Table S1: Detection of recombination breakpoints from *SAMD9* and *SAMD9L* genes alignment using GARD analysis

***SAMD9+SAMD9L* alignment**				
Breakpoint	LHS[a] Raw *p*	LHS[a] adjusted *p*	RHS[b] Raw *p*	RHS[b] adjusted *p*
1179	0.94650	1.00000	0.00010	0.00060
2404	0.00010	0.00060	0.40590	1.00000
4755	**0.00010**	**0.00060**	**0.00010**	**0.00060**

[a] LHS: segment to the left of the breakpoint

[b] RHS: segment to the right of the breakpoint