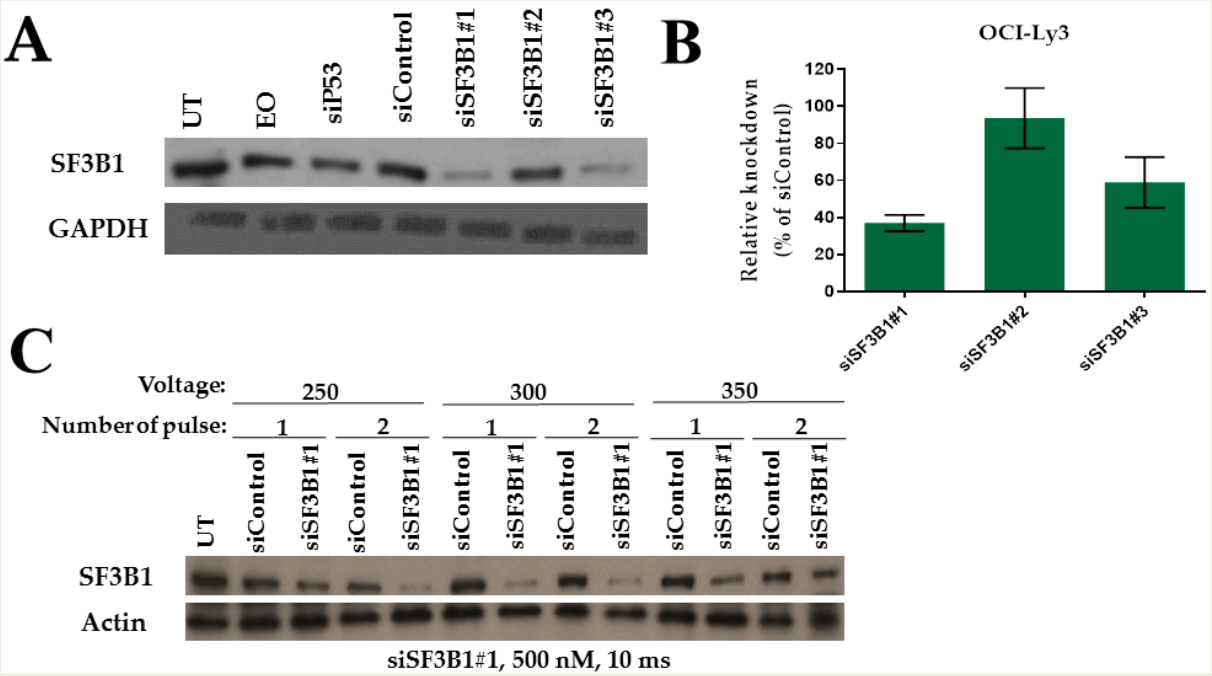
Supplementary Table S1. List of patients with CLL that carry *SF3B1* mutations.

Clinical information				p53		*SF3B1* mutation		
[1]Tumour ID	Age	Sex	Cytogenetic abnormalities	[2]*TP53* status	LC_{50} RG7388 (μM)	[3]Clone size (%)	[4]p_description	c_description
27	79	M	del(13q) del(11q)	WT		50	p.K700E	c.2098A>G
49	64	M	del(17p)	p.D208V (73%)		50	p.K700E	c.2098A>G
63	61	F	del(13q) del(11q) del(17p) 17%	WT		40	p.K700E	c.2098A>G
64	74	M	del(11q)	WT		50	p.K741N	c.2223G>T
81 (158,233)	60	M	del(13q) del(11q)	WT		30	p.K700E	c.2098A>G
88	60	M	None	WT		30	p.K741N	c.2223G>T
89(193)	60	M	del(13q)	WT		10	p.K700E	c.2098A>G
105	66	F	None	WT		50	p.G742D	c.2225G>A
158 (81,233)	61	M	del(13q) del(11q)	WT		50	p.K700E	c.2098A>G
169	57	M	del(13q)	WT		20; 30	p.K700E ; p.R775G	c.2098A>G ; c.2323C>G
183	67	F	None	WT		50	p.K666E	c.1996A>G
188	68	M	None	WT		30	p.G742D	c.2225G>A
193 (89)	63	M	del(13q)	WT		20	p.K700E	c.2098A>G
199	45	M	del(13q) del(17p)	c.375+2T>G p.?, Splice (39%)		50	p.K666T	c.1997A>C
207	81	F	del(13q)	WT		50	p.K700E	c.2098A>G
221	86	M	None	WT	0.17	50	p.W658C	c.1974G>T
225 (272)	66	F	None	WT	0.2	40	p.K700E	c.2098A>G
233 (81,158)	66	M	del(13q) del(11q)	WT	>10	50	p.K700E	c.2098A>G
240	72	F	None	WT	>10	20	p.K666E	c.1996A>G
243	76	F	None	WT	0.72	50	p.K700E	c.2098A>G
270	75	M	del(13q)	WT	0.35	50	p.Y623C	c.1868A>G
272 (225)	69	F	None	WT	0.33	50	p.K700E	c.2098A>G
283	69	F	None	p.R249G (48%)	9.2	30	p.G742D	c.2225G>A
287	69	M	del(13q) del(11q)	p.R175H (50%)	2.7	30	p.K700E	c.2098A>G
288	72	F	None	WT	>10	50	p.G740E	c.2219G>A
290	65	M	None	WT	>10	50	p.I704F	c.2110A>T
299	71	F	None		6	50	p.R775Q	c.2324G>A
305	81	M	None		0.3	50	p.K741N	c.2223G>C

[1]Numbers in brackets show the sequential samples from the same patient (e.g. 81(158, 233)).
[2]NGS was used to assess the mutational status of *TP53* (WT:wild-type, or mutation specified with mutant allele frequency in brackets).
[3]Sanger sequencing was used to detect *SF3B1* mutations. Approximate mutant clone percentages obtained from Sanger sequencing chromatograms are shown.
[4]Amino acid positions of the frequently mutated coding sites: 603-693 (exon14), 693-741 (exon15), 742-790 (exon16).
Blank boxes indicate that there is no data available.



Supplementary Figure S1. Optimization for siRNA delivery in OCI-Ly3 cells. (A) Silencing of SF3B1 using three different siRNA constructs (siSF3B1#1, siSF3B1#2, and siSF3B1#3) in OCI-Ly3 cells under the same electroporation conditions (500 nM siRNA; 300 volts; 1 pulse; 10 ms). Representative western blot shows the SF3B1 protein levels 24 hours after siRNA transfection. GAPDH was used as loading control. UT: untreated; EC: electroporation only control; siP53: control targeting different mRNA **(B)** SF3B1 protein levels were normalized to siControl and loading control for the three different siSF3B1 constructs. ImageJ 1.41 image processing was used to make quantitative measurement of detected protein bands of interest. Error bars show the mean±SEM for three independent repeats. **(C)** Knockdown of SF3B1 by 500 nM siSF3B1#1 was assessed for varied electroporation conditions including three different voltages (250, 300, or 350 volts) and two different number of pulses (1 or 2 pulse/s) by western blotting. Actin was used as loading control.