Table S1- Individuals examined and data generated in this study; related to Figure 2

Rearrangement Class	Number of Trios	SMS Probands	PTLS Probands	PacBio Seq.	Illumina Regional Trio Seq.	Exome Trio Seq.
Non-recurrent	26	12	14	26 probands	26	26
Recurrent	19	10	9	N/A	19	19
Control	10	N/A	N/A	N/A	10	10
Total	55	22	23	26	55	55

Table S4- *Alu-Alu* Microhomologies and microhomeologies at non-recurrent breakpoint junctions; Related to Table 1

First Identified	Sample	Total No. of Nucleotides	No. of matching Nucleotides	Identity Matching (%)	Putative donor sequence (Top) & Putative target sequence (Bottom) NA indicates no putative donor/target available
This Study	BAB641	11	9	82%	GG-ACAAATGT || || ||||| GGAACTAATGT
Liu *et al.* 2011	BAB649 DEL1	8	7	87.5%	CTCCAATT |||| ||| CTCCCATT
Shaw *et al.* 2005	BAB765	30	30 (*Alu*Y/*Alu*Sg)	*86%*	AGGAGGGTGGATCATGAGGTCAGGAGATCGAGACCCTCC || |||||||||||||||||||||||||||| ||| NA TGGCGGGTGGATCATGAGGTCAGGAGATCGAGACTATCC
Shaw *et al.* 2005	BAB1354	21	21 (*Alu*Sc/*Alu*Y)	*84%*	CACACGCCTGTAGTCCCAGCTACTCTGGTG || ||||||||||||||||||| || | NA CAGGCGCCTGTAGTCCCAGCTACTCGGGAG
Liu *et al.* 2011	BAB2564	10	8	80%	AGAGAACCAC ||| ||||| AGA-AACCAA
This Study	BAB6311	9	7	77.8%	ATGA-GGTG |||| | || ATGAaGCTG
This Study	BAB1615	6	4	66.7%	CCCAAG || || NA CCGCAG
Feng *et al.* 2009	BAB2695 TRP	31	31 (*Alu*Y/*Alu*Y)	*89%*	GTGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTG | || |||||||||||||||||||||||||||||| |||| NA GCGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGGCCA
Wang *et al.* 2015	BAB2695 DUP	6	6 (*Alu*Sx/*Alu*Y)	*81%*	GGATTTCAAGACCAGCCTGGG ||| || |||||| ||||| NA GGAGATCGAGACCATCCTGGC
This Study	BAB2543D UP1	29	29 (*Alu*Sz/*Alu*Sx)	*83%*	GTAGAGACGGGGTTTCACCATGTTGGCCAGGCTGGTCT ||| |||||||||||||||||||||||||||| || NA ATAGCGACGGGGTTTCACCATGTTGGCCAGGCTGCTCC
This Study	BAB2811	8	6	75%	CA-CA-CA || || || CAGCATCA
This Study	BAB3810	9	6	67%	AT-CATGAT || || || ATATAT-AT
This Study	BAB8123 DUP1	25	25 (*Alu*Y/*Alu*Y)	88.0%	AGCGAGACTCCGTCTCAAAAAAAAAAAAACAA || ||||||||||||||||||||||| || NA AGTGAGACTCCGTCTCAAAAAAAAAAAAAAA

Alu identity matching was calculated across the entirety of the aligned *Alu* sequences