Corrigendum

Two-polymerase mechanisms dictate error-free and error-prone translesion DNA synthesis in mammals

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Since the publication of this paper, the authors have noticed an error in Table I.

The correct table is shown here.

The authors apologize for any inconvenience caused.

Table I DNA sequence analysis of TLS events across BP-G and cisPt-GG in human U2OS cells, in which the expression of specific TLS DNA polymerases was knocked-down using siRNA

siRNA	Control	REV3L	POLK	POLH	POLK + REV3L	POLK + POLH
Nucleotide inserted opposite BP-G						
C	127 (74.3%)	52 (36.1%)	76 (68%)	65 (69.9%)	55 (42.3%)	83 (60.1%)
A	11 (6.4%)		5 (4.5%)	3 (3.2%)		2 (1.4%)
G	6 (3.5%)	2 (1.4%)			2 (1.5%)	1 (0.7%)
T	3 (1.8%)	2 (1.4%)	2 (1.8%)			1 (0.7%)
Deletion/insertion	24 (14%)	88 (61.1%)	29 (25.9%)	25 (26.9%)	73 (56.2%)	51 (37%)
Total number	171 (100%)	144 (100%)	112 (100%)	93 (100%)	130 (100%)	138 (100%)
TLS clones ^a	147	56	83	68	57	87
Mutagenic TLS (%) ^b	13.6%	7.1% <i>P</i> = 0.2 ^c	8.4% <i>P</i> = 0.2 ^c	4.4% <i>P</i> = 0.042^c	3.5% <i>P</i> = 0.037^c	4.6% <i>P</i> = 0.03^c

siRNA	Control	REV3L	POLK	POLH	POLH + REV3L	POLK + POLH
Nucleotide inserted opposite cisPt-GG						
CC	98 (78.4%)	53 (53%)	60 (87%)	59 (70.2%)	50 (58.1%)	44 (77.2%)
AC	15 (12%)	9 (9%)	2 (2.9%)	7 (8.3%)	4 (4.7%)	1 (1.8%)
TC	6 (4.8%)			3 (3.6%)		
CT	1 (0.8%)					
CA					2 (2.3%)	
Deletion/insertion	5 (4%)	38 (38%)	7 (10.1%)	15 (17.9%)	30 (34.9%)	12 (21.1%)
Total isolates	125 (100%)	100 (100%)	69 (100%)	84 (100%)	86 (100%)	57 (100%)
TLS clones ^a	120	62	62	69	56	45
Mutagenic TLS (%) ^b	18.3%	14.5%	3.2% <i>P</i> = 0.006^c	14.5%	10.7%	2.2% <i>P</i> = 0.01^c

U2OS cells were transfected with the indicated siRNAs. After incubation of 72 h, the plasmid mixtures containing the gap-lesion plasmid GP-BP-G1 or GP-cisPt-GG (kanR), along with the control gapped plasmid GP20 (cmR) and the carrier plasmid were introduced into the cells. After incubation of 8 h to allow TLS, the DNA was extracted and used to transform a *recA E. coli* indicator strain. GP-BP-G1 or GP-cisPt-GG (kanR) descendents were extracted from kanR colonies and subjected to DNA sequence analysis. Deletions and insertions are taken as non-TLS events.

^aThe number of clones, excluding clones having large deletions or insertions.

^bThe percent of mutagenic TLS is the fraction of events other than insertion of C opposite BP-G, or CC opposite cisPt-GG out of the total number of TLS events.

^c*P*-value is given compared with the results obtained with cells transfected with control siRNA. Analysis was performed using the χ^2 test. *P*-values that have reached statistical significance are presented in bold type.