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.

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<td>pol epsilon</td>
<td>1.22 (0.86-1.74)</td>
<td>0.59 (0.29-1.20)</td>
<td>0.33 (0.08-1.43)</td>
<td>2.12 (1.57-2.86)</td>
<td>1.68 (1.14-2.48)</td>
<td>2.44 (1.88-3.18)</td>
<td>2.03 (1.62-2.53)</td>
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<td>D1121</td>
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<td>1.33 (0.86-2.05)</td>
<td>0.62 (0.29-1.34)</td>
<td>0.99 (0.27-3.61)</td>
<td>2.28 (1.63-3.19)</td>
<td>3.74 (2.00-6.99)</td>
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<td>D1144</td>
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<td>0.82 (0.36-1.86)</td>
<td>4.94 (1.22-20.06)</td>
<td>1.70 (1.38-2.10)</td>
<td>1.90 (1.46-2.48)</td>
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<td>D132</td>
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<td>0.47 (0.28-0.8)</td>
<td>0.28 (0.07-1.20)</td>
<td>2.29 (1.75-3.00)</td>
<td>2.48 (1.32-4.66)</td>
<td>2.06 (1.75-2.42)</td>
<td>2.11 (1.87-2.38)</td>
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<td>D134</td>
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<td>0.44 (0.21-0.96)</td>
<td>0.66 (0.13-3.30)</td>
<td>1.75 (1.32-2.30)</td>
<td>1.68 (1.14-2.48)</td>
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<td>1.86 (1.52-2.27)</td>
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<td>0.51 (0.4-0.66)</td>
<td>2.37 (1.15-4.88)</td>
<td>2.34 (1.90-2.87)</td>
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<td>2.34 (2.05-2.68)</td>
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<td>1.84 (1.45-2.34)</td>
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<td>2.01 (1.64-2.46)</td>
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<td>0.44 (0.29-0.66)</td>
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<td>1.5 (1.01-2.21)</td>
<td>0.60 (0.51-0.71)</td>
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<td>0.92 (0.72-1.16)</td>
<td>1.31 (1.07-1.60)</td>
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