Table SI | Patient Characteristics

Study ID	Sex	Diagnosis	Age at diagnosis	Months since cytotoxic treatment
1	F	NB	15.4	64.3
2	M	RMS	11.1	21.7
3	F	ALL	5.7	132.4
4	NA	ALL	NA	NA
5*	F	ALL	1.1	106.4
6	F	ALL	6.1	80.3
7	M	NB	6.3	231.9
8§	M	NHL	4.7	176.2
9	f	ALL	1.7	52.6
10§	M	ALL	6.9	298.2
11	F	GCT	9.3	25.9
12	M	RMS	6.0	102.9
13	F	NHL	7.1	103.9
14	M	ALL	6.9	177.4
15	F	NHL	9.4	80.1
16	M	NB	0.6	94.0
17*	M	LL	5.8	55.4
18	M	HL	14.8	136.6
19	M	WT	0.8	57.3
20	M	RMS	3.1	47.6
21	F	ALL	9.1	35.7
22	M	HL	10.9	43.5
23	M	ALL	4.0	49.5
24	M	HL	14.2	42.5
25	M	HB	0.3	112.9
26*	M	ALL	0.6	81.1
27	M	HL	7.1	86.2
28	M	GCT	15.4	26.7
29	M	RMS	5.8	76.2
30§	M	NHL	15.5	46.6
31	M	HL	25.4	48.5
32§	M	ESFT	4.6	141.5
33	M	LL	9.3	112.9
34	F	ESFT	3.3	74.3
35*	M	NB	2.3	102.9
36	M	NHL	2.0	46.4
37	M	NB	3.4	166.4
38	F	NB	1.7	124.8
39*	M	LL	3.2	112.9
40§	M	NB	0.5	289.3
41	F	WT	3.1	105.9
42	M	NB	0.9	268.4
43	F	NB	0.6	238.8
44	M	NHL	5.8	183.2

45	M	RMS	8.4	192.2
46	M	NRSTS	4.3	105.9
47	M	ALL	3.0	58.3
48	M	ALL	3.9	35.7
49	M	NB	5.5	NA
50	F	ESFT	13.4	69.2
51*	M	ALL	4.7	89.1
52	F	CCA	12.8	41.5
53	M	NB	4.0	73.3
54	F	WT	4.8	63.4
55	M	HL	15.3	46.4
56*	M	ALL	1.5	44.5
57	M	NPC	15.9	35.4
58	F	NHL	8.7	25.7
59	M	ALL	4.5	59.4
60	M	ALL	3.6	35.9
61	M	NB	5.8	34.5
62	M	NHL	2.6	59.3
63	M	NHL	9.1	62.4
64	F	RMS	3.0	80.1
65	F	NB	0.3	138.6
66	F	RMS	1.1	45.4
67	F	ALL	2.4	54.4
68	M	NHL	3.7	212.9
69	F	NRSTS	11.0	38.1
70	M	NB	0.4	45.4
71	F	LCH	3.7	88.1
72*	F	LCH	3.1	69.2
73	F	WT	3.8	142.7
74	F	GCT	0.0	131.8
75	M	GCT	15.4	NA
76§	F	WT	4.9	96.1
77	F	ALL	8.2	45.4
78§	F	NB	1.1	39.6
79	M	ALL	4.5	77.2
80§	M	NB	1.3	194.1
81	M	ALL	3.3	48.5
82	F	NB	0.3	75.2
83	M	ALL	3.0	75.2
84	M	ESFT	10.7	100.0

RMS, rhabdomyosarcoma; ALL, acute lympoblastic leukaemia; NB, neuroblastoma; NHL, non-Hodgkin lymphoma; GCT, germ cell tumour; LL, lymphoblastic lymphoma; HL, Hodgkin lymphoma; WT, Wilm's tumour; ESFT, Ewing sarcoma; NRSTS, non-rhabdomyosarcoma soft tissue sarcoma; NPC, nasopharyngeal sarcoma; CCA, choriocarcinoma; LCH, Langerhans cell histiocytosis; NA, no data. Patients who received a haematopoietic stem cell transplant (HSCT) are indicated with the symbols * (allogeneic HSCT) or § (autologous HSCT).

Table SII | Primer Sequences

PLEX	PRIMER NAME	GENE	TARGETED EXON/CODON	PRIMER SEQUENCE3
1	ASXL1_exon12_a_F	ASXL1	exon12	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGGACCCTCGCAGACATTAmAA
1	ASXL1_exon12_a_R	ASXL1	exon12	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTGCTGTAGATCTGACGTACACmUT
1	ASXL1_exon12_b_F	ASXL1	exon12	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCAGTGGTGATGGTGGTGmAG
1	ASXL1_exon12_b_R	ASXL1	exon12	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTGGCATCTCCTAGCCCATmCT
1	ASXL1_exon12_c_F	ASXL1	exon12	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCTACTACAGAGGGCTACAGTmUG
1	ASXL1_exon12_c_R	ASXL1	exon12	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTCTTGCTCCTCATCATCACTTmUC
1	DNMT3A_p.R693C_F	DNMT3A	p.R693C	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCCTCATGTTCTTGGTGTTTTAT
1	DNMT3A_p.R693C_R	DNMT3A	p.R693C	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTTTTTCTCCCCCAGGGTATTTG
1	IDH1_p.R132H_F	IDH1	p.R132H	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTAAATGTGTGTAAATATACAGTTAT
1	IDH1_p.R132H_R	IDH1	p.R132H	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTATTATCTGCAAAAATATCCCCC
1	IDH2_p.R172K_IDH2_p.R140Q_F	IDH2	p.R172K, p.R140Q	ACACTCTTTCCCTACACGACGCTCTTCCGATCTAAGAGGATGGCTAGGCGAGGA
1	IDH2_p.R172K_IDH2_p.R140Q_R	IDH2	p.R172K, p.R140Q	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTCTCACAGAGTTCAAGCTGAAG
1	JAK2_p.V617F_F	JAK2	p.V617F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTAGTCTTTCTTTGAAGCAGCAAG
1	JAK2_p.V617F_R	JAK2	p.V617F	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTAGTTTACACTGACACCTAGCTG
1	KIT_exon17_F	KIT	exon17	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGGTTTTCTTTTCTCCTCCAAC
1	KIT_exon17_R	KIT	exon17	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTTCCTTTGCAGGACTGTCAAG
1	KRAS_p.G12R_F	KRAS	p.G12R	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGTTGGATCATATTCGTCCACA
1	KRAS_p.G12R_R	KRAS	p.G12R	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTAAGGTACTGGTGGAGTATTTGA
1	NPM1_p.L287fs*13_F	NPM1	p.L287fs*13	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGTTTGGAATTAAATTACATCTGA
1	NPM1_p.L287fs*13_R	NPM1	p.L287fs*13	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTAAAATTTTTAACAAATTGTTTAAACT
1	NRAS_p.G12D_F	NRAS	p.G12D	ACACTCTTTCCCTACACGACGCTCTTCCGATCTATGGGTAAAGATGATCCGACAA
1	NRAS_p.G12D_R	NRAS	p.G12D	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTCGCCAATTAACCCTGATTACTG
1	SF3B1_p.K666N_F	SF3B1	p.K666N	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACCCTGTCTCCTAAAGAAAAAA
1	SF3B1_p.K666N_R	SF3B1	p.K666N	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTTAGAGCTTTTGCTGTTGTAGC
1	SF3B1_p.K700E_F	SF3B1	p.K700E	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTAGTAATTTAGATTTATGTCGCC
1	SF3B1_p.K700E_R	SF3B1	p.K700E	TCGGCATTCCTGCTGAACCGCTCTTCCGATC

				TGGCATAGTTAAAACCTGTGTTT
1	SRSF2_p.P95L_F	SRSF2	p.P95L	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGCTTCGCCGCGGACCTTTGT
1	SRSF2_p.P95L_R	SRSF2	p.P95L	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTGAGGACGCTATGGATGCCATG
1	U2AF1_p.Q157R_F	U2AF1	p.Q157R	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGGGTTGGAAGGAGACATTTAmCT
1	U2AF1_p.Q157R_R	U2AF1	p.Q157R	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTGAAAAGGCTGTGATTGACTTmGA
1	U2AF1_p.S34F_F	U2AF1	p.S34F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCGATCACCTGCCTCACTATTmAT
1	U2AF1_p.S34F_R	U2AF1	p.S34F	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTTTTCAAAATTGGAGCATGTCmGT
2	PPM1D_exon1_a_F	PPM1D	exon1	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGAGCGCCTAGTGTGTCmUC
2	PPM1D_exon1_a_R	PPM1D	exon1	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTGCCTTTCCCCGAGACTmUC
2	PPM1D_exon1_c_F	PPM1D	exon1	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGTTCCTCCGTGGCCTTmUT
2	PPM1D_exon1_c_R	PPM1D	exon1	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTCAAACAAGCCAGGGAACTTmAC
2	PPM1D_exon3_F	PPM1D	exon3	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACTGAGCTATCTTAGTTGTTmGT
2	PPM1D_exon3_R	PPM1D	exon3	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTTGCCAAGTAAGGGTTTAGTTmCT
2	PPM1D_exon5_a_F	PPM1D	exon5	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACAGATGTAGTGGCAGCTAAmAT
2	PPM1D_exon5_a_R	PPM1D	exon5	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTGTCATCACACAGGTTTCTTGmAC
2	PPM1D_exon6_a_F	PPM1D	exon6	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGCATAGATTTGTTGAGTTCTmGG
2	PPM1D_exon6_a_R	PPM1D	exon6	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTTGGAAGGCTATTATTCAAAGAATmCA
2	PPM1D_exon6_c_F	PPM1D	exon6	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTTAGAAGAGTCCAATTCTGGmCC
2	PPM1D_exon6_c_R	PPM1D	exon6	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTTCAACATCGGCACCAAATTTmAA
2	TP53_exon1_F	TP53	exon1	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTTCAAAGACCCAAAACCCAAmAA
2	TP53_exon1_R	TP53	exon1	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTTTGATTTGAATTCCCGTTGTmCC
2	TP53_exon10_a_F	TP53	exon10	ACACTCTTTCCCTACACGACGCTCTTCCGATCTATTGAAGTCTCATGGAAGCCmAG
2	TP53_exon10_a_R	TP53	exon10	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTCGGACGATATTGAACAATGGmUT
2	TP53_exon10_b_F	TP53	exon10	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGAAGGGACAGAAGATGACAmGG
2	TP53_exon10_b_R	TP53	exon10	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTGACTGCTCTTTTCACCCATCmUA
2	TP53_exon11_F	TP53	exon11	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGGACTGTAGATGGGTGAAAAmGA
2	TP53_exon11_R	TP53	exon11	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTAGACCTATGGAAACTGTGAGmUG
2	TP53_exon12_F	TP53	exon12	ACACTCTTTCCCTACACGACGCTCTTCCGATCTAACGTTGTTTTCAGGAAGTCmUG

2	TP53_exon2_F	TP53	exon2	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGAGAATGGAATCCTATGGCmUT
2	TP53_exon2_R	TP53	exon2	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTCATGTTGCTTTTGTACCGTCmAT
2	TP53_exon3_F	TP53	exon3	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGGCTAGGCTAAGCTATGATGmUT
2	TP53_exon3_R	TP53	exon3	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTGCTCCTGGTTGTAGCTAACTmAA
2	TP53_exon5_F	TP53	exon5	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTTTCCACTTGATAAGAGGTCmCC
2	TP53_exon5_R	TP53	exon5	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTGAAGAGAATCTCCGCAAGAAmAG
2	TP53_exon7_F	TP53	exon7	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGAGAGGTGGATGGGTAGTAGmUA
2	TP53_exon7_R	TP53	exon7	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTATCTTGGGCCTGTGTTATCmUC
2	TP53_exon9_F	TP53	exon9	ACACTCTTTCCCTACACGACGCTCTTCCGATCTAATCAGTGAGGAATCAGAGmGC
2	TP53_exon9_R	TP53	exon9	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTTTTCAACTCTGTCTCCTTCCmUC
3	PPM1D_exon1_b_F	PPM1D	exon1	ACACTCTTTCCCTACACGACGCTCTTCCGATCTAACCGACGGCTGAAGAAmAA
3	PPM1D_exon1_b_R	PPM1D	exon1	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTCTTCTTGATGAAACCCCACAmAG
3	PPM1D_exon2_F	PPM1D	exon2	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACTTGCAAGAGTGAAATATTmUT
3	PPM1D_exon2_R	PPM1D	exon2	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTGAAAGAGAAAACGACAGAATmGT
3	PPM1D_exon4_F	PPM1D	exon4	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGCTTCCAACTAATACTTCTTGmCT
3	PPM1D_exon4_R	PPM1D	exon4	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTACCAAAACAATGTTTAGACAmAC
3	PPM1D_exon5_b_F	PPM1D	exon5	ACACTCTTTCCCTACACGACGCTCTTCCGATCTAGTGCCATAGTAATCTGCATmCT
3	PPM1D_exon5_b_R	PPM1D	exon5	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTTCGAGTTCAAATCCAAAATCCmUG
3	PPM1D_exon6_b_F	PPM1D	exon6	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTACCCTCAAAAGATCCAGAAmCC
3	PPM1D_exon6_b_R	PPM1D	exon6	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTTCGACTTAAGCCATTTCGTCmUA
3	TP53_exon12_R	TP53	exon12	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTGGATCCCCACTTTTCCTCTmUG
3	TP53_exon4_F	TP53	exon4	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTCAGGCAAAGTCATAGAACCmAT
3	TP53_exon4_R	TP53	exon4	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTTGACTGTTTTACCTGCAATTmGG
3	TP53_exon6_F	TP53	exon6	ACACTCTTTCCCTACACGACGCTCTTCCGATCTAGAGGCAAGGAAAGGTGATAmAA
3	TP53_exon6_R	TP53	exon6	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTTAGGACCTGATTTCCTTACTmGC
3	TP53_exon8_F	TP53	exon8	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTTGCACATCTCATGGGGTTAmUA
3	TP53_exon8_R	TP53	exon8	TCGGCATTCCTGCTGAACCGCTCTTCCGATCTTGATTCCTCACTGATTGCTCmUT

Nucleotide sequences for multiplexed primers used in plexes 1 - 3.
* Consecutive primers constitute forward (F) and reverse (R) primer pairs for the indicated loci

† Forward primers format: 5’ ACACTCTTTCCCTACACGACGCTCTTCCGATCT-[gene-specific forward] 3’,
Reverse primerformat:5’ TCGGCATTCCTGCTGAACCGCTCTTCCGATCT-[gene-specific reverse] 3’

‡ "m" denotes a single 2'-O-Methyl base in place of the DNA base, used in order to minimise potential primer dimers