

Table S1. Summary of multiple biopsies of unbalanced embryos derived from translocation carriers.

ID	Karyotype	Clinical TE	ICM	Second TE	Modified TE
1	46,XX,t(3;7)(p10;p10) 46,XY	dup(3)(p26.3-q11.2)(95.24Mb) del(7)(p12.1-q36.3)(107.52Mb)			
2	46,XX,t(3;7)(p10;p10) 46,XY	del(3)(q11.2-q29)(102.34Mb) dup(7)(p22.3-p12.1)(51.33Mb)			
3	46,XX 46,XY,t(7;18)(p13;q21.2)	dup(7)(p22.3-p12.2)(50.09Mb) del(18)(q21.2-q23)(25.20Mb)			
4	46,XX 46,XY,t(12;14)(q13;q11.2)	dup(12)(q13.12-q24.33)(83.39Mb) del(14)(q11.2-q32.33)(82.89Mb)			
5	46,XX,t(2;15)(q33;q24) 46,XY	del(2)(q33.1-q37.3)(41.71Mb) dup(15)(q24.2-q26.3)(26.51Mb)			
6	46,XX 46,XY,t(18;22)(q21.1;q11.2)	dup(18)(q21.2-q23)(29.50Mb) del(22)(q12.1-q13.33)(24.04Mb)			
7	46,XX 46,XY,t(2;10)(q31;p11.2)	del(2)(q31.1-q37.3)(69.31Mb) dup(10)(p15.3-p11.23)(29.96Mb)			
8	46,XX 46,XY,t(10;16)(q24;p13.1)	dup(10)(q24.32-q26.3)(30.39Mb) del(16)(p13.3-p13.13)(11.63Mb)			
9	46,XX 46,XY,t(10;16)(q24;p13.1)	del(10)(q24.32-q26.3)(30.98Mb) dup(16)(p13.3-p13.12)(12.83Mb)			NA
10	46,XX 46,X,Yqh-,t(4,16)(p16.2;q23)	dup(4)(p16.3-p15.33)(12.31Mb) del(16)(q21-q24.3)(27.71Mb)		NA	
11	46,XX,t(10;18)(p12;q21.3) 46,XY	del(10)(p15.3-p12.2)(23.96Mb) dup(18)(q21.1-q23)(31.30Mb)			NA
12	46,XX,t(15;17)(q24;q25) 46,XY	del(15)(q25.2-q26.3)(19.04Mb) dup(17)(q25.3-q25.3)(2.40Mb)			NA
13	46,XX 46,XY,t(7;12)(p12;q24.31)	del(7)(p22.3-p14.1)(37.20Mb) dup(12)(q24.33-q24.33)(1.48Mb)			NA
14	46,XX,t(11;22)(q23.3;q11.21) 46,XY	del(11)(q23.3-q25)(18.11Mb) dup(22)(q11.21-q13.33)(30.64Mb)		NA	
15	46,XX 46,XY,t(2;6)(q12;q12)	dup(2)(p11.2-q37.3)(158.96Mb) del(6)(p12.1-q27)(117.00Mb)		NA	
16	46,XX 46,XY,t(11;22)(q25;q13)	del(11)(q23.3-q25)(18.11Mb) dup(22)(q11.21-q13.33)(30.64Mb)			NA
17	46,XX 46,XY,t(18;20)(p11.3;p11.2)	del(18)(p11.32-q23)(75.60Mb) dup(20)(p11.23-q13.33)(43.11Mb)	NA		
18	46,XX,t(8;12)(p11.2;q15) 46,XY	del(8)(p23.3-p12)(34.93Mb) dup(12)(q21.31-q24.33)(52.19Mb)	NA		
19	46,XX,t(13;15)(q32;q15) 46,XY	del(13)(q12.11-q32.1)(78.09Mb) dup(15)(q11.2-q21.2)(26.96Mb)	NA		
20	46,XX 46,X,Yqh-,t(4,16)(p16.2;q23)	del(4)(p16.3-p15.33)(12.31Mb) dup(16)(q21-q24.3)(27.71Mb)	NA		
21	46,XX 46,XY,t(8;15)(q23;q21)	del(8)(q24.3-q24.3)(4.38Mb) dup(15)(q25.1-q26.3)(24.11Mb)	NA		



Perfect Concordant 34/50 (68%): cases presented with consistent segmental aneuploidies;



Partial Concordant 14/50 (28%): cases presented with almost consistent segmental aneuploidies;



Discordant 2/50 (4%): cases presented with different chromosomal aberrations;

NA: amplification failure or not obtained.