Table S2. Tandem repeat enrichment is associated with mutation mechanism. Related to Fig. 2.

		Variance explained		Test Statistic	
Class	Factor	Relative	Total	Corr. Coef.	p (F-test)
VNTR			43%	0.66	$<2.2\times10^{-16}$
	MR	6%			
	DSB	5.70%			
	MR x DNM	4.40%			
	MR X DSB	3.90%			
STR			25%	0.49	$<2.2\times10^{-16}$
	MR	6.60%			
	DSB	5.40%			
	MR x DSB	2.50%			
	DSB x DNM	1.60%			
No Repeat			24%	0.49	$<2.2\times10^{-16}$
	MR	4.20%			
	DSB	3.40%			
	DNM	3%			
	MR x DSB	2.10%			
All SVs			36%	0.60	$<2.2\times10^{-16}$
	MR	6.90%			
	DSB	5.20%			
	MR X DSB	3.50%			
	DNM	2.80%			

The genome-wide SV distribution is associated with several factors, and top correlations are found among male recombination (MR), double-strand breaks (DSB), de novo mutations (DNM), or a combination of these factors. For each SV class, the top four factors explaining observed variance in SV density (R^2) are shown.