SUPPLEMENTARY TABLES

Table S1: Anti-oxidant gene list used for gene set enrichment analysis of *Ppp2r1a*$^{fl/fl}$ B-ALL cells, Related to Figure 2.

Gene Symbol	**Description**
Aass	aminoadipate-semialdehyde synthase (Aass)
Alb	albumin (Alb)
Apc	adenomatosis polyposis coli (Apc)
Cat	catalase (Cat)
Ctsb	cathepsin B (Ctsb)
Epx	eosinophil peroxidase (Epx)
Ehd2	EH-domain containing 2 (Ehd2)
Ercc6	excision repair cross-complementing rodent repair deficiency, group 6 (Ercc6),
Gab1	growth factor receptor bound protein 2-associated protein 1 (Gab1)
Gpx1	glutathione peroxidase 1 (Gpx1)
Gpx2	glutathione peroxidase 2 (Gpx2)
Gpx3	glutathione peroxidase 3 (Gpx3), transcript variant 1
Gpx4-1	glutathione peroxidase 4 (Gpx4), transcript variant 2
Gpx4-2	glutathione peroxidase 4 (Gpx4), transcript variant 1
Gpx5	glutathione peroxidase 5 (Gpx5)
Gpx6	glutathione peroxidase 6 (Gpx6)
Gpx7	glutathione peroxidase 7 (Gpx7)
Gpx8	glutathione peroxidase 8 (putative) (Gpx8)
Gsta1-1	glutathione S-transferase, alpha 1 (Ya) (Gsta1)
Gsta1-2	glutathione S-transferase, alpha 1 (Ya) (Gsta1)
Gsta2	glutathione S-transferase, alpha 2 (Yc2) (Gsta2)
Gstk1	glutathione S-transferase kappa 1 (Gstk1), nuclear gene encoding mitochondrial protein
Gstm1	glutathione S-transferase, mu 1 (Gstm1)
Gstm5	glutathione S-transferase, mu 5 (Gstm5)
Gstm6	glutathione S-transferase, mu 6 (Gstm6)
Gsto1	glutathione S-transferase omega 1 (Gsto1)
Gstp1	glutathione S-transferase, pi 1 (Gstp1)
Gstp2-1	glutathione S-transferase, pi 2 (Gstp2)
Gstp2-2	glutathione S-transferase, pi 2 (Gstp2)
Gstt1	glutathione S-transferase, theta 1 (Gstt1)
Gstt2	glutathione S-transferase, theta 2 (Gstt2)
Gstt4	glutathione S-transferase, theta 4 (Gstt4)
Gsr	glutathione reductase (Gsr)
Idh1	isocitrate dehydrogenase 1 (NADP+), soluble (Idh1), transcript variant 2
Kif9	kinesin family member 9 (Kif9), transcript variant 2
Lpo	lactoperoxidase (Lpo)

Mpo	myeloperoxidase (Mpo), nuclear gene encoding mitochondrial protein
Mt1	metallothionein 1 (Mt1)
Mt2	metallothionein 2 (Mt2)
Nqo1	NAD(P)H dehydrogenase, quinone 1 (Nqo1)
Nudt15-1	nudix (nucleoside diphosphate linked moiety X)-type motif 15 (Nudt15)
Nudt15-2	nudix (nucleoside diphosphate linked moiety X)-type motif 15 (Nudt15)
Nxn	nucleoredoxin (Nxn)
Park7	Parkinson disease (autosomal recessive, early onset) 7 (Park7)
Prdx1-1	peroxiredoxin 1 (Prdx1)
Prdx1-2	peroxiredoxin 1 (Prdx1)
Prdx2-1	peroxiredoxin 2 (Prdx2), nuclear gene encoding mitochondrial protein
Prdx2-2	peroxiredoxin 2 (Prdx2), nuclear gene encoding mitochondrial protein
Prdx3	peroxiredoxin 3 (Prdx3), nuclear gene encoding mitochondrial protein
Prdx4	peroxiredoxin 4 (Prdx4)
Prdx5	peroxiredoxin 5 (Prdx5), nuclear gene encoding mitochondrial protein
Prdx6	peroxiredoxin 6 (Prdx6)
Prdx6-ps1	peroxiredoxin 6, pseudogene 1 (Prdx6-ps1)
Prnp	prion protein (Prnp)
Ptgs1	prostaglandin-endoperoxide synthase 1 (Ptgs1)
Ptgs2	prostaglandin-endoperoxide synthase 2 (Ptgs2)
Serpinb1b	serine (or cysteine) peptidase inhibitor, clade B, member 1b (Serpinb1b)
Slc41a3	solute carrier family 41, member 3 (Slc41a3), transcript variant 1
Sod1	superoxide dismutase 1, soluble (Sod1)
Sod2	superoxide dismutase 2, mitochondrial (Sod2)
Sod3	superoxide dismutase 3, extracellular (Sod3)
Srxn1	sulfiredoxin 1 homolog (S. cerevisiae) (Srxn1)
Tmod1	tropomodulin 1 (Tmod1)
Tpo	thyroid peroxidase (Tpo)
Txnrd1	thioredoxin reductase 1 (Txnrd1), transcript variant 1
Txnrd2	thioredoxin reductase 2 (Txnrd2), nuclear gene encoding mitochondrial protein
Txnrd3	thioredoxin reductase 3 (Txnrd3), transcript variant 1
Xpa	xeroderma pigmentosum, complementation group A (Xpa)
Zmynd17	zinc finger, MYND domain containing 17 (Zmynd17)

Table S2: Patient-derived pre-B ALL samples used in this study, Related to Figure 3.

Case	**Cytogenetics**	**Oncogene**	**Clinical course**	**Gender/Age**
ICN1	t(9;22)(q34;q11)	*BCR-ABL1;* p210	At diagnosis	m
LAX2	t(9;22)(q34;q11)	*BCR-ABL1;* p210 protein, T315I mutation	Relapse (Imatinib)	m/38
PDX2	der(9)(q10),t(9;22)(q34;q11)	*BCR-ABL1*	At diagnosis	f/52
MXP2	t(9;22)(q34;q11)	*BCR-ABL1*; p190	At diagnosis	6
BLQ5	FISH der(9),der(22)	*BCR-ABL1;* p190, T315I mutation	Relapse (Imatinib)	f

Notes: All primary samples are bone marrow biopsies, blast content >80%; ICN, Seoul; LAX, Los Angeles; PDX, Portland; MXP, Milan; f, female; m, male

Table S3: Patient-derived B-cell lymphoma samples used in this study, Related to Figure 3.

Case	**WHO Classification**	**Cytogenetics**	**Mutations**	**Clinical course**	**Gender/Age**
BOS4	Mantle cell lymphoma	t(11;14)(q13;q32) *IGH-CCND1*	*NOTCH1*$^{\text{P2514fs*4}}$ *KRAS*$^{\text{S136R}}$	Relapse	m/81
BOS5	Mantle cell lymphoma	t(11;14)(q13;q32) *IGH-CCND1*	*ATM*$^{\text{V1671fs*}}$ *TP53*$^{\text{R248W}}$ *WHSC1*$^{\text{E1099K}}$ *ATM*$^{\text{R2459P}}$ *CREBBP*$^{\text{Q2257H}}$	Relapse	m/63
BOS6	Mantle cell lymphoma	N/A	N/A	Progressive	m/76
BOS10	DLBCL	*MYC*, *BCL2*	*MLL2*$^{\text{P1460fs}}$ *MLL2*$^{\text{Q4609*}}$ *TP53*$^{\text{C277F}}$	Relapse	m/77
BOS12	DLBCL	*MYC*, *BCL2*	N/A	At diagnosis	m/64

Notes: All primary samples are from peripheral blood, BOS, Boston; f, female; m, male

Table S4: Patient-derived chronic myeloid leukemia samples used in this study, Related to Figure 3.

ID	**Cytogenetics**	**Oncogene**	**Clinical course**	**Gender/Age**
34903803	t(9;22)(q34;q11)	*BCR-ABL1;* b2a2	At diagnosis	m/36
34932094	t(9;22)(q34;q11)	*BCR-ABL1;* e1a2	At diagnosis	m/75
34947803	t(9;22)(q34;q11)	*BCR-ABL1;* b3a2	At diagnosis	f/27
35041796	t(9;22)(q34;q11)	*BCR-ABL1;* b3a2	At diagnosis	m/26
35124465		*BCR-ABL1;* b3a2	At diagnosis	f/71
35671299	t(9;22)(q34;q11)	*BCR-ABL1;* b3a2	At diagnosis	f/63
34932375	t(9;22)(q34;q11)	*BCR-ABL1;* b3a2, b2a2	At diagnosis	f/52
35250994	t(9;22;2)(q34;q11.2;q33)	*BCR-ABL1;* b2a2	At diagnosis	f/30
33822816	t(9;22)(q34;q11)	*BCR-ABL1;* b2a2	At diagnosis	m/64
33758468	t(9;22)(q34;q11)	*BCR-ABL1;* b3a2	At diagnosis	m/72

Notes: CP, chronic phase; f, female; m, male

Table S5: PFK1 mutations found in B-cell tumor cell lines and PDX, Related to Figure 5

Gene Name	Sample Name	AA	CDS	Sample	Histology
PFKL	HT	p.Y561N	c.1681T>A	Cell line	B-cell, DLBCL
PFKL	L1236	p.A436T	c.1306G>A	Cell line	B-cell, Hodgkin's lymphoma
PFKL	GR-ST	p.L737P	c.2210T>C	Cell line	B-cell, ALL
PFKM	WSU-DLCL2	p.G342E	c.1025G>A	Cell line	B-cell, DLBCL
PFKM	SFO1	p.E512Q	c.1808G>C	PDX	B-cell, ALL
PFKM	SFO1	p.E441Q	c.1506G>C	PDX	B-cell, ALL
PFKM	BLQ6	p.T503K	c.1693C>A	PDX	B-cell, ALL
PFKP	JEKO-1	p.?	c.9-1G>C	Cell line	B-cell, Mantle cell lymphoma
PFKP	DG-75	p.?	c.431-7C>T	Cell line	B-cell, Burkitt's lymphoma
PFKP	SUP-HD1	p.?	c.846+5G>A	Cell line	B-cell, Hodgkin's lymphoma
PFKP	NALM-6	p.R567Q	c.1700G>A	Cell line	B-cell, ALL
PFKP	SUP-HD1	p.A590S	c.1768G>T	Cell line	B-cell, Hodgkin's lymphoma
PFKP	SUP-HD1	p.E734E	c.2202G>A	Cell line	B-cell, Hodgkin's lymphoma
PFKP	LAX7	p.Q99R	c.332A>G	PDX	B-cell, ALL
PFKP	ICN3	p.Q99R	c.332A>G	PDX	B-cell, ALL
PFKP	SFO3	p.Q99R	c.332A>G	PDX	B-cell, ALL
PFKP	RS4-11	p.R49Q	c.146G>A	Cell line	B-cell, ALL
PFKP	ROS-50	p.D159E	c.477T>A	Cell line	B-cell, ALL
PFKP	Daudi	p.Q498L	c.1493A>T	Cell line	B-cell, Burkitt's lymphoma

Table S6: Oligonucleotide sequences of primers and gRNA sequences for CRISP-Cas9 mediated gene disruption, Related to Figure7

Experiment	**Name**	**Sequence (5’ to 3’)**
Ppp2r1a$^{fl/fl}$ mice genotyping	loxP sites flanked allele Forward	AGGACAAGTCTTGGCGTG
Ppp2r1a$^{fl/fl}$ mice genotyping	loxP sites flanked allele Reverse	GAATTAAACCCAGGACCCCTGG
Ppp2r1a$^{fl/fl}$ mice genotyping	Cre-deleted allele Forward	CAGCACCAGGATATCAGGATCCG
Ppp2r1a$^{fl/fl}$ mice genotyping	Cre-deleted allele Reverse	TGCAGGGCCTTGTACTGTACTTATGAG
Mb1-Cre mice genotyping	Targeted allele Forward	CCCTGTGGATGCCACCTC
Mb1-Cre mice genotyping	Targeted allele Reverse	GTCCTGGCATCTGTCAGAG
Mb1-Cre mice genotyping	Wild type allele Forward	TTCAGCCTTCAGTCTAACATC
Mb1-Cre mice genotyping	Wild type allele Reverse	ATCTGTGAAGACAGGGTGC
Quantitative ChIP	*G6PD* Promoter Forward	ACAGCTATGACACCGGAAGC
Quantitative ChIP	*G6PD* Promoter Reverse	AAAGGACCACACCTGTCAGC
Quantitative ChIP	*CD19* Promoter Forward	ACCACCGCCTTCCTCTCTG
Quantitative ChIP	*CD19* Promoter Reverse	TGGCATGGTGGTCAGACTCT
Quantitative ChIP	*ACTA1* Promoter Forward	AGAGTCAGAGCAGCAGGTAG
Quantitative ChIP	*ACTA1* Promoter Reverse	CAAGGCTCAATAGCTTTCTT
gRNA target sequence (no PAM)	*PPP2R1A*-1	GCGCAGAGTGGGCATCACCA
gRNA target sequence (no PAM)	*PPP2R1A*-2	ACTTGTCAGCCACCATGTAG
gRNA target sequence (no PAM)	*PPP2R1A*-3	GGTGGCTGACAAGTTCACAG
gRNA target sequence (no PAM)	Non-targeting	GGAGCGCACCATCTTCTTCA

Table S7: Combination Index (CI) values of combined treatment with LB-100 and 6-AN, Related to Figure 7.

		Combination Index values			
Cell	**Combination**	**ED_{50}**	**ED_{75}**	**ED_{90}**	**ED_{95}**
PDX2 (*Ph*$^+$ ALL)	LB-100 + 6-AN (1:4)	0.06953	0.03037	0.01352	0.00784
	LB-100 + 6-AN (1:6)	0.29489	0.24600	0.20572	0.18243
MXP2 (*Ph*$^+$ ALL)	LB-100 + 6-AN (1:4)	0.49049	0.38942	0.31530	0.27584
	LB-100 + 6-AN (1:6)	0.47072	0.36051	0.27701	0.23199
SP53 (Mantle cell lymphoma)	LB-100 + 6-AN (1:6)	0.02438	0.02366	0.02394	0.02469
OCI-Ly10 (DLBCL)	LB-100 + 6-AN (1:6)	0.22545	0.24767	0.27933	0.30676