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Supplemental Data

Using Somatic Mutations from Tumors to Classify Variants in Mismatch Repair Genes

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Supplemental Tables:

Table S1: Z-score calculations for changes at canonical splice sites defined by MaxEnt score distributions for all MMR genes

See Excel file.

Table S2: Variant counts used to derive likelihood ratios where loss of heterozygosity is observed and where no loss of heterozygosity is observed

Loss of heterozygosity present, variant read fraction cutoff = 0.8

All tumors	Below	Above
Known Pathogenic and Loss of Function	7	37
Intronic	244	8

Colorectal only	Below	Above
Known Pathogenic and Loss of Function	4	28
Intronic	155	6

Endometrial only	Below	Above
Known Pathogenic and Loss of Function	2	9
Intronic	71	2

No loss of heterozygosity present, variant read fraction cutoff = 0.35

	Below	Above
Known Pathogenic and Loss of Function	9	100
Intronic	209	299

	Below	Above
Known Pathogenic and Loss of Function	2	41
Intronic	43	82

	Below	Above
Known Pathogenic and Loss of Function	6	53
Intronic	164	215

Table S3: Multifactorial likelihood calculations for 165 variants in *MLH1*, *MSH2*, *MSH6*, and *PMS2*
See Excel file.