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Supplementary Table S1. Breakpoints of the chromosomes involved in the chromosomal rearrangements of the studied patients, considering their locations in the A and B compartments and repeated regions.

Patient	Breakpoint Position [GRCh37]	A. c	B. c	Repeat Annotation
P1	2p24.2p16.3(17,447,798_49,515,986)x3	-	B	-
	2p24.2p16.3(17,447,798_49,515,986)x3	-	B	-
P2	10q11.22q22.3(49,378,356_81,617,607)x3	n.c	n.c	Segmental duplication
	10q11.22q22.3(49,378,356_81,617,607)x3	A	-	Segmental duplication
P3	16p12.3p11.1(19,708,014_34,727,349)x3	-	B	-
	16p12.3p11.1(19,708,014_34,727,349)x3	-	B	-
P4	22q12.2q13.33(31,993,312_51,197,838)x3	A	-	-
	22qter	n.a	n.a	-
P5	6p22.3p12.3(24,239,091_50,209,146)x3	-	B	CR1 (Class LINE)
	6p22.3p12.3(24,239,091_50,209,146)x3	-	B	-
P6	10q21.3q23.31(68,449,230_90,962,409)x3	-	B	-
	10q21.3q23.31(68,449,230_90,962,409)x3	A	-	-
P7	3q25.2 (154,846,050)	-	B	-
	3qter	n.a	n.a	-
P8	12p13.33p12.1(173,786_24,336,114)x3	A	-	-
	12pter	n.a	n.a	-
P9	10q23.31q26.3(91,217,474_135,427,143)x3	A	-	-
	10qter	n.a	n.a	-
P10	4q28.3q35.2(139,305,925_190,957,473)x3	-	B	-
	15p (acrocentric)	n.a	n.a	-
P11	5p15.33p11(113,577_46,100,000)x3	-	B	-
	14p (acrocentric)	n.a	n.a	-
P12	7p22.3p15.2(43,360_26,417,503)x3	A	-	-
	15p (acrocentric)	n.a	n.a	-
P13	1q41q44(216,531,592_249,212,668)x3	-	B	-
	4q34.2q35.2(177,357,703_190,469,337)x1	-	B	-
P14	5p15.33p13.3(15,519_30,629,115)x3	-	B	-
	15q26.3(99,829,402_102,400,037)x1	A	-	-
P15	6q25.2q27(153,640,498_170,919,483)x3	-	B	ERV1 (Class LTR)
	9p24.3p24.1(177,044_6,341,615)x1	A	-	L1 (Class LINE)
P16	1p36.33p36.32(849,466_2,419,139)x1	A	-	-
	13q32.3q34(100,357,543_115,107,733)x3	A	-	L1 (Class LINE)
P17	1q32.1q44(202,430,499_249,224,684)x3	A	-	Segmental duplication MIR (Class SINE)
	18q23(77,381,997_78,013,728)x1	-	B	-
P18	9p24.3p13.1(203,310_38,914,934)x3	n.c	n.c	Segmental duplication ERV1 (Class LTR)
	18p11.32p11.31(136,227_6,433,650)x1	-	B	-
P19	1q32.3q44(212,508,954_249,224,376)x3	A	-	-
	11q25(132,927,027_134,944,770)x1	-	B	Alu (Class SINE)
P20	1q41q44(220,462,071_249,224,684)x3	A	-	Alu (Class SINE)
	4q34.3q35.2(179,058,723_190,957,460)x1	-	B	ERV1 (Class LTR)
P21	4q32.1q35.2(159,863,373_190,469,337)x3	A	-	-
	5q35.3(177,570,036_180,696,806)x1	A	-	-

P22	2q34q37.3(209,479,612_243,089,444)×3	-	B	Alu (Class SINE)
	8p23.3(161,221_1,829,244)×1	-	B	-
P23	18q21.33q23(60,803,693_77,756,508)×3	A	-	L2 (Class LINE)
	20p13(668,559_1,418,229)×1	A	-	L1 (Class LINE)
P24	7p22.3(43,360_1,696,632)×1	A	-	L1 (Class LINE)
	12q24.22q24.33(116,927,065_133,777,902)×3	A	-	-
P25	5p15.33p14.2(113,576_24,272,820)×1	-	B	-
	18q12.1q23(29,782,990_78,013,728)×3	-	B	-
P26	5p15.33p15.1(15,519_17,447,645)×3	-	B	-
	5q35.3(178,908,634_180,719,790)×1	-	B	ERV1 (Class LTR)
P27	9p24.3p24.1(203,861_7,193,123)×3	A	-	-
	9q34.3(140,034,826_141,020,389)×1	A	-	-
P28	17p13.3p12(525_12,675,313)×3	-	B	-
	17q25.3(80,520,618_81,041,938)×1	A	-	-
P29	9p24.3q21.11(46,586_69,978,010)×3	n.c	n.c	ALR/Alpha (Class Satellite)
	15p (acrocentric)	n.a	n.a	-
P30	9p24.3q21.11(203,862_70,990,047)×3	n.c	n.c	Segmental duplication ERV1-MaLR (Class LTR)
	21p (acrocentric)	n.a	n.a	-
P31	7q35q36.3(143,425,873_158,949,365)×4	n.c	n.c	-
	7qter	n.a	n.a	-

P: Patient; A.c: A compartment; B.c: B compartment; Repeat Annotation: Segmental Duplication and/or repetitive element; n.c: no compartment defined; n.a: not available; -: none; bold writing refers to the analysed breakpoint.