

Patient ID	Protocol	Chr	Gene or Fusion	Karyotype	Start	Reference Sequence	Alternate Sequence	Transcript ID	Class	AAChange
PARCVS	AAML0531	chr16	CREBBP	44,X,-Y,der(8)t(8;21)(q22;q22),-21,der(21)t(8;21)(q22;q22)(21)(q10)[20]	3830795	A	AC	NM_004380	frameshift	G587fs
PABLDZ	CCG-2961	chr16	CREBBP	Unknown	3831230	G	T	NM_004380	missense	L551I
PANGJY	AAML03P1	chr16	CREBBP	46,XX,der(15)t(1;15)(q12;q26)[12]	3779615	CTTGCCTTTCAGCCCT	C	NM_004380	inframe deletion	HT1804P
PARGVC	AAML0531	chr16	CREBBP	45,X,-Y,t(8;21)(q22;q22),add(13)(p11.2),add(22)(p11.2)	3778966	G	GA	NM_004380	frameshift	P2027fs
PARDRM	AAML0531	chr16	CREBBP	46,XX,t(7;11-9)(p15;p15;q22)[23]	3832802	C	CATGGGCCT	NM_004380	inframe insertion	Y485RP
PARFMY	AAML0531	chr16	CREBBP	46,XY[20]	3801796	C	T	NM_004380	missense	C1237Y
PARMGH	AAML0531	chr16	CREBBP	46,XY,add(14)(q32)[6]/46,XY[33]	3819294	C	T	NM_004380	missense	A981T
PARVZU	AAML0531	chr16	CREBBP	46,XX,t(4;11)(p11.2;q23)[10]/46,XX[10]	3817732	GGCTGC	G	NM_004380	frameshift	P1080fs
PASLPU	AAML0531	chr16	CREBBP	46,XY,ins(8;21)(q22;q22)1,del(9)(q13q22)[20]	3795345	A	ACC	NM_004380	frameshift	C1283fs
PASRR	AAML0531	chr16	CREBBP	46,XY[20]	3819294	C	T	NM_004380	missense	A981T
PASVSS	AAML0531	chr16	CREBBP	47,XY,+21[17]/46,XY[3]	3807828	TC	T	NM_004380	frameshift	G1197fs
PARWNS	AAML0531	chr16	CREBBP	46,XY[20]	3831230	G	T	NM_004380	missense	L551I
PAVTDU	AAML1031	chr16	CREBBP	46,XX,der(8)inv(8)(p22q24.2)inv(8)(q12q22)inv(8)(q21.3q24.2)[20]	3749641	G	O	NM_004380	frameshift	T1274fs
PAWNYX	AAML1031	chr16	CREBBP	46,XX,t(9;11)(p22;q23)[20]	3729746	-	T	NM_004380	frameshift	S1767fs
PAUUCG	AAML1031	chr16	CREBBP	46,XX,inv(11)(p15q24),add(17)(p11.2)[18]/46,XX[14]	3793624	-	AA	NM_004380	frameshift	S326fs
PAUZRX	AAML1031	chr16	CREBBP	46,XY,t(8;16;21)(q22;p11.2;q22)[16]/47,idem,+21[4]	3749641	-	G	NM_004380	frameshift	T1274fs
PAVPXS	AAML1031	chr16	CREBBP	47,XY,+X,t(4;11)(q21;q23)[20]	3767804	-	TATCC	NM_004380	frameshift	K1056fs
PAVRGN	AAML1031	chr16	CREBBP	45,X,-Y,t(8;21)(q22;q22)[16]/46,XY[4]	3793399	-	CCCAG	NM_004380	frameshift	A400_G401fs
PAWDNF	AAML1031	chr16	CREBBP	45,X,-X,t(8;21)(q22;q22)[46]	3767738	-	ATGGCCC	NM_004380	frameshift	T873fs;S1078fs
PAWWEI	AAML1031	chr16	CREBBP	47,XX,+11[17]/46,XX[3]	3728439	-	TGC	NM_004380	inframe insertion	Q2203>QQ
PAXLFG	AAML1031	chr16	CREBBP	46,XY[20]	3729762	-	TTTGG	NM_004380	frameshift	K1762fs
PARUNX	AAML0531	chr16	CREBBP	48,XX,+der(6)t(1;6)(q21;q27),t(7;12)(q36;p13),+19[18][t(7;12) nuc ish ETV6 sep]	3788657	A	G	NM_004380	missense	Y1433>H
PATDHA	AAML0531	chr16	CREBBP	46,XX,t(8;21)(q22;q22)[18]/46,idem,del(9)(q12q22)[2]	3799632	C	A	NM_004380	nonsense	E1278>*
PAWWEI	AAML1031	chr16	CREBBP	46,XX, cryp ins(21;8)(q22;q22q22)[15]/47,idem,+mar[5]	3843495	G	A	NM_004380	nonsense	R370>*
PANGCM	AAML03P1	chr16	CREBBP	46,XY,inv(16)(p13.1q22)[13]/46,XY[6]	3778297	G	A	NM_004380	nonsense	Q2251>*
PAPVCN	AAML0531	chr16	CREBBP	46,XY,inv(16)(p13.1q22)[20]	3929862	G	T	NM_004380	nonsense	S19>*
PAVAWS	AAML1031	chr16	CREBBP	46,XY,add(10)(p11.2)[4]/48,idem,+6,del(13)(q12q22),+21[cp16]	3778672	C	T	NM_004380	missense	G2126fs
PAUJAD	AAML1031	chr16	CREBBP	47,XX,dup(1)(q21q44),t(2;8)(q21;q21.2),r(11)(p15q21),del(16)(q13),+22[21]	3794894	C	T	NM_004380	splice	R1328_E23splice
PAUPYX	AAML1031	chr16	CREBBP	46,XX,t(11;17)(q23;q12)[3]/46,idem,add(7)(q36)[2]/46,idem,+1,der(1;18)(q10;q10)[3]/46,XX[12]	3807323	G	A	NM_004380	missense	P1222S
PAUPYX	AAML1031	chr16	CREBBP	46,XX,t(11;17)(q23;q12)[3]/46,idem,add(7)(q36)[2]/46,idem,+1,der(1;18)(q10;q10)[3]/46,XX[12]	3807323	G	A	NM_004380	missense	E664K
PAUTWE	AAML1031	chr16	CREBBP	46,XY,inv(9)(p22q34)[19]/46,XY[1]	3843606	C	T	NM_004380	missense	G333R
PAUWCF	AAML1031	chr16	CREBBP	46,XY,t(2;7)(p15;p22)[20]	3900776	G	A	NM_004380	missense	P107L
PAUWKY	AAML1031	chr16	CREBBP	45,XY,t(3;8)(q27;q24),-7[13]	3789658	C	T	NM_004380	missense	E1401K
PAUZXP	AAML1031	chr16	CREBBP	46,XY[22]	3789709	C	T	NM_004380	missense	E1384K
PAVPKA	AAML1031	chr16	CREBBP	47,XX,+21[15]/46,XX[5]	3900974	G	A	NM_004380	missense	P41L
PAWUUY	AAML1031	chr16	CREBBP	45,X,-X,t(8;21)(q22;q22)[19]/46,XX[1]	3817736	GC	GAGC	NM_004380	frameshift	S1078_Q1079fs
PAWXIA	AAML1031	chr16	CREBBP	46,XX,dup(8)(q11.2q24)[2]/46,XX[18]	3830825	TAT	TCTT	NM_004380	frameshift	IS77fs
PAUIRJ	AAML1031	chr16	KAT6A-CREBBP	46,XX,t(8;16)(p11.2;p13.3)[20]	Unknown				fusion	
PAXCKX	AAML1031	chr16	KAT6A-CREBBP	46,XY,der(8)add(8)(p11.2)ins(8;7)(q22;?),add(14)(q11.2),der(16)t(8;16)(p11.2;p13.3)[5]/46,XY[15]	3901010				fusion	
PAXDXW	AAML1031	chr16	KAT6A-CREBBP	46,XX,dic(1,5)[5pter->5q13;5q21->5q13;7;1p13->1qter],add(5)(q13),+10,der(17)t(5;17)(q13;q22)[4]/49,idem,+X,+8,+15[7]/46,XX[8]	Unknown				fusion	
PALZWS	CCG-2961	chr16	KAT6A-CREBBP	46,XY,t(8;16)(p11.2;p13.3)[20]	3929832				fusion	
PANRBV	AAML03P1	chr16	KAT6A-CREBBP	46,XY,t(3;6)(q25;q23),t(8;16)(p11.2;p13.3)[14]/46,XY[5]	3901010				fusion	
PARHSA	AAML0531	chr16	KAT6A-CREBBP	46,XX,t(8;16)(p11.2;p13.3)[19]/46,XX[1]	Unknown				fusion	
PASNKC	AAML0531	chr16	KAT6A-CREBBP	46,XX,t(8;16)(p11.2;p13.3)[20]	Unknown				fusion	
PASNLR	AAML0531	chr16	KAT6A-CREBBP	46,XY,del(4)(p12p15.2),der(8)(pter->8p22;1;16q22->16q24;1;16q12.1->16q23;4;p12->4p15.2;8p11.2->8qter),der(16)(16pter->16q12.1;8p12->8p22;1;16q23->16qter),del(16)(q22q24)[14]/46,XY[7]	Unknown				fusion	
PASSVI	AAML0531	chr16	KAT6A-CREBBP	46,X,t(X;16;8)(q22;p13.3;p11.2)[14]/46,XX[6]	3901010				fusion	
PATANY	AAML0531	chr16	CREBBP-ANK1	46,XX,der(7)t(6;7)(q15;q32),t(8;16)(p11.2;p13.3)[14]	Unknown				fusion	
PATGIG	AAML0531	chr16	KAT6A-CREBBP	46,XX,t(3;21)(q21;q22),t(8;16)(p11.2;p13.3),der(16)t(8;16)(p11.2;p13.3)[20]/46,XX[20]	3929832				fusion	
PAUUKK	AAML1031	chr16	KAT6A-CREBBP	47,XX,t(8;16)(p11.2;p13.3),+der(8)t(8;16)(p19)/46,XX[1]	3901010				fusion	
PAVYKS	AAML1031	chr16	KAT6A-CREBBP	46,XX,t(8;16)(p11.2;p13.3)[3]/46,XX[17]	3901010				fusion	
PAXBVX	AAML1031	chr16	KAT6A-CREBBP	46,XX,t(8;14;16)(p11.2;q32;p13.3)[22]/46,XX[1]	3901010				fusion	
PAXGVS	AAML1031	chr16	KAT6A-CREBBP	46,XX,t(8;16)(p11.2;p13.3)[17]/46,XX[2]	3901010				fusion	
PAVKMI	AAML1031	chr16	KAT6A-CREBBP	47,XX,+8,t(8;16)(p11.2;p13.3)[20]	Unknown				fusion	

Multivariable Cox analysis for EFS from study entry				
	N	HR	95% CI	p
CREBBP				
neg	2164	1		
fus	16	0.96	0.52 - 1.80	0.903
mut	36	1.71	1.18 - 2.47	0.005
Cytogenetics/Fusion/Molecular risk group				
standard	659	1		
low	819	0.52	0.45 - 0.61	<0.001
high	738	1.67	1.46 - 1.90	<0.001