

Supplementary Table S2. Genomic status results based on next-generation sequencing and methylation-specific multiplex ligation-dependent probe amplification (n=124).

N (% of total)	<i>MLH1</i> (mut/met)	<i>MLH1</i> (only met)	<i>MLH1</i> (only mut)	<i>PMS2</i> (mut)	<i>MSH2</i> (mut)	<i>MSH6</i> (mut)	Double alteration
Altered	36 (29.0)	28 (22.6)	4 (3.2)	8 (6.5)	7 (5.6)	18 (14.5)	6 (4.8)

Two cases (1.6% of 126) had no available data and were therefore not considered for the descriptive calculations.

Mut, mutated; met, methylated.