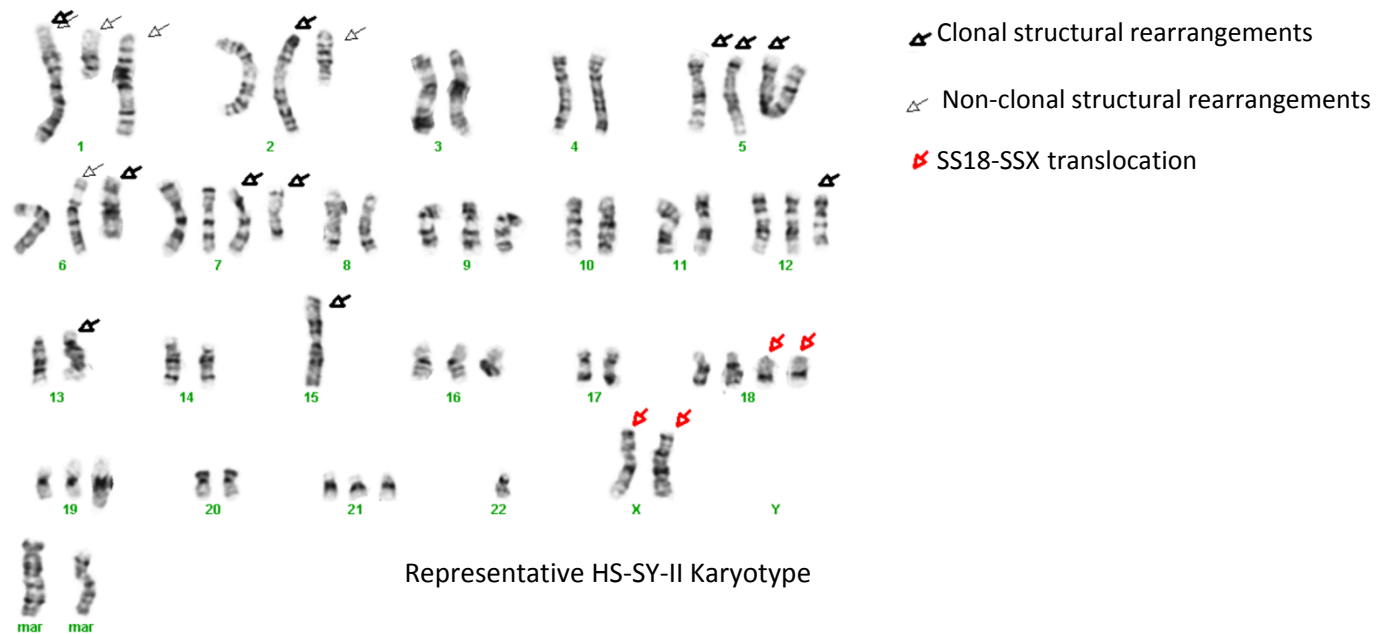


S4A Fig

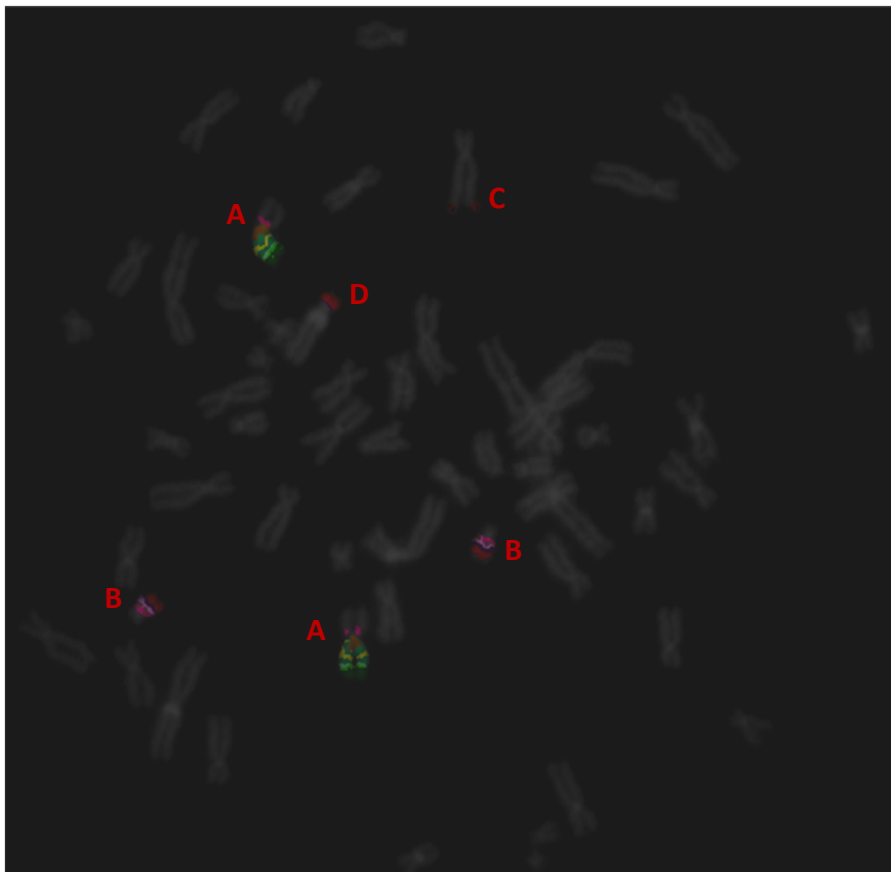
A Karyotype of HS-SY-II:

52~61<2n>,t(X;18)(p11.2;q11.2)x2[12],add(1)(q11)[9],+del(1)(p13)[7],add(2)(p23)[9],add(3)(p12)[2],del(4)(p13)[2],add(5)(q21)[5],add(5)(q31)[9],+der(5)t(1;5)(q33;q12)[12],+add(6)(q13)[11],+del(6)(p21.3)[6],+add(7)(p11)[12],+add(7)(q11.1)[6],del(8)(p21)[10],+add(8)(q11.2)[8],+9[6],+10[3],+add(12)(q13)[10],-13[8],add(13)(p11)[2],der(15)t(15;15)(p13;q11.2)[11],+16[10],-18[5],add(19)(q13.4)[9],-20[3],-21[3],22[12],del(22)(q11.2)[7],+mar1[4],+3-10mar[cp12]

Number in brackets represents number of clones in which rearrangement was observed out of 12.



S4B Fig



Metaphase spread 25: **X** MBAND

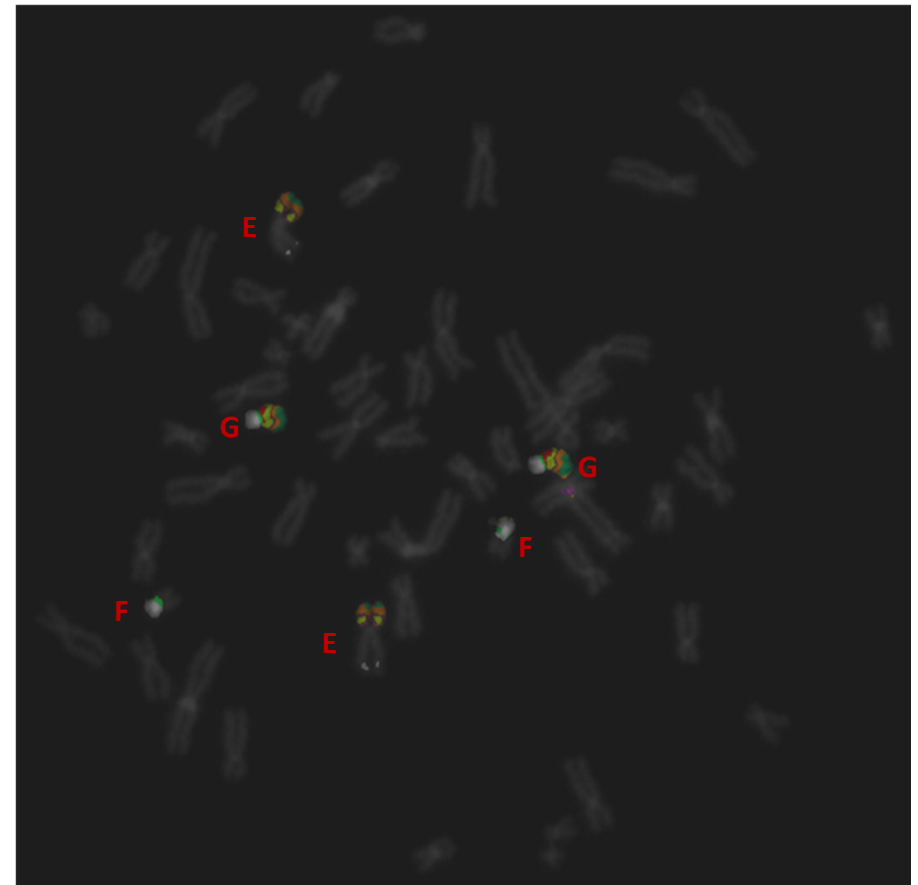
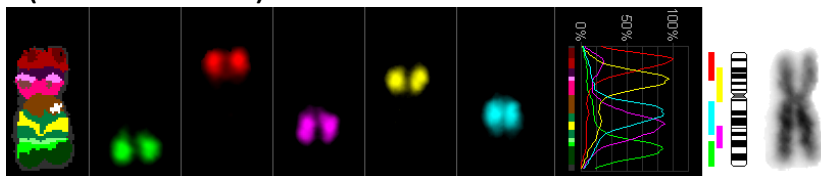
A=der(X)t(X;18) x2

B=der(18)t(X;18) x2

C=der(?)t(X;?) x1 (present in all cells)

D=different der(?)t(X;?) x1 (in 2cells)

(No normal X)



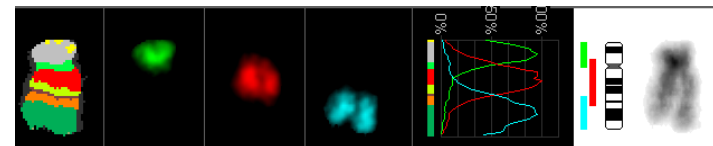
Metaphase spread 25a: **18** MBAND

E=der(X)t(X;18) x2

(note the small region on the opposite end which classifies as 18pter-q11; not consistently seen)

F=der(18)t(X;18) x2

G= normal 18 x2



S4C and S4D Figs

