Supplemental Table S2.

Replication asymmetry in the most extreme bin and in the entire dataset for bMMRD cancers (5 exomes with mutated pol epsilon and 2 exomes with mutated pol delta). The values in brackets are 95% confidence intervals. Asterisks denote significance of the deviation from 1.

*p:<0.05, **:p< 0.001,***:p<0.001.

	Mutated pol epsilon		**Mutated pol delta**	
	Rightmost bin	**Entire dataset**	**Rightmost bin**	**Entire dataset**
A→G/T→C	1.21 (1.03-1.42)*	1.07 (1.00-1.14)*	2.00 (1.75-2.28)***	1.30 (1.23-1.36)***
A→C/T→G	0.55 (0.40-0.75)***	0.74 (0.66-0.83)***	1.53 (1.05-2.23)*	1.20 (1.04-1.39)*
A→T/T→A	0.90 (0.49-1.63)	1.06 (0.87-1.29)	0.63 (0.54-0.74)***	0.84 (0.79-0.90)***
C→G/G→C	0.69 (0.27-1.76)	0.75 (0.49-1.15)	0.63 (0.25-1.57)	0.82 (0.58-1.15)
DpC→DpA/GpH→TpH	1.95 (1.73-2.20)***	1.27 (1.21-1.32)***	0.41 (0.34-0.51)***	0.71 (0.66-0.76)***
CpC→CpA/GpG→TpG	1.97 (1.65-2.34)***	1.23 (1.15-1.31)***	0.55 (0.45-0.66)***	0.78 (0.73-0.84)***
HpC→HpT/GpD→ApD	2.10 (1.96-2.25)***	1.30 (1.27-1.34)***	0.99 (0.84-1.16)	0.95 (0.89-1.01)
GpC→GpT/GpC→ApC	1.92 (1.80-2.06)***	1.27 (1.24-1.30)***	1.22 (1.02-1.46)*	1.11 (1.03-1.19)**