Supplemental Table S10.

The ratios of complementary mutation rates on the leading strand in regions belonging to the most extreme replication direction bin in MSI cancers genomes for individual samples. The values in brackets are 95% confidence intervals.

Sample	**A→G**	**A→C**	**A→T**	**C→G**	**C→A**	**CpC→CpA**	**C→T**	**GpC→GpT**
TCGA-A5-A0G9	1.80 (1.58-2.06)	1.16 (0.86-1.56)	0.93 (0.78-1.12)	1.07 (0.74-1.55)	0.92 (0.76-1.12)	0.55 (0.43-0.69)	0.99 (0.84-1.16)	1.39 (1.20-1.60)
TCGA-A5-A0GA	1.63 (1.45-1.83)	1.15 (0.82-1.62)	0.78 (0.61-0.99)	1.29 (0.89-1.88)	0.79 (0.62-1.02)	0.54 (0.45-0.66)	1.12 (0.96-1.31)	1.68 (1.48-1.92)
TCGA-A5-A0GG	1.91 (1.65-2.20)	1.34 (0.89-2.03)	0.91 (0.66-1.26)	1.43 (0.97-2.12)	0.80 (0.59-1.09)	0.46 (0.35-0.59)	1.02 (0.84-1.23)	1.56 (1.32-1.83)
TCGA-AP-A054	2.34 (2.25-2.44)	1.88 (1.69-2.10)	1.47 (1.35-1.60)	1.35 (1.07-1.70)	0.96 (0.81-1.14)	0.42 (0.35-0.50)	1.11 (0.97-1.25)	1.73 (1.55-1.93)
TCGA-AP-A0LD	2.10 (1.92-2.30)	1.81 (1.44-2.28)	0.89 (0.73-1.08)	1.52 (1.05-2.21)	0.80 (0.64-1.01)	0.46 (0.38-0.56)	1.12 (0.97-1.30)	1.65 (1.45-1.88)
TCGA-AP-A0LE	1.67 (1.53-1.83)	1.26 (0.97-1.63)	0.87 (0.72-1.06)	1.11 (0.80-1.55)	0.82 (0.67-1.00)	0.40 (0.34-0.47)	1.18 (1.04-1.35)	1.73 (1.56-1.92)
TCGA-AX-A05S	1.73 (1.54-1.95)	1.41 (1.09-1.83)	0.88 (0.72-1.07)	1.04 (0.74-1.46)	0.89 (0.69-1.14)	0.61 (0.50-0.75)	1.03 (0.90-1.17)	1.57 (1.40-1.76)
TCGA-AA-3516	1.36 (1.29-1.42)	1.35 (1.24-1.46)	0.73 (0.67-0.81)	0.82 (0.72-0.94)	0.79 (0.72-0.88)	0.50 (0.45-0.55)	0.90 (0.84-0.97)	1.32 (1.25-1.39)
TCGA-AA-A01R	1.70 (1.60-1.80)	1.64 (1.47-1.83)	0.82 (0.74-0.91)	1.05 (0.86-1.28)	0.83 (0.73-0.94)	0.47 (0.42-0.52)	1.07 (1.00-1.15)	1.53 (1.44-1.63)
TCGA-D5-6540	1.71 (1.59-1.84)	1.38 (1.20-1.58)	0.61 (0.54-0.70)	1.07 (0.85-1.35)	0.81 (0.73-0.90)	0.50 (0.45-0.56)	1.00 (0.92-1.09)	1.47 (1.38-1.57)