Core Transcriptional Regulatory Circuit Controlled by the TAL1 Complex in Human T Cell Acute Lymphoblastic Leukemia

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SUMMARY

The oncogenic transcription factor TAL1/SCL is aberrantly expressed in over 40% of cases of human T cell acute lymphoblastic leukemia (T-ALL), emphasizing its importance in the molecular pathogenesis of T-ALL. Here we identify the core transcriptional regulatory circuit controlled by TAL1 and its regulatory partners HEB, E2A, LMO1/2, GATA3, and RUNX1. We show that TAL1 forms a positive interconnected autoregulatory loop with GATA3 and RUNX1 and that the TAL1 complex directly activates the MYB oncogene, forming a positive feed-forward regulatory loop that reinforces and stabilizes the TAL1-regulated oncogenic program. One of the critical downstream targets in this circuitry is the TRIB2 gene, which is oppositely regulated by TAL1 and E2A/HEB and is essential for the survival of T-ALL cells.

INTRODUCTION

In human T cell acute lymphoblastic leukemia (T-ALL), the normal molecular events contributing to thymocyte development are interrupted by genetic lesions that induce arrested differentiation, dysregulated proliferation, and aberrant survival, leading to clonal expansion of the fully transformed leukemic cells (Armstrong and Look, 2005; Look, 1997). TAL1/SCL, one of the most prevalent oncogenic transcription factors in T-ALL, is overexpressed in 40%–60% of T-ALL cases, owing to chromosomal translocations, an activating interstitial deletion (SIL-TAL1 deletion), or undefined trans-acting mechanisms (Brown et al., 1990; Ferrando and Look, 2000; Ferrando et al., 2002). Results from gene expression analysis have demonstrated that TAL1 overexpression is associated with a differentiation block at the CD4+CD8+ double-positive (DP) stage of thymocytes in both human tumors and murine models (Ferrando et al., 2002; Larson et al., 1996; Tremblay et al., 2010).

TAL1 is a class II basic helix-loop-helix (bHLH) transcription factor that forms an obligate heterodimer with the class I bHLH E-proteins, which include TCF3/E2A and TCF12/HEB (Hsu et al., 1991, 1994). In hematopoietic cells, TAL1 regulates the
transcription of its target genes by binding to E-box motifs and nucleating a large complex that includes the E-proteins, GATA family members, and several non-DNA-binding LMO proteins (Lécuyer et al., 2002; Wadman et al., 1997; Xu et al., 2003). TAL1 expression is normally silenced during early thymocyte development (Herblot et al., 2000); thus, its expression and the regulatory complex it recruits to its direct target genes are clearly aberrant in DP thymocytes. By contrast, E-proteins act as homo- or heterodimers to regulate gene expression (Kee, 2009) and are required for thymocyte development in a stage-specific manner (Bernard et al., 1998; Herblot et al., 2000). A number of genes have been implicated as direct targets of TAL1 and its regulatory partners in human T-ALL (Bernard et al., 1998; Herblot et al., 2000; Ono et al., 1998; Palii et al., 2011b; Palomero et al., 2006). Studies in murine models have shown that E2A and HEB are highly dosage dependent, in that haplo-insufficiency for either gene accelerates the onset of TAL1-induced T-ALL (O’Neil et al., 2004). Hence, although E2A and HEB are critical for the formation of the TAL1 transcriptional complex, a change in the relative dosage of each member can affect the onset and severity of leukemia, through mechanisms that remain to be elucidated.

Recently, several groups have identified high-level expression of genes encoding multiple transcription factors in the TAL1-overexpressing T-ALL subgroup, including RUNX1, MYB, NKK3-1, and ETS family members, such as ERG and ETS1 (Clappier et al., 2007; Kusy et al., 2010; Lahortiga et al., 2007; O’Neil et al., 2007; Thoms et al., 2011). However, it has been difficult to integrate them into a unified network of altered gene regulation that promotes thymocyte transformation. The present study was designed to elucidate the role of TAL1 in this aberrant transcriptional circuitry.

RESULTS

TAL1 Binding Is Highly Overlapping in Multiple T-ALL Cell Lines and Primary T-ALL Cells

We generated high-resolution maps of the genomewide occupancy of TAL1 by chromatin immunoprecipitation coupled to massively parallel DNA sequencing (ChIP-seq; Table S1 available online). Multiple TAL1-expressing T-ALL samples were analyzed, which included two cell lines (Jurkat and CCRF-CEM; Figures S1A and 1B) and two “primagraft” samples (“Prima 2” and “Prima 5”) derived from primary T-ALL cells expanded in immunocompromised mice without any exposure to in vitro culture. Aberrant expression of TAL1 in both primagrafts and the CCRF-CEM cell line is due to an ~90-kb SIL-TAL deletion. The activity of the TAL1 antibody used was validated by ChIP followed by western blot analysis with a different specific antibody (Figure S1C). Of note, TAL1 was enriched in chromatin precipitated with anti-HEB and anti-E2A antibodies (Figure S1C) that do not cross-react (Figure S1D), consistent with its ability to heterodimerize with each of these E-proteins.

We first examined the results for known TAL1 target genes, including CD69, TCRA enhancer, and NKK3-1 (Bernard et al., 1998; Kusy et al., 2010; Palii et al., 2011b), and detected TAL1 binding at sites in the regulatory regions of each gene (Figure 1A). Our results agree with previously reported TAL1 binding sites except for NKK3-1 (Kusy et al., 2010), where we found that TAL1 occupied a region consistent with a candidate distal enhancer in each of the four T-ALL samples but not the previously identified promoter region (Figure 1A, right). We then investigated the relative overlap of high-confidence TAL1-bound regions across all four T-ALL samples. Pairwise comparisons of the top 200 TAL1-bound regions showed a high degree of agreement, compared with the results for NRSF-bound regions in Jurkat cells as a negative control (Figure 1B). Nearest neighbor analysis confirmed this result (Figure 1C). When we compared the relative distribution of TAL1-bound regions with the locations of protein-coding genes, the majority of the bound regions were within the gene body and intergenic regions of known protein-coding genes, consistent with the location of enhancer elements, as opposed to sites in the proximal or distal promoter (Figure 1D). Hence, the TAL1-binding sites identified in multiple T-ALL cell samples overlapped substantially at known and candidate regulatory elements.

We next sought to identify DNA motifs that were statistically overrepresented within 200 base pairs (bp) of the peak of TAL1 binding in each T-ALL sample. Four transcription factor binding motifs were enriched in TAL1-bound regions, including E-box (5’-CAG/GTG-3’), GATA (5’-AGATAA-3’), RUNX (5’-TGTGG TC-3’), and motifs recognized by the ETS family of transcription factors (5’-GGAAA-3’) (Figure 1E). This complement of motifs is highly similar to the TAL1 motifs identified by ChIP-seq in normal murine hematopoietic progenitors and red cells (Kassouf et al., 2010; Wilson et al., 2010) and in human hematopoietic cells (Novershtern et al., 2011; Palii et al., 2011b; Tijssen et al., 2011). We expect that TAL1 is likely coregulating its target genes in T-ALL in a complex analogous to that identified in normal hematopoietic cells.

TAL1 Complex Controls Genes Involved in T Cell Homeostasis

To identify the regulatory network controlled by the TAL1 transcriptional complex in human T-ALL cells, we performed ChIP-seq analysis for TAL1 and its regulatory partners HEB, E2A, GATA3, RUNX1, and LMO1/2 in Jurkat and CCRF-CEM cells, which express high levels of LMO1 and LMO2, respectively (Figures S1A–S1C). The genomic sites occupied in T-ALL samples showed remarkable concordance for TAL1, its regulatory partners, and the transcriptional coactivator CBP, as illustrated for a known TAL1 complex target, the TRCA enhancer (Bernard et al., 1998; Hollenhorst et al., 2007) (Figure 2A). The E2A-bound regions we identified included a number of E2A target genes reported in murine thymocytes, including PTCRA, NOTCH3, RAG1, RAG2, and GFI1 (Miyazaki et al., 2011).

Examination of the overlap among regions enriched for TAL1, HEB, E2A, LMO1/2, GATA3, or RUNX1 revealed that TAL1 binds to the majority of HEB- and E2A-enriched regions, which frequently overlap with the LMO1/2-, GATA3-, and RUNX1-enriched regions (Figures 2B and S2A). We next investigated the relative binding overlap of these factors within high-confidence enriched regions (Table S2), identifying three different classes of regulatory elements in both Jurkat (Figure 2C) and CCRF-CEM cells (Figure S2B). One showed concordant enrichment for multiple TAL1 complex members (Group 1), a second was predominantly occupied by GATA3 alone (Group 2), and a third was mainly occupied by RUNX1 alone (Group 3).
Several groups have reported that the TAL1 complex frequently contains ETS family members (e.g., ETS1) in multiple hematopoietic cell types (Palli et al., 2011b; Soler et al., 2010; Wilson et al., 2010). By comparing the ChIP-seq binding profiles for TAL1 complex members determined in our study with those described by three other groups (Hollenhorst et al., 2009; Palii et al., 2011b; Valouev et al., 2008), we determined that ETS1 occupancy correlates with the binding of other members of the TAL1 complex, as compared with two non-ETS transcription factors, SRF and NRSF (Figure S2 C). For TAL1 complex members determined in our study with those described by three other groups (Hollenhorst et al., 2009; Palii et al., 2011b; Valouev et al., 2008), we determined that ETS1 occupancy correlates with the binding of other members of the TAL1 complex, as compared with two non-ETS transcription factors, SRF and NRSF (Figure S2 C). ERG, an ETS family member, is also highly expressed and regulated by the TAL1 complex in human T-ALL cells (Thoms et al., 2011).

Analysis by the de novo motif discovery method, based on regions we have segregated into three groups, identified E-box, GATA, and RUNX motifs, as well as known motifs for the ETS family of transcription factors in Group 1, GATA and ETS motifs in Group 2, and RUNX, ETS, and SP1 motifs in Group 3 (Figure 2D). The distribution of consensus motifs for E-box, GATA, RUNX, and ETS motifs was centered under the peak of ChIP-seq enrichment within these three groups (Figure S2D). Moreover, the majority of enriched regions in Group 1 contained at least one E-box or one GATA motif within 200 bp of the center (n = 8,245/12,748 in Jurkat and n = 9,005/14,745 in CCRF-CEM). Many of the motifs enriched in E2A-bound regions had been identified in murine lymphocytes (Lin et al., 2010), where they also were frequently associated with ETS and RUNX binding sites.

To determine the dominant functions of the genes occupied by the TAL1 complex, we compared target genes (Table S3) to identify overrepresented functional groups (Figures S2E–S2G and Table S4). TAL1 complex targets were enriched in molecular pathways that regulate cell development, growth, and death, as well as those known to contribute to cancer and to hematological and immune diseases (Figures S2E and S2F). It is important to note that enriched genes include those regulating T cell development, differentiation, morphology, cell number, and activation (Figure S2G). These observations indicate that, in transformed thyocytes, the TAL1 complex sits at the apex of a network that drives aberrant proliferation, differentiation, and survival.

TAL1, GATA3, and RUNX1 Form a Positive Interconnected Autoregulatory Loop

It is important to note that we found that members of the TAL1 complex frequently occupy known and candidate regulatory regions of their own and each other’s genes (Figure 3A). For example, members of the TAL1 complex co-occupy enhancers that have been identified by others in normal hematopoietic cells, including the GATA3 3’ T cell-specific enhancer (Hosoya-Ohmura et al., 2011), the RUNX1 +23 enhancer (Nottingham et al., 2007) (Figure 3A), and the LMO2 –24 enhancer (Landy
downregulated (Figure 3C). Similarly, knockdown of Jurkat cells showed that GATA3 and RUNX1 were significantly regulated upon knockdown (Figure S3C and Table S5).

To further dissect the function of the TAL1 complex, we used two independent short-hairpin RNAs (shRNAs) to knockdown the level of TAL1 expression in T-ALL cell lines (Figure S3A). In this context, there was significant downregulation of a known target gene, ALDH1A2 (Ono et al., 1998), which was rescued by re-expression of the TAL1 cDNA (Figure S3B). Several cell surface markers related to T cell activation (CD69 and CD84) or cell survival in vivo (CD47) were also downregulated upon TAL1 knockdown (Figure S3C and Table S5). Analysis of gene expression changes after TAL1 knockdown in Jurkat cells showed that GATA3 and RUNX1 were significantly downregulated (Figure 3C). Similarly, knockdown of GATA3 or RUNX1 (Figure S3A) resulted in the coordinate downregulation of expression of each of these factors (Figure 3C). We observed the same relationships in CCRF-CEM cells (Figure S3D), except that knockdown of GATA3 or RUNX1 did not affect the levels of TAL1 expression, which was expected because in this cell line TAL1 expression is controlled by the SIL promoter. These alterations in expression after gene knockdown demonstrate the presence of a positive interconnected autoregulatory loop involving TAL1, GATA3, and RUNX1 and support the critical role of TAL1 overexpression in initiating the formation of the loop.

The knockdown of TAL1 in Jurkat cells reduced the growth rate of these cells (Figures 3D and S3E), consistent with our previous study using TAL1 shRNA #2 (Palmero et al., 2006) and published results of Pali and coworkers (Pali et al., 2011b). TAL1 shRNA #1 induced similar growth inhibition of multiple T-ALL cell lines expressing TAL1 (Figure S3F and Table S5). We also detected increased fractions of apoptotic cells after transduction with shRNA #1, but not with shRNA #2 (Figure S3G), indicating that higher levels of TAL1 knockdown are needed to detect cell death. Of note, knockdown of GATA3 and RUNX1 also inhibited cell growth and induced apoptosis (Figure 3D), indicating that each of these three components of the autoregulatory loop is required for cell growth and survival. Taken together, our results indicate that components of the TAL1 complex positively regulate each other in T-ALL and act to promote the growth and survival of T-ALL cells (Figure S3E), underscoring the importance of this positive interconnected autoregulatory loop in maintaining the malignant state.

Expression Levels of High-Confidence TAL1 Targets Classify T-ALL Subtypes

We next performed microarray gene expression analysis after knockdown of each transcription factor gene in Jurkat cells (Table S6). Gene set enrichment analysis (GSEA) revealed that genes enriched for TAL1 binding by ChIP-seq analysis were more likely to be downregulated upon TAL1 knockdown than
Figure 3. TAL1, GATA3, and RUNX1 Form a Positive Interconnected Autoregulatory Loop

(A) Gene tracks represent binding of TAL1, GATA3, RUNX1, and CBP at the TAL1 (right), RUNX1 (middle), and GATA3 (left) loci in Jurkat cells. See Figure 1A legend for details.

(B) Co-occupancy by TAL1, GATA3, and RUNX1 at the TAL1, RUNX1, and GATA3 gene loci in multiple T-ALL cells. Enrichment of regions indicated in panel A (TAL1 enhancer, RUNX1 +23, and GATA3 +280) in four T-ALL cell samples (Jurkat, CCRF-CEM, Prima 2, and Prima 5) was analyzed by ChIP-PCR. The NANOG promoter was used as a negative control. The error bars represent the SD of the fold enrichment. The red line represents the 2-fold enrichment detection for the negative control.

(C) mRNA (left) and protein (right) levels of TAL1, GATA3, and RUNX1 after knockdown (KD) of each of these factors in Jurkat cells. The data are means ± SD of duplicate experiments. *p < 0.05, **p < 0.01, and ***p < 0.001 by two-sample, two-tailed t test.

(D) Growth inhibition and apoptosis induction after knockdown of TAL1, GATA3, and RUNX1 in Jurkat cells. Cell viability was measured after 3 and 7 days of lentivirus infection. The growth rate (Day 7/Day 3) is reported as means ± SD percentage of that for control shRNAs (GFP and Luc) in triplicate experiments.
genes lacking TAL1 occupancy (Figure 4A). This difference was statistically significant (p < 2.2E-16 by the Kolmogorov–Smirnov test), indicating that TAL1 acts predominantly as a positive regulator of the expression of its direct target genes in T-ALL.

Further analyses were based on high-confidence TAL1 target genes (n = 302) that showed TAL1 binding and significant alterations in expression (p < 0.05 with an absolute log₂-fold change ≥ 0.24) upon TAL1 knockdown (Figure 4B and Table S7). Since the TAL1 gene was reduced by 1.89-fold, we were expecting modest but consistent expression changes in other target genes. The distribution of expression changes of genes selected was statistically different when compared to all genes (p < 2.2E-16; see also Figures S4A–S4C for details). The percentage of genes within the high-confidence targets occupied by TAL1 across the four T-ALL cells (Jurkat, CCRF-CEM, Prima 2, and Prima 5) showed that 90% of genes occupied in Jurkat cells were occupied by TAL1 in at least one of the other T-ALL samples (Figure 4C). To address whether the target genes that are directly regulated by TAL1 in Jurkat cells are similarly regulated in TAL1-positive T-ALL cells, we analyzed gene expression profiles in other TAL1-positive T-ALL cell lines and primary T-ALL samples. We observed consistent downregulation of selected TAL1 target genes upon TAL1 knockdown in two additional T-ALL cell lines (CCRF-CEM and RPMI-8402; Figure 4D). Principal-component analysis of gene expression levels in 75 primary T-ALL samples and seven BM samples based on the expression profile of high-confidence TAL1 target genes. Primary T-ALL samples were classified into three groups (TAL1/LMO, TLX, and HOXA) based on the genetic alterations reported in the original article (Homminga et al., 2011). The analysis was performed with a set of 238 genes that are bound by TAL1 and significantly downregulated after TAL1 knockdown (see Figure 4B, left). See also Figure S4 and Tables S6 and S7.

Apoptosis was analyzed at Day 4 after lentiviral infection by flow cytometric analysis of cells stained with AnnexinV-fluorescein isothiocyanate (FITC). The values are means ± SD of duplicate experiments. Asterisks denote p values as described for (C).

(E) Positive interconnected autoregulatory loop formed by TAL1, GATA3, and RUNX1. Genes are represented by rectangles, and proteins are represented by ovals.

See also Figure S3 and Table S5.

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when targets of RUNX1 were equally likely to be up- or downregulated regulator of their expressions in T-ALL. By contrast, direct knockdown (Figure 5A), implicating GATA3 as a positive GATA3 analyzed by GSEA, most of them were downregulated after in T-ALL cells. When genes enriched for GATA3 binding were and RUNX1 coordinately regulate gene expression with TAL1 An important question in this study was whether GATA3 is commonly found in T-ALL (Clappier et al., 2007; Lahortiga et al., 2007; O’Neil et al., 2007) (Figure S5 A). Interrogation of the effects of GATA3 or RUNX1 depletion on the expression of the 238 high-confidence TAL1 target genes revealed that the genes downregulated upon loss of TAL1 expression were generally also downregulated by the loss of GATA3 or RUNX1 (Figures S5C–S5E), implicating GATA3 as a positive regulator of their expressions in T-ALL. By contrast, direct targets of RUNX1 were equally likely to be up- or downregulated when RUNX1 was depleted (Figure 5B).

Interrogation of the effects of GATA3 or RUNX1 depletion on the expression of the 238 high-confidence TAL1 target genes revealed that the genes downregulated upon loss of TAL1 expression were generally also downregulated by the loss of GATA3 or RUNX1 expression (Figures S5C–S5E), indicating that TAL1 acts in concert with GATA3 and RUNX1 to positively regulate the majority of its direct target genes in T-ALL.

**MYB Oncogene Coordinately Regulates TAL1 Target Genes**

MYB overexpression, mediated in part through gene duplication, is commonly found in T-ALL (Clappier et al., 2007; Lahortiga et al., 2007; O’Neil et al., 2007) (Figure S5A). Interrogation of ChIP-seq data across the MYB locus indicated that MYB was a common target of the TAL1 complex in TAL1-positive T-ALL cell lines (Figure 6A), indicating that it is directly upregulated by the TAL1 complex due to the aberrant expression of TAL1. The TAL1-occupied regions included the known locus control region located 77 kb upstream of Myb in mice (Ramsay and Gonda, 2008) and a candidate regulatory element within intron 8 (+14) co-occupied by the TAL1 complex in T-ALL cells (Figure 6A). Co-occupancy of the TAL1 complex was observed at this candidate regulatory element in T-ALL primagrafts and cell lines by ChIP-PCR (Figure 6B). In all cases, MYB gene expression was sensitive to the reduction of multiple TAL1 complex members in Jurkat and CCRF-CEM cells (Figures 6C and S5B).

Since MYB is a known transcriptional regulator of normal and malignant hematopoiesis (Ramsay and Gonda, 2008), a reduction of its expression could indicate the transcriptional relationship between the TAL1 complex and this gene in T-ALL. We therefore performed knockdown analysis of MYB (Figure S5C), followed by microarray gene expression analysis. The result showed that many TAL1 targets were also significantly downregulated by MYB knockdown (Figures 6D and S5D), indicating that MYB not only is induced by TAL1 but also acts to coordinately upregulate overlapping sets of target genes controlled by TAL1. Thus, the MYB oncogene appears to reinforce the activities of the TAL1-regulated oncogenic network through a feed-forward circuit that maintains the gene expression program in T-ALL cells (Figure 6E).

**HEB and E2A Oppose Positive Regulation by TAL1 at Critical Target Genes**

Several groups have postulated that the ectopic expression of TAL1 in normal thymocytes may antagonize the physiologic activities of E2A or HEB in thymocyte development by recruiting them into the TAL1 complex, where they could deregulate key target genes (Bain et al., 1997; Herblot et al., 2000; O’Neil...
et al., 2004). Hence, we next interrogated the effects of HEB and E2A knockdown (Figure S6) on the expression of their direct target genes. GSEA revealed that genes enriched for HEB or E2A binding by ChIP-seq analysis could be either down- or up-regulated after knockdown of each gene (Figures 7A and 7B). As expected, 40% of the TAL1 target genes that were downregulated after TAL1 knockdown were also downregulated by the knockdown of either E2A or HEB (Figures 7C–7E, left). By contrast, 25% of the TAL1 target genes that were downregulated by TAL1 knockdown were upregulated by the loss of either E2A or HEB expression (Figures 7C–7E, right), indicating that they can act to repress gene expression in the absence of TAL1. Only 50 of the 238 genes that were downregulated after TAL1 knockdown were significantly upregulated after knockdown of HEB and/or E2A, and an even smaller group of seven TAL1 target genes showed the inverse relationship (Table S8).

**TRIB2 Is a Critical Target of TAL1 and Is Required for the Survival of T-ALL Cells**

We also conducted an inducible RNA interference screen (Ngo et al., 2006) in two TAL1-positive T-ALL cell lines (Jurkat and CCRF-CEM) and identified four genes that were required for T-ALL growth among the high-confidence targets: STAT5A, TNFSF4, PI3KC2B, and TRIB2 (Table S9). An especially attractive candidate target of the TAL1 complex is TRIB2 (Figure 8A), whose expression was downregulated by TAL1 knockdown and upregulated by E2A knockdown in multiple TAL1-positive T-ALL cell lines (Figure 8B). After 3 weeks of culture, Jurkat or CCRF-CEM cells expressing two different shRNAs targeting TRIB2 were depleted (Figure 8C). This result was validated by knockdown of TRIB2 using another shRNA (Figure 8D), which was partially rescued by the ectopic expression of the TRIB2 cDNA (Figure 8E). TRIB2 knockdown inhibited the growth of additional TAL1-positive T-ALL cell lines (Figure 8F) and induced apoptosis in each cell line (Figure 8G) but did not affect the cell cycle phase distribution (Figure S7), indicating that this factor is required for the survival of T-ALL cells. A reasonable hypothesis is that TRIB2 is transcriptionally repressed by E-proteins and the aberrant expression of TAL1 by translocation or intrachromosomal rearrangement upregulates TRIB2 expression by heterodimerizing with E2A and HEB, thus actively opposing their repressive effects on the TRIB2 locus (Figure 8H).

**DISCUSSION**

We have identified a set of transcriptional regulators that collaborate with TAL1 to generate a “core” regulatory circuit that contributes to the initiation and maintenance of human T-ALL. Critically, we found that TAL1, GATA3, and RUNX1 co-occupy the MYB locus (Figure 8H). This result was validated by knockdown of MYB using another shRNA (Figure 8D), which was partially rescued by the ectopic expression of the MYB cDNA (Figure 8E). MYB knockdown inhibited the growth of additional TAL1-positive T-ALL cell lines (Figure 8F) and induced apoptosis in each cell line (Figure 8G) but did not affect the cell cycle phase distribution (Figure S7), indicating that this factor is required for the survival of T-ALL cells. A reasonable hypothesis is that MYB is transcriptionally repressed by E-proteins and the aberrant expression of MYB by translocation or intrachromosomal rearrangement upregulates MYB expression by heterodimerizing with E2A and HEB, thus actively opposing their repressive effects on the MYB locus (Figure 8H).
malignant transformation. Indeed, such regulatory structures have been shown to reinforce and increase the stability of gene expression programs (Alon, 2007), which, in turn, act to establish and maintain critical cell states, such as pluripotency in embryonic stem cells (Young, 2011).

Expression of GATA3 and RUNX1 is required in normal T-lineage commitment to CD4 or CD8 single-positive cells, respectively (Collins et al., 2009; Ho et al., 2009). TAL1-sustained upregulation of GATA3 and RUNX1 may therefore contribute to the differentiation block at the DP stage. Thus, overexpression of RUNX1 appears to contribute to thymocyte transformation in TAL1-positive T-ALL, in marked contrast to its role as a tumor suppressor whose loss of function promotes the onset of acute myeloid leukemia (AML) and myelodysplastic syndromes. Two groups have also recently reported inactivating RUNX1 mutations in the early thymocyte precursor (ETP) subgroup of T-ALL (Della Gatta et al., 2012; Grossmann et al., 2011). ETP leukemia is distinct from TAL1-positive T-ALL, which generally shows a block at the DP stage of thymocyte development and involves different aberrant molecular pathways leading to transformation (Coustan-Smith et al., 2009; Gutierrez et al., 2010; Zhang et al., 2012). Thus, despite the presence of inactivating RUNX1 mutations in ETP T-ALL, our data show that, in T-ALLs blocked in a later DP stage of thymocyte development, RUNX1 serves as a key member of an interconnected autoregulatory loop involved in reinforcing and stabilizing the malignant cell state.

We also identified an oncogenic transcription factor gene, *MYB*, as a direct target of TAL1 that is expressed at high levels in TAL1-positive T-ALL cases. It integrates with the TAL1-controlled transcriptional network through a positive feed-forward loop that likely acts to stabilize the TAL1 oncogenic program, similar to mechanisms first identified in model organisms (Alon, 2007). The *Myb* gene was reported as a *Tal1* target in murine hematopoietic progenitor cells (Wilson et al., 2009), which may reflect an important regulatory module shared by leukemic and normal stem cells. MYB has recently been implicated in the control of aberrant self-renewal programs in AML (Zuber et al., 2011), reinforcing its potential importance as the target of a feed-forward regulatory motif mediated by the TAL1 complex in T-ALL. This transcriptional regulatory circuit is also implicated in normal hematopoiesis (Novershtern et al., 2011) and presumably contributes to the establishment and stability of the transformed state in TAL1-overexpressing thymocytes.

It will be important to confirm and extend our results with shRNA knockdown as we have done with ChIP-seq analysis in primary T-ALL cells. Several groups have reported success with shRNA gene knockdown in primary T-ALL cells (Gerby et al., 2010; Kusy et al., 2010; Paliii et al., 2011a, 2011b). These procedures involve both improved lentivirus production using the new-generation plasmids (Paliii et al., 2011a, 2011b) and the new pseudotyping vector, resulting in interleukin 7 (IL-7)-displaying lentiviral vectors that promote efficient gene transfer into primary T cells (Gerby et al., 2010; Kusy et al., 2010; Verhoeven et al., 2003). We are now attempting to optimize these procedures for shRNA transduction into primary T-ALL cells explanted from our primagraft models. When established, this approach should be helpful in tracing the regulatory circuits in de novo T-ALL leukemias.

We also present a comprehensive analysis of the gene set that is differentially regulated by TAL1 and its partners, HEB and E2A. Many of the direct targets of these three interacting proteins are coordinately upregulated as a consequence of binding to key regulatory regions. Only a small subset of these
Mammalian genes of the Tribbles family (TRIB1, TRIB2, and TRIB3) encode proteins that contain pseudokinase domains that are unable to directly phosphorylate target proteins but rather appear to act as adaptors that negatively regulate key cellular signaling pathways (Yokoyama and Nakamura, 2011). Overexpression of TRIB2 by retroviral transduction in murine hematopoietic stem cells identified it as an oncogene that contributes to AML (Keeshan et al., 2006). Our data indicate that TRIB2 is required for the survival of T-ALL cells. Until our analysis, there had been no evidence implicating TRIB2 in T-ALL pathogenesis, although this role was not entirely unexpected given the expression of this gene as a target of NOTCH1 (Wouters et al., 2007). Since TRIB2 is a direct target for upregulation by both the NOTCH1 complex in T-ALL (right).

See also Figure S7 and Table S9.
and TAL1 transcription factors, our data suggest that a progressive increase in its expression levels contribute to the collaboration between aberrant TAL1 expression and mutually activated NOTCH1 in the pathogenesis of T-ALL.

EXPERIMENTAL PROCEDURES

T-ALL Cell Samples

Human T-ALL cell lines were maintained in RPMI-1640 medium (Invitrogen, Carlsbad, CA, USA) supplemented with 10% fetal bovine serum (Sigma-Aldrich, St Louis, MO, USA), L-glutamine, and penicillin/streptomycin (Invitrogen). Diagnostic T-ALL samples were obtained with informed consent and institutional review board (IRB) approval from children treated in Dana-Farber Cancer Institute Study 05-01 and were used with existing IRB approval by the University of California, San Diego (UCSD), Human Research Protections Program, titled “Protocol 070678: Permission to Collect Blood and/or Bone Specimens and/or Tumor Samples and/or Saliva from Patients with Hematologic Malignancies.” The Human CD34+ T-ALL cells were transplanted into Rag2−/−γ−/− mice to propagate the cells as “primagrags.”

ChIP

ChIP was performed according to previously described methods (Lee et al., 2008). The antibodies and detailed ChIP conditions can be found in the Supplemental Experimental Procedures. For ChIP-seq analysis, Solexa/Illumina sequencing and analysis were conducted according to the protocol described by Marson et al. (2008).

shRNA Knockdown Analysis

shRNA sequences were cloned into the lentiviral vector pLKO.1-puro. Each construct was cotransfected into 293T cells with delta 8.9 and VSV-G using FuGENE 6 reagent (Roche, Indianapolis, IN, USA). Supernatants containing the lentiviruses were collected, filtered, and added to T-ALL cell lines in the presence of polybrene. The level of knockdown was verified by qRT-PCR for RNA or by western blot.

RNA Extraction, cDNA, and Expression Analysis

We extracted mRNA by Trizol (Invitrogen) followed by column purification using the RNeasy Mini Kit (Qiagen, Valencia, CA, USA). Purified RNA was reverse-transcribed using QuantiTect (Qiagen). Quantitative real-time qPCR was performed on the AB7300 Detection System (Applied Biosystems, Foster City, CA, USA) using gene-specific primers and Power SYBR Green PCR Master Mix (Applied Biosystems).

Microarray Expression Analysis

Total RNA samples from two biological replicates performed in Jurkat cells were used to assess gene expression change for two target shRNAs per transcription factor versus two control shRNA performed in duplicate on Affymetrix HG U133 2.0 plus microarrays. The detailed analysis can be found in the Supplemental Experimental Procedures. GSEA (Broad Institute, Cambridge, MA, USA) was performed for direct targets identified by ChIP-seq by comparing control samples with knockdown samples. The genes, which are direct TAL1 targets identified by ChIP-seq based on a significant gene expression change upon shRNA knockdown (absolute log2-fold change ≥ 0.24; p < 0.05), were defined as the high-confidence TAL1 targets and used as a gene set.

ACCESSION NUMBERS

Expression data and ChIP-seq can be found at http://www.ncbi.nlm.nih.gov/geo/ under superseries accession number GSE29181.

SUPPLEMENTAL INFORMATION

Supplemental Information includes seven figures, nine tables, and Supplemental Experimental Procedures and can be found with this article online at http://dx.doi.org/10.1016/j.ccr.2012.06.007.

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REFERENCES


