Variable Retention of Differentiation-specific DNA Replication Timing in Human Pediatric Leukemia

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ABSTRACT

Human B-lineage precursor acute lymphoid leukemias (BCP-ALLs) comprise a group of genetically and clinically distinct disease entities with features of differentiation arrest at known stages of normal B-lineage differentiation. We previously showed BCP-ALL cells display unique and clonally heritable DNA-replication timing (RT) programs; i.e., programs describing the variable order of replication of megabase-scale chromosomal units of DNA in different cell types. To determine the extent to which BCP-ALL RT programs mirror or deviate from specific stages of normal human B-cell differentiation, we transplanted immunodeficient mice with quiescent normal human CD34+ cord blood cells and obtained RT signatures of the regenerating B-lineage populations. We then compared these with RT signatures for leukemic cells from a large cohort of BCP-ALL patients. The results identify BCP-ALL subtype-specific features that resemble specific stages of B-cell differentiation and features that appear associated with relapse. These results suggest the genesis of BCP-ALL involves alterations in RT that reflect clinically relevant leukemia-specific genetic and/or epigenetic changes.

SUMMARY

Genome-wide DNA replication timing profiles of >100 pediatric leukemic samples and normally differentiating human B-lineage cells isolated from xenografted immunodeficient mice were generated. Comparison of these identified potentially clinically relevant features that both match and deviate from the normal profiles.

INTRODUCTION

B-lineage precursor acute lymphoid leukemia (BCP-ALL) cells from pediatric patients retain many characteristics of normal B-cell precursors including clonotypic immunoglobulin rearrangements (Korsmeyer et al., 1983) and a phenotype suggestive of an "arrested" state of pre-B cell differentiation (Felix and Poplack, 1991). However, the genesis of BCP-ALL has also been shown to be a multi-step process, in which genomically and epigenomically variant subclones continuously arise and evolve in ways that may impact their response to therapeutic interventions (Beishuizen et al., 1994; Gawad et al., 2012) by continuously altering mechanisms regulating cell proliferation, survival, and differentiation (Wong et al., 2012). However, the degree to which apparently abnormal features of the leukemic cells may also reflect transient cell states that occur during normal hematopoietic cell differentiation and are then fixed or reactivated, is unclear (Ntziachristos et al., 2013). Most cancers can be traced to a single genetically altered somatic cell whose progeny, at least initially, retain many of its characteristics and properties. BCP-ALL is considered a prototype of this situation as most of the leukemic cells retain a close resemblance both biologically and phenotypically to a narrow window in the B-cell differentiation process (Felix and Poplack, 1991). In the specific case of *TCF3-PBX1* BCP-ALL, the therapeutic effect of inhibiting the pre-B-pre-BCR signaling complex is believed to reflect the arrest of the leukemic cells at an intermediate/late stage of B-lineage differentiation where cells are dependent on the pre-BCR signaling pathway (Bicocca et al., 2012; Geng et al., 2015). On the other hand, many cancers, including pediatric BCP-ALL, also contain genetic mutations in epigenetic regulatory pathways (Ntziachristos et al., 2013) likely to produce aberrant epigenetic states with broad biological consequences or even a generalized epigenetic instability (Hansen et al., 2011). These findings suggest that some malignant cells may acquire mechanisms normally used by stem cells to relax the stringency of chromatin states and make them more permissive to the activation of multiple lineage differentiation programs (Pujadas and Feinberg, 2012; Timp and Feinberg, 2013).

These possibilities raised interest in examining DNA replication timing (RT) programs in normal and leukemic B-lineage cells as a surrogate indicator of how cellular states might be altered in BCP-ALL. Changes in RT affect at least half of the genome during the normal development and differentiation of tissues (Hiratani et al., 2008; Ryba et al., 2010; Hiratani et al., 2010) and RT profiles are robustly characteristic of a given cell type with consistent changes between even closely related cell types (Pope et al., 2010; Hiratani et al., 2009; Rivera-Mulia et al., 2015;

Dileep et al., 2015). RT profiles are also closely related to the large-scale 3D organization of chromosomes with the units of RT showing a close correspondence to so-called topologically-associating domains (TADs) that are organized into separate spatial compartments in the nucleus historically identified as early and late replicating chromatin (Ryba et al., 2010; Pope et al., 2014). Early replication also correlates with transcription, but there are many exceptions and it is more likely that RT reflects large scale chromatin architectural features that are indirectly related to transcription (Rivera-Mulia and Gilbert, 2016a; b). A recent analysis of RT profiles in cells from individuals with premature aging diseases identified “RT signatures” that distinguish these from cells that have undergone “natural” aging. This observation, in turn, led to the discovery of the first molecular marker common to progeroid diseases of different genetic origin; thus demonstrating the ability of RT analysis to identify novel biomarkers not identified by standard transcriptome analyses (Rivera-Mulia et al., 2017a; 2018).

In a previous report, we described disease-specific features in the RT profiles of BCP-ALL leukemic cells (Pope et al., 2014; Ryba et al., 2012) and showed these remained stable in serially passed patient-derived xenografts (PDX) in immunodeficient mice (Sasaki et al., 2017). Comparison of RT differences between cells from 19 BCP-ALL patients and 26 human cell types in our RT database (replicationdomain.org) further revealed that most of the differences between these populations were in regions of DNA that are affected by RT changes during normal differentiation (Ryba et al., 2012). Here we investigated the relationship of different categories of BCP-ALL cells to developmentally similar proliferating cells at different stages of normal human B-lineage precursor differentiation using cells from immunodeficient mice engrafted with human cord blood (CB) cells as a source of these in a proliferating mode (Laurenti et al., 2013; Miller et al., 2017). Genome-wide RT measurements obtained on these cells, as well as co-isolated proliferating myeloid cells, and T-cells activated to divide *in vitro*, were then compared to RT profiles generated from 106 patients’ leukemic cells and various related cell lines (**Supplemental Table 1)**. The results identify new features of specific normal cell types, and establish the existence of leukemia-specific RT signatures that include previously unknown associations with specific BCP-ALL subtypes and their responses to therapy.

RESULTS

RT signatures of normal human hematopoietic cell types

Determination of RT changes that occur during the neonatal differentiation of primitive normal human hematopoietic cells, including early stages of B-cell differentiation, requires these cells to be proliferating under *in vivo* conditions that mimic those operative physiologically. To meet these constraints, we transplanted normal human CD34+ CB cells into sub-lethally irradiated Non-obese diabetic-*Rag1*$^{-/-}$*IL2Rγc*$^{-/-}$ (NRG) mice and isolated human CD34+CD38-, CD34+CD19+, CD34-CD19+ and total CD34+ (mixed progenitors) cells by fluorescent activated cell sorting (FACS) from their bone marrow and spleens 2-3 months later (**Figure 1A**). Biological replicates consisted of cells regenerated from different pooled sources of CB cells. The CD34+CD19+ and CD34-CD19+ cells obtained in one of the replicate experiments were also sorted for the presence or absence of *ROR1* expression. As expected (Hudecek et al., 2010), CD34+CD19+ROR1+ cells were rare allowing only 300 cells from the early and late S-phase fractions to be obtained. Analysis of such low numbers of cells required the development of a modified protocol in which the cells were simultaneously sorted for surface marker expression and DNA content, from which good quality Repli-seq profiles were then also obtained.

RT profiles were generated by Repli-chip (Ryba et al., 2011) or Repli-seq (Marchal et al., 2018) as described in the Methods and illustrated in **Figure 1B** and **1C**. RT signatures specific to differentiating B-cells were derived by comparisons with similarly generated RT profiles obtained for other normal human hematopoietic cells, including our previously reported data for granulopoietic and erythroid cells generated from adult mobilized peripheral blood cells, stimulated adult T-cells, and a series of Epstein Barr virus (EBV)-immortalized B-cell lines (Rivera-Mulia et al., 2015) with a stringent quality control cut-off (Marchal et al., 2018; Ryba et al., 2011).

We then derived RT “signatures” using a pipeline that identifies regions of the genome that replicate at times unique to each of 26 normal human cell types (Rivera-Mulia et al., 2015). In brief, after removing reads from the sex chromosomes, remaining mappable reads for each cell type were first divided into 55,940 50-kb segments each of which was then assigned an RT value. This showed an expectedly high correlation in the genome-wide RT programs of all the different hematopoietic cell types compared (**Supplemental Figure S1A**). We then applied an unsupervised K-means clustering analysis to all 50-kb genomic segments that changed their RT from a $\log_2$ ratio ≥0.5 to ≤–0.5 (or vice versa) (Rivera-Mulia et al., 2015) to identify features

that replicate significantly differently between cell types (p-value <$2x10^{-16}$ using T-tests). This identified 10,350 variable segments (18.5% of the genome), consistent with results for other closely related normal cell types (Rivera-Mulia et al., 2015) and different BCP-ALL leukemias (Ryba et al., 2012; Sasaki et al., 2017). Correlation matrix (**Supplemental Figure S1B**) and dendrogram (**Figure 1D**) analyses of all samples using only these RT-variable regions confirmed the close matching of data from separately analyzed biological replicates (cells generated from different donor pools) and the clustering of samples by hematopoietic cell type to yield 14 RT signatures (**Figure 1D and Supplemental Figure S1C-D**). Interestingly, some of the RT-variable regions displayed multiple RT switches between sequential early stages of normal human B-cell differentiation. Gene expression changes for each of these signatures, derived from published human hematopoiesis transcriptome data (Laurenti et al., 2013) were generally coordinated with their RT changes (**Figure 1D-F)**. Moreover, multiple known key regulators of hematopoiesis were found in each signature with coordinated changes in RT and gene expression; for example, *HMGA2, KIT* and *HOX* genes that are required for self-renewal activity in hematopoietic stem cells (Copley et al., 2013; Edling and Hallberg, 2007); *CREB5* linked to quiescence of early precursors; *RUNX2* required for HSC differentiation (De Bruijn and Dzierzak, 2017); and *CD79B* is required for the pro-B/pre-B transition (Benschop and Cambier, 1999) (**Figure 1D-F and Supplemental Table S2**). Together, these results indicate that RT features can discriminate different phenotypically distinguished hematopoietic cell types.

BCP-ALL-specific RT signatures

Genome-wide RT profiles generated on a panel of **97** BCP-ALL patient samples and cell lines, and more limited numbers of pediatric AML and T-ALL patient samples and cell lines are shown in **Supplemental Table S1**. Although our standard E/L method (**Figure 2A**) performs well on samples of freshly obtained leukemic cells from patients (Ryba et al., 2012) or transplanted mice (Sasaki et al., 2017), the numbers of viable cells or cells able to incorporate BrdU that we obtained from many of the frozen banked samples were very low, consistent with S-phase specific replication fork collapse (Falk et al., 2018). Therefore, to analyze these we first sorted unlabeled S-phase and G1 phase cells by FACS based on their DNA content (**Figure 2A**). We then used microarray or whole genome sequencing (WGS) to obtain the relative copy numbers of each 50-kb sequence in S and G1 and derived RT profiles from the fact that earlier replicating sequences are higher in copy number than late replicating sequences in S phase, but are at equal copy number in G1 phase (**Figure 2A; S/G1 Repli-seq**) (Gilbert, 2010; Sasaki et al.,

2017). Since the dynamic range of G1/S data is inherently <2-fold, a large number of sequenc-
125 ing reads is needed to quantify copy numbers (160 million per sample), making it expensive as a routine assay. Thus, we designed a set of capture oligonucleotides spaced evenly throughout the genome (see Materials and Methods) that significantly reduced the sequence depth required to cover the breadth of the genome (10^7 mappable reads) and also enabled high resolution RT profiles to be obtained, scaled and normalized sufficiently to identify RT differences
130 between the different closely related samples examined here (**Figure 2B**). Clustering of all samples demonstrated a high concordance between replicate datasets and confirmed a lack of bias from the different methods used to generate the full set of RT profiles on the leukemic cells analyzed (**Figure 2C**).

Comparison of the RT programs from the leukemia patient samples and cell lines with one
135 another using the same pipeline revealed 3,540 50-kb variable segments (6.3% of the autosomal genome) that showed significant differences and generated 14 RT signatures (**Figure 3A**). Six of these were linked to patients and cell lines containing the t(1;19) translocation that encodes the TCF3-PBX1 fusion protein (#1 to #6 in **Figure 3A** and **3B).** *TCF3* (also known as E2A) is a transcription factor required for normal B- (and T-) cell differentiation and has been
140 implicated in many lymphoid malignancies (Santos et al., 2011; Xu et al., 2013). *PBX1* is a proto-oncogene with a critical role in hematopoiesis and lymphopoiesis (Sanyal et al., 2007). The *TCF3-PBX1* fusion gene is believed to be a driver mutation in the BCP-ALLs in which it is found (Nourse et al., 1990). The #1 and #2 RT signatures were early replicating and #6 was late replicating uniquely in the *TCF3-PBX1*-positive samples. The fact that all 3 *TCF3-PBX1*-
145 positive cell lines shared the same RT signatures as the patients' *TCF3-PBX1*-positive leukemic cells underscores the epigenetic stability of their identified RT signatures. Interestingly, signatures #3, #4 and #5 sub-stratified the *TCF3-PBX1* samples, with signatures #3 and #5 found to be shared with an established cell line from an AML patient (MOLM1), but not with any of the two other AML patients' samples. In addition, most of the regions in RT signature #1 that were
150 early replicating uniquely in the *TCF3-PBX1*-positive patients' cells were also very late in both T-ALL and AML cells. However, these commonalities between T-ALL and AML cells may not be driven by similarities known to exist between AML and Early T-cell precursor T-ALL (ETP ALL) (Zhang et al., 2012), since T-ALL sample 10-799 is not categorized as ETP ALL (**Supplemental Table S1**). Moreover, RT signatures #3 and #5, which were common to the AML and
155 some *TCF3-PBX1*-positive samples, also distinguished AML from T-ALL.

The other RT signatures (#8-#14) were found in other groups of patient samples. RT signature #8 was early replicating in a group of BCP-ALL samples of unknown genotype, and #9 was shared between these and certain AML samples. RT signatures #10, #11, and #12 identified known subsets of BCP-ALL samples. Signature #13 was late in one case and #14 was late in 2 others. The exclusivity of these RT signatures for specific subsets of patients can be further probed by clustering all patient samples using only the 50-kb chromosomal segments (features) found in each of the RT signatures. In fact, clustering analysis of patient samples using the chromosomal segments from RT signature #1 identified the patients carrying the *TCF3-PBX1* translocation (**Figure 3C**). Heat maps and dendrograms for each RT signature from **Figure 3A** are shown in **Supplemental Figure S2**.

Interestingly, RT signatures #1, #2 and #6 (**Figure 3A**) identified two BCP-ALLs exhibiting an RT signature of *TCF3-PBX1*-positive cells despite the samples being designated as "not otherwise specified" (NOS; cannot be classified into typical genetic subtypes including those with a t[1;19] karyotype). To determine whether these samples might have an undetected *TCF3-PBX1* fusion, we performed reverse transcriptase (RT)-PCR on mRNA isolated from these samples. Interestingly, this revealed a *TCF3-PBX1* fusion mRNA in sample PALCRG but not in sample 10-795 (**Figure 3D**), which also did not contain a *TCF3-TFPT* fusion gene (**Supplemental Table S1**) (Brambillasca et al., 1999). Next, we analyzed the gene expression patterns within these RT signatures using transcriptome data from 508 B-ALL samples generated by the Therapeutically Applicable Research to Generate Effective Treatments (TARGET) from patients enrolled in Children's Oncology Group clinical trials (Ma et al., 2018). This analysis identified the genes with coordinated changes in transcriptional activity and RT (**Figure 3C and Supplemental Figure S3)**. Among the genes overexpressed in RT signature #1 we identified *WNT16*, *GLT1D1*, *ROR1* and others (**Figure 3D**). *WNT16* has been shown to be a target of the TCF3-PBX fusion protein and is associated with the leukemogenesis of this BCP-ALL subtype (Mazieres et al., 2005). *GLT1D* is also upregulated in *TCF3-PBX1*-positive cells but not in patients with TCF3-HLF translocation (Kachroo et al., 2018). *ROR1* encodes for the receptor orphan tyrosine kinase receptor 1 and it enhances the viability of *TCF3-PBX1*-positive cells (Bicocca et al., 2012; Geng et al., 2015). **Supplemental Table S3 contains the** complete gene list for all B-ALL RT signatures shown in **Figure 3C**.

To investigate the possible role of the *TCF3-PBX1* fusion protein in determining the RT signatures of *TCF3-PBX1*-positive leukemic cells, we transfected two *TCF3-PBX1*-positive cell lines (Kasumi and RCH-ACV) each with a pair of *TCF3-PBX1*-siRNA oligonucleotides (Casagrande et al., 2006). Despite evidence of significant specific reduction of the TCF3-PBX1 RNA in both lines (**Figure 4A-B**), very strong genome-wide correlations in RT (≥ 0.85) were observed after downregulation of *TCF3-PBX1* (**Figure 4C-D**) and no significant changes were observed in their RT profiles (**Figure 4E-F**). Additionally, we over-expressed a TCF3-PBX1 cDNA in the mature *TCF3-PBX1*-negative GM12878 B-cell line (**Figure 4G**) and detected no change in its original RT profile (**Figure 4H-I**). Together, these results argue against a direct or continuing action of the *TCF3-PBX1* fusion gene or the protein it encodes on the RT features unique to *TCF3-PBX1*-positive leukemic cells.

RT signatures associated with CNS relapse in *TCF3-PBX1*-positive BCP-ALL patients

Although most *TCF3-PBX1-positive* BCP-ALL patients are cured with current therapies, ~10% currently relapse and then respond poorly to subsequent treatment. Moreover, a high incidence of central nervous system (CNS) relapse has been observed in *TCF3-PBX1-positive* patients (Jeha et al., 2009; van der Velden et al., 2016; Irving et al., 2016). To determine whether specific RT alterations are associated with CNS relapse we analyzed WGS data (28X coverage) derived from 21 *TCF3-PBX1*-positive BCP-ALL patients at diagnosis by the St. Judes Pediatric Cancer Genome Project (PCGP). First, we identified differences in copy number variation (CNV) and detected multiple amplified loci in all *TCF3-PBX1-positive* patients but we did not detected differences that distinguished patients with CNS relapse (**Supplemental Figure S4**). Next we exploited the deep coverage of this sequencing WGS data to generate RT profiles based on the fact that earlier replicating sequences are higher in copy number than late replicating sequences (**Figure 5A**) even without prior purification of S and G1 cells (Koren et al., 2014). RT datasets were derived from the 16 highest quality WGS data based on the correlation values between each other (**Supplemental Figure S4**). RT profiles across all patient samples confirmed the high concordance of the RT programs derived from WGS data (**Figure 5B**). This group of *TCF3-PBX1-positive* patients included 2 patients that had an isolated CNS relapse and 1 that developed an unrelated secondary AML (likely due to etoposide exposure). Clustering analysis of variable chromosomal segments revealed RT signatures that were shared by the 2 CNS relapse samples (**Figure 5C**) and these features were not shared in the AML relapse sample (**Figure 5C** and **5D**).

RT signature #1 contained features that were early replicating in the cells from the CNS relapse samples but late in all other *TCF3-PBX1*-positive BCP-ALL patients. Gene ontology (GO) analysis of these chromosomal segments indicated that genes within this signature are associated with neurological regulation (**Figure 5E)**; specifically, this ontology term is linked to genes from the opiorphin family (*SMR3A*, *SMR3B* and *OPRPN*) which are up-regulated in head and neck squamous cell carcinoma (HNSCC) (Grünow et al., 2017). Additionally, odontogenesis regulation was also associated with this RT signature, derived from genes *AMBN*, *AMTN*, *ODAM*, *ENAM*, which are evolutionarily related genes all located within 500 kb of each other on chromosome 4 (Sire et al., 2007). RT signature #2 contained features that were later replicating in samples from patients that developed CNS relapse but early in samples derived from patients in remission. GO analysis indicated that genes within this signature were associated with glial cell fate determination (Gene *CTNNB1*), neural plate development (Gene *CTNNB1*), establishment of endothelial blood-brain barrier (Gene *CTNNB1*) and regulation of neuron migration (Gene *ULK4*) (**Figure 5E**). *CTNNB1* and *ULK4* are located within 500 kb of each other on chromosome 3 (**Figure 5D)**. *CTNNB1* encodes for the β-catenin, is among the most frequently mutated genes in human cancer (Grossman et al., 2016) and is the gene with the highest mutation frequency within the RT signatures #1 and #2 (**Figure 5F)**. It is important to keep in mind that other genes reside in the domains with these GO-term driving genes, so further investigation must be done to confirm any link between these genes and cellular phenotypes. **Supplemental Table S4** contains the complete gene list for these RT signatures.

RT signatures associated with relapse in NOS patients

A total of 120 NOS samples were obtained from the Children's Oncology Group (COG) bank. 60 of these were from patients classified as high risk; 30 from patients that relapsed within 3 years and 30 from patients who were still in remission after at least 3 years. Because most of these samples had too few cells to support the generation of high-quality RT profiles, we selected the 5 highest quality datasets each from paired set of relapse and remission samples and generated RT signatures for all of these (**Figure 6A**). This analysis revealed 4 RT relapse-specific signatures, one of which was found in all relapses, one in 3 relapse samples and the other 2 in the other 2 relapse samples (**Figure 6B**). For all 4 signatures, all remission samples were identical. Thus, despite the high degree of genomic heterogeneity of these samples, their relapse RT signatures showed several associated features. Genes found within these RT signatures are listed in **Supplemental Table S5**. GO analysis identified genes associated with

250 interleukin-5 signaling and B-cell activation for RT signature #1; and leukocyte tethering, interleukin-35 and interleukin-21 signaling for RT signature #3 (**Figure 6C**). GO terms derived from genes *IL5RA* and *ITPR1*, which are required for B-cell development and are among the genes with the highest mutation frequency within the NOS-RT signatures (**Figure 6D**).

Matching leukemia-specific RT signatures to RT profiles of normal human hematopoietic
255 **cell types**

To identify features of the leukemic cell RT signatures that might match those of normal hematopoietic cells and or subsets of these at different stages of differentiation, we performed a hierarchical clustering analysis of the RT data for the subsets of genomic segments from the RT signature #1 that distinguish the *TCF3-PBX1*-positive samples including the normal blood
260 cell types (**Figure 3A**). The genomic regions from this RT signature display heterogenous patters of RT in mature B-cells and T-cells (**Figure 7A**). Thus, we identified sub-signatures by further dividing this subset of genomic regions by k-means clustering analysis (**Figure 7B**). This analysis identified three groups of features within signature #1, one shared with normal pre-B cells (late B-precursors) but not normal pro-B or mature B cell lines (**1A in Figure 7AB**), a
265 second set shared with mature B-cell lines but not normal pre- or pro-B cells (**1B in Figure 7AB**), and a third set not shared with any of the nonleukemic B-cells analyzed (**1C in Figure 7AB**). When these three separate sets of features were used to subdivide signature #1, the *TCF3-PBX1* patients' cells and cell lines, and related patient samples continued to form a closely related cohort. Additionally, *TCF3-PBX1* patient samples also cluster tightly with the RT
270 features of the pre-B cell samples using signature #1A and with the B-cell lines using signature #1B (**Figure 7B**). Importantly, signature #1A includes the gene for the receptor orphan tyrosine kinase receptor 1 (ROR1) (**Figure 3B** and **Supplemental Table S2**). ROR1 is highly expressed in t(1;19) BCP-ALL blasts and is required for their viability, even though ROR1 is not directly regulated by either the TCF3-PBX1 fusion protein or the pre-B cell receptor (pre-BCR) (Bicocca
275 et al., 2012; Geng et al., 2015).

DISCUSSION

In previous studies we have shown that different BCP-ALL leukemic cells display different RT features that are highly stable and patient-specific. Here, we expanded the numbers and types of leukemic cell samples and examined their normal counterparts to determine the extent of this heterogeneity and relationship to near and distally related normal hematopoietic subsets. The results confirm the ability of RT profiles to identify markers characteristic of BCP-ALL sub-types and to sub-stratify those sub-types by outcome. This included the identification of several groups of domains that replicate together uniquely and consistently in TCF3-PBX1 leukemic cells as compared to other BCP-ALL subsets (**RT signatures**). These TCF3-PBX1-associated RT signatures were also found in cell lines established from TCF3-PBX1 patients' cells but were not affected by inducing gain or loss of TCF3-PBX1 by genetic strategies, confirming their remarkable clonal stability previously implied by serial passage in PDX (Sasaki et al, 2017), and indicating independence of the TCF3-PBX1 fusion gene itself. Evidence that these instead reflect a retained epigenetic state of the normal cells they resemble is provided by the demonstration of a subset of individual domains (**RT features**) with correlates in normal CD19+CD34- pre-B cells, but not more primitive normal CD19+CD34+ pro-B cells or more mature B cells. Interestingly, the feature shared with normal CD19+CD34- pre-B cells included ROR1, a gene that is uniquely expressed in the TCF3-PBX1 subtype of BCP-ALL where it is a therapeutic target (Bicocca, 2012). We also discovered signatures that sub-stratify the already narrowly defined TCF3-PBX1 patient samples that we hypothesized might be linked to different biological or clinically relevant phenotypes. As a preliminary test of this concept, we examined cells from a collection of TCF3-PBX1 patients that included 2 who suffered a CNS relapse, and were able to identify a pair of RT signatures specific to and shared by the relapse cells. Similarly, a comparison of NOS BCP-ALL samples from patients that suffered relapse or not also identified RT signatures selectively associated with the relapse cells. Other subtypes of BCP-ALL cells also contained a variety of distinguishing features. Taken together, these results indicate that the RT profiles of BCP-ALL cells have stable prevalent clonotypic features some of which likely reflect a retention of mechanisms operative in the normal phenotypes they resemble. Nevertheless, many others are different, likely reflecting an epigenetically perturbed state that includes elements with potential prognostic import.

We also report here the successful application of a variety of methodologies for expanding the use of RT to analyze normal differentiating hematopoietic cells and leukemic samples from BCP-ALL patients. These show that the method of choice for fresh or viably cryopreserved samples is to label cells with BrdU and perform E/L Repli-seq (Marchal et al., 2018). Here we also describe a protocol that yields good quality RT profiles from as few as 300 early and late S phase cells directly co-sorted for surface markers and DNA content, permitting rare populations to be analyzed. Cryopreserved samples, which often have significantly reduced numbers of viable cells (Falk et al., 2018), can also be sorted for total S- and G1-phase cells and RT profiles generated from the increased copy number of early replicating vs. late replicating sequences in S phase but not G1 phase cells. Samples with low viability can also be expanded as PDX in immunodeficient mice permitting E/L Repli-seq to be used to obtain their clone-specific RT signatures (Sasaki et al., 2017). Finally, when deep WGS is available, RT profiles can be derived from samples with sufficient S-phase cells to exhibit a measurably higher copy number for early vs. late replicating sequences (Koren et al., 2014). We demonstrate that all of these methods can be normalized together for comparative analyses.

The biological significance of RT signatures in related normal and BCP-ALL populations will clearly require further interrogation. In some cases, early replication is likely to be associated with increased transcription, as for *ROR1* in TCF3-PBX1 RT signature 1. However, transcription levels do not always correlate with RT alterations. For example, aberrant early replication of *TP63* in premature aging diseases is associated with a change in promoter usage that creates an altered N-terminal coding exon without affecting transcription levels as detected by RNA-seq (Rivera-Mulia et al., 2017). The mechanisms regulating RT are also only just beginning to be revealed. Deletion of *cis*-elements known as Early Replication Control Elements (ERCEs) leads to large shifts from early to late replication of entire chromosome domains and influences their 3D architecture and sub-nuclear positioning (Sima et al., 2019). These ERCEs have properties of enhancers but also make strong 3D loops and contain binding sites for core transcriptional regulatory factors. In fact, bipartite networks linking transcription and RT changes during human stem cell differentiation through multiple lineages predicted novel edges (interactions) between core transcriptional regulatory factors and sites within unlinked domains that coordinately change their RT (Rivera-Mulia et al., 2017b). Together, these findings suggest that RT signatures of BCP-ALL may reflect altered cellular transcriptional regulatory networks.

In summary, we find RT signatures of neonatal human hematopoietic cells and their B-lineage leukemic derivatives to reflect highly stable and consistent cell states with shared and distinguishing features. Some of these may also point to new prognostic or therapeutic strategies, warranting their further investigation.

MATERIALS AND METHODS

Patient Samples. Primary BCP-ALL patient samples were obtained with informed consent according to protocols approved by the Institutional Review Boards of Oregon Health & Science University and St. Jude's Childrens Research Hospital. Mononuclear cells were obtained from
345 bone marrow aspirates by Ficoll density gradient centrifugation, and viably frozen cells were stored in 90% fetal bovine serum, 10% DMSO for sample preparation as described below.

Normal Cells. Normal human cord blood samples were obtained with informed consent, anonymyzed and used in the present studies according to procedures approved by the Research Ethics Board of the University of British Columbia. Low density CD3-CD19-CD11b- cells simul-
350 taneously depleted of neutrophils and red cells were isolated on Lymphoprep using RosetteSep™ and the >90% pure CD34+ cells isolated using EasySep (both sets of reagent and protocols used from STEMCELL Technologies). Cells were stored frozen at -176 ^{o}C in DMSO with 90% fetal bovine serum (STEMCELL Technologies). Prior to use for transplanting mice the cells were thawed in Iscove's modified Dulbecco medium with 10% FBS (both STEMCELL
355 Technologies) and 10 mg/mL DNase I (Sigma Aldrich), centrifuged, and re-suspended in Hanks balanced salt solution (STEMCELL Technologies) with 2% FBS.

Xenografts. 2-10 x 10^4 normal human CD34+ CB cells (2 biological replicates consisting of pooled CB cells from 3 individuals) were intravenously injected into 8-12 week adult female NRG mice within a few hours of being exposed to 8.5 cGy of ^{137}Cs γ-rays delivered over 3
360 hours. These mice were bred in the Animal Resource Centre of the British Columbia Cancer Research Centre and used experimentally according to procedures approved by the Animal Care Committee of the University of British Columbia. 10-15 weeks later, pelvic, femoral and tibial bone marrow and spleen cells were isolated, and sorted for subsets by FACS, as described (Beer et al., 2014).

365 **Simultaneous Sorting for Surface Markers and DAPI.** To reduce the cell number requirements and demonstrate that S-phase cells have the same distribution of cell surface markers as those not in-S-phase, cells were first stained surface marker antibodies and then gently permeabilized with digitonin to permit staining of DNA with 4′,6-diamidino-2-phenylindole (DAPI) but still permit the detection of surface markers unique to each cell type. Cells were
370 directly sorted for the desired cell surface phenotype and simultaneously for either early or late S-phase DNA content based on DAPI staining, and sorted directly into the DNA extraction

buffer. This protocol yields high quality RT profiles from as few as 300 cells per early and late S-phase fraction and was used to profile CD34+CD19+ pro-B cells and CD34-CD19+ pre-B cells. Red blood cell lysis was first performed using Ammonium Chloride solution from STEM-
375 CELL Technologies for 10 minutes on ice. Cells were then washed a crude enrichment for human cells was performed using an EasySep™ Mouse/Human Chimera Isolation Kit (STEM-CELL Technologies) as per manufacturer instructions but with only a single separation on the magnet and with an extra wash of the mouse cells retained on the magnet during the pour off. Cells were then spun down and resuspended in Iscove's Modified Dulbecco's Medium (IMDM)
380 supplemented with 10% Fetal Bovine Serum (both from STEMCELL Technologies) and 100 μM Bromodeoxyuridine (BrdU, BD Pharmingen) and were placed in a humidified 37 °C (5% CO2 in air) for 2 hours. Following incubation, cells were washed once with Dulbecco's phosphate-buffered saline (PBS) + 2% FBS, and stained with 1:25 anti-human CD45 FITC (clone 2D1, STEMCELL Technologies), 1:50 anti-human CD45 APC-ef780 (clone HI30, eBiosci-
385 ences), 1:100 anti-human CD34 AlexaFluor 647 (clone 581), 1:50 anti-human CD19 PE-Cy7 (clone HIB19), and 1:800 anti-human ROR1 PE (clone 2A2, all from Biolegend) for 30 minutes on ice. Cells were once again washed, then resuspended in 8 mg/mL DAPI (Sigma) + 200 mg/mL Digitonin (Sigma) in PBS + 2% FBS. Cells were then sorted on a BD FACSAria™ Fusion sorter directly into Qiagen Buffer AL for downstream processing.

390 **Repli-chip and Repli-seq.** Repli-ChIP (Ryba et al., 2011) and Repli-seq (Marchal et al., 2018) were performed as detailed elsewhere. Genome-wide RT profiles were constructed as previously described (Marchal et al., 2018; Ryba et al., 2011). Briefly, cells were pulse labeled with bromodeoxyuridine (BrdU), separated into early and late S-phase fractions by flow cytometry, and then nascent (BrdU-substituted) DNA from each fraction was immunoprecipitated. The
395 abundance of sequences in the nascent DNA from either early or late is quantified by microarray (Repli-chip) or next generation sequencing (Repli-seq), and the RT of any given sequence is expressed as a log2 ratio of enrichment in early S to enrichment in late S (E/L) (**Figure 1C**). Microarray hybridization and data extraction were performed according to standard NimbleGen procedures. For Repli-seq, sequencing libraries were prepared by NEBNext Ultra DNA Library
400 Prep Kit for Illumina (E7370; New England Biolabs) and ~8 million uniquely mapped reads obtained on an Illumina-HiSeq 2500 sequencing system by 50-bp single-end reads. Results are reproducible and comparable between platforms, and after appropriate scaling datasets can be pooled for analysis (Rivera-Mulia et al., 2015; Marchal et al., 2018; Sasaki et al., 2017).

Capture Repli-seq. *Design of sequence capture libraries:* Roche SeqCap EZ Developer Library (cat # 06471684001, IRN/Design Name:4000016400) was designed to tile a 250 bp capture region within the central 4-kb target region from each 10-kb window of hg19 avoiding non-specific sequences by Roche so that the maximum distance between 2 capture regions is 14 kb, with a 6-kb minimum distance between 2 capture regions. *Preparation of captured sequencing libraries:* For Capture Repli-seq, G1 and S phase total genomic DNA libraries (average 150 bp insert size) were made from cells isolated by FACS from each patient sample using NEBNext Ultra DNA Library Prep Kit for Illumina (NEB E7370) and single indexed using NEB E7335 or NEB E7500. Up to 12 each of these indexed libraries were pooled and representative 250 bp regions from each 10-k window throughout the genome captured using the Roche SeqCap EZ Developer Library (cat # 06471684001, IRN/Design Name:4000016400), the SeqCap EZ Pure Capture Bead Kit (cat #06 977 952 001), and the SEQCAP EZ REAGENT KIT PLUS (cat #06 953 212 001), according to the manufacturer's instructions. After capture, enrichment of the target region was confirmed by qPCR. The target region was 51-221 times enriched compared with the pre-capture library and non-target regions were reduced by 0.02-0.16 times of pre-capture library.

RT Profiles from Deep WGS. Paired-end WGS on diagnostic leukemic blasts and matched germ line DNA samples from TCF3-PBX1 patients treated at St. Jude Children's Research Hospital was performed using the Illumina sequencing platform (Illumina Inc., San Diego, CA). The leukemic genomes had an average haploid coverage of 28x. DNA copy number was estimated and replication timing was inferred as previously described (Koren et al., 2014). Briefly, we counted the number of sequencing reads in segments of 2.5 Kb of uniquely aligned sequence, corrected for local GC content in 400 bp windows, and removed regions of copy number variation identified as near-integer changes in read coverage, as well as outlier data points and data points spanning gaps in the reference genome. The data was then smoothed using a cubic smoothing spline.

RT Signatures: These were identified as described (Rivera-Mulia et al., 2015). Briefly, RT profiles were expressed as numeric vectors. Nonoverlapping and variable regions (50-kb windows) were defined as those with differences ≥1 in pairwise comparisons between all samples. Unsupervised hierarchical and k-means clustering analyses were performed using the RT variable

regions in Cluster 3.0 (de Hoon et al., 2004). Heatmaps and dendrograms were generated in
435 Java TreeView (Saldanha, 2004).

TCF3-PBX1 siRNA Transfection. Cell lines were transfected using the Lonza Amaxa Nucleofector kit CA 137 program with 6 µg each of 2 separate E2A-PBX1-specific siRNAs (Eurofins/Operon): CUC CUA CAG UGU UUU GAG U and CAG UGU UUU GAG UAU CCG. These siRNA's were tagged at the 3'end with Cyanine-3 NHS Ester (Cy-3) and Cyanine-5 NHS Ester
440 (Cy-5), respectively, to enable transfection efficiency to be measured by fluorescence microscopy.

SUPPLEMENTAL MATERIAL

Supplemental Figure S1. Correlation matrix of normal blood cell types. (A) Whole genome correlations. **(B)** Correlations using only the RT variable genome segments. **(C-D)** RT signatures per Cord Blood.

Supplemental Figure S2. Hierarchical clustering analysis for each BCP-ALL RT signature from main Figure 3A.

Supplemental Figure S3. Gene expression patterns of genes within the BCP-ALL RT signature from main Figure 3A. Transcriptome data from 508 B-ALL samples was obtained from the Therapeutically Applicable Research to Generate Effective Treatments (TARGET) (Ma et al., 2018).

Supplemental Figure S4. Analysis of whole genome sequencing (WGS) data (28X coverage) from TCF3-PBX1-positive BCP-ALL patients. **(A)** Copy number variation (CNV) per chromosome across TCF3-PBX1-positive patients identified multiple loci amplifications. **(B)** Correlation matrix of the RT programs derived from WGS of TCF3-PBX1-positive BCP-ALL patients. WGS data was obtained from the St. Judes Pediatric Cancer Genome Project (PCGP).

Supplemental Table S1. Cell samples and dataset list.

Supplemental Table S2. Normal blood cell types RT signatures.

Supplemental Table S3. B-ALL RT signatures.

Supplemental Table S4. TCF3_PBX1 outcome Rt signatures.

Supplemental Table S5. NOS outcome RT signatures.

AUTHOR CONTRIBUTIONS

J.C.R.-M., D.M.G. and C.E. designed research; J.C.R.-M., T.S., C.T.-G., N.N., D. K., C.H., K.K., V.S. and D.M.G. performed experiments; B.C., J.W.T., B.D., T.G., C.E. provided patient samples; J.C.R.-M., J.Z. and A.K. analyzed and interpreted data; J.C.R.-M. and D.M.G. wrote the manuscript with input from all authors.

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ABBREVIATIONS

695 AML: Acute myeloid leukemia.

BCP-ALL: Human B-lineage precursor acute lymphoid leukemia.

CB: cord blood.

CNS: central nervous system.

EBV: Epstein Barr virus.

700 FACS: fluorescent activated cell sorting.

GO: Gene ontology

HSC: hematopoietic stem cells.

PDX: patient-derived xenografts.

RT: DNA-replication timing program.

705 T-ALL: T-cell Acute Lymphoblastic Leukemia.

WGS: whole genome sequencing.

FIGURE LEGENDS

710 **Figure 1. RT changes during B-cell development**. **(A)** HSCs extracted from cord blood (CB) were expanded in xenografted mice and developmental intermediates of B-cell differentiation were extracted from xenografted mice by FACS using the cell surface markers shown in distinct colors. The approximate temporal expression patterns during differentiation are shown. (**B**) RT profiling method. **(C)** Exemplary RT profiles highlighting in pink differences between immature
715 (red) and mature B-cells (blue). **(D)** Unsupervised clustering analysis of RT-variable regions identified specific RT signatures (labeled in gray boxes). Dendrogram at the top shows the correlation of all samples based on the 10,350 RT-variable 50kb segments identified. The heat map shows the RT ratios [= log2(early/late)]. (**E**) Early human hematopoiesis transcriptome data (Laurenti et al., 2013) was used to measure gene expression patterns within each RT
720 signature. RT signatures from (D) contained 274 genes with transcriptional patterns coordinated with their RT program. (**F**) Heatmap of expression patterns for known hematopoietic regulators within the RT signatures from (D). Two exemplary genes for each RT signature are shown.

Figure 2. Protocols for genome-wide RT profiling. (A) Bone marrow samples were collected
725 from pediatric BCP-ALL patients and analyzed by one of the methods shown. Samples with high viability were analyzed by E/L methods while samples with poor viability were either analyzed by S/G1 methods or they were expanded in patient derived xenografts (PDX) to rejuvenate their viability for analysis by E/L methods (Sasaki et al., 2017). RT was measured using either E/L or S/G1 methods (Gilbert, 2010; Sasaki et al., 2017). In the E/L method, asynchro-
730 nously growing cells are pulse-labeled with 5'-bromo-2'-deoxyuridine (BrdU) and separated by FACS into early and late S phase populations. BrdU-substituted DNA is immunoprecipitated with an anti-BrdU antibody and subjected to either microarray analysis (E/L Repli-chip; Ryba et al., 2011) or NextGen sequencing (E/L Repli-seq; (Marchal et al., 2018) to obtain a replication timing ratio [=$\log_2$(Early/Late)] along each chromosome. For the S/G1 method, unlabeled cells
735 are sorted into S phase and G1 phase fractions, the relative abundance of genomic sequences is quantified by either microarray (S/G1 Repli-chip) or evenly spaced segments of genomic DNA are captured using oligonucleotides and subject to NGS (Repli-CaptureSeq). **(B)** Exemplary RT profiles showing the similarity in results using the various methods after appropriate

local polynomial-smoothing (Loess). **(B)** Hierarchical clustering analysis of all patient datasets
740 based on their genome-wide RT programs confirms that there is. no bias from the different methods exploited for RT profiling.

Figure 3. Establishing BCP-ALL RT Signatures. (A) patient BCP-ALL stratification using RT profiling data. RT signatures are first identified by unsupervised K-means clustering of all 50 kb genomic segments that change between early and late replication from RT log2 ratio ≥ +0.5
745 to/from ≤ –0.5 respectively (Rivera-Mulia et al., 2015). These stringent criteria identify features that replicate significantly different in specific clusters of patients (p-value <2x10-16 using T-tests). Branches of the dendrogram were constructed based on correlation values (distance = 1 minus the correlation value). **(B)** Exemplary RT profiles of RT signatures. The top panel show an example of an RT feature (containing the ROR1 gene) of TCF3-PBX1 (red) vs. non-TCF3-
750 PBX1 BCP-ALL cells (grey). **(C)** Hierarchical clustering of BCP-ALL samples for RT signature #1. **(D)** RT-PCR to determine the TCF3-PBX1 fusion mRNA in patient samples classified as NOS (PALCRG and 10-795). Specific primers for the TCF3-PBX1 fusion mRNA and for ABL as a control were used. Two TCF3-PBX1-positive cell lines were used as positive controls (RCH-ACV and Kasumi2). Normal B-lymphoid cells (GM12878) was used as negative control.

755 **Figure 4. TCF3-PBX1 fusion gene does not cause the RT alterations observed in TCF3-PBX1-positive patient cells. (A)** Down-regulation of TCF3-PBX1 fusion protein with siRNA oligonucleotides in Kasumi2 cell line. **(B)** Down-regulation of TCF3-PBX1 fusion protein with siRNA oligonucleotides in RCH cell line. **(C-D)** Genome-wide correlation matrices of Kasumi2 and RCH cells before and after down-regulation of TCF3-PBX1 fusion protein. **(E-F)** Exemplary
760 RT profiles at two distinct chromosomal regions confirms that the RT program is preserved after down-regulation of TCF3-PBX1 fusion protein in Kasumi2 (E) and RCH (F) cell lines. **(G)** Over-expression of TCF3-PBX1 cDNA in normal B-cells (GM12878). **(H)** Genome-wide correlation matrix of normal B-cells with and without over-expression of TCF3-PBX1 cDNA. **(I)** Exemplary RT profiles confirm that the RT program is preserved after over-expression of TCF3-PBX1 fu-
765 sion protein in normal B-cells.

Figure 5. RT signatures linked to CNS relapse of TCF3-PBX1 patients. (**A)** Patient samples were subject to whole genome sequencing (WGS) at 28X depth. These sequences were subjected to a pipeline that converts their relative copy number into RT profiles (Koren et al., 2014). WGS data for 21 patients was obtained and the 16 with highest quality RT profiles (based on

770 genome-wide correlations to each other; **Supplementary Figure S4**) were chosen for analysis. Of these, 2 samples were from patients that later suffered CNS relapse, and one was from a patient that developed a secondary AML; the remaining sampled were from patients who were in remission. **(B)** Exemplary profiles of all patient samples from a typical genomic region that shows no variance between sample profiles. **(C)** Clustering analysis of differences between
775 relapses vs remission. 2 RT signatures distinguish patients who developed CNS relapse from those in remission. **(D)** RT profiles of each signature shown in (C). **(E)** Ontology analysis of RT signatures shown in (C). **(F)** Mutation frequencies for the genes in the RT signatures shown in (C). Mutation frequencies were obtained from the National Cancer Institute Genomic Data Commons Data Portal (Grossman et al., 2016).

780 **Figure 6. RT signatures of NOS relapse.** 60 NOS samples (30 relapse; 30 remission) were obtained from the Children's Oncology Group (COG). Many of these samples were non-viable and had to be analyzed by the repli-capture-seq S/G1 method (Figure 2), which frequently yielded a low signal to noise ratio. The 5 highest quality relapse and remission samples (based on their correlation to normal B-cells) were subjected to hierarchical clustering to identify RT
785 signatures. **(A)** 4 RT signatures distinguish patients with relapse from those in remission. The first one includes all relapses, the 2nd only 3 relapses, and 3rd and 4th are specific for 2 relapses. **(B)** RT profiles of each signature shown in (A). **(C)** Ontology analysis of RT signatures shown in (A). **(F)** Mutation frequencies for the genes in the RT signature #1 shown in (A). Mutation frequencies were obtained from the National Cancer Institute Genomic Data Commons
790 Data Portal (Grossman et al., 2016).

Figure 7. Tracking the origin of TCF3-PBX1 RT abnormalities. (**A**) Hierarchical analysis of RT signature #1 from Figure 3 clustered TCF3-PBX1 with normal B-cells. This RT signature can be sub-classified in 3 RT sub-signatures: **(B)** RT Signature #1A: TCF3-PBX1 specific RT changes that track with normal pre-B cells (late B-precursors, CD34negCD19posROR1pos
795 cells). RT Signature #1B: TCF3-PBX1 specific RT changes that track with EBV-B cells. RT Signature #1C: TCF3-PBX1 specific RT changes that do not track with any of the B cells and substratify the patient samples.

Figure 1

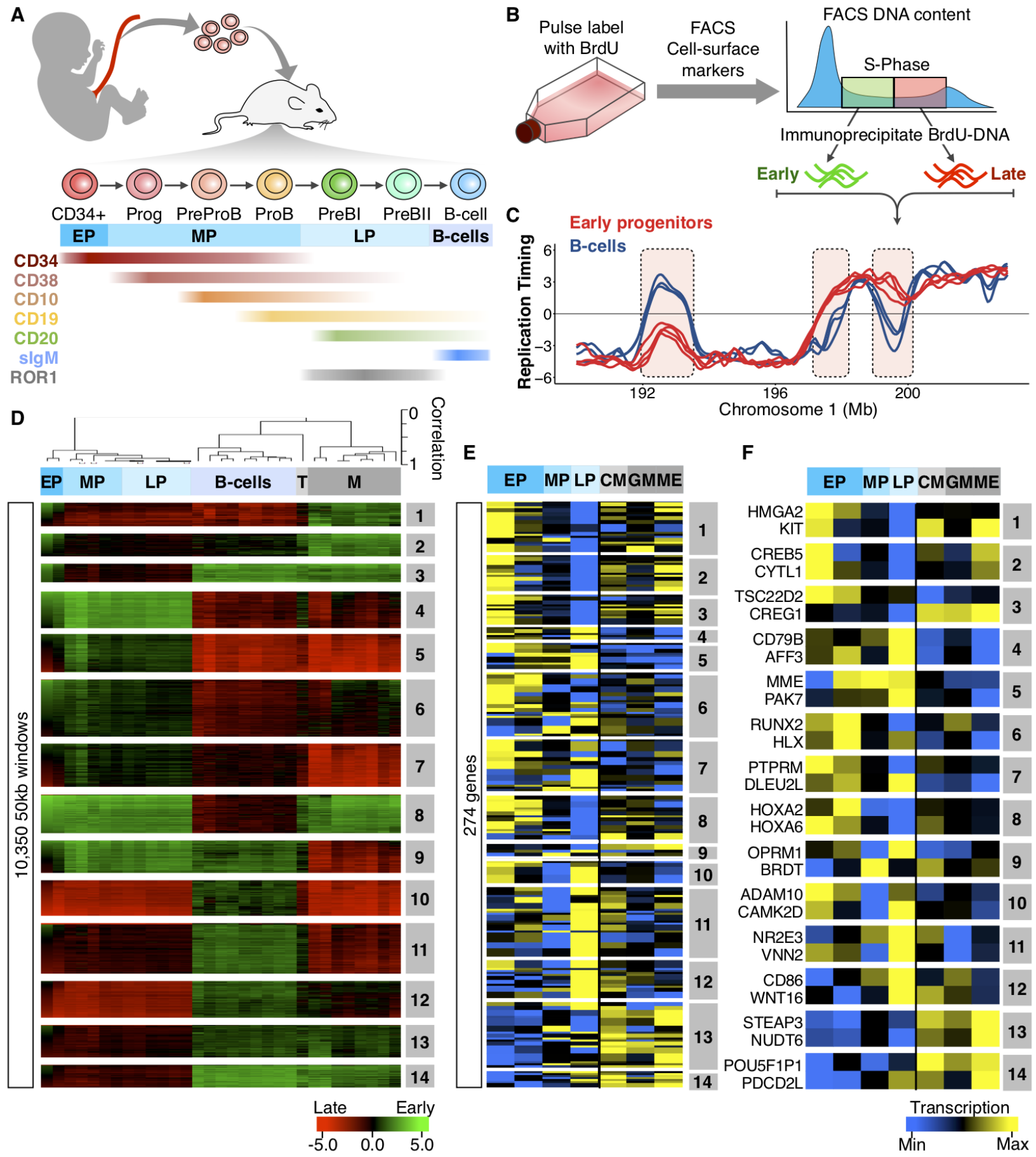

A
CD34+
Prog
PreProB
ProB
PreBI
PreBII
B-cell
EP
MP
LP
B-cells
CD34
CD38
CD10
CD19
CD20
sIgM
ROR1
B
Pulse label with BrdU
FACS Cell-surface markers
FACS DNA content
S-Phase
Immunoprecipitate BrdU-DNA
Early
Late
C
Early progenitors
B-cells
Replication Timing
Chromosome 1 (Mb)
D
Correlation
10,350 50kb windows
Late
Early
E
274 genes
F
HMGA2
KIT
CREB5
CYTL1
TSC22D2
CREG1
CD79B
AFF3
MME
PAK7
RUNX2
HLX
PTPRM
DLEU2L
HOXA2
HOXA6
OPRM1
BRDT
ADAM10
CAMK2D
NR2E3
VNN2
CD86
WNT16
STEAP3
NUDT6
POU5F1P1
PDCD2L
Transcription
Min
Max

Figure 2

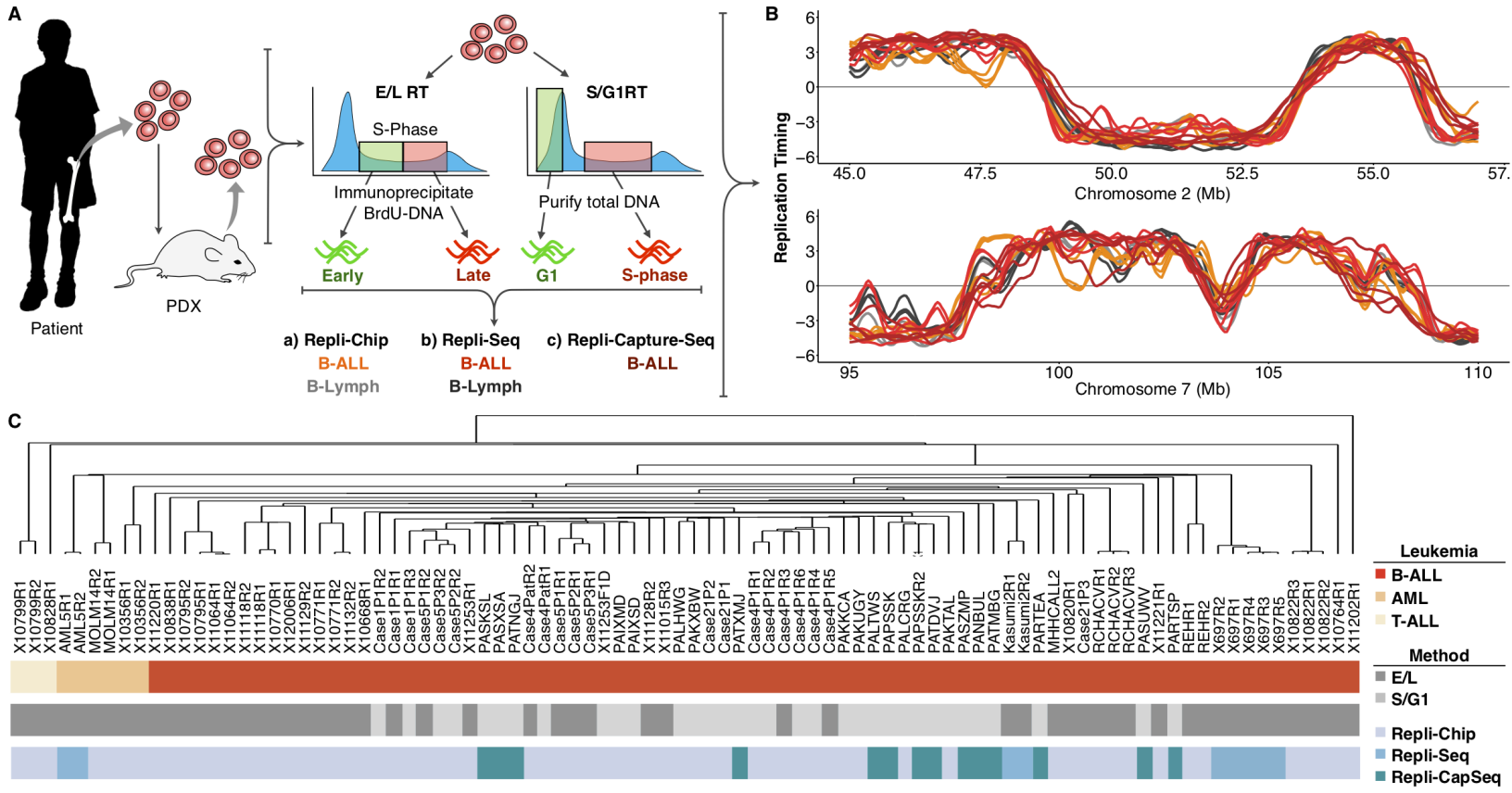

A
Patient
PDX
E/L RT
S-Phase
S/G1RT
Immunoprecipitate
BrdU-DNA
Purify total DNA
Early
Late
G1
S-phase
a) Repli-Chip
B-ALL
B-Lymph
b) Repli-Seq
B-ALL
B-Lymph
c) Repli-Capture-Seq
B-ALL
B
Replication Timing
Chromosome 2 (Mb)
Chromosome 7 (Mb)
C
Leukemia
B-ALL
AML
T-ALL
Method
E/L
S/G1
Repli-Chip
Repli-Seq
Repli-CapSeq

Figure 3

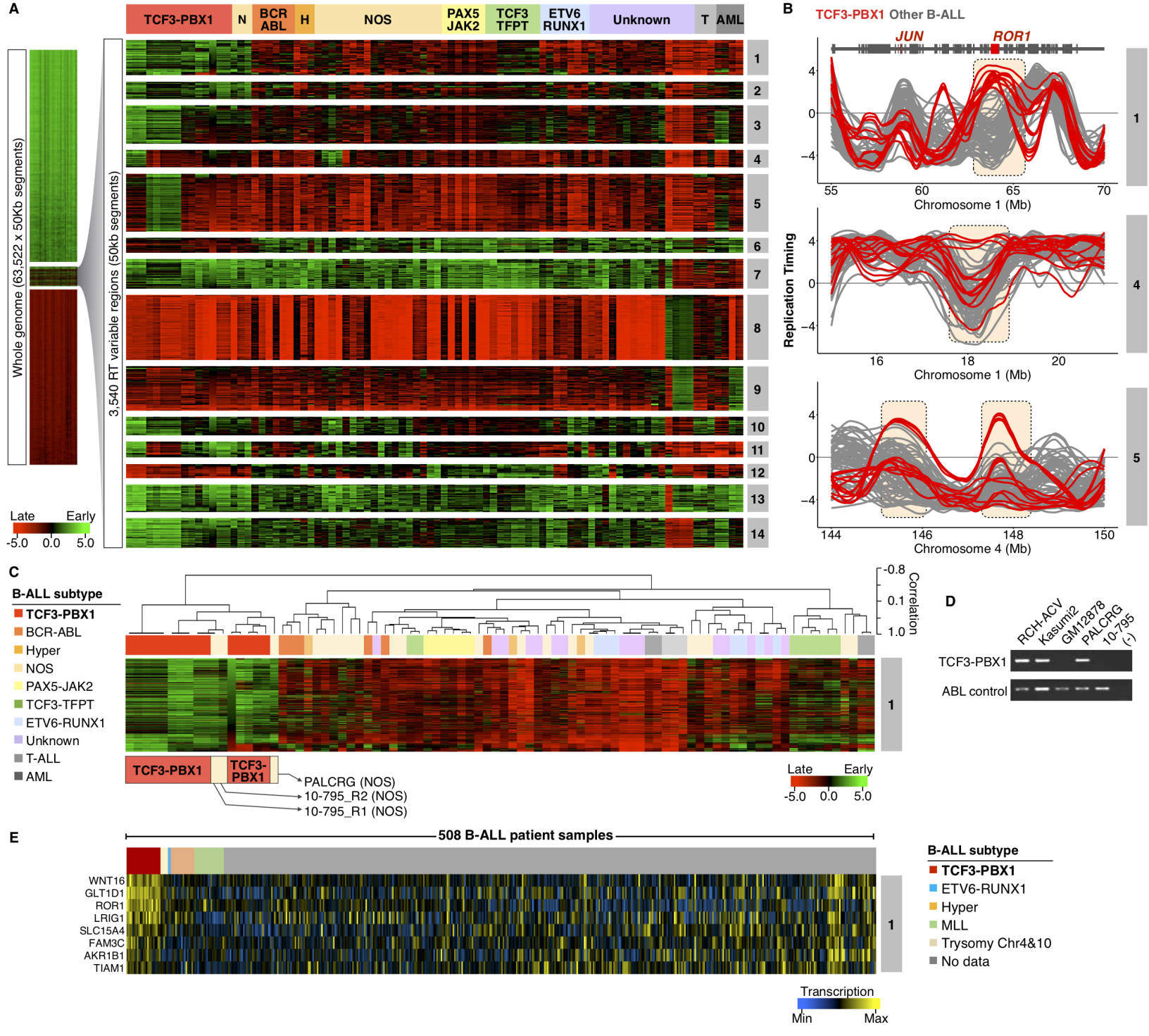
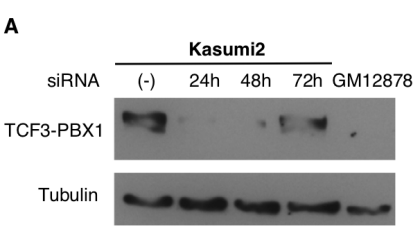
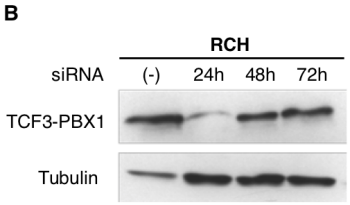
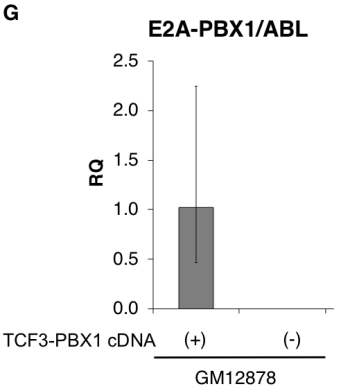
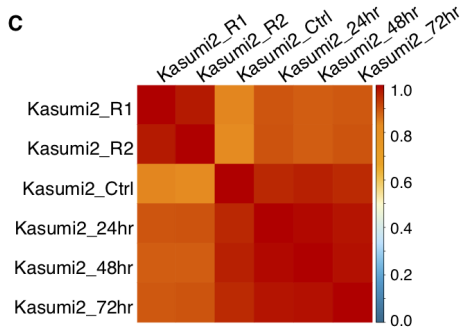

A
TCF3-PBX1
N
BCR ABL
H
NOS
PAX5 JAK2
TCF3 TFPT
ETV6 RUNX1
Unknown
T
AML
Whole genome (63,522 x 50Kb segments)
3,540 RT variable regions (50kb segments)
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Late
Early
-5.0
0.0
5.0
B
TCF3-PBX1 Other B-ALL
JUN
ROR1
Replication Timing
Chromosome 1 (Mb)
Chromosome 4 (Mb)
C
B-ALL subtype
TCF3-PBX1
BCR-ABL
Hyper
NOS
PAX5-JAK2
TCF3-TFPT
ETV6-RUNX1
Unknown
T-ALL
AML
Correlation
-0.8
0.1
1.0
PALCRG (NOS)
10-795_R2 (NOS)
10-795_R1 (NOS)
D
RCH-ACV
Kasumi2
GM12878
PALCRG
10-795
(-)
TCF3-PBX1
ABL control
E
508 B-ALL patient samples
WNT16
GLT1D1
ROR1
LRIG1
SLC15A4
FAM3C
AKR1B1
TIAM1
B-ALL subtype
TCF3-PBX1
ETV6-RUNX1
Hyper
MLL
Trysomy Chr4&10
No data
Transcription
Min
Max

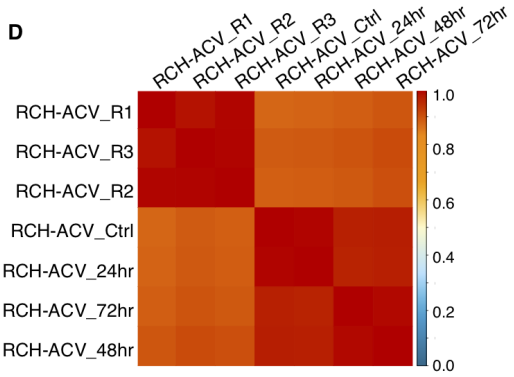
Figure 4

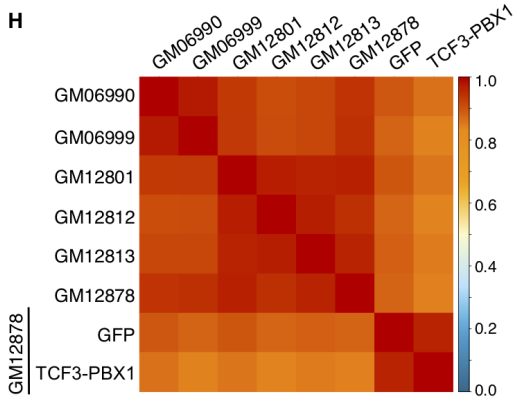

A
Kasumi2
siRNA
(-)
24h
48h
72h
GM12878
TCF3-PBX1
Tubulin

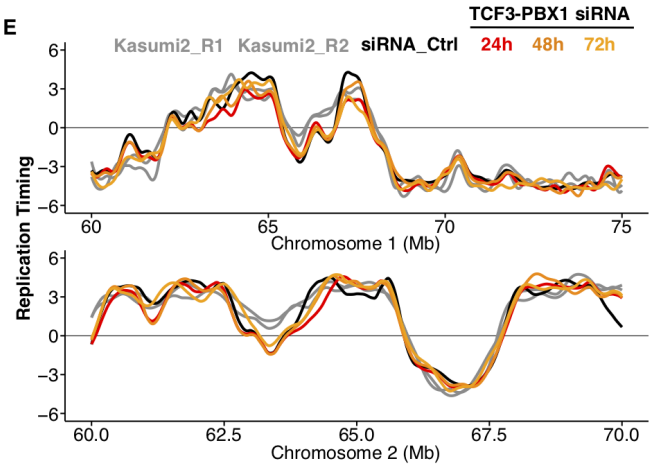

B
RCH
siRNA
(-)
24h
48h
72h
TCF3-PBX1
Tubulin

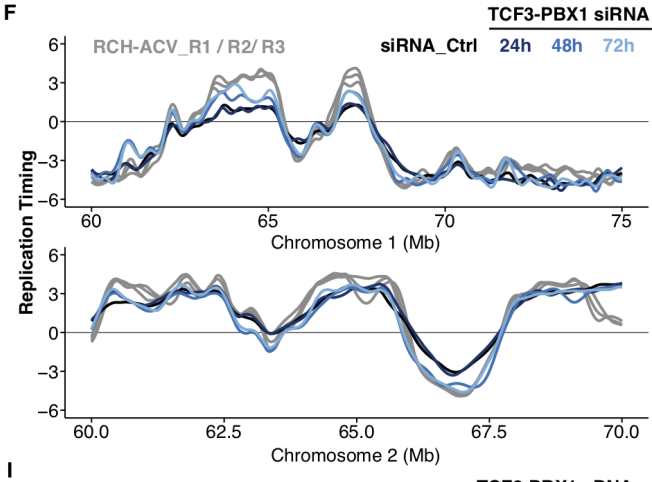

G
E2A-PBX1/ABL
RQ
2.5
2.0
1.5
1.0
0.5
0.0
TCF3-PBX1 cDNA
(+)
(-)
GM12878


C
Kasumi2_R1
Kasumi2_R2
Kasumi2_Ctrl
Kasumi2_24hr
Kasumi2_48hr
Kasumi2_72hr
1.0
0.8
0.6
0.4
0.2
0.0


D
RCH-ACV_R1
RCH-ACV_R2
RCH-ACV_R3
RCH-ACV_Ctrl
RCH-ACV_24hr
RCH-ACV_48hr
RCH-ACV_72hr
1.0
0.8
0.6
0.4
0.2
0.0


H
GM06990
GM06999
GM12801
GM12812
GM12813
GM12878
GFP
TCF3-PBX1
GM12878
1.0
0.8
0.6
0.4
0.2
0.0


E
TCF3-PBX1 siRNA
Kasumi2_R1
Kasumi2_R2
siRNA_Ctrl
24h
48h
72h
Replication Timing
Chromosome 1 (Mb)
Chromosome 2 (Mb)


F
TCF3-PBX1 siRNA
RCH-ACV_R1 / R2/ R3
siRNA_Ctrl
24h
48h
72h
Replication Timing
Chromosome 1 (Mb)
Chromosome 2 (Mb)

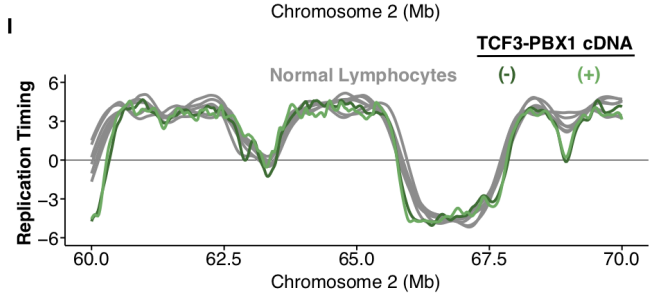

I
TCF3-PBX1 cDNA
Normal Lymphocytes
(-)
(+)
Replication Timing
Chromosome 2 (Mb)

Figure 5

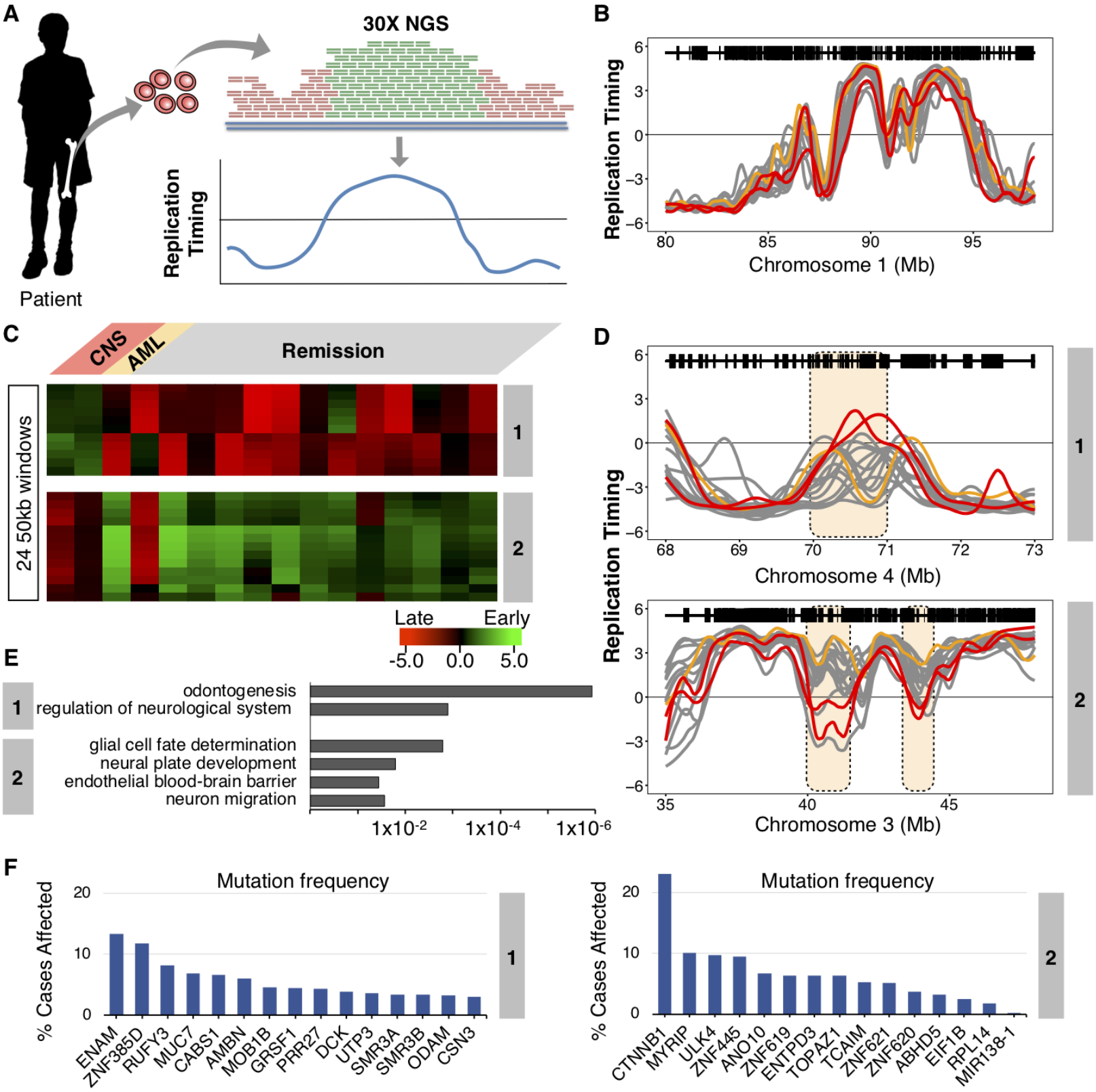

A
30X NGS
Replication Timing
Patient
B
Replication Timing
Chromosome 1 (Mb)
C
CNS
AML
Remission
24 50kb windows
1
2
Late
Early
-5.0
0.0
5.0
D
Replication Timing
Chromosome 4 (Mb)
Chromosome 3 (Mb)
E
odontogenesis
regulation of neurological system
glial cell fate determination
neural plate development
endothelial blood-brain barrier
neuron migration
1x10-2
1x10-4
1x10-6
F
Mutation frequency
% Cases Affected
ENAM
ZNF385D
RUFY3
MUC7
CABS1
AMBN
MOB1B
GRSF1
PRR27
DCK
UTP3
SMR3A
SMR3B
ODAM
CSN3
CTNNB1
MYRIP
ULK4
ZNF445
ANO10
ZNF619
ENTPD3
TOPAZ1
TCAIM
ZNF621
ZNF620
ABHD5
EIF1B
RPL14
MIR138-1

Figure 6

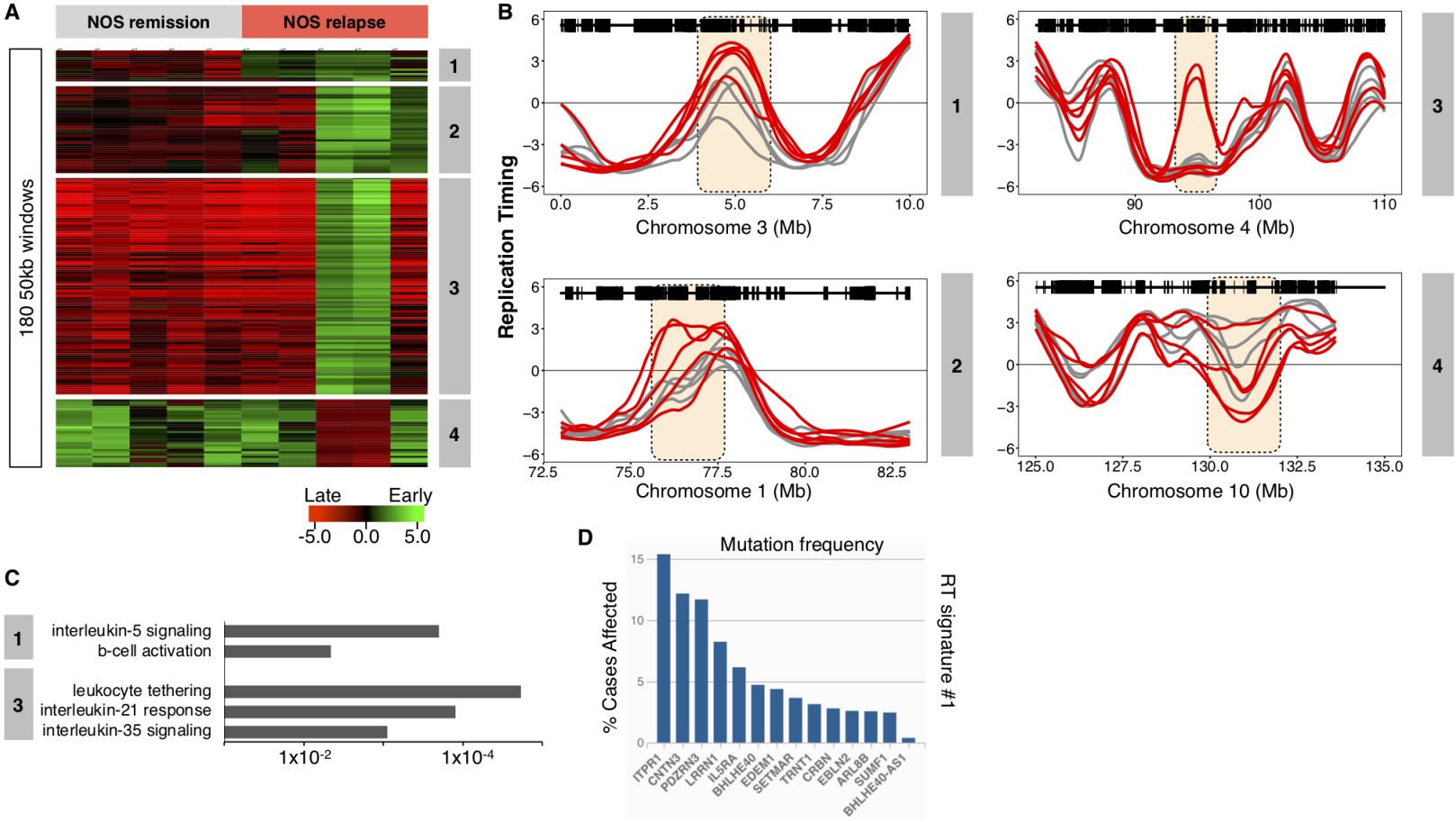
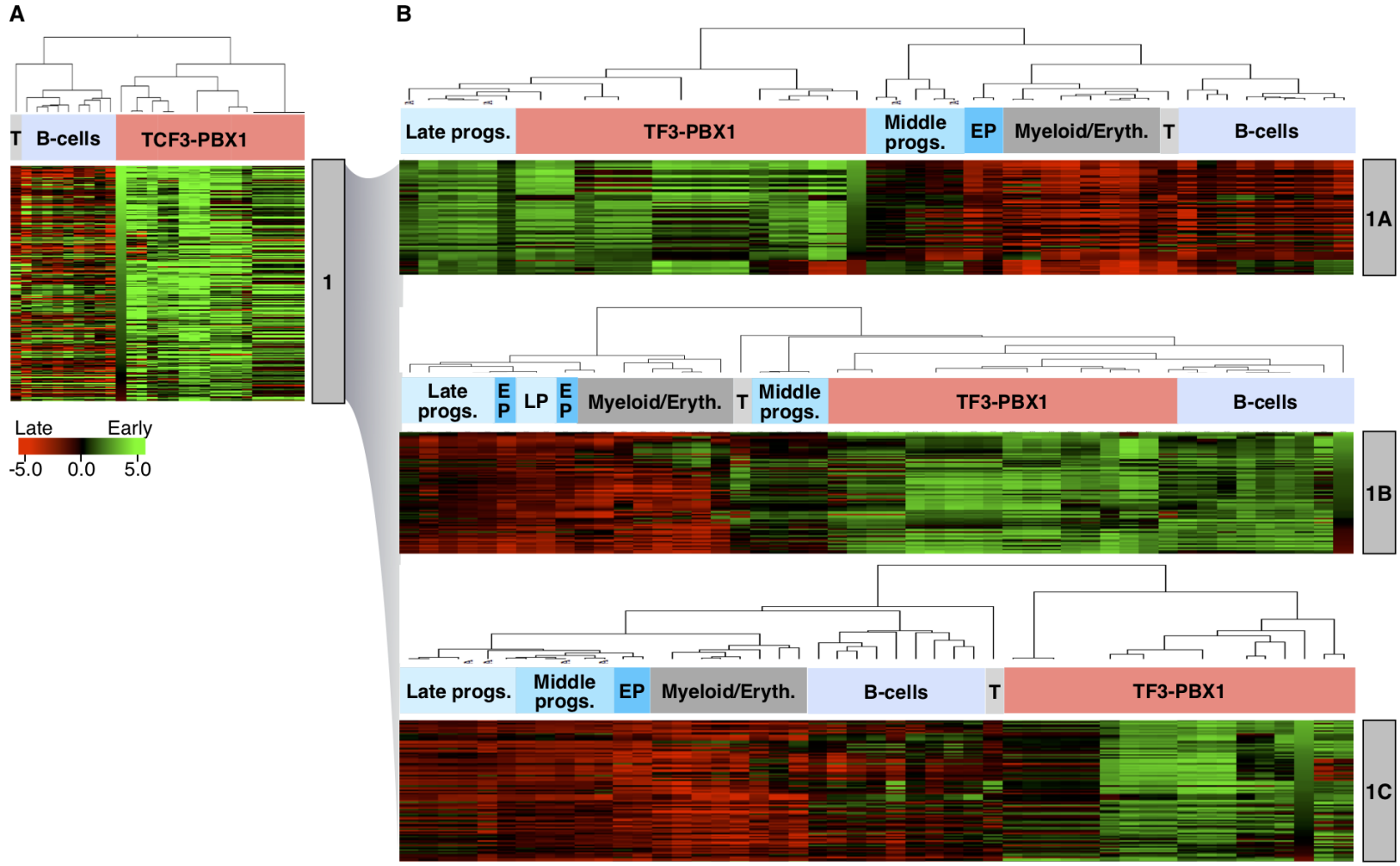

A
NOS remission
NOS relapse
180 50kb windows
1
2
3
4
Late
Early
-5.0
0.0
5.0
B
Replication Timing
Chromosome 3 (Mb)
Chromosome 4 (Mb)
Chromosome 1 (Mb)
Chromosome 10 (Mb)
C
interleukin-5 signaling
b-cell activation
leukocyte tethering
interleukin-21 response
interleukin-35 signaling
1x10-2
1x10-4
D
Mutation frequency
% Cases Affected
RT signature #1
ITPR1
CNTN3
PDZRN3
LRRN1
IL5RA
BHLHE40
EDEM1
SETMAR
TRMT1
CRBN
EBLN2
ARL8B
SUMF1
BHLHE40-AS1

Figure 7


A
T
B-cells
TCF3-PBX1
1
Late
Early
-5.0
0.0
5.0
B
Late progs.
TF3-PBX1
Middle progs.
EP
Myeloid/Eryth.
T
B-cells
1A
Late progs.
E P
LP
E P
Myeloid/Eryth.
T
Middle progs.
TF3-PBX1
B-cells
1B
Late progs.
Middle progs.
EP
Myeloid/Eryth.
B-cells
T
TF3-PBX1
1C