

Supplemental Table S5. Number of insertion and deletion events per indel type analyzed on chromosome 1.

Indel type	Insertions	Deletions
Chromosome 1 ^a	3840	8107
Chromosome 1 size 1-bp	2181	3934
Chromosome 1 polymorphic ^b	1534	1559

^aevent size ≤ 30-bp, restricted to chromosome 1 (a subset of those analyzed in main text).

^bPolymorphic insertions and deletions were obtained from (Mills et al 2006; see SOM text).

Supplemental Table S6. Motifs displaying significant enrichment profiles in 5' and 3' regions flanking insertions and deletions on chromosome 1.

Scale (bp)	Insertions		Deletions	
	5' flanks	3' flanks	5' flanks	3' flanks
10	NS	NS	NS	NS
20	NS	Deletion Hotspot 3_c (<10-16/R)	NS	NS
	NS	Dna Pol Pause/Frameshift Hotspot 5_r (0.0315/R)	NS	NS
		Dna Pol Pause/Frameshift Hotspot 6_c (0.042/R)		
40		Dna Pol Pause/Frameshift Hotspot 8_c (<10-16/R)		
		Dna Pol Pause/Frameshift Hotspot 8_rc (0.042/R)		
80	NS	NS	NS	NS
160	Dna Pol Pause/Frameshift Hotspot 4 (0.042/R)	NS	NS	NS
	X-like Site 4 (<10-16/R)			
	Topoisomerase Cleavage Site 6_c (<10-16/R)	NS	NS	Dna Pol Pause/Frameshift Hotspot 1 (<10-16/R)
320	Topoisomerase Cleavage Site 6_rc (<10-16/R)			Dna Pol Pause/Frameshift Hotspot 2_c (<10-16/R)
				Translin Target 2_rc (0.042/R)
640	NS	NS	NS	Dna Pol Pause/Frameshift Hotspot 9_rc (<10-16/R)

P-values given in parentheses are reported after adjustment to control FDR at threshold of 5% (see Methods). Thus, NS: Non-significant at FDR of 0.05. L, left tail test; R, right tail test.

Motif matches are coded as follows: r, reverse; c, complement; rc, reverse complement.

Supplemental Table S7. Motifs displaying significant enrichment profiles in 5' and 3' regions flanking insertions and deletions of size 1-bp on chromosome 1.

Scale (bp)	Insertions		Deletions	
	5' flanks	3' flanks	5' flanks	3' flanks
10	NS	NS	NS	NS
20	NS	NS	NS	NS
40	NS	Dna Pol Pause/Frameshift Hotspot 7_c (<10-16/R)	NS	NS
80	NS	NS	NS	NS
160	X-like Site 4 (<10-16/R)	NS	NS	NS
320	NS	Dna Pol Pause/Frameshift Hotspot 3 (<10-16/R)	Dna Pol Pause/Frameshift Hotspot 2_c (<10-16/R)	NS
		Translin Target 2_rc (0.042/R)	Dna Pol Pause/Frameshift Hotspot 3_c (<10-16/R)	
		X-like Site 1_r (<10-16/R)		
640	NS	NS	Deletion Hotspot 1_r (<10-16/R)	NS

P-values given in parentheses are reported after adjustment to control FDR at threshold of 5% (see Methods). Thus, NS: Non-significant at FDR of 0.05. L, left tail test; R, right tail test.

Motif matches are coded as follows: r, reverse; c, complement; rc, reverse complement.

Supplemental Table S8. Motifs displaying significant enrichment profiles in 5' and 3' regions flanking polymorphic^a insertions and deletions on chromosome 1.

Scale (bp)	Insertions		Deletions	
	5' flanks	3' flanks	5' flanks	3' flanks
10	NS	NS	NS	NS
20	NS	NS	NS	NS
40	Dna Pol Pause/Frameshift Hotspot 8_c (<10-16/R)	NS	NS	NS
	Dna Pol Pause/Frameshift Hotspot 8_rc (<10-16/R)			
80	Dna Pol Pause/Frameshift Hotspot 9 (<10-16/R)	Dna Pol Pause/Frameshift Hotspot 9 (<10-16/R)	Topoisomerase Cleavage Site 1_c (<10-16/R)	NS
	Topoisomerase Cleavage Site 6_c (0.0315/R)	Topoisomerase Cleavage Site 6_rc (<10-16/R)		
	Topoisomerase Cleavage Site 6_rc (<10-16/R)			
160	NS	NS	NS	NS
320	NS	Dna Pol Pause/Frameshift Hotspot 1 (<10-16/R)	NS	Dna Pol Pause/Frameshift Hotspot 1 (<10-16/R)
640	NS	X-like Site 4_rc (<10-16/R)	NS	Topoisomerase Cleavage Site 3_rc (<10-16/R)

P-values given in parentheses are reported after adjustment to control FDR at threshold of 5% (see Methods). Thus, NS: Non-significant at FDR of 0.05. L, left tail test; R, right tail test.

Motif matches are coded as follows: r, reverse; c, complement; rc, reverse complement.

^aPolymorphic insertions and deletions were obtained from (Mills et al 2006; see SOM text)