Table S1. Specificity of Detectable Coding Region Mutational Events for $[GT]_{10}$, $[TC]_{11}$, and $[T]_8$ Microsatellite-Containing Templates

	HSV-tk Mutation Frequency x 10^{-4}		
	Pol δ4	**Pol κ**	**Pol η**
Coding Pol EFest (No. obs.)	**4.5 (27)**	**120 (219)**	**380 (157)**
FRAMESHIFT (No. obs.)	**1.3 (8)**	**104 (190)**	**180 (76)**
Tandem Repeat	0.50	72	85
Mononucleotide Monitors	0.50	72	80
Deletion	***0.50***	***70***	***68***
AA	---	8.2	46
GG	0.17	28	7.3
CC	---	31	4.8
TT	0.33	2.2	4.8
CCC	---	0.55	4.8
Insertion	***---***	***1.6***	***12***
AA	---	---	2.4
GG	---	---	2.4
CC	---	---	2.4
TT	---	1.6	---
CCC	---	---	4.8
Dinucleotide Monitors	---	0.55	4.8
Non repeated sequences	0.83	32	99
Deletion	***0.67***	***28***	***85***
-A	0.50	1.6	27
-G	---	16	19
-C	---	3.3	7.3
-T	0.17	7.1	31
Insertion	***0.17***	***3.3***	***15***
BASE SUBSTITUTION (No. obs.)	**2.0 (12)**	**13 (23)**	**150 (62)**
Transition	1.5	5.5	75
T → C	---	---	29
C → T	1.3	3.8	31
G → A	0.17	1.1	4.8
A → G	---	0.55	9.7
Transversion	0.50	7.1	75
T → G	---	0.55	12
T → A	---	---	2.4
A → T	---	---	27
A → C	---	---	12
G → T	0.50	3.8	9.7
G → C	---	1.6	2.4
C → A	---	1.1	4.8
C → G	---	---	4.8
OTHER[a] (No. obs.)	**1.2 (7)**	**3.3 (6)**	**46 (19)**

[a]Other mutational events include large deletions, large insertions, rearrangements, and tandem events.

Table S2. Number of dinucleotide microsatellite alleles in the human reference genome (hg18)

Number of Units	[GT/CA] count [a]	Total count [b]
5	91,745	238,803
6	39,388	95,589
7	19,190	47,059
8	10,606	25,375
9	7,107	15,590
10	5,555	10,705
>10	53, 394	73,135
Sum	58,949	506, 256

[a] Enumeration of pure, uninterrupted microsatellites above the threshold length

[b] Includes dinucleotides of all sequences: [GT/CA], [TC/AG], [AT/TA], and [GC/CG].