Supplemental Table S3.

The ratios of complementary mutation rates on the leading strand in regions belonging to the most extreme replication direction bin for individual exomes of bMMRD cancers with mutated polymerases. The values in brackets are 95% confidence intervals. For C→G mutations, there was not enough data for individual patient to estimate the asymmetry level.

Sample	Mutated polymerase	A→G	A→C	A→T	DpC→DpA	CpC→CpA	HpC→HpT	GpC→GpT
D1119	pol epsilon	1.22 (0.86-1.74)	0.59 (0.29-1.20)	0.33 (0.08-1.43)	2.12 (1.57-2.86)	1.68 (1.14-2.48)	2.44 (1.88-3.18)	2.03 (1.62-2.53)
D1121	pol epsilon	1.33 (0.86-2.05)	0.62 (0.29-1.34)	0.99 (0.27-3.61)	2.28 (1.63-3.19)	3.74 (2.00-6.99)	2.38 (1.84-3.08)	1.83 (1.46-2.30)
D1144	pol epsilon	1.20 (0.82-1.77)	0.82 (0.36-1.86)	4.94 (1.22-20.06)	1.70 (1.38-2.10)	1.90 (1.46-2.48)	2.24 (1.89-2.65)	1.80 (1.61-2.00)
D132	pol epsilon	1.20 (0.91-1.57)	0.47 (0.28-0.8)	0.28 (0.07-1.20)	2.29 (1.75-3.00)	2.48 (1.32-4.66)	2.06 (1.75-2.42)	2.11 (1.87-2.38)
D134	pol epsilon	1.12 (0.73-1.71)	0.44 (0.21-0.96)	0.66 (0.13-3.30)	1.75 (1.32-2.30)	1.68 (1.14-2.48)	1.83 (1.50-2.24)	1.86 (1.52-2.27)
60001	pol epsilon	2.19 (1.69-2.82)	0.51 (0.4-0.66)	2.37 (1.15-4.88)	2.34 (1.90-2.87)	2.20 (1.30-3.70)	2.34 (2.05-2.68)	1.99 (1.62-2.43)
60003	pol epsilon	0.99 (0.69-1.42)	0.47 (0.26-0.84)	1.29 (0.64-2.62)	2.34 (1.82-3.02)	1.95 (1.36-2.8)	2.18 (1.75-2.73)	1.83 (1.51-2.21)
60004	pol epsilon	1.65 (1.18-2.31)	0.41 (0.24-0.69)	0.58 (0.23-1.42)	1.84 (1.45-2.34)	1.78 (1.24-2.55)	2.28 (1.80-2.88)	2.01 (1.64-2.46)
D1120	pol delta	2.03 (1.60-2.58)	1.98 (0.54-7.21)	1.25 (0.69-2.26)	0.44 (0.29-0.66)	0.65 (0.49-0.85)	0.49 (0.33-0.73)	0.89 (0.58-1.36)
D1122	pol delta	1.99 (1.70-2.32)	1.5 (1.01-2.21)	0.60 (0.51-0.71)	0.41 (0.32-0.52)	0.47 (0.36-0.62)	0.92 (0.72-1.16)	1.31 (1.07-1.60)