Supplemental Table S9.

The ratios of complementary mutation rates on the leading strand in regions belonging to the most extreme replication direction bin in MSI and MSS cancers for different cancer types. Asterisks denote mutation types where asymmetry estimates are unreliable because there were few mutations (<100). The values in brackets are 95% confidence intervals. COAD, colon adenocarcinoma; STAD, stomach adenocarcinoma; UCEC, uterine corpus endometrial carcinoma.

Whole-exomes data

	COAD		UCEC		STAD	
Type	**MSI**	**MSS**	**MSI**	**MSS**	**MSI**	**MSS**
A→C/T→G	*1.60 (1.11-2.30)	*1.08 (0.79-1.46)	*0.89 (0.63-1.28)	*0.88 (0.55-1.41)	1.53 (1.28-1.83)	1.21 (1.08-1.36)
A→G/T→C	1.55 (1.33-1.82)	0.90 (0.75-1.09)	1.96 (1.74-2.21)	1.18 (0.89-1.55)	2.01 (1.87-2.16)	1.07 (0.95-1.21)
A→T/T→A	*0.94 (0.66-1.34)	*0.90 (0.67-1.22)	*0.89 (0.65-1.22)	*1.28 (0.82-2.01)	0.64 (0.52-0.77)	1.17 (0.97-1.40)
C→A/G→T	0.74 (0.61-0.88)	0.89 (0.76-1.04)	0.68 (0.58-0.79)	0.90 (0.74-1.09)	0.73 (0.66-0.80)	0.92 (0.81-1.04)
C→T/G→A	1.18 (1.09-1.27)	0.94 (0.87-1.02)	1.25 (1.16-1.34)	0.88 (0.78-0.99)	1.21 (1.17-1.26)	0.84 (0.78-0.90)
C→G/G→C	*0.94 (0.60-1.47)	0.98 (0.78-1.24)	*0.79 (0.52-1.19)	0.75 (0.59-0.96)	1.07 (0.83-1.39)	0.91 (0.78-1.07)

Whole-genomes data

	COAD		UCEC	
	MSI	**MSS**	**MSI**	**MSS**
A→C/T→G	1.43 (1.35-1.52)	1.12 (1.05-1.20)	1.53 (1.43-1.64)	0.94 (0.80-1.11)
A→G/T→C	1.54 (1.49-1.59)	1.03 (0.97-1.05)	1.99 (1.94-2.04)	1.03 (0.92-1.15)
A→T/T→A	0.73 (0.69-0.78)	0.94 (0.87-1.03)	1.06 (1.01-1.12)	1.01 (0.87-1.16)
C→A/G→T	0.62 (0.60-0.65)	0.95 (0.90-1.00)	0.65 (0.62-0.68)	0.88 (0.80-0.97)
C→T/G→A	1.24 (1.22-1.27)	0.94 (0.90-0.99)	1.30 (1.27-1.34)	0.87 (0.81-0.94)
C→G/G→C	0.92 (0.83-1.01)	0.72 (0.65-0.79)	1.24 (1.11-1.38)	0.93 (0.80-1.06)