Supplementary Table 1. FISH results performed on a peripheral blood specimen.

Targeted abnormality	Interphase nuclei analyzed (#)	Result	Abnormal (%)	Cutoff (%)
6q23 (D6Z1x2,MYBx1)	200	Normal	-	<4
-11q22.3 (D11Z1x2,ATMx1)	200	Normal	-	<7.5
+12 (D12Z3,MDM2)x3	200	Normal	-	<2.5
-13q14.3 (D13S319x1,LAMP1x2)	200	Abnormal	74.5	<7
-13q14.3x2 (D13S319x0,LAMPx2)	200	Normal	-	<1.5
t(11;14) CCND1-XT/IGH-XT fusion	500	Normal	-	<0.6
+14q32 (IGH-XTx3)	500	Abnormal	59.6	<3
-17p13.1 (TP53x1,D17Z1x2)	200	Abnormal	77	<9.5
-17 (TP53,D17Z1)x1	200	Normal	-	<5.5
t(14;18) IGH/BCL2 fusion	500	Normal	-	<0.6
t(14;19) IGH/BCL3 fusion	500	Normal	-	<0.6
+19q13.1-q13.2 (BCL3x3)	500	Abnormal	19.2	<1.4
+19q13.1-q13.2 (BCL3x4)	500	Abnormal	40.6	<10
11q13 (CCND1 sep)	200	Normal	-	<5.5

Supplementary Table 2. List of 61 targeted genes by NGS, including gene coverage.

Gene name	***Chromosome***	***Transcript or genomic posittion***	***Exon or introns covered***
AKT1	14	NM_001014432.1	Ex3-Ex15
AKT2	19	NM_001626.5	Ex2-Ex14
AKT3	1	NM_001206729.1	Ex2-Ex14
AKT3	1	243668551-243668636	Intron 13
ATM	11	NM_000051.3	Ex2-Ex63
B2M	15	NM_004048.2	Ex1-Ex3
BIRC2	11	NM_001166.4	Ex2-Ex9
BIRC3	11	NM_001165.4	Ex2-Ex9
BRAF	7	NM_004333.4	Ex1-Ex18
CCND1	11	NM_053056.2	Ex1-Ex5
CD38	4	NM_001775.3	Ex1-Ex8
CDK4	12	NM_000075.3	Ex2-Ex8
CDK7	5	NM_001799.3	Ex1-Ex12
CDKN1B	12	NM_004064.4	Ex1-Ex2
CDKN2A	9	NM_000077.4	Ex1-Ex3
CDKN2A	9	21994138-21994330	Intron 0
CRBN	3	NM_016302.3	Ex1-Ex11
CUL4A	14	NM_001008895.2	Ex2-Ex20
CUL4B	X	NM_003588.3	Ex2-Ex22

CXCR4	2	NM_003467.2	Ex1-Ex2
DIS3	13	NM_014953.4	Ex1-Ex21
DIS3	13	73355427-73355494	Intron 1
EGFR	7	NM_005228.3	Ex1-Ex28
FAM46C	1	NM_017709.3	Ex2
FGFR3	4	NM_001163213.1	Ex2-Ex18
FGFR3	4	1805419-1805563	Intron 8
GRB2	17	NM_002086.4	Ex2-Ex6
IDH1	2	NM_005896.3	Ex3- Ex10
IDH2	15	NM_002168.3	Ex2-Ex11
IDH3A	15	NM_005530.2	Ex2-Ex11
IFNGR2	21	NM_005534.3	Ex2-Ex7
IGF1R	15	NM_000875.4	Ex1-Ex21
IKZF1	7	NM_006060.5	Ex2-Ex8
IKZF3	17	NM_012481.4	Ex1-Ex8
IL6	7	NM_000600.4	Ex1-Ex5
IL6R	1	NM_000565.3	Ex2-Ex10
IRF4	6	NM_002460.3	Ex2-Ex9
JAK2	9	NM_004972.3	Ex3-Ex25
KDM6A	X	NM_021140.2	Ex1-Ex29
KDM6A	X	44919854-44920009	Intron 13
KRAS	12	NM_033360.2	Ex2-Ex5
MYC	8	NM_002467.4	Ex1-Ex3
MYD88	3	NM_002468.4	Ex1-Ex5
NFKB2	10	NM_001077494.3	Ex2-Ex23
NR3C1	5	NM_000176.2	Ex2-Ex9
NRAS	1	NM_002524.4	Ex2-Ex5
NSD2	4	NM_001042424.2	Ex2-Ex22
PIK3CA	3	NM_006218.2	Ex2-Ex21
PIK3CG	7	NM_001282426.1	Ex2-Ex11
PIK3R1	5	NM_181523.2	Ex2-Ex16
PIK3R1	5	67584564-67584579 and 67586557-67586662	Intron 7a and 7b
PIK3R2	19	NM_005027.3	Ex2-Ex16
PIM1	6	NM_001243186.1	Ex1-Ex6
PIM2	X	NM_006875.3	Ex1-Ex6
PIM3	22	NM_001001852.3	Ex1-Ex6
PSMA1	11	NM_148976.2	Ex2-Ex11
PSMB5	14	NM_002797.4	Ex1-Ex3
PSMB5	14	23497038-23496954	Intron 2
PSMD1	2	NM_002807.3	Ex1-Ex24
PSMG2	18	NM_020232.4	Ex1-Ex7
PTPN11	12	NM_002834.3	Ex2-Ex15
RB1	13	NM_000321.2	Ex1-Ex27
STAT3	17	NM_139276.2	Ex2-Ex24

TGFBR2	3	NM_001024847.2	Ex1-Ex8
TLR4	9	NM_138554.4	Ex1-Ex3
TP53	17	NM_001126113.2	Ex2-Ex10
TRAF3	14	NM_145725.2	Ex3-Ex12
XBP1	22	NM_001079539.1	Ex1-Ex6

Supplementary Table 3. Mate-pair and Sanger sequencing results for the *CCND1* insertion and subsequent 12p/der(14q) translocation.

Event description	***Mate-pair event/Position***	***Breakpoint by Sanger [hg38]***	***Breakpoint by MPseq [hg38]***	***Gene/ Locus***	***Primer sequence***	***Primer Direction***
CCND1 insertion	FR/position A	chr11:69625958	chr11:69626008	No gene	CTAGTTCTAAATGCACC CTGCTATTG	Reverse
	FR/position B	chr14:105863765	chr14:105863688	No gene	AGTAATCACAATGGCA GAATGTCCA	Forward
	RF/position A	chr11:69655212	chr11:69655053	No gene	TGTTTGCTCTGGATGA ATCATGGTC	Forward
	RF/position B	chr14:106335081	chr14:106335048	*IGH* locus	TGAATGATGGAATTACT ACCAGTCTCC	Reverse
t(12;14)/ *CCND1* 3'UTR rearrangement	FF/position A	chr11:69651484	chr11:69651701	*CCND1*	AAATCCTCTATCATCTG TAGCACAACC	Reverse
	FF/position B	chr12:33700719	chr12:33700732	No gene	AACTTCTTACAACTTCT TGTCCCCATC	Reverse
	RR/position A	chr11:69651450	chr11:69651701	*CCND1*	GGCTTAGTCTTGCTCTT ATAAAGGCTT	Forward
	RR/position B	chr12:33700531	chr12:33700732	No gene	CATTTCTACTCGACTCT CTTCTGAAAC	Forward

Supplementary Table 4. Mutations detected from the 61-gene NGS panel.

Variant; genomic position	***Gene***	***Variant; cDNA position***	***Variant; protein***	***Percentage (%)***	***Classification***
Chr1(GRCh37):g.243663089C>T	*AKT3*	NM_001206729.1(AKT3):c.1355-1G>A	p.?	21	VUS
Chr11(GRCh37):g.69456102C>T	*CCND1*	NM_053056.2(CCND1):c.21C>T	p.Cys7=	20	Benign
Chr11(GRCh37):g.69456220T>A	*CCND1*	NM_053056.2(CCND1):c.139T>A	p.Cys47Ser	19	Likely pathogenic
Chr17(GRCh37):g.7577538C>T	*TP53*	NM_001126113.2(TP53):c.743G>A	p.Arg248Gln	49	Pathogenic

VUS, variant of unknown significance