Supplementary Table 2 – Next Generation Sequencing (NGS) result of MMR-deficient cases (excluding cases with *MLH1* promoter hypermethylation)

Variants are either likely pathogenic (class 4) or pathogenic (class 5) unless otherwise specified.

Abbreviations: VAF = Variant allele frequency. LOH = Loss of heterozygosity. SNP = Single Nucleotide Polymorphism. NP = not performed. VAF = Variant allele freque

Immunohistochemistry results: + = normal nuclear staining. - = loss of staining in neoplastic cells with positive internal controls. +/++ = weak staining in neoplastic ce

* since germline variants may be unique to a family/person, only a general description of the germline variant type is given to protect privacy and maintain data and

Study ID	Resection or biopsy	Immunohistochemistry pattern				NGS results neoplastic tissue				Variant detected in non-neoplastic tissue
		PMS2	MLH1	MSH6	MSH2	Gene	Variant	VAF : coverage	LOH	
3	Resection	+	np	+/++	-	MSH2	Nonsense variant*	0.779:715	Probable based on 1 SNP and VAF	Yes
18	Biopsy	-	-	+	np		No relevant variants detected			
33	Resection	+	np	-	+/++	MSH2	NM_000251.2:c.1777C>T	0.480:125	No	No
							Deletion exon 1			No
46	Resection	-	+	+	np		NGS data of insufficient quality			
48	Resection	-	+	+	+	MLH1	NM_000249.3:c.112A>C	0.48:448	No informative SNPs	Normal tissue not available
71	Resection	+	np	-	+/++		No relevant variants detected			
85	Resection	Failed	np	-	+	MLH1	Missense variant classified as pathogenic by InSiGHT	0.479:1308	No informative SNPs	Yes
							NM_000249.3:c.1513_1520dup	0.168:1985		No
						MSH6	C-deletion			
94	Resection	-	-	+	np	MLH1	NM_000249.3:c.676C>T		yes	Not performed
98	Resection	+	np	-	+/++	MSH6	Frameshift variant*	0.483:1989	No	Yes
							NM_000179.2:c.3743del	0.329:1989		No
118	Resection	+	np	-	-		NGS data of insufficient quality			
119	Resection	-	+	+	np	PMS2	Frameshift variant*	0.498:1933	yes	Yes

119	Resection	-	+	+	np	MSH2	NM_000251.2:c.187dup	0.204:1967		No
124	Resection	+	np	-	failed		No relevant variants detected			According to PA-report this is a Lynch
156	Resection	+	np	-	-	MSH2	NM_000251.2:c.2027C>G	0.219:283	No informative SNPs	Not performed
206	Resection	-	-	+	np	MLH1	Frameshift variant*	0.429:1919	No informative SNPs	Yes
211	Resection	-	-	+	np	MLH1	NM_000249.3:c.454-13A>G	0.918:244	No informative SNPs, VAF is however	Normal tissue not available
214	Resection	subclonal -	+	+	np	MSH2	NM_000251.2:c.1414C>T (class 3 VUS)	0.156:257		Not performed
236	Resection	+	np	-	-	MSH6	Frameshift variant*	0.511:1621		Yes
							NM_000179.2:c.3172G>T (class 3 VUS)	0.313:1995		No
249	Resection	-	+	+	np	PMS2	NM_000535.5:c.2287G>T	0.159:1233	No informative SNPs	Normal tissue not available
							NM_000535.5:c.1882C>T	0.397:315		
316	Resection	+	np	+/++	-	MSH2	Exon deletion*	Not applicable	Yes	Yes
325	Resection	+	np	-	-		No relevant variants detected			
333	Resection	+	np	-	-	MSH6	NM_000179.2:c.3128del	0.185:352	No informative SNPs	Not performed
335	Resection	+	np	-	-	MSH2	Missense variant classified as likely pathogenic by InSiGHT*	0.520:1997	LOH probable based on 1 informative SNP	Yes
344	Resection	-	-	+	np	MLH1	NM_000249.3:c.94_110del	0.341:1510	No informative SNPs	Not performed
363	Resection	+	np	-	-	MSH2	Frameshift variant*	0.499:914	No based on 1 SNP	Yes
379	Resection	-	+	+	np	PMS2	Nonsense variant*	0.500:1225	No	Yes
							NM_000535.5:c.1802C>G	0.421:680		No
414	Resection	+	np	-	+/++	MSH6	Frameshift variant*	0.481:1795	No based on 1 SNP	Yes
							NM_000179.2:c.3533del	0.239:1980		No

426	Resection	-	-	+	np	MLH1	Frameshift variant*	0.539:1990	No informative SNPs	Yes
453	Resection	-	-	+	np	MLH1	NM_000249.3:c.791-2A>C (class 3 VUS)	0.634:1994	No informative SNPs	No
460	Resection	+	np	+/++	-	MSH2	NM_000251.2:c.2557G>T	0.241:1312	Unlikely based on 1 SNP	Not performed
466	Resection	-	-	+	np		No relevant variants detected			
474	Resection	+	np	-	-	MSH2	Frameshift variant*	0.691:676	Probable based on 1 SNP	Yes
480	Resection	-	-	Subclonal	np	MLH1	Nonsense variant*	0.744:1999	yes	Yes
				-		MSH6	No relevant variants detected		yes	
526	Resection	+	np	-	-		No relevant variants detected			
551	Resection	-	-	+	Np	MLH1	NM_000249.3:c.2145_2168del	0.578:211	No informative SNPs	Normal tissue not available
558	Resection	-	+	Subclonal -	+/++	PMS2	NM_000535.5:c.638del	0.378:1995	Possibly based on 3 SNPs	No
568	Resection	-	+/++	+	np	PMS2	NM_000251.2:c.2458+1G>A	0.381:1998	No	Not performed
595	Resection	+	np	-	+/++	MSH6	Frameshift variant*	0.453:1190	No	Yes
							NM_000179.2:c.2232G>T (class 3 VUS)	0.169:349		No
596	Resection	+	np	-	-	MSH2	NM_000251.2:c.1861C>T	0.491:1611	No	Normal tissue not available
							NM_000251.2:c.2458+1G>A	0.271:399		
601	Resection	+	np	-	-	MSH2	NM_000251.2:c.1601G>A	0.346:619	No informative SNPs	Not performed
						MSH6	NM_000179.2:c.1436_1440del	0.35:1980	Yes	
687	Resection	-	np	-	-		NGS data of insufficient quality			
698	Resection	+	np	Subclonal	+		NGS data of insufficient quality			
710	Resection	-	+	+	np	PMS2	NM_000535.5:c.1405A>T	0.522:1994	No	Normal tissue not available

720	Resection	+	np	-	-	MSH2	Nonsense variant*	0.678:1772	No	Yes
722	Resection	+	np	-	+/++	MSH6	Frameshift variant*	0.532:342	no	Yes
							NM_000179.2:c.1444C>T	0.285:895		No
723	Resection	-	-	+	np	MLH1	Frameshift variant*	0.937:1449	Probable based on one SNP and VAF of	Yes
746	Resection	-	-	+	np	MLH1	Frameshift variant*	0.594:1721	Yes	Yes
748	Resection	+	np	-	-		NGS data of insufficient quality			
760	Resection	-	-	+	np	MLH1	NM_000249.3:c.252del	0.498:601	yes	No