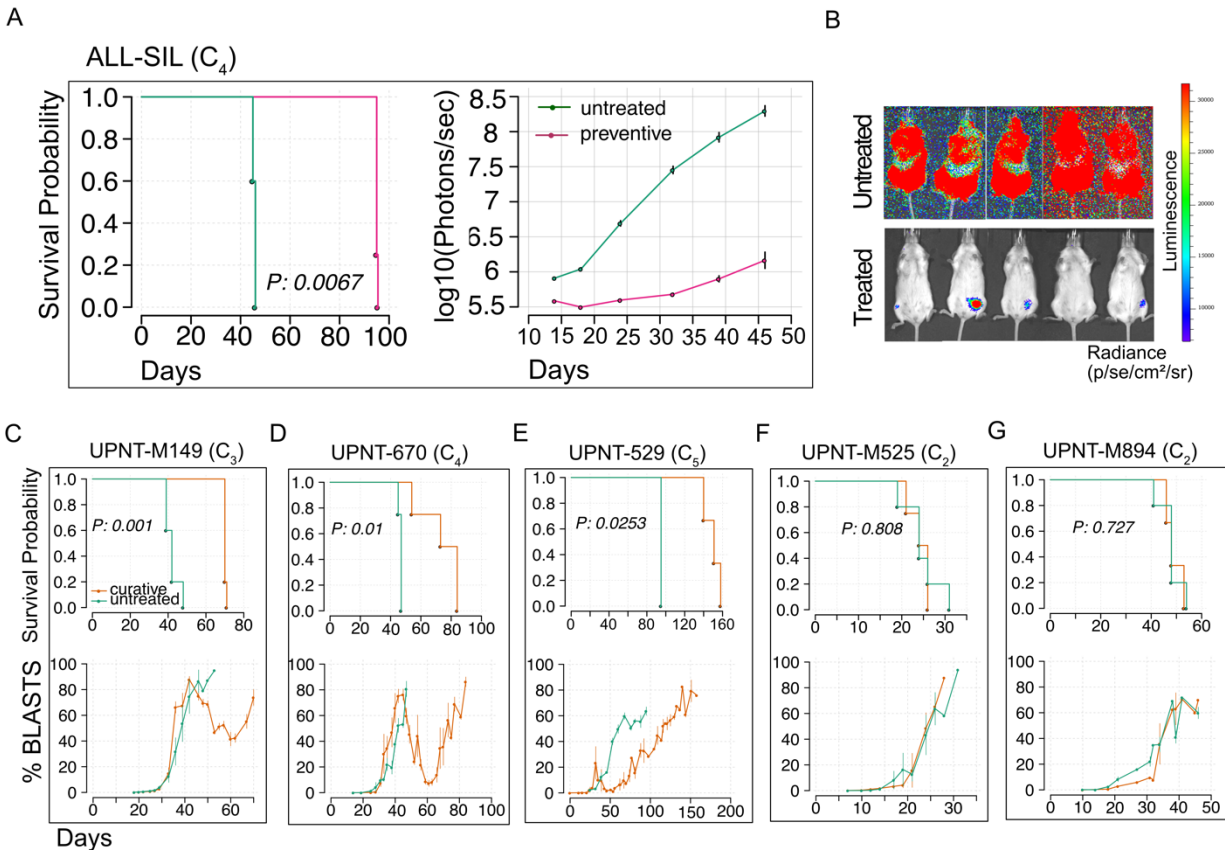
1 (C1-C5). Dark gray color indicates genes also found to be significantly differentially expressed  
 2 (FDR < 0.1; from panel C). Selected genes known to be associated with the T-ALL pathogenesis  
 3 are highlighted in red and annotated.

4 \*Promoter DNAm is estimated by averaging the beta values from probes within 1200 bp upstream  
 5 and 800 bp downstream of known TSS.

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 9 **Figure-5: Prognostic impact of DNA methylation. A.** Overall Survival (OS) for patients  
 10 classified into hypomethylated ( $C_{1+2}$ ), intermediate hypermethylated ( $C_{3+4}$ ), and  
 11 hypermethylated ( $C_5$ ) subgroups. Risk table indicates number of individuals at risk for a  
 12 given time point. *P*-values are derived from log-rank test. **B.** Event Free Survival (EFS) for  
 13 patients classified into  $C_{1+2}$ ,  $C_{3+4}$ , and  $C_5$  subgroups.



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2 **Figure-6: Efficacy of 5-Azacytidine treatment among T-ALL clusters.** 5-Azacytidine  
3 treatment in PDX mice models. Leukemic cells ( $n = 1,000,000$ ) were injected into NSG mice (day-  
4 0). **A.** Survival (left panel) and tumor burden measured by bioluminescence (right panel) for NSG  
5 mice injected with ALL-SILL cell line (predicted cluster C<sub>4</sub>;  $n = 5$  for untreated;  $n = 4$  for treated)  
6 after 2 weeks of preventive treatment with 5-Azacytidine (treatment initiation at day 2 post-  
7 injection, 5mg/kg/day for 5 days a week for two weeks) (red line) or NaCl (green line). Tumor  
8 burden was measured as a function of luminescence (Y-axis) from tumor cells at different time  
9 points (X-axis). **B.** Bioluminescence radiance signals (photons/cm<sup>2</sup>/sr) for mice treated with 5-  
10 Azacytidine or NaCl (untreated) at day 45 post-transplantation for ALL-SIL cell line.. **C-G.**  
11 Survival (top panel) and leukemic burden (%blast cells) measured by flow cytometry in peripheral  
12 blood (bottom panel) for five PDX mice models. **C.** UPNT-M149 (predicted C<sub>3</sub>;  $n = 4$  to 5 per  
13 group), **D.** UPNT-670 (cluster C<sub>4</sub>;  $n = 4$  to 5 per group), **E.** UPNT-529 (C<sub>5</sub>;  $n = 3$  per group), **F.**  
14 UPNT525 (cluster C<sub>2</sub>;  $n = 4$  to 5 per group) and **G.** UPNT-894 (cluster C<sub>2</sub>;  $n = 3$  to 5 per group)  
15 under untreated (NaCl; green line) or treated for 2 weeks with 5-Azacytidine in a curative-like  
16 manner (when blasts count reached 1% in blood, 5mg/kg/day for 5 days a week for two weeks)  
17 (orange line). *P*-values are calculated by comparing untreated group with rest of the groups using  
18 log-rank test.

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1 **Table 1: Characteristics of the 143 T-ALL patients<sup>^</sup>**

Characteristic	Value
Median age at study entry (range) – year	29.9 (16.3-59.1)
Sex ratio (Male/Female) – no.	107/36
T-cell Receptor subsets analyzed – no./total no. (%)	
Immature (IM0. IMδ. IMγ)	33/127 (26)
IMβ/pre-αβ	66/127 (52)
TCRαβ+	14/127 (11)
TCRγδ+	14/127 (11)
Early T-cell precursor (ETP) Immunophenotype – no./total no. (%)	25/125 (20)
High risk patients* – no./total no. (%)	61/143 (43)
Oncogenetic category – no./total no. (%)	
<i>TLX1</i>	28/137 (20)
<i>TLX3</i>	19/137 (14)
<i>SIL-TAL1/TAL1</i> -neoenhancer	17/137 (12)
<i>CALM-AF10</i>	6/137 (4)
None of the above	67/137 (49)
HOXA deregulation <sup>+</sup> – no./total no. (%)	
<i>Cis</i>	7/127 (6)
<i>Trans</i>	17/127 (13)
Unknown	11/127 (9)
Mutations in epigenetic factors – no./total no. (%)	
<i>DNMT3A</i>	20/143 (14)
<i>IDH1</i>	3/143 (2)
<i>IDH2</i>	6/143 (4)
<i>TET2</i>	7/143 (5)
<i>TET3</i>	4/143 (3)
Early response – no./total no. (%)	
Prednisone response	80/143 (56)
Bone marrow response	78/140 (56)
Complete remission	134/143 (94)

<sup>^</sup>Percentages may not total 100 because of rounding up.

\*High risk: *NOTCH1/FBXW7*<sup>WT</sup> OR *NOTCH1*<sup>mut</sup> + [*KRAS, NRAS, PTEN*]<sup>mut</sup>

<sup>+</sup>Cis: *HOXA* over expression under the influence of TCRβ enhancer

Trans: *HOXA* over expression under the influence of *SET-NUP214, MLLT10* or MLL fusion

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**Table 2: Clinical characteristics of the three prognostic subgroups**

	<b>C(1+2)</b>	<b>C(3+4)</b>	<b>C(5)</b>	<b>P-value<sup>†</sup></b>
	<b>N= 48</b>	<b>N=63</b>	<b>N=32</b>	
<b><i>Clinical Subsets Analyzed</i></b>				
Median age in years (range)	26.2 (16.3-59.1)	30.5 (16.4-57.2)	31.4 (18.8-59)	0,3
age >45 years- no./total no. (%)	6/48 (13%)	6/63 (10%)	5/32 (15%)	0,67
Sex ratio, Male/Female- no.	38/10	46/17	23/9	0,7
WBC (G/L), median (range)	69.9 (0.9-604.4)	37 (4.1-645)	31.2 (2.2-241.6)	0,3
CNS involvement- no./total no. (%)	7/48 (15%)	8/63 (13%)	5/32 (16%)	0,9
<b><i>Early Response</i></b>				
Prednisone response- no./total no. (%)	26/48 (54%)	44/63 (70%)	9/32 (28%)	<b>0,001</b>
Bone marrow response- no./total no. (%)	30/45 (67%)	41/63 (65%)	7/32 (22%)	<b>&lt;0,001</b>
MRD (TP1) <10-4- no./total no. (%)	18/23 (78%)	33/39 (85%)	8/21 (38%)	<b>0,001</b>
Complete remission- no./total no. (%)	44/48 (92%)	61/63 (99%)	29/32 (94%)	0,4
WBC (G/L), white blood cells; CNS, central nervous system; MRD (TP1), post-induction minimal residual disease; †Fisher's exact test or Mann-Whitney tests were used where appropriate.				

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1 **Supplementary Material**

2 **Epigenetic blueprint identifies poor outcome and hypomethylating agent-responsive T-**  
3 **ALL subgroup**

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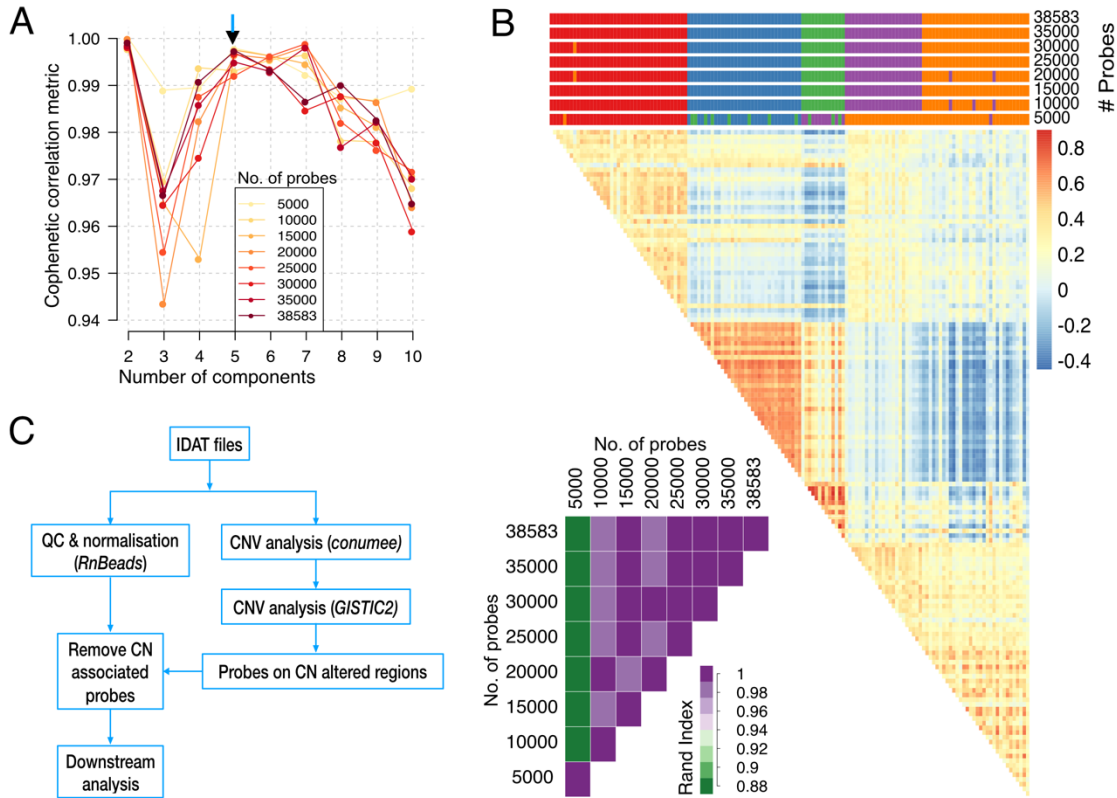
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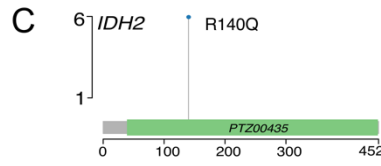
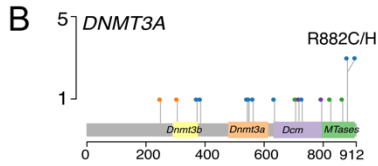
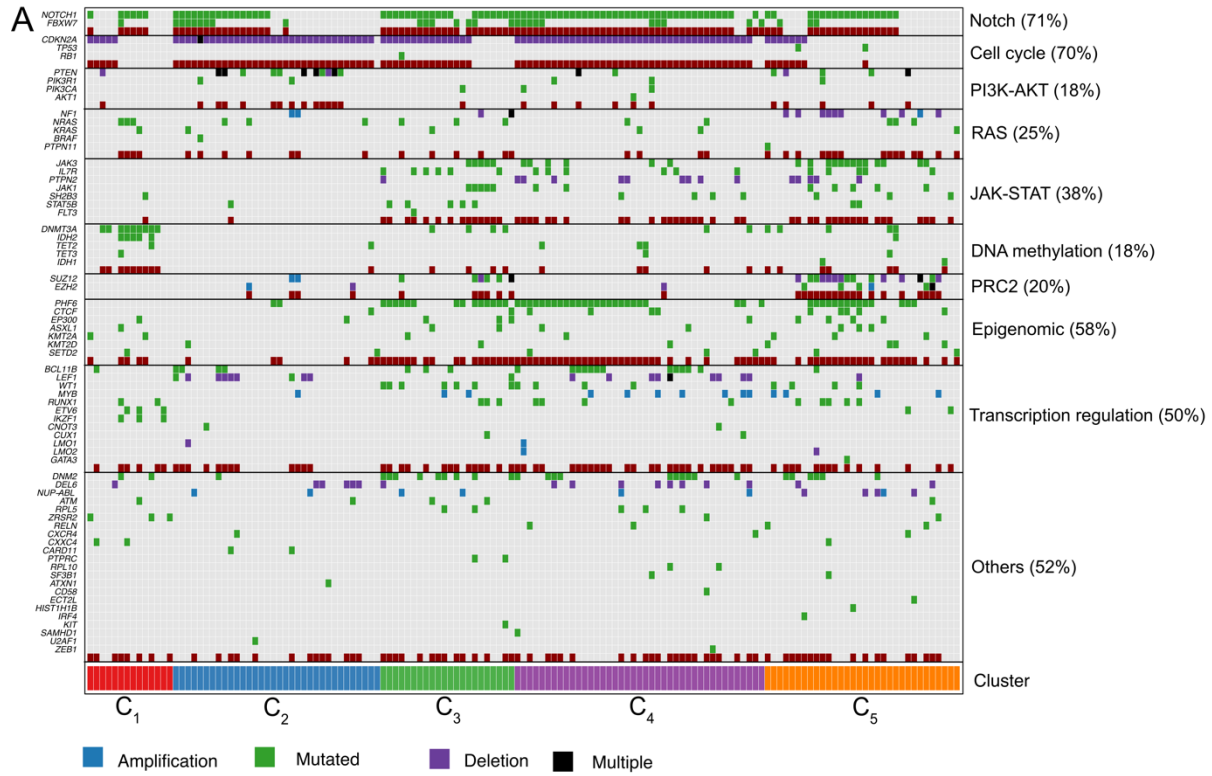
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30 **Table of Contents:**

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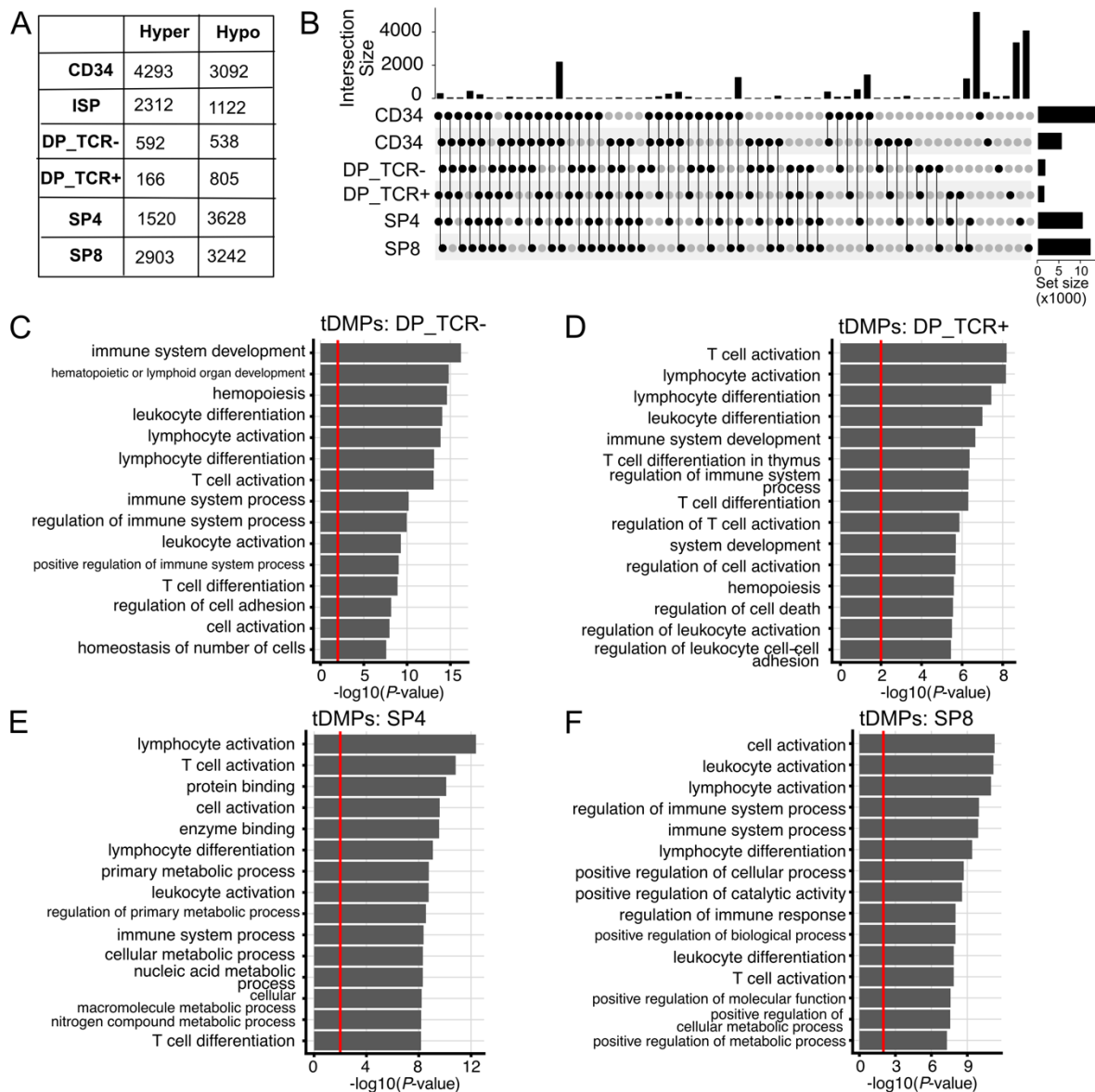


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**Supplementary Figure-S1: Identification of epigenetic clusters.** **A.** Cophenetic correlation (Y-axis) measured for a range of values (2...10, X-axis). Optimum value is chosen at which the correlation value reaches maximum followed by no-change or decrease in correlation metric. Same step was performed for varying number of probes as represented by the lines with color gradient. Arrowhead represents the optimal value chosen for downstream analysis ( $N = 5$ ). **B.** Cluster stability was measured by re-running clustering with  $n=5$  for different number of probes as indicated in the top annotation bar. Heatmap represents spearman-correlation coefficient between samples. Inner panel shows pairwise Rand-index values which indicates similarity between two clustering results. **C.** Pre-processing and QC steps involved in analyzing raw Illumina EPIC arrays. R packages used in particular steps are mentioned within parenthesis in italics.

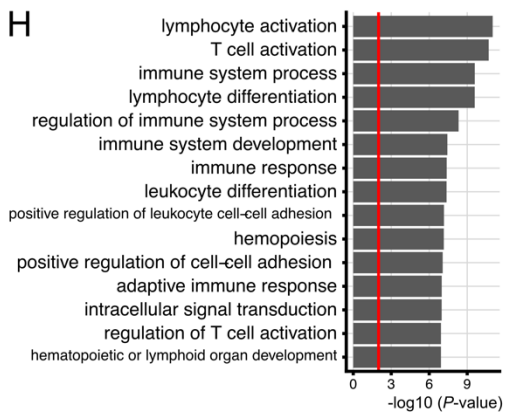
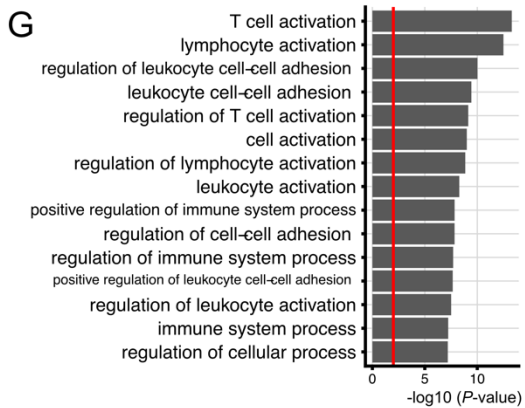
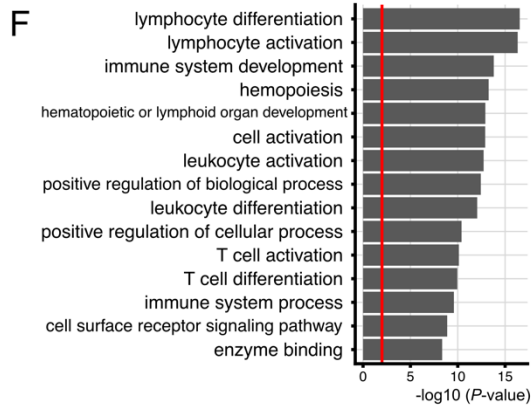
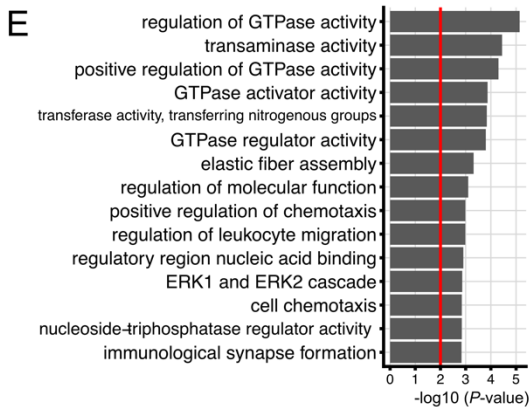
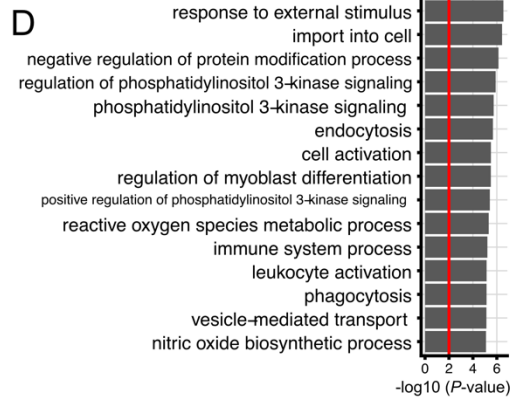
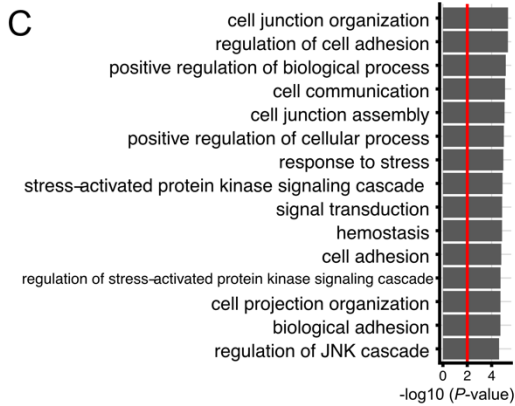
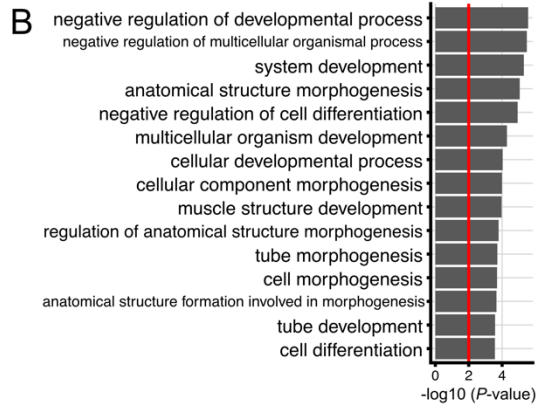
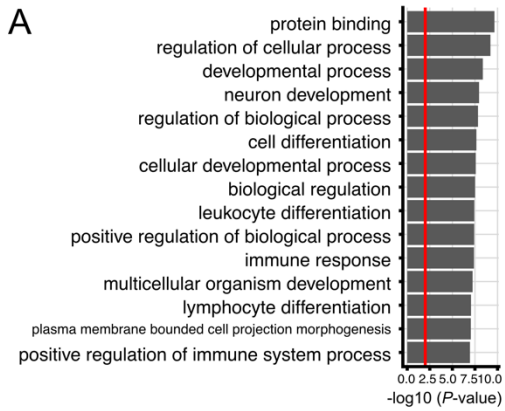


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3 **Supplementary Figure-S2: Genomic landscape of adult T-ALL.** **A.** Oncoplot depicting genetic alterations for the  
4 targeted panel of genes known to be frequently altered in T-ALL. Each row represents a gene and each column  
5 represents a sample. Genes are grouped according to the pathway as annotated to the right. Samples are sorted  
6 according to the clusters - indicated by the bottom annotation bar. Cells are color coded for mutation and copy-number  
7 status. **B and C.** Lollipop plot for *DNMT3A* (B) and *IDH2* (C). Recurrent R882 and R140 mutational hotspots in  
8 *DNMT3A* and *IDH2* are named.  
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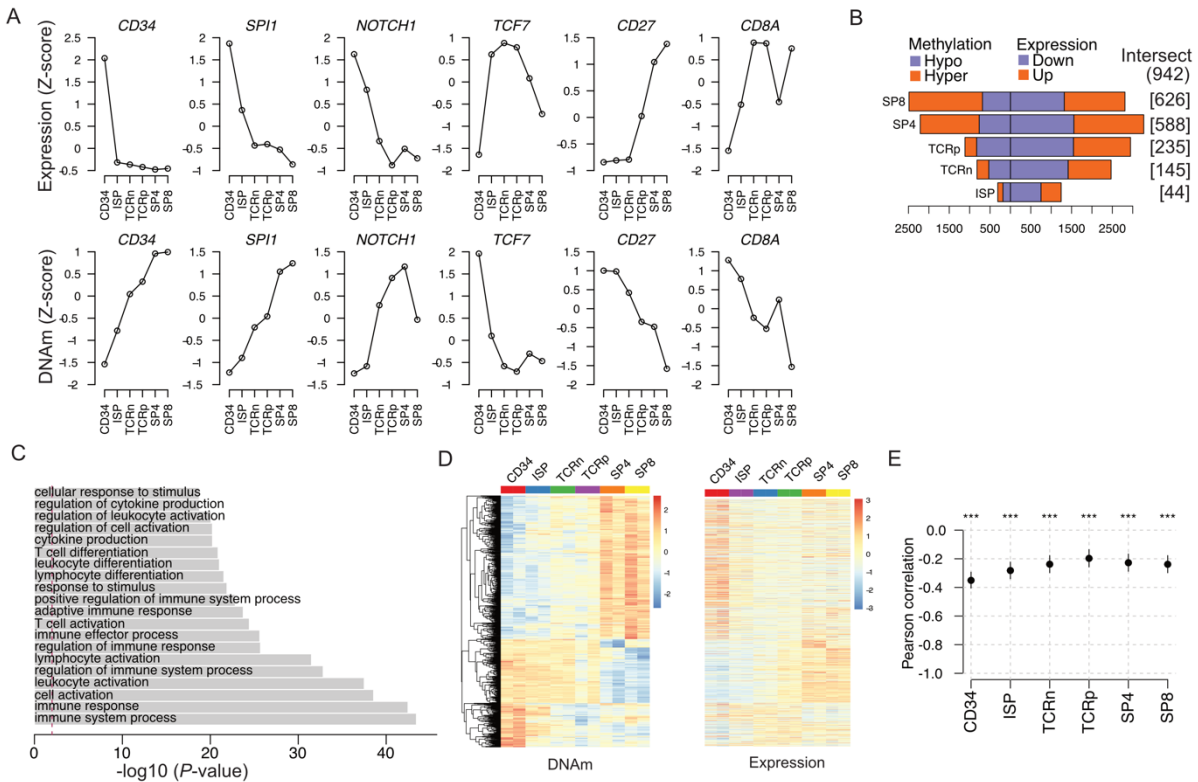
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**Supplementary Figure-S3: Differentially Methylated Probes associated with T-cell maturation (tDMPs).** **A.** Number of hyper- and hypo methylated tDMPs identified for each thymic cell type at various T-cell maturation stages. **B.** Upset plot showing overlap of tDMPs between T-cell subtypes. **C-F.** Gene ontology terms enriched for tDMPs associated with DP\_TCR- (C), DP\_TCR+ (D), SP4 (E), and SP8 T-cell subtypes (F). Vertical red bar indicates  $P = 0.001$  (Hypergeometric test).



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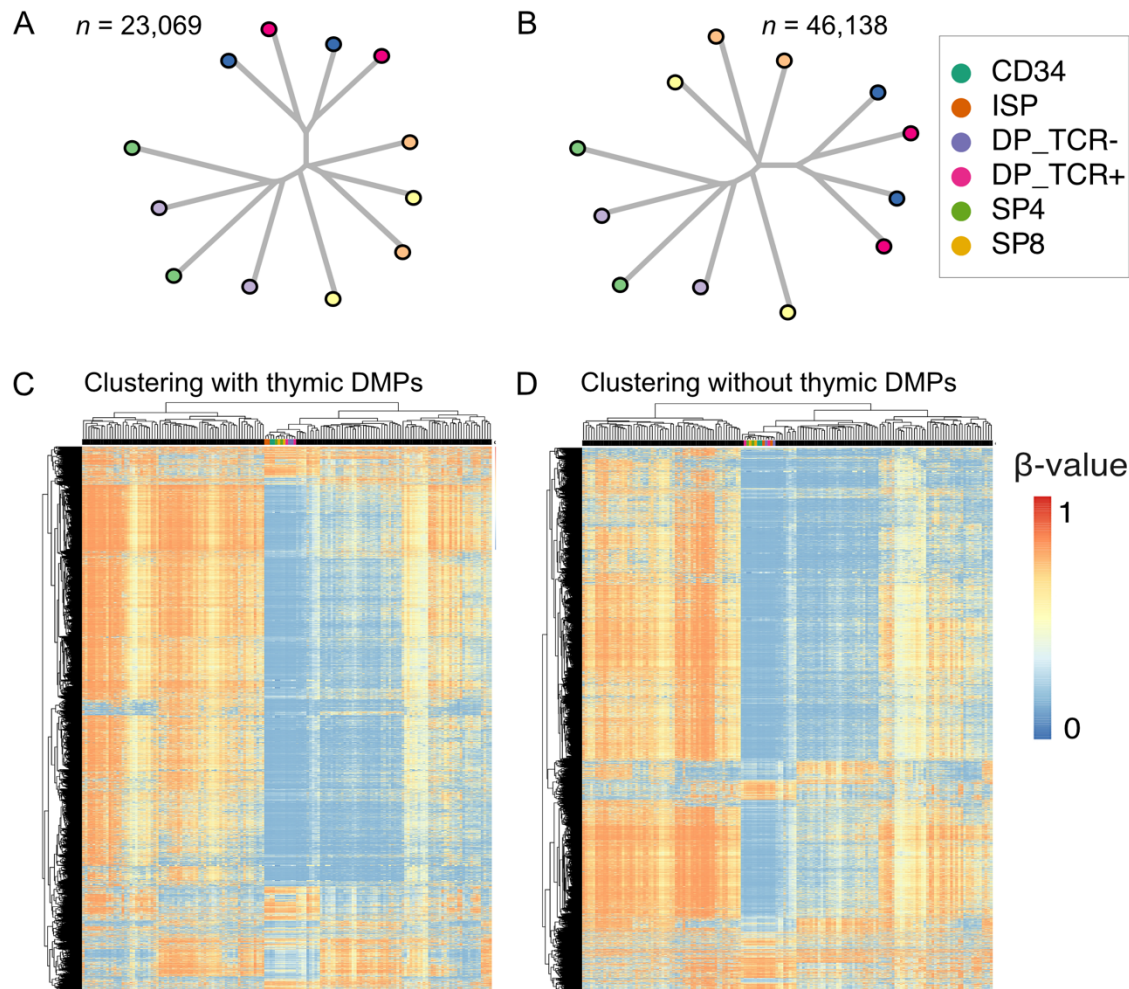
**Supplementary Figure-S4: Characterization of Differentially Methylated Probes associated with T-cell maturation (tDMPs) based on methylation dynamics. A-H.** Gene ontology terms enriched among tDMPs classified into 8 subgroups (tDMP1-tDMP8 respectively). Vertical red bar indicates  $P = 0.001$  (Hypergeometric test).



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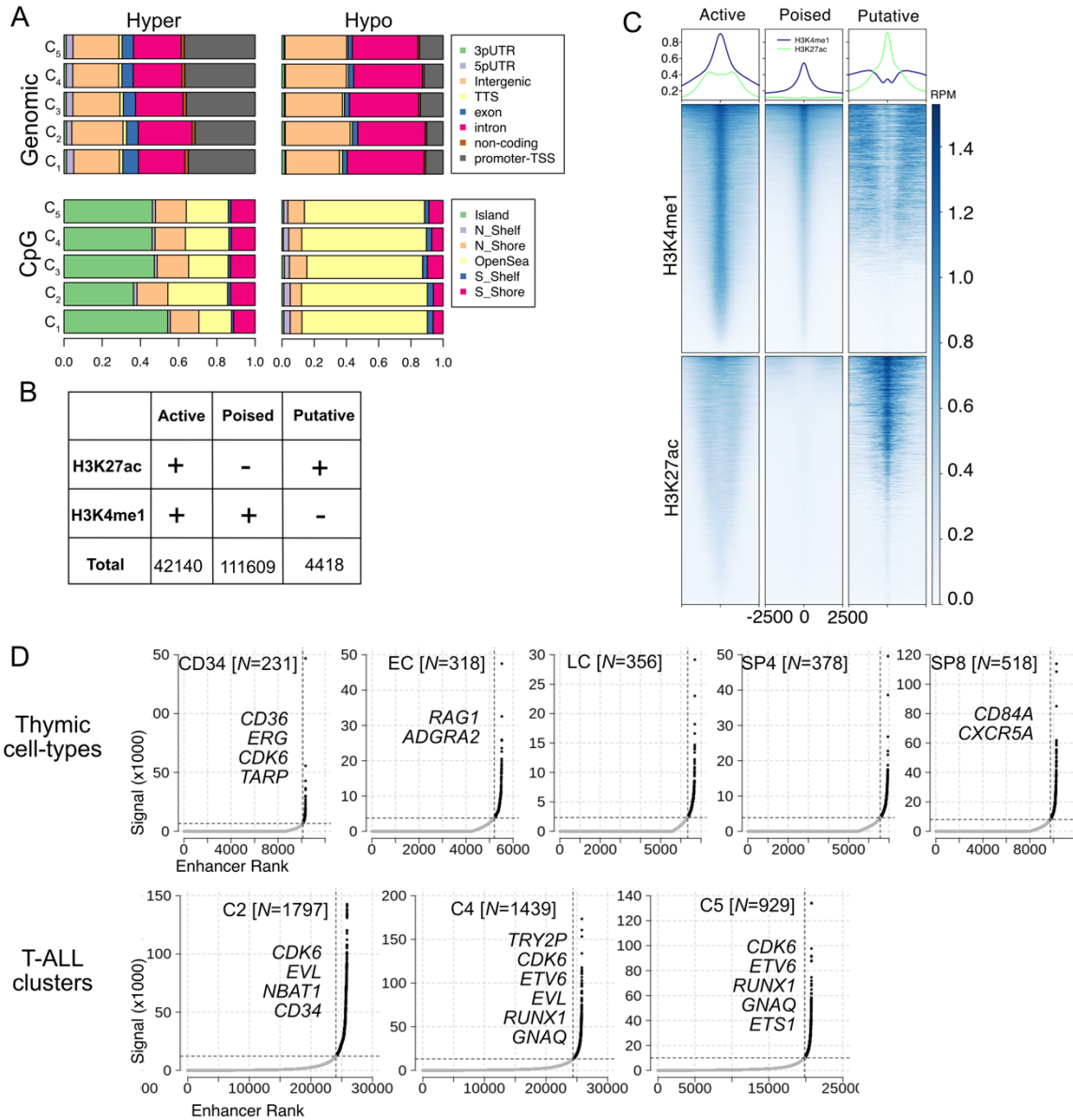
**Supplementary Figure-S5: Gene expression dynamics during Thymopoiesis A.** Gene expression profiles of selected marker genes and their corresponding promoter DNAm dynamics associated with the specific thymic cell types. Centered and scaled data are plotted. (Gene expression data obtained from gene expression omnibus dataset with accession number GSE151081). **B.** Number differentially methylated promoters, and differentially expressed genes for each mature thymic cell type compared to CD34 positive ETP cells. Number in parenthesis indicate common genes showing differential expression as well as differential promoter DANm.  $N = 942$  indicates unique genes from all 5 cell types. **C.** Gene ontology terms associated with the common genes which show both differential promoter methylation and expression ( $N = 942$ ). **D.** Heatmaps of promoter DNAm and their corresponding gene expression profiles indicate inverse correlation as quantified by Pearson correlation (**E**). \*\*\*  $P < 0.001$ ; Bars indicate 95% confidence interval of correlation coefficient.





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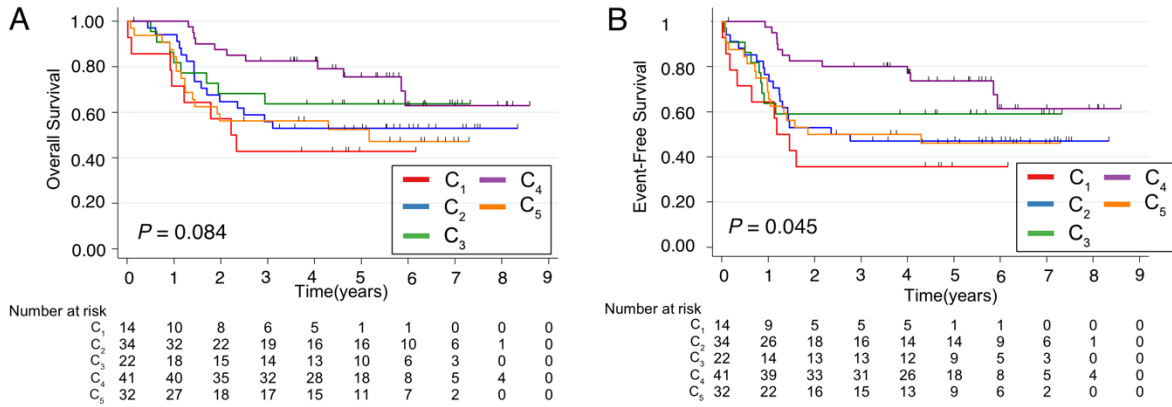
**Supplementary Figure-S6: Influence of thymic maturation associated Differentially Methylated Probes (tDMPs).** **A.** Unsupervised T-cell phylogenetic tree constructed from randomly selected probes ( $n = 23,069$  corresponding to number of unique tDMPs identified during T-cell development) from EPIC arrays fail to infer known T-cell developmental trajectories. **B.** Unsupervised T-cell phylogenetic tree constructed from randomly selected probes ( $n = 46,138$  corresponding to twice the number of unique tDMPs identified during T-cell development) from EPIC arrays fail to infer known T-cell developmental trajectories. **C and D.** Unsupervised clustering (top 5% of most variable methylation probes) of normal thymic subpopulations and T-ALL samples with (C) and without (D) tDMPs associated with T-cell maturation respectively. T-ALL samples are annotated in black in top annotation bar.



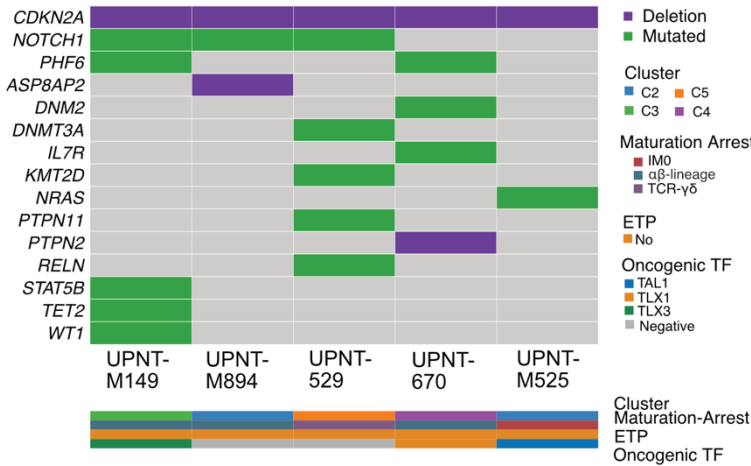
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**Supplementary Figure-S7: Defining normal and disease associated enhancers.** **A.** CpG and genomic annotations of hyper and hypo differentially methylated probes identified in each cluster compared to pooled normal thymic cells. **B.** Number of active, poised, and putative enhancers identified based on the presence or absence of H3K4me1 and H3K27ac histone marks in Thymic cell types. **C.** ChIP-seq binding profiles of H3K4me1 and H3K27ac histone marks for three distinct regulatory genomic regions (Active, Poised and Putative enhancers) in CD34+ thymic cells. Regulatory regions are displayed as 5 kb regions centered around the peak. Top line plot shows average signal density whereas bottom heat maps display ChIP-seq signal for individual peaks. Color gradient reflects the density of ChIP-seq signal. **D.** Super Enhancers (SEs) identified for each thymic subpopulation (top panel), and T-ALL clusters (bottom panel) respectively. Key SE associated genes are highlighted in italics. SEs are highlighted in black whereas typical enhancers

1 are in gray; EC = Early Committer [CD3<sup>-</sup>CD4<sup>+</sup>CD8<sup>+</sup>]; LC = Late Committer [CD3<sup>+</sup>CD4<sup>+</sup>CD8<sup>+</sup>];  
 2 SP4 = Single CD4 Positive [CD4<sup>+</sup>], SP8 = Single CD8 Positive [CD8<sup>+</sup>].  
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 6 **Supplementary Figure-S8: Overall Survival (OS) and Event Free Survival (EFS) of**  
 7 **methylation clusters. A and B. OS (A) and EFS (B) for five epigenetic clusters (C<sub>1</sub>-C<sub>5</sub>). P-values**  
 8 **are estimated from log-rank test.**  
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 11 **Supplementary Figure-S9: Key genetic alterations and cluster associations of the xenografted**  
 12 **samples.**  
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**Supplementary tables:**

- **Supplementary Table S1:** Significantly mutated genes in every cluster compared to rest of the clusters (Related to Figure 1H). (XLSX)
- **Supplementary Table S2:** Differentially methylated probes identified in each of the normal thymic cell-types (Related to Figure-2). (XLSX)
- **Supplementary Table S3:** Differentially methylated probes identified in each of the normal thymic cell-types classified into 8 subgroups based on methylation dynamics (Related to Figure-2D, E, and Supplementary Figure S4). (XLSX)
- **Supplementary Table S4:** Genes which are both differentially expressed and showing a differential promoter methylation in normal thymic cell types (Related to Supplementary Figure S5B). (XLSX)
- **Supplementary Table S5:** Differentially methylated probes found in each cluster along with the genomic annotations (Related to Figure 3A). (XLSX)
- **Supplementary Table S6:** Super and Typical Enhancers identified in normal thymic cell-types, and in T-ALL clusters (Related to Figure 3D, and Supplementary Figure S7D). (XLSX)
- **Supplementary Table S7:** Significantly enriched TF motifs detected within 100 base pair vicinity of hypo-methylated probes located within the super or typical enhancer regions from T-ALL clusters (Related to Figure 3F). (XLSX)
- **Supplementary Table S8:** Differentially expressed genes in cluster compared to total thymus (Related to Figure 4C). (XLSX)

Univariate and multivariate analysis						
EFS	Univariate			Multivariate		
	HR	95%CI	p	HR	95%CI	p
Age*	1.03	( 1.00 ; 1.05 )	0.019	1.03	( 1.01 ; 1.06 )	0.004
Log(WBC)*	1.28	( 0.84 ; 1.95 )	0.243	-	-	-
Prednisone response	0.55	( 0.34 ; 0.89 )	0.016	0.67	( 0.37 ; 1.21 )	0.18
Bone marrow response	0.62	( 0.38 ; 1.02 )	0.06	0.70	( 0.39 ; 1.26 )	0.234
CNS involvement	1.74	( 0.95 ; 3.20 )	0.073	2.11	( 1.14 ; 3.93 )	0.018
C(3+4) (baseline)	1	-	-	1	-	-
C(1+2)	2.02	( 1.14 ; 3.58 )	0.016	2.19	( 1.22 ; 3.94 )	0.009
C(5)	1.93	( 1.02 ; 3.66 )	0.045	1.37	( 0.68 ; 2.77 )	0.38
OS	HR	95%CI	p	HR	95%CI	p
Age*	1.03	( 1.00 ; 1.05 )	0.018	1.03	( 1.01 ; 1.06 )	0.009
Log(WBC)*	1.26	( 0.82 ; 1.94 )	0.291	-	-	-
Prednisone response	0.55	( 0.33 ; 0.92 )	0.024	0.57	( 0.33 ; 0.99 )	0.046
Bone marrow response	0.67	( 0.40 ; 1.12 )	0.129	-	-	-
CNS involvement	1.86	( 0.98 ; 3.51 )	0.056	1.92	( 1.01 ; 3.63 )	0.046
C(3+4) (baseline)	1	-	-	1	-	-
C(1+2)	1.93	( 1.06 ; 3.52 )	0.033	1.92	( 1.05 ; 3.54 )	0.036
C(5)	2.04	( 1.05 ; 3.97 )	0.035	1.56	( 0.77 ; 3.16 )	0.22

**Supplementary Table S9:** Univariate and Multivariate analyses of EFS and Overall Survival: \*continuous variables. Abbreviations: EFS: event-free survival, OS: overall survival, HR: hazard ratio, CI: confidence interval, CNS: central nervous system

GRAALL(2003/05)	Study Cohort (N=143)	Non-investigated (N=194)	P-value
Baseline characteristics			
Male	107	132	0.18
Median Age (range) - Years	29.9 (16.3-59.1)	34.1 (16.8-59.5)	0.01
Median WBC count (Range)	40.5 (0.9-645.0)	19.8 (0.9-573.0)	<0.001
CNS involvement – no/total (%)	20/143 (14%)	15/194 (8%)	0.07
Outcome characteristics			
Prednisone response – no/total (%)	79/143 (55%)	126/194 (65%)	0.09
CR -- no/total (%)	134/143 (94%)	181/194 (93%)	0.99
Allo-SCT - - no/total (%)	53/143 (37%)	48/194 (30%)	0.20
5y-EFS (95%CI)	55% (47-63)	57% (50-64)	0.72
5y-OS (95%CI)	60% (51-68)	67% (60-73)	0.30

**Supplementary Table S10:** Clinical characteristics and outcome of the study cohort versus non-investigated patients (GRAALL-2003/05 trials). WBC, white blood cell count; CNS, central nervous system; CR, complete remission; EFS, event-free survival; OS, overall survival; CI, confidence interval; Allo-SCT, allogeneic stem cell transplantation.