Table S1. V_H region genes in human Ph^- ALL cells

Case	V_H	D_H	J_H	Mutation frequency [per 10^3 bp]	Cytogenetics	Genes involved
1	V6-1	D2-2	J4	0	Hyperdiploid	N.N.
2	V4-61	none	J4	26	t(9;15)(p2;q1)	N.N.
3	V3-13	D2-15	J5	0	Hyperdiploid	N.N.
4	V3-66	none	J4	67	Hyperdiploid ; del(6)(q2)	N.N.
5	V4-34	none	J6	0	Hyperdiploid	N.N.
6	V4-34	D3-22	J4	30	del(6)(q2q5)	N.N.
7	V4-39	D3-22	J6	4	Hyperdiploid, trisomy 14	N.N.
8	V4-59	D3-10	J6	0	Hyperdiploid	N.N.
9	V3-64	none	J5	19	t(17;22)(q25;q11)	*BCR* locus
	V7-4	D6-19	J2	22		
	V1-18	D3-3	J6	11		
10	V3-33	D2-2	J6	0	t(3;12)(p11;p13)	*TEL* rearranged
	V4-4	none	J1	4		
11	V4-34	D1-20	J4	0	Hyperdiploid	N.N.
12	V1-3	D6-6	J5	0	Hyperdiploid	N.N.
13	V6-1	D2-8	J6	4	Hyperdiploid	N.N.
14	V5-a	D2-15	J6	4	t(4;11)(q21;q23)	*MLL-AF4*
15	V3-74	D2-2	J4	0	t(1;12)(p32;p12),t(7;7)(q22;q36)	*TEL* rearranged
16	V3-33	none	J6	0	no gross abnormality	N.N.
17	V6-1	D2-21	J6	0	t(2;14)(q23;q32); t(12;21)(p13;q22)	*IGH* locus; *TEL-AML1*
18	V6-1	D3-10	J6	0	Hyperdiploid	N.N.
19	V4-34	D3-16	J4	4	Hyperdiploid	N.N.
20	V1-3	none	J4	4	del1(q?)	N.N.
21	V2-5	D5-12	J5	7; 69-bp in V_H	Hyperdiploid	N.N.
22	V2-70	D3-10	J4	4	der(9)t(9;22)(p11;q11)	*BCR* locus
23	V3-9	D3-3	J6	7	Hyperdiploid	N.N.
24	V1-58	none	J6	4, 70-bp in V_H	Hyperdiploid	N.N.
25	V2-5	D2-15	J4	0	Hyperdiploid	N.N.
26	V2-5	D3-10	J6	7	t(11;19)(q23;p13.3)	*MLL-ENL*
27	V3-23	D2-2	J6	4	Hyperdiploid	N.N.
28	V2-5	D3-10	J6	0	Hyperdiploid	N.N.
29	V4-34	D6-19	J4	4	Hyperdiploid	N.N.
30	V3-53	D2-21	J4	4	Hyperdiploid	N.N.
31	V6-1	D2-2	J6	0	Hyperdiploid	N.N.
32	V4-34	D3-9	J6	0	no gross abnormality	N.N.
33	V1-8	D3-3	J4	4	t(1;19)(q23;p13)	*E2A-PBX1*
	V3-66	D2-2	J4	0		
34	V2-70	D3-10	J6	0	der(12)t(12;14)(p12;q11)	*TEL* rearranged
35	V6-1	D2-2	J6	0	del(10)(p11)	N.N.
36	V3-21	none	J6	0	del(9)(p11),del(17)(p11)	N.N.
37	V3-9	D2-15	J4	0	Hyperdiploid	N.N.
38	V3-30	D3-10	J6	0	Hyperdiploid	N.N.
39	V2-5	D2-2	J3	0	t(12;21)(p13;q22)	*TEL-AML1*
	V3-15	D3-19	J6	4		
40	V4-34	D2-15	J6	4	t(12;21)(p13;q22)	*TEL-AML1*
	V4-39	none	J6	0		
41	V3-13	D3-22	J6	7	t(4;11)(q21;q23)	*MLL-AF4*
	V2-5	D2-2	J6	0		
42	V3-20	D2-8	J5	0	t(4;11)(q21;q23)	*MLL-AF4*
	V6-1	D1-7	J4	0		
43	V3-15	D3-10	J6	4	t(12;21)(p13;q22), t(16;21)(q24 ;q22)	*TEL-AML1*
44	V4-34	D3-22	J2	0	t(1;19)(q23;p13), del(6)(q21)	*E2A-PBX1*
	V2-26	D2-2	J4	4		
45	V3-7	D3-10	J4	4	t(1;19)(q23;p13), t(3;14)(q27;q24)	*E2A-PBX1*
46	V3-15	D3-16	J5	0	t(1;19)(q23;p13); t(9;9)(q21;q11)	*E2A-PBX1*
47	V1-69	D3-10	J6	7	t(5 ;12)(q33 ;p13)	*TEL-PDGFRB*
48	V6-1	D5-5	J6	0	Hyperdiploid	N.N.
	V4-59	D2-8	J6	0		
49	V1-8		J5	34	Hyperdiploid	N.N.
50	V1-8	D2-15	J6	0	Hyperdiploid	N.N.
51	V3-13	D3-22	J6	4	Hyperdiploid	N.N.
52	V1-18	D3-10	J4	0	Hyperdiploid	N.N.
53	V3-23	D3-16	J4	0	Hyperdiploid	N.N.
54	V3-9	D3-22	J4	0	Hyperdiploid	N.N.
55	V1-18	D2-8	J6	0	Hyperdiploid	N.N.
56	V3-15	D2-2	J4	7	Hyperdiploid	N.N.
57	V1-2	D3-22	J5	0	Hyperdiploid	N.N.
58	V6-1	D3-16	J4	0	Hyperdiploid	N.N.
59	V1-45	D3-9	J5	7	Hyperdiploid	N.N.
60	V3-53	D6-19	J6	10	Hyperdiploid	N.N.
Mean ± S.E.M.:				4.85 ± 1.23 mutations per 10^3 bp		

Cases 1–9 were previously described (Height, S.E., G.J. Swansbury, E. Matutes, J.G. Treleaven, D. Catovsky, and M.J. Dyer. 1996. *Blood*. 87:5242–5250). Sequence data were reanalyzed based on the full sequence of human germline *IGHV* genes according to Matsuda et al. (Matsuda, F., K. Ishii, P. Bourvagnet, K. Kuma, H. Hayashida, T. Miyata, and T. Honjo. 1998. *J. Exp. Med.* 188:2151–2162). Cases 1–40 and 49–60 are primary cases of Ph^- leukemia. Cases 41–48 represent leukemia cell lines BEL1 (41), RS4;11 (42), REH (43), 697 (44), Kasumi-2 (45), MHH-CALL3 (46), Nalm-6 (47), and HPB-Null (48). Deletions were counted as one mutation.

Table S2. V_H region genes in human Ph^+ ALL cells

Case	V_H	D_H	J_H	Mutation frequency [per 10^3 bp]	Cytogenetics	Genes involved
1	V3-66	D3-3	J4	44	t(9;22)(q34;q11)	*BCR-ABL1*
2	V3-49	D2-21	J4	78	t(9;22)(q34;q11), add(2)(q37), add(4)(q33)	*BCR-ABL1*
	V3-48	D6-13	J4	181		
3	V4-30	D4-23	J6	26	t(9;22)(q34;q11)	*BCR-ABL1*
4	V2-70	D2-2	J6	30; 87-bp in V_H	t(9;22)(q34;q11), add(9)(p2)	*BCR-ABL1*
5	V4-59	D3-9	J4	0	t(9;22)(q34;q11), +15, +18	*BCR-ABL1*
6	V1-18	D3-3	J3	15	t(9;22)(q34;q11)	*BCR-ABL1*
	V3-74	D4-17	J4	11		
	V3-7	D6-13	J4	37		
	V3-53	D3-22	J6	59		
7	V4-31	D2-2	J4	48	t(2;9;22)(p11;q34;q11)	*BCR-ABL1*
8	V4-34	D5-12	J2	63	t(9;22)(q34;q11), +der(22)	*BCR-ABL1*
	V4-31	D2-2	J4	48		
9	V3-7	D6-13	J5	15	t(9;22)(q34;q11), i(17)(p10)	*BCR-ABL1*
	V1-2	none	J5	15		
	V3-74	D3-3	J5	48		
10	V3-49	D7-27	J6	81	t(9;22)(q34;q11)	*BCR-ABL1*
	V1-46	D5-5	J4	22		
11	V3-49	none	J5	78	t(9;22)(q34;q11), add(3)(q29), +mar	*BCR-ABL1*
12	V4-34	D6-13	J5	15	t(9;22)(q34;q11)	*BCR-ABL1*
13	V4-61	D2-2	J4	0	t(9;22)(q34;q11)	*BCR-ABL1*
14	V3-33	D3-22	J4	0	t(9;22)(q34;q11)	*BCR-ABL1*
15	V5-51	D3-22	J4	15	t(9;22)(q34;q11)	*BCR-ABL1*
	V5-51	D6-19	J3	11	t(9;22)(q34;q11)	*BCR-ABL1*
16	V5-51	D1-26	J1	19	t(9;22)(q34;q11)	*BCR-ABL1*
17	V3-30	D3-22	J3	15	t(9;22)(q34;q11)	*BCR-ABL1*
18	V1-46	D6-13	J4	0	t(9;22)(q34;q11)	*BCR-ABL1*
	V1-2	D3-10	J5	15	t(9;22)(q34;q11)	*BCR-ABL1*
19	V2-5	D3-22	J3	11	t(9;22)(q34;q11)	*BCR-ABL1*
20	V1-46	D3-10	J5	22	t(9;22)(q34;q11)	*BCR-ABL1*
21	V1-18	D2-2	J6	26; ID	t(9;22)(q34;q11)	*BCR-ABL1*
	V3-21	D6-25	J6	15		
22	V1-3	D1-14	J4	7; ID		
	V3-7	D2-2	J6	15; ID	t(9;22)(q34;q11)	*BCR-ABL1*
	V3-30	D5-5	J4	41		
23	V1-8	D5-18	J6	0	t(9;22)(q34;q11)	*BCR-ABL1*
	V1-46	D2-21	J5	133; ID		
24	V3-33	D2-2	J4	89; ID	t(9;22)(q34;q11)	*BCR-ABL1*
	V3-30	D6-6	J4	78; ID		
	V3-33	D1-20	J5	0		
	V3-30	D2-15	J6	63; ID		
25	V2-5	none	J5	7	t(9;22)(q34;q11)	*BCR-ABL1*
26	V3-21	D2-15	J3	22; ID	t(9;22)(q34;q11), add(1)(q42), add(8)(p23), +mar	*BCR-ABL1*
27	V4-34	D2-8	J2	22	t(9;22)(q34;q11), t(6 ;7)(q24 ;q35), del(11)(q22.3)	*BCR-ABL1*
	V3-74	none	J5	137; ID		
28	V3-43	none	J4	11	t(9;22)(q34;q11), -3, -13, -18, del(9)(p11),	*BCR-ABL1*
	V6-1	D3-9	J6	22	t(15 ;18)(q21 ;q12)	
29	V1-8	none	J2	37; ID	t(9;22)(q34;q11) , dup(13)(q21)	*BCR-ABL1*
	V2-70	D3-16	J4	26; ID		
	V3-43	D3-9	J5	11		
	V3-9	D2-21	J5	22; ID		
	V4-31	D3-16	J4	26; ID		
	V4-59	D3-16	J4	22; ID		
30	V1-46	none	J4	22	t(9;22)(q34;q11)	*BCR-ABL1*
	V3-30	none	J5	44		
	V3-30	D6-13	J3	41; ID		
	V4-34	none	J5	52		
31	V1-2	D2-2	J6	70; ID	t(9;22)(q34;q11), t(1;1)(p11;q31), t(1;4)(q11;q35)	*BCR-ABL1*
	V3-53	D2-8	J6	11	add(10)(q25), del(14)(q23q31), t(9;16)(q11;p13)	
	V4-4	none	J6	44		
32	V1-69	D3-22	J6	15	t(9;22)(q34;q11), +8, +16, del(7)(p14), del(9)(q13q34)	*BCR-ABL1*
	V4-55	D3-22	J6	7		
33	V1-2	D2-21	J5	144	t(9;22)(q34;q11)	*BCR-ABL1*
34	V1-3	D5-24	J6	96; ID	t(9;22)(q34;q11)	*BCR-ABL1*
35	V1-3	D2-21	J6	11	t(9;22)(q34;q11)	*BCR-ABL1*
36	V1-45	D1-26	J3	141	t(9;22)(q34;q11)	*BCR-ABL1*
37	V3-43	D1-26	J4	7	t(9;22)(q34;q11)	*BCR-ABL1*
38	V3-43	D3-9	J5	0	t(9;22)(q34;q11)	*BCR-ABL1*
39	V1-3	D3-10	J5	0	t(9;22)(q34;q11)	*BCR-ABL1*
40	V1-2		J4	30; ID	t(9;22)(q34;q11)	*BCR-ABL1*
41	V3-11	D3-16	J6	7	t(9;22)(q34;q11)	*BCR-ABL1*
42	V1-69	D3-9	J4	7	t(9;22)(q34;q11)	*BCR-ABL1*
43	V3-66	D3-22	J4	4	t(9;22)(q34;q11)	*BCR-ABL1*
44	V1-2	D2-2	J4	7	t(9;22)(q34;q11)	*BCR-ABL1*
45	V1-46	D1-20	J4	0	t(9;22)(q34;q11)	*BCR-ABL1*
46	V1-2	D3-16	J4	7	t(9;22)(q34;q11)	*BCR-ABL1*
Mean ± S.E.M.:				34.45 ± 4.42 mutations per 10^3 bp		

Cases 1–10 were previously described (Height, S.E., G.J. Swansbury, E. Matutes, J.G. Treleaven, D. Catovsky, and M.J. Dyer. 1996. *Blood*. 87:5242–5250). Sequence data were reanalyzed based on the full sequence of human germline *IGHV* genes according to Matsuda et al. (Matsuda, F., K. Ishii, P. Bourvagnet, K. Kuma, H. Hayashida, T. Miyata, and T. Honjo. 1998. *J. Exp. Med.* 188:2151–2162). Cases 1–25 and 33–46 are primary cases of Ph^+ leukemia. Cases 21–25 represent lymphoid blast crisis of chronic myeloid leukemia (LBC cases in Table II and Table S3). Cases 26–32 represent cell lines BV173 (26), CMLT1

(27), K562 (28), Nalm1 (29), SD1 (30), SUP-B15 (31), and TOM1 (32). Intraclonal diversity (ID) denotes the presence of multiple sequences for one VH gene rearrangement, which share common mutations but differ in diversifying mutations. Deletions were counted as one mutation. N.N., unknown

Table S3. Somatic mutations within non-Ig loci

Cell type	*BCL6*[a]		*MYC*[a]		*TCRB*		*TCRG*	
	Mutation frequency	Mutated clones	Mutation frequency	Mutated clones	Mutation frequency	Mutated clones	Mutation frequency	Mutated clones
BV173	1.41	6/9	0.91	2/13	germline		6.05[b]	4/4
CMLT1[c]	2.31	15/22	1.05	4/9	11.56[d]	4/4	7.44[b]	3/5
NALM1	0.36	3/15	0.47	2/7	germline		5.15[b]	2/4
SD1	0.84	5/13	0.09	1/16	n.d.		n.d.	
SUP-B15	0.49	3/11	0.24	2/13	n.d.		n.d.	
TOM1	0.72	6/15	0	0/7	germline		n.d.	
LBCII	1.12	12/16	1.21	2/4	germline		0	0/2
LBCIII	2.10	13/20	0.40	2/9	8.67[d]	4/5	2.23[b]	2/4
LBCIV	0	0/14	0.18	1/10	2.52[d]	3/6	7.45[b]	6/6
LBCV	1.31	11/19	n.d.	n.d.	2.21[d]	3/3	0	0/4
Ph^+ ALL	1.07 ± 0.23	74/154	0.51 ± 0.15	16/88	6.21 ± 2.31	14/18	5.66 ± 0.96	17/29
Mutated cases	7/10		3/9		4/4		5/7	
697	0	0/11	0	0/8	n.d.		n.d.	
HBP-NULL	0.56	2/8	0.56	4/10	n.d.		n.d.	
NALM6	0	0/4	0	0/8	germline		germline	
REH	0	0/7	0.13	2/8	n.d.		n.d.	
RS4.11	0	0/14	0.11	1/10	germline		germline	
Ph^- ALL	0.11 ± 0.11	2/44	0.16 ± 0.11	7/44				
Mutated cases	1/5		1/5		not applicable		not applicable	
$CD3^+$ T cells[e]	n.d.		n.d.		0.17 ± 0.14	2/30	0.18 ± 0.18	1/16

[a] *BCL6* and *MYC* alleles were amplified by PFU DNA polymerase and sequenced from both DNA strands. *BCL6* or *MYC* alleles amplified from ALL cases were considered mutated if at least two mutated sequences were amplified per case with an average mutation frequency of all amplified sequences significantly ($P < 0.01$) above the error rate of PFU DNA polymerase.

[b] The following *TCRG* gene rearrangements were amplified and sequenced: V3-1 J2 (1 mutation) and V8-1 Jp1 (2 mutations) from subclones of BV173, V4-2 J2 (0 mutations), and V4-2 J1 (1 mutation) from CMLT1; V5-1 J2 (2 mutations) and V5-1 Jp1 (unmutated) from subclones of NALM1; V3-1 J2-1 (unmutated) from LBCII; V3-1 J2 (unmutated) and V8-1 J2 (1 mutation) from LBCIII; V2-2 J2 (3 mutations) and V4-2 J2 (1 mutation) from LBCIV; and V3-1 J2 and V4-2 J2 (both unmutated) from LBC V.

[c] CMLT1 are heterogenous with respect to expression of B cell (CD19), T cell (CD3) and myeloid (CD13) antigens. For this experiment, $CD19^+$ $CD13^-$ cells were sorted and analyzed.

[d]The following *TCRB* gene rearrangements were amplified and sequenced: V4-2 D2 J2-3 (3 mutations) and V18-1 D2 D2-7 (5 mutations, with intraclonal diversity) from CMLT1 cells; V6-5 D1 J1-1 (1 mutation), V20 D1 J1-2 (0 mutation), and V28 D2 J2-5 (8 mutations, with intraclonal diversity) from case LBCIII; V28 D2 J2-7 (0 mutation) and V12-5 DD2 J2-3 (3 mutations) from case LBCIV; and V20-1 D2 J2-7 (1 mutation) and a *TCRB* germline allele were amplified from case LBCV.
[e]As control for Taq DNA polymerase error, *TCRB* and *TCRG* gene rearrangements were amplified and sequenced from normal peripheral blood T cells. *TCRB* and *TCRG* gene rearrangements amplified from ALL cases were considered mutated if at least two mutated sequences were amplified per case with an average mutation frequency of all amplified sequences significantly ($P < 0.01$) above the error rate of Taq DNA polymerase.

Table S4. Summary of oligonucleotides used for DNA-mutation analysis, RT-PCR, RNA interference and ligation-mediated PCR

***IGHV* and *IGHC* primers**

V_H1 F	5′-CAGTCTGGGGCTGAGGTGAAGA-3'
V_H2 F	5′-GTCCTRCGCTGGTGAAACCCACACA-3′
V_H3 F	5′-GGGGTCCCTGAGACTCTCCTGTGCAG-3′
V_H4 F	5′-GACCCTGTCCCTCACCTGCRCTGTC-3′
V_H5 F	5′-AAAAAGCCCGGGGAGTCTCTGARGA-3′
V_H6 F	5′-ACCTGTGCCATCTCCGGGGACAGTG-3′
J_H1.4.5 R	5′-GACGGTGACCAGGGTKCCCTGGCC-3′
J_H2 R	5′-GACAGTGACCAGGGTGCCACGGCC-3′
J_H3 R	5′-GACGGTGACCATTGTCCCTTGGCC-3′
J_H6 R	5′-GACGGTGACCGTGGTCCCTTKGCC-3′
C R	5′-AGACGAGGGGGAAAAGGGTT--3′
Cδ R	5′-AGAGCTGGCTGCTTGTCATG-3′
Cγ1 R	5′-GAGTTTTGTCACAAGATTTGGGCT-3′
Cγ2 R	5′-GCACTCGACACAACATTTGCG-3′
Cγ3 R	5′-TCACCAAGTGGGGTTTTGAGC-3′
Cγ4 R	5′-ATGGGCATGGGGGACCATTT-3′
Cα2 R	5′-TGTTGGCGGTTAGTGGGGTC-3′
Cε R	5′-GAGGTGGCATTGGAGGGAAT-3′

***TCRBV* and *TCRGV* primers**

TCRBV 1/5	5′-ACAGCAAGTGACDCTGAGATGCTC-3′
TCRBV 2	5′-GAGTGCCGTTCCCTGGACTTTCAG-3′
TCRBV 3	5′-GTAACCCAGAGCTCGAGATATCTA-3′
TCRBV 4	5′-TCCAGTGTCAAGTCGATAGCCAAGTC-3′
TCRBV 6.1	5′-ATGTAACTYTCAGGTGTGATCCAA-3′
TCRBV 6.2	5′-GTGTGATCCAATTTCAGGTCATAC-3′
TCRBV 7	5′-TACGCAGACACCAARACACCTGGTCA-3′
TCRBV 8	5′-GGTGACAGAGATGGGACAAGAAGT-3′
TCRBV 9	5′-CCCAGACTCCAAAATACCTGGTCA-3′
TCRBV 10	5′-AAGGTCACCCAGAGACCTAGACTT-3′
TCRBV 11	5′-GATCACTCTGGAATGTTCTCAAACC-3′
TCRBV 12	5′-CCAAGACACAAGGTCACAGAGACA-3′
TCRBV 13	5′-GTGTCACTCAGACCCCAAAATTCC-3′
TCRBV 14	5′-GTGACCCAGAACCCAAGATACCTC-3′
TCRBV 15	5′-GTTACCCAGACCCCAAGGAATAGG-3′
TCRBV 16	5′-ATAGAAGCTGGAGTTACTCAGTTC-3′
TCRBV 17	5′-CACTCAGTCCCCAAAGTACCTGTT-3′
TCRBV 18	5'-TGCAGAACCCAAGACACCTGGTCA-3′
TCRBV 19	5′-ACAAAGATGGATTGTACCCCCGAA-3′
TCRBV 20	5′-GTCAGATCTCAGACTATTCATCAATGG-3′
TCRBV 21	5′-CAGTCTCCCAGATATAAGATTAYAGAG-3′
TCRBV 22	5′-GGTCACACAGATGGGACAGGAAGT-3′
TCRBV 23	5′-CTGATCAAAGAAAAGAGGGAAACAGCC-3′

***TCRBV* and *TCRGV* primers (continued)**

TCRBV 24	5′-CAAGATACCAGGTTACCCAGTTTG-3′
TCRBV 25	5′-GACAGAAAGCAAAATTATATTGTGCC-3′
TCRBJ 1.2	5′-TACAACGGTTAACCTGGTCCCCGA-3′
TCRBJ 1.3	5′-CACCTACAACAGTGAGCCAACTT-3′
TCRBJ 1.5	5′-CCAACTTACCTAGGATGGAGAGTCGA-3′
TCRBJ 1.6	5′-CCTGGTCCCATTCCCAAAGTGGA-3′
TCRBJ 2.2	5′-CCTTACCCAGTACGGTCAGCCTA-3′

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TCRBJ 2.3            5’-TCCCGGGGCGCCCCCTCCCCAGTT-3’
TCRBJ 2.6            5’-CAGCCGCCGCCTTCCACCTGAAT-3’
TCRBJ 2.7            5’-TCCATCGTTCACCTTCTCTCTAAACA-3’
TCRGV11 F       5’-TCAGGAGTTATAAGCATTCACC-3’
TCRGV1-9 F      5’-ACGGCGTCTTCAGTACTATGAC-3’
TCRGJ1 R        5’-TTACCAGGCGAAGTTACTATGAGC-3’
TCRGJ3 R        5’-GTGTTGTTCCACTGCCAAAGAG-3’
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MYC and *BCL6*

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MYC1 F                    5’-CACCGGCCCTTTATAATGCG-3’
MYC1 R                    5’-CGATTCCAGGAGAATCGGAC-3’
MYC2 F                    5’-CTTTGTGTGCCCCGCTCCAG-3’
MYC2 R                    5’-GCGCTCAGATCCTGCAGGTA-3’
BCL6 F                    5’-ATGCTTTGGCTCCAAGTT-3’
BCL6 R                    5’-CACGATACTTCATCTCATC-3’
```

Human RT-PCR primers

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GAPDH F                   5’-TTAGCACCCCTGGCCAAG-3’
GAPDH R                   5’-CTTACTCCTTGGAGGCCATG-3’
BCR-ABL1 F      5’-ACCTCACCTCCAGCGAGGAGGACTT-3'
BCR-ABL1 R      5'-TCCACTGGCCACAAAATCATACAGT-3'
AID F           5'-TGCTCTTCCTCCGCTACATC-3'
AID R           5'-CCTCATACAGGGGCAAAAGG-3'
ID2 F                     5'-TACAACATGAACGACTGCTACTC-3'
ID2 R                     5'-TTGCTGTCATTTGACATTAACTC-3'
```

Mouse RT-PCR primers

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mAid F          5'- AAATGTCCGCTGGGCCAA-3'
mAid R          5'- CATCGACTTCGTACAAGGG-3'
mObf1 F         5'-AGCTCCCTGACCATTGAC-3'
mObf1 R         5'-CTGTCCCATCCCCCTGTAA-3'
mOct2 F         5'-ATCGAGACGAATGTCCGCTT-3'
mOct2 R         5'-GTAGCTGGTCGGCTTTCC-3'
mHprt                     5’-GGGGGCTATAAGTTCTTTGC-3’
mHprt           5’-TCCAACACTTCGAGAGGTCC-3’
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siRNA duplices

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Non-targeting siRNA       5’-UUGUACCUAAUUUCGUCCCAC-3’
                          3’-CAUGGAUUAAAGCAGGGUGUU-5’
AID siRNA              5'-UUGCUCUUCCUCCGCUACAUC-3'
                          3'-CGAGAAGGAGGCGAUGUAGUU-5'
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LM-PCR primers

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CDKN2A F      5’-CCAGGAATAAAATAAGGGGAATA-3’
CDKN2A F2     5’-GGAATAAAATAAGGGGAATAGGG-3’
CDKN2A R      5’-CTTTCCTACCTGGTCTTCTAGG-3’
CDKN2B F1     5’-GTGAACATTCCCAAAATATTAGC-3’
CDKN2B F2     5’-AAAATATTAGCCTTGGCTTTACTG-3’
CDKN2B R      5’-AGACTCCTGTACAAATCTACATCG-3’
V3-21 R       5’-CTCTCGCACAGTAATACACAGC-3’
V1-2 R        5’-CTCTCGCACAGTAATACACGAC-3’
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V1-69 R	5’-TCTCTCGCACAGTAATACACG-3’
V3-73 R	5’-GGTTTTCAGGCTGTTCATTT-3’
V3-53_R	5’-CACCTTTTAAAATAGCAACAAGG-3’
V3-30_R	5’-AGCATAGCTACTGAAGGTGAAT-3’
Linker F1	5’-CTGCTCGAATTCAAGCTTCT-3’
Linker F2	5’-GCTTCTAACGATGTACGGGG-3’
Linker R1	5’-GTACATCGTTAGAAGCTTGAA-3’
Linker R2	5’-GTTAGAAGCTTGAATTCGAGC-3’