Functional loss of IκBε leads to NF-κB deregulation in aggressive chronic lymphocytic leukemia

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NF-κB is constitutively activated in chronic lymphocytic leukemia (CLL); however, the implicated molecular mechanisms remain largely unknown. Thus, we performed targeted deep sequencing of 18 core complex genes within the NF-κB pathway in a discovery and validation CLL cohort totaling 315 cases. The most frequently mutated gene was NFKBIE (21/315 cases; 7%), which encodes IκBε, a negative regulator of NF-κB in normal B cells. Strikingly, 13 of these cases carried an identical 4-bp frameshift deletion, resulting in a truncated protein. Screening of an additional 377 CLL cases revealed that NFKBIE aberrations predominated in poor-prognostic patients and were associated with inferior outcome. Minor subclones and/or clonal evolution were also observed, thus potentially linking this recurrent event to disease progression. Compared with wild-type patients, NFKBIE-deleted cases showed reduced IκBε protein levels and decreased p65 inhibition, along with increased phosphorylation and nuclear translocation of p65. Considering the central role of B cell receptor (BcR) signaling in CLL pathobiology, it is notable that IκBε loss was enriched in aggressive cases with distinctive stereotyped BcR, likely contributing to their poor prognosis, and leading to an altered response to BcR inhibitors. Because NFKBIE deletions were observed in several other B cell lymphomas, our findings suggest a novel common mechanism of NF-κB deregulation during lymphomagenesis.
Consisting of five members, NFKB1 (p50), NFKB2 (p52), RELA (p65), RELB, and c-REL (REL), the NF-κB signaling pathway regulates many cellular processes, including cell cycle progression, differentiation, and apoptosis (Bonizzi and Karin, 2004). These proteins form homo- and heterodimers that are held in the cytoplasm by inhibitor proteins (IkB) and function by activating or suppressing target genes (Bonizzi and Karin, 2004). The IkBs (α, β, δ, ε, and θ) are regulated by the IkB kinase complex, which, when activated, phosphorylates the IkBs, leading to their degradation; this culminates in the translocation of transcription factors to the nucleus. In B cells, the canonical NF-κB pathway can be activated through numerous upstream signals including B cell receptor (BcR) or TLR signaling, whereas the noncanonical pathway is primarily activated through BAFF receptor–CD40 interaction (Bonizzi and Karin, 2004; Höming-Hölzel et al., 2008).

Deregulated NF-κB signaling appears to be particularly important in B cell malignancies, with recurrent activating mutations identified in both the canonical and the noncanonical NF-κB pathways (Compagno et al., 2009; Staudt, 2010; Rossi et al., 2013a). In chronic lymphocytic leukemia (CLL), NF-κB activation is known to be present in virtually all cases (Herrishanu et al., 2011). That notwithstanding, the extent to which genetic aberrations contribute to NF-κB activation in CLL remains largely unknown except for low-frequency (<3%) mutations in BIRC3 (noncanonical NF-κB pathway) and MYD88 (TLR signaling; Bialiakas et al., 2015). Very recently, a recurrent 4-bp truncating mutation within the NFKBIE gene, which encodes IkBe, a negative regulator of NF-κB in B cells, has been reported as frequent in advanced stage CLL (Damm et al., 2014). However, the precise functional impact of this mutation and, especially, the extent to which it contributes to constitutional NF-κB activation in CLL remain unexplored.

To gain insight into these issues, we undertook a combined genetic and functional approach for investigating the NF-κB signaling pathway in CLL. Taking advantage of HaloPlex technology (Agilent Technologies), we designed a targeted gene panel and performed deep sequencing of 18 members of the NF-κB pathway in 315 CLL cases. The most striking observation was the finding of the recurrent frameshift deletion within the NFKBIE gene that resulted in profound functional consequences. In particular, patients carrying this truncating mutation displayed lower IkBe expression and reduced IkBe–p65 interactions, as well as increased levels of phosphorylated p65 and nuclear p50/p65. Because we also detected this truncating event in other lymphoma entities, our finding implies that the loss of IkBe may be a common mechanism contributing to the sustained survival of malignant B cells, thus also shaping disease evolution and ultimately impacting disease progression.

RESULTS AND DISCUSSION
Targeted sequencing identifies NFKBIE mutations as a recurrent event in CLL
We performed targeted deep sequencing of 18 NF-κB core complex genes (Table S1) within a discovery cohort of 124 CLL patients (Table S2). Sequencing resulted in a mean read depth of 656 reads/base and 97% of the targeted coding regions being covered (Table S1). By applying a conservative cutoff of >10% for the mutant allele, we identified 26 mutations in 11/18 NF-κB genes analyzed within 24/124 (19%) CLL patients (Table S3); 16/16 selected mutations were validated by Sanger sequencing. IkBe (encoded by NFKBIE) was the most frequently mutated, being altered in eight patients (6.5%); notably, three/eight patients carried an identical 4-bp frameshift deletion in NFKBIE exon 1 (Fig. 1A). When considering mutations with a low mutant allele frequency (<10%), this 4-bp deletion within NFKBIE was found in eight additional cases (Table S4).

NFKBIE mutations predominated in CLL cases with unmutated Ig heavy variable (IGHV) genes (U-CLL) belonging to certain subsets with restricted BcR IgG (stereotyped BcRs), for which we and others have reported distinct, subset-biased profiles regarding their biological background and clinical course (Stamatopoulos et al., 2007; Agathangelidis et al., 2012; Strefford et al., 2013; Bialiakas et al., 2014). Prompted by this observation, we again performed targeted resequencing of NF-κB genes using HaloPlex technology within a validation CLL cohort (n = 191) enriched for cases assigned to poor-prognostic stereotyped subsets (Tables S5 and S6). We found 30 mutations in 10/18 NF-κB genes analyzed within 28 CLL patients; strikingly, 13/30 mutations were in IkBe with 10/13 patients carrying the 4-bp NFKBIE deletion (Fig. 1B and Table S7). This deletion was also detected at a low mutant allele frequency (<10%) in 18 additional cases (Table S4).

Because germline DNA was lacking for the vast majority of patients (because of the retrospective nature of the study), we were limited in our ability to confirm the somatic nature of mutations. That said, we could verify that mutations within the NFKBIE gene were somatic and not germline variants in all cases with available material (Tables S3 and S7). For the remaining NF-κB mutations, we cannot formally exclude the possibility that they are rare germline variants (despite extensive filtering against various SNP databases) and hence decided to focus on NFKBIE, which, importantly, was also the most frequently mutated NF-κB gene.

Enrichment of NFKBIE aberrations in poor-prognostic subsets of CLL
We next developed a GeneScan assay specific for the 4-bp NFKBIE deletion and studied 377 additional CLL cases, including (a) patients from a population-based cohort (Table S8), where U-CLL accounted for 32% of cases, with the remaining cases carrying mutated IGHV genes (M-CLL); (b) patients with stage B/C disease; and (c) patients assigned to stereotyped subsets. Overall, 22 additional NFKBIE-deleted patients were identified (Table S9). Collectively, this amounted to 43/692 (6.2%) CLL patients carrying NFKBIE aberrations (i.e., mutations and/or deletions), of whom 37/43 concerned U-CLL. A significant enrichment of NFKBIE aberrations was observed in certain poor-prognostic stereotyped CLL subsets, especially subset #1 (17/112 cases, 15%) and the less
populated subset #6 (5/35 cases, 14%; Fig. 1 B), further supporting the concept that the subclassification of CLL based on BcR stereotypy may supersede the more generic discrimination into U-CLL or M-CLL (Baliakas et al., 2014). A considerably lower frequency of NFKBIE aberrations was observed within our population-based cohort (4/236, 1.7%; Smedby et al., 2005), whereas advanced stage B/C patients carried NFKBIE aberrations at a frequency of 6.1% (12/198), thus lower than recently reported (10%; Damm et al., 2014).

In Fig. 2 A, we depict coexisting cytogenetic/molecular lesions in the 43 patients with NFKBIE aberrations; although a small proportion of cases carried concomitant poor-prognostic TP53 (7%), NOTCH1 (14%), and SF3B1 (9%) mutations, the majority of cases did not carry mutations within these genes. Because mutations have been described in two other NF-κB pathway genes in CLL, MYD88 and BIRC3, albeit at a low frequency (Baliakas et al., 2015), we also sequenced the hotspot p.L265P MYD88 mutation and exons 6–9 of BIRC3. In total, 4/495 (0.8%) patients carried a p.L265P MYD88 mutation, none of which co-occurred with a mutation in NFKBIE, whereas 8/568 (1.4%) patients harbored mutations within BIRC3, with only 1 of these patients carrying the 4-bp deletion within NFKBIE. In addition, we analyzed copy number data for 369 CLL cases obtained from SNP arrays (250K) and found only 3 cases showing a potential monoallelic deletion covering the NFKBIE gene (on chromosome 6p21.1); none of these cases had a truncating NFKBIE mutation (not depicted).

The remarkable enrichment of NFKBIE aberrations in poor-prognostic subset #1 (17/43 NFKBIE-mutated/deleted cases, 39.5%) recalls the significantly higher frequency of SF3B1 mutations in poor-prognostic stereotyped subset #2 compared with all remaining CLL (∼44% vs. ∼5%; Rossi et al., 2013b; Strefford et al., 2013). This subset-biased distribution of genomic aberrations in different poor-prognostic stereotyped subsets supports the existence of distinct mechanisms underlying clinical aggressiveness in CLL and could perhaps result from particular modes of BcR-mediated signaling, which could shape the evolution of each individual subset. In other words, the enrichment seen in stereotyped subsets might primarily be linked to the particular BcR configuration of each subset rather than merely attributed to IGHV gene mutational status.

NFKBIE aberrations are linked to rapid disease progression and poor outcome

The presence of NFKBIE aberrations was associated with a significantly shorter time to first treatment (TTFT) similar to IGHV-unmutated or 17p-deleted patients (Fig. 2 B), which was perhaps expected given the preference toward clinically aggressive CLL subsets (Stamatopoulos et al., 2007; Baliakas et al., 2014). In multivariate analysis including established risk factors, NFKBIE aberrations did not hold as an independent factor; however, when IGHV mutational status (one of the strongest molecular predictors of TTFT in CLL [Baliakas et al., 2015]) was removed from the model, NFKBIE aberrations regained significance (Table S10). Taking into account that almost all cases with NFKBIE aberrations concerned U-CLL, this could be the overarching reason behind this latter finding, along with the comparatively lower number of cases in the NFKBIE-mutated/deleted group (relative to IGHV-unmutated CLL). Despite a limited number of cases showing
coexisting TP53, SF3B1, or NOTCH1 aberrations, no other clinicobiological factor was identified that could explain the poor outcome seen for the vast majority of cases with NFKBIE aberrations, thus implying an important role as a driver mutation during disease evolution.

Because NFKBIE aberrations were linked to inferior outcome and considering the finding of low-frequency (<10%) 4-bp NFKBIE deletions in a considerable proportion of cases (Table S4), we also investigated longitudinal samples available from 14 treated CLL cases. These cases exhibited varying allelic frequencies in the initial sample investigated (8/14 cases <10%, range 1–8%), and an increase in the allelic frequency of the NFKBIE mutations and/or deletions was observed over time and at relapse in 6/14 cases (Fig. 2 C). Such temporal dynamics is indicative of clonal evolution and potentially links these aberrations to disease progression. Admittedly, this has to be studied in more detail, in particular because the variant allele frequency of several cases with low-frequency NFKBIE aberrations was found to remain stable or essentially unaltered at relapse.

Considering our findings in CLL and the sparse reporting of NFKBIE mutations in other lymphomas (Emmerich et al., 2003; Gunawardana et al., 2014), we performed a comprehensive screening of 372 additional mature B cell lymphomas by either targeted sequencing or GeneScan analysis. NFKBIE deletions were detected in 7/136 (5.1%) mantle cell lymphomas, 3/66 (4.5%) diffuse large B cell lymphomas (DLBCLs), and 3/170 (1.8%) splenic marginal zone lymphomas. These results are highly indicative of a common mechanism for NF-kB deregulation within at least a subset of mature B cell malignancy cases (Fig. 1 B).

IkBε disruption results in reduced inhibition and increased nuclear p65 levels
In normal B cells, IkBε provides negative regulation upon BcR/TLR stimulation by limiting nuclear migration of Rel-containing NF-kB dimers (e.g., p65 and REL) through protein binding via the ankyrin repeat region (Fig. 1 A), thus ensuring temporal control of NF-kB activation (Alves et al., 2014). Furthermore, IkBε loss was reported to result in increased B cell proliferation and survival of stimulated B cells in IkBε−/− mice (Alves et al., 2014). To understand the functional consequence of truncating NFKBIE mutations for the NF-kB signaling pathway in CLL, the three IkB members (α, β, and ε) were investigated together with the transcription factor p65 using Western blot analysis. Significantly lower IkBε protein levels were observed in NFKBIE-deleted (n = 7, mean allele frequency 45%, range 28–61%) versus WT patients (n = 7; P < 0.001), whereas no differences were detected for either IkBα or IkBβ (Fig. 3, A–C). Accordingly, phosphorylated p65 levels were significantly higher in NFKBIE-deleted versus WT patients (Fig. 3, A–C; P < 0.05).
this domain, which is a prerequisite for binding to p65 (and other transcription factors). Although both the mutant and WT alleles were expressed at the RNA level in **NFKBIE**-deleted patient samples (Table S11), Western blot analysis for low-molecular mass proteins did not reveal any truncated form of IkB\(\alpha\) in **NFKBIE**-deleted cases besides that corresponding to the WT protein (41 kD; Fig. 3 D). Because the truncated form does not appear to render a stable protein, this suggests that the **NFKBIE** deletion may represent a loss-of-function mutation. Regarding the other **NFKBIE** mutations, all of which were missense mutations, these were predominantly located in the ankyrin domain and were deemed as deleterious using various prediction tools (Fig. 1 A).

To further explore how the interaction between IkB\(\alpha\) and p65 is influenced, coimmunoprecipitation (co-IP) experiments with p65 demonstrated a lower pull-down of IkB\(\alpha\) in **NFKBIE**-deleted (\(n = 3\)) versus WT (\(n = 2\)) cases (Fig. 4, A and B), indicating reduced interaction between IkB\(\alpha\) and p65. Seeking further support for the latter finding, we studied the physical interaction between IkB\(\alpha\), IkB\(\beta\) and IkB\(\varepsilon\), and p65 using an alternative approach by applying proximity ligation assays, a highly sensitive method for real-time visualization of protein–protein interactions in situ (Söderberg et al., 2006). In six **NFKBIE** WT CLL cases, although interactions were detected for all IkBs in unstimulated CLL cells, IkB\(\varepsilon\) exhibited the greatest number of interactions with p65 per cell analyzed, supporting its important role in CLL (Fig. 4 C).

Upon stimulation with \(\alpha\)IgM or CD40 ligand (CD40L), although the interactions between all IkBs and p65 were reduced, IkB\(\varepsilon\) was predominantly affected (Fig. 4, C–F). In contrast, in six **NFKBIE**-deleted cases, IkB\(\varepsilon\) and p65 interactions in unstimulated CLL cells were notably reduced, thus resembling stimulated WT cells (Fig. 4, C–F); however, this finding did not reach statistical significance (\(P = 0.15\)), probably because of the low number of cases available for analysis.

Altogether, our data indicates that these truncating mutations reduce IkB\(\varepsilon\) levels, in turn leading to reduced IkB\(\varepsilon\)–p65 interactions, and, consequently, increasing phosphorylated p65, which is potentially underlying a more activated state. This was further supported by subsequent fractionation experiments.
Figure 4. Interactions between IkBs and p65 in CLL. (A) Co-IP to study the interaction between p65 and IkBe in NFKBIE-deleted (n = 3) versus WT (n = 2) CLL. The bottom panel indicates TCL from samples used in the co-IP assay. (B) Mean values for IkBe pull-down in NFKBIE-deleted versus WT CLL. (C) Proximity ligation assay to study the physical interaction between IkBα, IkBβ and IkBe, and p65 in six NFKBIE WT CLL patients. Interactions were assessed in unstimulated (U), α-IgM-stimulated, and CD40L-stimulated cells. For IkBα and IkBe, six NFKBIE WT CLL patients were analyzed, whereas for IkBβ only four NFKBIE WT CLL patients were assessed. (D) The interaction between IkBe and the transcription factor p65 in six NFKBIE WT CLL patients and six NFKBIE-deleted patients. Interactions were again assessed in unstimulated (U), α-IgM-stimulated, and CD40L-stimulated cells. Error bars indicate standard error. (E and F) Fluorescent microscope images of the interaction between IkBe and the transcription factor p65 in cells from a NFKBIE WT CLL patient (E) and an NFKBIE-deleted CLL patient (F). Blue color indicates cell nuclei, whereas each red dot represents a single interaction. Bars, 20 µm.

for NFKBIE-deleted (n = 3) and WT (n = 2) samples, which revealed an increase in the nuclear fraction of p50 and p65 in NFKBIE-deleted patients (Fig. 5, A–D). Hence, loss of IkBe inhibitory function increased nuclear p50/p65 translocation and consequent NF-κB activation.

**NFKBIE deletion has limited impact on the global gene expression profile**

To further investigate the impact of this truncating mutation, using shRNA, we knocked down the expression of IkBe (by 56% and 60%, in two independent experiments) in the HG3 CLL cell line (Rosén et al., 2012), which revealed differential gene expression profiles between the knockdowns and the parental as well as the mock-transfected cell line (Fig. 5, E and F; and Table S12). Gene annotation enrichment analysis using the DAVID Bioinformatics Resources revealed that the top annotation clusters included regulation of apoptosis and cell death and regulation of the NF-κB signaling pathway (Table S13). Because the HG3 cell line is EBV transformed, which may seriously interfere with BcR signaling (Siemer et al., 2008), we next studied the global gene expression patterns in primary CLL cells from nine NFKBIE-deleted (mean allele frequency 45%, range 28–61%) and nine WT patients. Although an interesting up-regulation of several small nuclear RNAs (i.e., SNORD66, SNORD114-1, and SNORA80-B), previously linked to cancer (Gao et al., 2015), was observed in the NFKBIE-deleted group, only a few genes were significantly differentially expressed between the subgroups (Table S14). This finding might reflect previous gene expression profiling studies in U-CLL and M-CLL, showing only subtle differences in gene expression signatures in these clinically distinct subgroups (Klein et al., 2001; Rosenwald et al., 2001); along this line, one gene known to be up-regulated in U-CLL is ZAP70, and this gene also showed a higher expression in NFKBIE-deleted patients. In addition, as constitutive NF-κB activation has been observed in most, if not all, CLL patients, this may also override potential relevant yet subtler differences in gene expression between NFKBIE-deleted and WT patients.

**Altered response to ibrutinib in NFKBIE-deleted cases**

Finally, because truncating IkBe mutations appeared to lead to constitutive NF-κB activation independent of BcR signaling, we hypothesized that for NFKBIE-deleted patients no difference should be observed in the tumor cell response to ibrutinib.
the BcR inhibitor ibrutinib after αIgM stimulation. To test this hypothesis, we treated primary CLL cells from four NFKBIE-deleted and four NFKBIE WT patients with ibrutinib, in the presence or absence of αIgM stimulation. A difference in cell survival was observed between unstimulated versus stimulated IκBe- WT cells, whereas no such difference was seen in IκBe-mutated cases (Fig. 5 G), which were generally more sensitive to ibrutinib than WT patients. Although at first sight the finding that NFKBIE-deleted cases were generally more sensitive to ibrutinib than WT patients may seem counterintuitive, a similar observation has been reported for the ABC type of DLBCL and has been attributed to tonic activation of the BcR–NF-κB signaling pathway. Thus, along the same lines, one could reasonably hypothesize that because of tonic BcR signaling, NFKBIE mutant CLL cases could be more dependent on external stimulation and, hence, more sensitive to BTK inhibition (Davis et al., 2010; Mathews Griner et al., 2014).

In summary, we provide for the first time a novel genetic basis for NF-κB activation with the prime finding being recurrent mutations in genes belonging to the NF-κB pathway and in particular within the NFKBIE gene not only in CLL but also in other B cell–derived malignancies. In CLL, we show that NFKBIE aberrations were highly enriched in poor-prognostic, stereotyped subsets, potentially contributing to their adverse prognosis, and resulted in reduced IκBe

Figure 5. Functional analysis of the NFKBIE deletion in CLL. (A) Cytoplasmic (C) and nuclear (N) expression of p50, p65, and PARP in CLL patients. For the nuclear fraction, the expression ratio to PARP is provided. (B) Expression levels for p50, p65, and GAPDH in TCLs for the same patient. Normalized nuclear expression for p50 and p65 is provided. (C and D) Mean normalized nuclear expression of p50 (C) and p65 (D) in CLL. Error bars indicate standard error. (E) Western blot showing IκBe expression for the mock-transfected cells as well as the two independent knockdown clones (KD c1 and c2) in the HG3 cell line. All samples were run on the same gel but not in adjacent lanes and have therefore been quantified using the same exposure time. (F) Gene expression patterns in two independent CLL HG3 cell lines (c1 and c2) with partial knockdown (KD) of IκBe compared with the mock-transfected and untransfected (UT) HG3 cell lines. Genes that showed at least 50% difference in both c1 and c2 compared with either Mock or UT were selected. The list of genes is provided in Table S12. (G) Dose–response curves to the BTK inhibitor ibrutinib in primary CLL samples with WT NFKBIE (n = 4) and deleted NFKBIE (n = 4). Data were normalized against ibrutinib-naive CLL cells in culture. In NFKBIE WT cases, borderline significance was observed when comparing αIgM-stimulated versus unstimulated cells (P = 0.07 at 0.1 μM concentration, P = 0.06 at 1 μM concentration, and P = 0.05 at 2.5 μM concentration). Error bars indicate standard error.
protein levels and diminished interactions between IkBα–p65, as well as increased p65 phosphorylation and nuclear translocation. Notably, minor clones and/or clonal evolution were also observed, thus potentially linking IkBα loss to disease progression. Considering the central role of BcR stimulation in the natural history of CLL, the functional loss of IkBα may significantly contribute to sustained CLL cell survival in these patients. On these grounds, components of the NF-kB signaling pathway may emerge as possible targets for future therapies in CLL and, possibly, also other mature B cell lymphomas.

MATERIALS AND METHODS

Patient samples. In total, 692 CLL samples were collected from collaborating institutions in Sweden, Greece, Italy, France, Czech Republic, the Netherlands, the USA, and the UK. All cases were diagnosed according to the iwCLL criteria, displayed a typical CLL immunophenotype, and contained >70% tumor cells (Hallek et al., 2008). Clinicobiological characteristics of the discovery and validation cohorts are summarized in Tables S2 and S5. Mantle cell lymphoma (n = 136), DLBCL (n = 66), and splenic marginal zone lymphoma (n = 170) samples were diagnosed according to the WHO classification. The study was approved by the local Ethics Review Committees (Bmo: NT13493–4/2012, Milan: VIVI-CLL, New York: 08–202A, Thessaloniki: CERTH/EHT2, Uppsala: 214/33, Southampton: 06/Q2202/30, and Stockholm: 2006/964–31/2).

Targeted enrichment and library construction. We applied HaloPlex technology (Agilent Technologies) for targeted enrichment. For the discovery cohort, an earlier version of the current HaloPlex protocol was used. Biotin-labeled probes were designed for 18 NF-kB genes that targeted all coding exons with a high coverage (Tables S1 and S6). In brief, genomic DNA was fragmented using a combination of restriction enzymes. Biotin-labeled HaloPlex probes were hybridized to the target DNA and acted as template for a second universal DNA oligonucleotide, which contains primer sites, sequencing barcodes, and adapter sequences. The target DNA and the hybridized molecules were captured using streptavidin-labeled magnetic beads and circularized after a ligation reaction. The circularized DNA was amplified using universal primers. For the validation cohort, we took advantage of the automated HaloPlex protocol (http://www.chem.agilent.com/Library/usermanuals/Public/G9900-90020.pdf) using a Bravo Automated Liquid Handling Platform (Agilent Technologies). The libraries were subsequently sequenced using a HiSeq 2000 sequencing system (Illumina).

Targeted sequencing data analysis. Illumina adapters were trimmed using Cutadapt, and the reads were aligned to the human genome reference hg19/NCBI GRCh37 using the MOSAIK alignment tool version 2.2 (Martin, 2011). SAMTools was used for file format conversion and sorting. Using a modified version of GATK-lite, the aligned reads were mapped to their corresponding HaloPlex fragment. Variants were detected using an in-house, purpose-built variant caller (SNPmana) and annotated using ANNOVAR (Wang et al., 2010). Exonic variants were kept if they fulfilled the following criteria: (a) having a variant allele ratio of ≥0.1, (b) not in dbSNP and/or 1,000 genomes unless annotated in the Cosmic database, and (c) supported by at least two amplicons unless the position was covered by a single amplicon only.

Sanger sequencing and GeneScan analysis. Selected variants were sequenced using the BigDye Terminator v3.1 Cycle Sequencing kit and an ABI 3730 DNA Analyzer (Life Technologies) using standard protocols. For GeneScan analysis, the following oligonucleotides were used for the analysis of the 4-bp deletion in NFKBIE: forward primer, 5′-[Hex]CCTCAAAAAGTGGGCTTAGGA-3′; and reverse primer, 5′-CAAGGACACGAGGAAAGG-3′. Genomic DNA was amplified by hot-start PCR with Platinum-Taq DNA Polymerase (Invitrogen) and 60°C as annealing temperature. The fragment length of the PCR products was assessed by capillary electrophoresis with ABI3730XL DNA Analyzer (Applied Biosystems) and analyzed with Peak Scanner Software v1.0 (Applied Biosystems).

Western blots, co-IP assays, and cell fractions. Primary CLL cells were washed in PBS and lysed for 10 min in ice-cold RIPA buffer supplemented with phosphatase/protease inhibitors (Roche). Crude cell lysates were cleared by centrifugation and supernatants were transferred to new tubes. For collection of total cell lysates (TCLs), the supernatants were immediately mixed with 4× NuPAGE LDS sample buffer (Life Technologies) with DTT and treated at 95°C for 5 min. For co-IP assays, supernatants were first incubated 2 h at 4°C (end-over-end rotation) with 1:100 addition of either an anti-p65 antibody (a detailed list of all antibodies used is provided in Table S15) or a non-p65–targeting control antibody (AML1) followed by addition of protein A agarose beads (Cell Signaling Technology) and an extra hour of incubation. Beads were collected by centrifugation and washed three times in ice-cold RIPA buffer before being diluted in NuPAGE LDS Sample buffer (Life Technologies) supplemented with DTT and heated at 95°C for 5 min. Nuclear and cytoplasmic cell fractions were obtained as previously described by Andrews and Faller (1991). Denatured samples were separated on NuPAGE Novex 4–12% Bis-Tris Gels (Life Technologies) and transferred to nitrocellulose membranes using iBlot (Life Technologies). Blocking was performed at room temperature by incubating membranes for 1 h in 5% wt/vol nonfat dry milk (Bio-Rad Laboratories) or 5% wt/vol BSA (Sigma–Aldrich) in TBS buffer. Primary antibodies were diluted in TBS-T (0.1% Tween-20) with 5% wt/vol nonfat dry milk (Bio-Rad Laboratories) or 5% wt/vol BSA (Sigma–Aldrich) and were incubated together with the blocked membranes at 4°C over night. Before imaging, membranes were washed (3× 20 min) in TBS-T (0.1% Tween-20), incubated 1 h with secondary antibodies (1:10,000/1:20,000) of the IRDye 800CW goat anti-rabbit IgG and/or 1:20,000 of the IRDye 680RD donkey anti–mouse IgG (LI-COR Biosciences) in TBS-T (0.1% Tween-20) with 5% wt/vol BSA, washed (3× 15 min) in TBS-T (0.1% Tween-20), and finally rinsed 5 min in TBS buffer only. All incubation steps were performed at room temperature. Membranes were scanned and imaged using the Odyssey CLx Infrared Imaging System (LI-COR Biosciences). Protein bands were quantified using ImageJ software (National Institutes of Health).

Stimulation of BcR and CD40 signaling pathways. Two million viable primary CLL cells per milliliter were grown in RPMI medium supplemented with 10% FBS (Gibco), 1% PEST (Gibco), and 1% l-glutamine (Gibco). supplemented with 25% vol/vol serum-free supernatant from the T cell hybridoma cell line MP6 (Rosén et al., 1986), as a source of thioredoxin (Soderberg et al., 1999; Nilsson et al., 2000). For stimulation of the BcR, the modified RPMI medium was supplemented with 3 µg/ml AffiPure Fab(’a)2 fragment rabbit anti–human IgM (Jackson ImmunoResearch Laboratories, Inc.), 10 ng/ml IL-2 (GE Healthcare), and 1 µg/ml streptavidin (Roche). To stimulate the CD40 signaling pathway, cells were treated with the modified RPMI medium supplemented with 100 ng/ml sCD40L (Enzo Life Sciences), 25 ng/ml IL-4 (R&D Systems), and 100 ng/ml IL-10 (R&D Systems). Cells were stimulated for 15 min at 37°C (5% CO2). Cytospins were prepared using 150,000 cells per slide and a Cellspin I cytocentrifuge (Thar mac) at 500 rpm for 2 min.

Proximity ligation assay. The cells were fixed in 3.7% formaldehyde solution (Sigma–Aldrich) for 15 min at room temperature and permeabilized in 0.5% Triton X-100 (GE Healthcare) for 2 min at room temperature. All washing steps were performed twice for 5 min in 1× TBS with 0.05% Tween (Sigma–Aldrich) unless stated otherwise. First, the samples were incubated in a blocking solution (Olink Biosciences) for 1 h at 37°C. The primary antibodies were diluted as follows, p65 (Cell Signaling Technology) 1:400, 1kBe (Cell Signaling Technology) 1:50, 1kBB (Santa Cruz Biotechnology, Inc.) 1:50, 1kBE (Santa Cruz Biotechnology, Inc.) 1:200, and 1kBB (Cell Signaling Technology) 1:50 in antibody diluent solution (Olink Biosciences) and applied to the samples for incubation overnight at 4°C. The samples were then washed and incubated with DsRedIn Situ PLA Probe

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anti–mouse MINUS Affinity donkey anti–mouse IgG and DuoLink In Situ PLA Probe anti–rabbit PLUS Affinity donkey anti–rabbit IgG (Olink Biosciences) diluted 1:5 in antibody diluent solution (Olink Biosciences) for 1 h at 37°C, followed by washing. A hybridization solution containing 0.25 mg/ml BSA (New England Biolabs, Inc.), 25 mM NaCl, 0.05% Tween-20 (Sigma-Aldrich), 10 mM TrisAc, 10 mM MgAc, 50 mM KAc, and 125 mM of circularization oligonucleotides (5′-GGGCTGCTATATTTAAGTGCTTTCAAT-3′ and 5′-CTATTAGCGTCCAGTGAATGCGAGTCGTTGCAAGGACTGCT-3′; Integrated DNA Technology) at pH 7.5 were applied to the sample for 30 min incubation at 37°C, followed by washing. Both oligonucleotides were phosphorylated in the 5′ end. Ligation of the circularization oligonucleotides were performed in 1× T4 DNA ligase buffer (Fermentas, Thermo Fisher Scientific), 0.05 U/µl T4 DNA ligase (Fermentas), and ddH2O for 30 min at 37°C, followed by washing. Rolling circle amplification was performed by incubating the samples in 0.25 mg/ml BSA (New England Biolabs, Inc.), 300 ng/ml poly-adenosine, 1× phi29 DNA polymerase buffer (Fermentas), 0.25 mM dNTP (Thermo Fisher Scientific), 1 µM Hoechst 33342 (Sigma-Aldrich), 0.25 U/µl phi29 DNA polymerase (Fermentas), and a BODYPH TR–labeled oligonucleotide (5′-CAGTGAGATCCCGATCCGCTUUUU-3′, U represents Uracil 2′O methyl RNA group; Trilink) for 90 min at 37°C. Finally, the samples were washed twice in 1× TBS supplemented with TWEEN (Sigma-Aldrich) and once in 1× TBS, followed by centrifugation of the slides. SlowFade Gold antifade reagent (Life Technologies) was used for mounting of the slides. Images were acquired with an Axioplan 2 imaging microscope (Carl Zeiss) using 40× objectives and an AxioCam MRm camera (Carl Zeiss). Exposure times, number of z-levels, and distance between z-levels were kept the same for all patients within each assay. CellProfiler version one was used to quantify number of signals per cell in raw images. The interactions between the IgBs and p56 were normalized against the number of interactions between p65 and p50 for each sample.

**Stable knockdown of IκBε.** Stable knockdown of IκBε in the HG3 CLL cell line was established using the pGPZ lentiviral vector (V3LHS_365665) and the mature antisense sequence 5′-TGCTCCAGATGTCAAGGCCA-3′ (GE Healthcare). The plasmid was linearized using SpI restriction enzyme (Fermentas). HG3 cells were transfected with 3 µg of plasmid DNA per 106 cells by electroporation using the Neon Transfection System (Thermo Fisher Scientific) and standard parameters. Puroycin selection was started 48 h after transfection and cells were kept under Puroycin selection. Additional selection for positive clones was performed by FACS sorting for cells expressing tGFP, expressed from the same promoter as the shRNA and the Puroycin resistance gene.

**Gene expression analysis.** Gene expression was studied using Affymetrix GeneChip Human Gene 2.0 ST Arrays (Affymetrix) and 250 ng total RNA according to standard protocols. Data were analyzed in R (The R Project for Statistical Computing) using packages from the Bioconductor project and normalized using the robust multi-array average method (Irizarry et al., 2003). To search for differentially expressed genes, an empirical Bayes moderated Student’s t test was used applying the “limma” package. The p-values were adjusted using the method of Benjamini and Hochberg to address potential problems with multiple testing (Benjamini and Hochberg, 1995). Genes with an adjusted p-value <0.05 were regarded as differentially expressed. Gene annotation enrichment analysis was performed using the DAVID Bioinformatics Resources.

**Ibrutinib treatment and cell viability test.** Unstimulated and aIgM-stimulated (10 µg/ml for 15 min) primary CLL cells from four NFLKBIΕ WT patients and four NFLKBIΕ-deleted patients were plated in quadruplicate wells at a density of 100,000 cells per well in 96-well plates followed by ibrutinib (PCI-32765; Selleckchem) treatment at 0, 0.1, 1, 2.5, and 10 µM concentration for 72 h. Alamar Blue (Life Technologies) was added, and cell viability was measured after 24 h using a VICTOR plate reader (PerkinElmer) and standard protocols. Data were normalized against ibrutinib naive matched controls.

**Statistical analysis.** Paired Student’s t test was used to assess differences between subgroups with at least four patients in each subgroup. Friedman ANOVA was used to study differences in NFLKBIΕ mutation frequency among CLL subset cases. Kaplan–Meier analysis was performed to construct survival curves for TTFT, defined as the time interval from the diagnosis date until date of initial treatment, and the log-rank test was used to assess differences. All statistical analyses were performed using Statistica version 12 (StatSoft).

**Online supplemental material.** Table S1 shows the 18 NF-κB core complex genes targeted for deep sequencing in the discovery cohort. Table S2 shows the clinical and biological characteristics of CLL patients in the discovery cohort. Table S3 shows a summary of mutations found in the discovery cohort (n = 124) with additional molecular data. Table S4 shows low-frequency NFLKBIΕ deletions (<10%) detected in the discovery (n = 124) and validation cohorts (n = 191). Table S5 shows clinical and biological characteristics of CLL patients in the validation cohort. Table S6 shows the 18 NF-κB core complex genes targeted for deep sequencing in the validation cohort. Table S7 shows a summary of mutations found in the validation cohort (n = 191). Table S8 shows clinical and biological characteristics of the population-based CLL cohort. Table S9 shows a summary of NFLKBIΕ deletions detected by GeneScan analysis (n = 383). Table S10 shows multivariate analyses for TTFT (A) and for TTFT excluding IGHV mutation status (B). Table S11 shows allelic ratio of the deleted NFLKBIΕ allele detected by GeneScan analysis. Table S12 shows differentially expressed genes in the HG3 cell line after NFLKBIΕ knockdown. Table S13 shows gene annotation enrichment analysis performed using the DAVID Bioinformatics Resources for differentially expressed genes in HG3 cell line after NFLKBIΕ knockdown. Table S14 shows a list of significantly differentially expressed genes in NFLKBIΕ-deleted versus NFLKBIΕ WT cases. Table S15 shows the list of antibodies used. Online supplemental material is available at http://www.jem.org/cgi/content/full/jem.20142009/D1C1.

Sequencing was performed by the SNP&SEQ Technology Platform, Science for Life Laboratory at Uppsala University, a national infrastructure supported by the Swedish Research Council (VRFFI) and the Knut and Alice Wallenberg Foundation. The computations were performed on resources provided by SNIC through Uppsala Multidisciplinary Center for Advanced Computational Science (UPPMAX) under Project b2011080. Gene expression profiling was performed at Uppsala Array Facility, and FACS-sorting was performed at the BioVis imaging facility, Science for Life Laboratory, Uppsala University.

This research project was supported by the Nordic Cancer Union, the Swedish Cancer Society, the Swedish Research Council, the Lion’s Cancer Research Foundation, Selandor’s Foundation, Uppsala, the Hans von Kantzow Foundation, The Cancer Society in Stockholm, The Stockholm County Council, Leukemia and Lymphoma Research, The Kay Kendal Leukaemia Fund, The National Cancer Institute, National Institutes of Health (NIH), USA (CA181554), R01 grant CA081554 from the NIH National Cancer Institute to N. Chiorazzi, and the European Community’s Seventh Framework Program (FP7/2007–2013) under grant agreement no. 259796 (DiTools), Associazione Italiana per la Ricerca sul Cancro (AIRC; Investigator Grant and Special Program Molecular Clinical Oncology–IG and 5 per mille #9965) and Ricerca Finalizzata 2010 (RF-2010-2318823)–Ministero della Salute, Roma; IGA MZ CR NT13493-4, CEITEC project CZ.1.05/1.1.00/02.0068, and Swedish Research Council (VRRFI) and the Knut and Alice Wallenberg Foundation. The computations were performed on resources provided by SNIC through Uppsala Multidisciplinary Center for Advanced Computational Science (UPPMAX) under Project b2011080. Gene expression profiling was performed at Uppsala Array Facility, and FACS-sorting was performed at the BioVis imaging facility, Science for Life Laboratory, Uppsala University.
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