

Figure S5

	SV_num	Breakpoint_id	Mate-pairs	TC (from MPs)	TC (from gel)	TC (from qPCR)	TC (from cnv)
Tandem duplication	SV1	B_8_128-8_128	212	72%	92%, 72%	33%, 37%	
Coupled inversion	SV2	B_1_198-1_203	216	56%	88%, 88%	21%, 56%	
	SV3	B_1_197-1_198	199		91%	104%, 81%	
	SV8	B_1_197-1_203	75		81%, 49%	80%, 39%	
Duplicative translocation	SV4	B_1_154-8_128	204	70%	34%	42%	56%, 64%
Coupled inversion	SV5	B_11_95-11_102	155	52%	71%, 81%	50%, 25%	
	SV6	B_11_101-11_102	157		34%, 77%	104%, 44%	
	SV7	B_11_95-11_101	141		81%, 44%	32%, 65%	
Deletion	SV9	B_2_66-2_66	184	63%	137%, 141%	66%, 54%	
Deletion	SV10	B_1_155-1_155	145	50%	58%	47%	