Germline variants in the mismatch repair genes: Detection and phenotype

Suerink, M.

Prevalence of mismatch repair deficiency and Lynch syndrome in a cohort of unselected small bowel adenocarcinomas

Journal of Clinical Pathology, online ahead of print 2020

Manon Suerink, Gül Kilinç, Diantha Terlouw, Hristina Hristova, Lily Sensuk, Demi van Egmond, PALGA-group, Arantza Farina Sarasqueta, Alexandra MJ Langers, Tom van Wezel, Hans Morreau, Maartje Nielsen

ABSTRACT

Aims

Previous estimates of the prevalence of mismatch repair (MMR) deficiency and Lynch syndrome in small bowel cancer have varied widely. The aim of this study was to establish the prevalence of MMR deficiency and Lynch syndrome in a large group of small bowel adenocarcinomas.

Methods

To this end, a total of 400 small bowel adenocarcinomas (332 resections, 68 biopsies) were collected through PALGA (Dutch Pathology Registry). No preselection criteria, such as family history, were applied, thus avoiding (ascertainment) bias. MMR deficiency status was determined by immunohistochemical staining of MMR proteins, supplemented by *MLH1* promoter hypermethylation analysis and Next Generation Sequencing (NGS) of the MMR genes.

Results

MMR deficiency was observed in 22.3% of resected and 4.4% of biopsied small bowel carcinomas. Prevalence of Lynch syndrome was 6.2% in resections and 0.0% in biopsy samples. Patients with Lynch syndrome-associated small bowel cancer were significantly younger at the time of diagnosis than patients with MMR-proficient and sporadic MMR-deficient cancers (mean age of 54.6 years versus 66.6 years and 68.8 years, respectively, $p<0.000$).

Conclusions

The prevalence of MMR deficiency and Lynch syndrome in resected small bowel adenocarcinomas is at least comparable to prevalence in colorectal cancers, a finding relevant both for treatment (immunotherapy) and family management. We recommend that all small bowel adenocarcinomas should be screened for MMR deficiency.

INTRODUCTION

Small bowel cancer is a rare form of cancer, with an incidence of less than 1.0 per 100,000,[1] and little is known about the risk factors for development of this rare disease. However, monogenic cancer predisposition syndromes, such as familial adenomatous polyposis (FAP) and Lynch syndrome, are known to be responsible for a proportion of small bowel adenocarcinomas.[2] While FAP, which is caused by a germline pathogenic variant in the *APC* gene, is characterized by the presence of polyposis coli, Lynch syndrome may be harder to recognize.[3,4]

Lynch syndrome is caused by germline pathogenic variants in one of four mismatch repair (MMR) genes (*MLH1, MSH2 (EPCAM), MSH6* and *PMS2*) and predisposes carriers to the development of mainly colorectal and endometrial cancer.[4] In addition, risk for several other malignancies is increased, including risk for small bowel adenocarcinomas, currently estimated to be between 0.4% and 12% for *MLH1* and *MSH2* variant carriers.[5] Unlike FAP, there are no overt clinical characteristics that distinguish a small bowel malignancy in a Lynch syndrome patient from a sporadic case, although a personal or family history of a Lynch syndrome-associated cancer may be suggestive. Surveillance of the duodenum is generally not recommended in Lynch syndrome due to lack of evidence supporting its effectiveness.[6] Nonetheless, identification of a Lynch syndrome family via a small bowel cancer case may provide the patient and other family members with the opportunity for surveillance of the colon, which has proven value as a screening strategy [7,8].

A hallmark of Lynch syndrome-related tumours is the presence of MMR deficiency, which results from biallelic inactivation of one of the MMR genes and can be demonstrated by immunohistochemical staining of tumour tissue for the MMR proteins, and/or microsatellite instability (MSI) analysis.[9,10] Lack of nuclear staining of neoplastic cells or presence of MSI are indicative of MMR deficiency. MMR deficiency in Lynch syndrome occurs due to a second somatic hit in neoplastic cells, in addition to a germline variant. MMR deficiency may also occur in sporadic cases due to somatic inactivation of both alleles.[11] The presence of MMR deficiency might also be relevant to patient treatment, given that PDL1-blockers produce a good response in MMR-deficient (colorectal) cancers regardless of sporadic or hereditary aetiology.[11,12] Universal screening for MMR deficiency in small bowel cancers, as introduced for colorectal cancer and endometrial cancer in many countries,[13,14] may therefore be warranted. The potential benefit of a comparable screening strategy can only be accurately assessed if the prevalence of MMR deficiency and Lynch syndrome in unselected small bowel cancer is first reliably estimated. Previous estimates of the prevalence of MMR deficiency were

based on small cohorts and consequently showed wide variability (0-35%).[2,15] Few data are available on the prevalence of Lynch syndrome in these cohorts. In this study, a large, unbiased collection of small bowel cancers was used to reliably establish the prevalence of MMR deficiency and Lynch syndrome in this rare tumour group.

METHODS

Cohort

The nationwide network and registry of histo- and cytopathology in the Netherlands, known as PALGA, was consulted in 2017 in a nationwide search of tumour samples from small bowel cancer patients.[16] All excerpts labelled by the reporting pathologist as a neoplasm of the small bowel were extracted for the five-year period 2012-2016. The conclusions of the resulting pathology reports were then screened for:

1. All resected primary small bowel adenocarcinomas within the five-year time frame. This resulted in the selection of 411 eligible tumour specimens.
2. The hundred most recent samples that included a biopsy of an adenocarcinoma with a (possible) primary origin in the small bowel. This second category of samples was added to ensure inclusion of unresectable cases (some duodenal adenocarcinomas present at an advanced stage and are not resectable due to the high morbidity of surgery).

Formalin-fixed paraffin-embedded (FFPE) material representative of these adenocarcinomas was then requested. Material from 332 resection specimens and 68 biopsy samples was obtained. A favourable ethical opinion was received from the Medical Ethical Review Board of Leiden University Medical Centre (reference number P16.313). Due to the anonymous nature of the samples and the rules and regulations of the PALGA-network, obtaining consent was not possible or required.

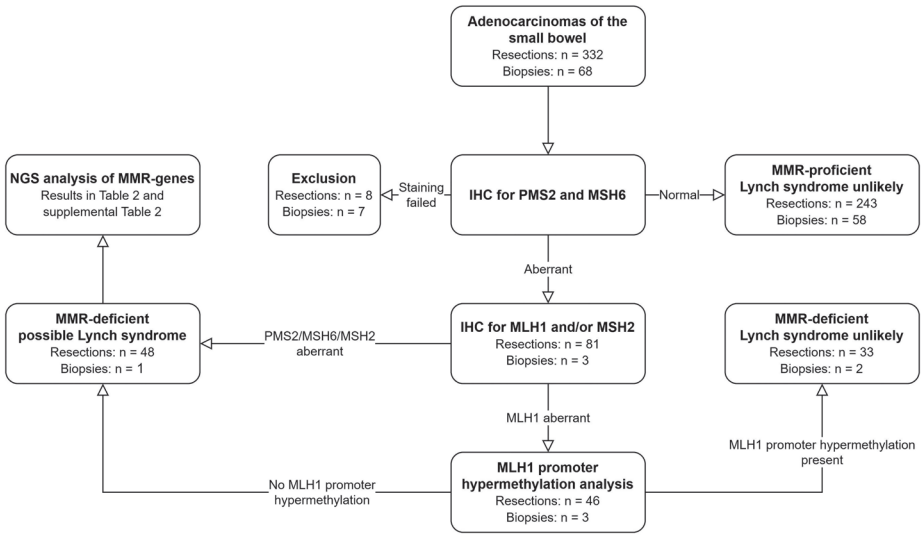
Study procedures

The study flow is visualized in Figure 1. Upon receipt, 4µm sections were taken from the FFPE blocks and subjected to haematoxylin and eosin staining (H&E) and immunohistochemical staining of the MMR proteins. Additionally, depending on tumour size and histology, 10µm sections or punches from the tumour were taken for later DNA isolation. Guided by a matching H&E slide, the 10µm sections were micro-dissected to enrich for tumour. All samples were coded for complete anonymity

according to Dutch guidelines. Anonymous basic personal data (age at diagnosis and gender) was available for each patient, in addition to historical pathology reports. No other clinical data were available.

All adenocarcinomas were initially immunohistochemically stained for PMS2 and MSH6 protein expression.[17] Subsequent immunohistochemical staining for MLH1 and/or MSH2 was performed if the tumour was PMS2- or MSH6-deficient. This approach is more cost-effective than using a four-antibody panel and has good sensitivity. The rationale for this approach is that functionally, MLH1 forms a heterodimer with PMS2, while MSH2 forms a heterodimer with MSH6, and mutations in *MLH1* or *MSH2* result in degradation of their heterodimer partners. Hence, use of PMS2 and MSH6 antibodies as a first screening step will generally identify loss of protein expression of MLH1 or MSH2.[17,18] In cases with MLH1 deficiency, *MLH1* promoter hypermethylation analysis was performed. In cases with loss of expression of MLH1 in the absence of *MLH1* promoter hypermethylation or in cases with MSH2, MSH6 and solitary PMS2 expression loss, the MMR genes were further analysed using Next Generation Sequencing (NGS). If NGS identified a variant with an allele frequency of >40%, DNA from matching non-neoplastic tissue (when available) was isolated to determine whether the variant was germline or somatic in origin.

Figure 1 Study procedures. IHC = immunohistochemistry. MMR = mismatch repair. NGS = next generation sequencing



Immunohistochemical staining

Details on the immunohistochemical staining procedures can be found in the Supplemental Methods. The immunohistochemically stained samples were examined by an experienced pathologist (HM or AFS) using light microscopy to evaluate MMR status. MMR proficiency was defined as the presence of nuclear staining within neoplastic cells, as well as within adjacent non-neoplastic cells. MMR deficiency was defined as an absence of nuclear staining within neoplastic cells, together with positive expression in non-neoplastic cells. A third category, subclonal loss of protein expression, was defined for those adenocarcinomas harbouring a subpopulation of cancer cells with loss of expression together with cells retaining expression of an MMR protein.

DNA isolation using the Tissue Preparation System

DNA was isolated using the Tissue Preparation System with VERSANT Tissue Preparation Reagents (Siemens Healthcare Diagnostics, Tarrytown, NY), as previously described.[19]

MLH1 promoter hypermethylation analysis

Cases with loss of MLH1 expression were analysed for *MLH1* promoter hypermethylation by methylation-specific PCR (MSP).[20,21] Bisulphite conversion was carried out using the EZ DNA Methylation-Lightning Kit (D5031; Zymo Research) according to manufacturer's instructions.

Targeted Next Generation Sequencing

Adenocarcinomas with aberrant expression of at least one of the MMR proteins in the absence of *MLH1* promoter hypermethylation underwent DNA variant analysis using an NGS panel. This panel consists of 20 colorectal cancer- and polyposis-associated genes, and hotspot regions of the *CTNNB1* gene (see Supplemental Table 1 for all genes and panel coverage). For the purposes of this study, analysis of NGS results was restricted to *MLH1*, *MSH2*, *MSH6* and *PMS2*. Sequencing was performed using the Ion Torrent platform according to the manufacturer's recommendations. Details can be found in the Supplemental Methods.

The unaligned sequence reads generated by the sequencer were mapped against a human reference genome (hg19) using the Burrows-Wheeler aligner (BWA). VarScan and ANNOVAR software were used for variant calling and annotation, respectively, and Integrative Genomics Viewer (IGV) software was used to visualize the read alignment and presence of variants. Additionally, the Leiden Open Variant Database (LOVD),

ClinVar and Alamut software were used whenever additional variant interpretation was needed.

Statistical analysis

Using IBM SPSS Statistics 24, the chi-square test and one-way ANOVA test were performed as appropriate to compare patient and tumour characteristics of MMR-proficient cases with sporadic MMR-deficient cases and Lynch syndrome-associated cases. A *p*-value <0.05 was considered to be statistically significant. Cases with subclonal loss of one of the MMR proteins were excluded from these analyses.

RESULTS

Immunohistochemistry

The prevalence of MMR deficiency, as determined by immunohistochemical staining, was 22.3% in resected small bowel adenocarcinomas and 4.4% in biopsies (Table 1). Additionally, seven (2.1%) resected samples showed subclonal loss of at least one MMR protein. Eight resected adenocarcinomas and seven adenocarcinoma biopsy samples had to be excluded from further analysis because no (representative) tumour tissue was present in the available FFPE blocks.

Table 1. Prevalence of mismatch repair (MMR) deficiency and immunohistochemical staining patterns in resected and biopsied adenocarcinoma samples

Immunohistochemistry results	Resections *N (%)*	Biopsies *N (%)*
MMR-proficient	**243 (73.2)**	**58 (85.3)**
MMR deficiency - complete tumor	**74 (22.3)**	**3 (4.4)**
- MLH1/PMS2	42	3
- PMS2 only	7	0
- MSH2/MSH6	19	0
- MSH6 only	6	0
Subclonal MMR deficiency	**7 (2.1)**	**0 (0)**
- MLH1/PMS2	4	
- MSH6 only	1	
- All four deficient	2	
No tumor, excluded from further analysis	8 (2.4)	7 (10.3)
Total	332	68

The most common cause of MMR deficiency was *MLH1* promoter hypermethylation (40.5% of MMR-deficient resections and 66.7% of MMR-deficient biopsies, Table 2). In more than a quarter of MMR-deficient resection samples the MMR deficiency was related to Lynch syndrome (27%, Table 2 and Supplemental Table 2). The prevalence of Lynch syndrome within the total resection cohort was therefore at least 20/324 (6.2%). The true number might in fact be higher, because in six cases an MMR gene variant with a high allele frequency (>40% of reads) was identified within the tumour, but matched normal tissue was not available to confirm or refute germline origin of the variant.
A comparison of patient and tumour characteristics of MMR-proficient, (apparently) sporadic MMR-deficient and Lynch syndrome-associated cases included only the resected adenocarcinoma cases, as they represent the largest subcohort and have a documented primary tumour location within the small bowel. The six cases carrying a high allele frequency variant but without available matched normal tissue were excluded due to uncertainty regarding their status as Lynch syndrome or sporadic MMR-deficient cases. Cases with an unexplained MMR deficiency and those with subclonal MMR deficiencies were also excluded from this analysis.

Table 2. Causes of mismatch repair (MMR) deficiency

	MMR-deficient tumors		Subclonal loss
	Resections *N (%)*	Biopsies *N (%)*	Resections *N (%)*
MLH1 promoter hypermethylation	30 (40.5)	2 (66.7)	3 (42.9)
Two somatic hits	10 (13.5)	0	1 (14.3)
Lynch syndrome - MLH1 variant - MSH2 variant - PMS2 variant - MSH6 variant	20 (27.0) 6 7 2 5	0	0
MMR variants identified in tumor, normal tissue not available, but high variant allele frequency	6 (8.1)	0	0
MMR deficiency molecularly unexplained (no or only one somatic hit identified)	8 (10.8)	1 (33.3)	3 (42.9)
Total	74	3	7

Table 3. Cohort characteristics for Lynch syndrome versus mismatch repair (MMR) proficient versus MMR-deficient cases

		MMR-proficient *N*=243	Sporadic MMR-deficient carcinomas *N*= 44	Lynch syndrome *N*=20	*P*-value
Gender – male		126 (51.9%)	23 (52.3%)	13 (65.0%)	0.525
Mean age at diagnosis in years (range)		66.6 (27-91)	68.8 (43-90)	54.6 (35-77)	<0.000
Location (%)	Duodenum	126 (51.9%)	26 (59.1%)	12 (60.0%)	0.893
	Jejunum	51 (21.0%)	7 (15.9%)	3 (15.0%)	
	Ileum	33 (13.6%)	4 (9.1%)	3 (15.0%)	
	Small bowel not otherwise specified	33 (13.6%)	7 (15.9%)	2 (10.0%)	
Previous history of Lynch syndrome-associated* cancer		28 (11.5%)	8 (18.2%)	13 (65.0%)	<0.000
Previous history of other cancer type(s)# (non-Lynch)		27 (11.1%)	6 (13.6%)	6 (30.0%)	0.050
Crohn's disease - yes		8 (3.3%)	0 (0%)	0 (0%)	0.339
Coeliac disease - yes		3 (1.2%)	3 (6.8%)	0 (0%)	0.039

** Lynch syndrome-associated cancers: colorectal cancer, endometrial cancer, ovarian cancer, gastric cancer, cancer of the bile duct or gallbladder, pancreatic cancer or urothelial cancer (Moller et al. 2018). # Excluding basal cell cancer of the skin*

Mean age at cancer diagnosis was significantly lower in the Lynch syndrome patients (Table 3), and a previous history of a Lynch syndrome-associated cancer was significantly elevated in Lynch syndrome patients. Interestingly, coeliac disease (diagnosed based on pathology reports of small bowel biopsies unconnected to the small bowel cancer diagnosis) was significantly more common in sporadic MMR-deficient cases. No other significant associations were identified (e.g. location, gender, other cancer history,[22] Crohn's disease).

DISCUSSION

In a large group of resected primary small bowel adenocarcinomas, we found complete MMR deficiency in 22.3% and subclonal deficiency in 2.1% of cases, while biopsied small bowel adenocarcinomas showed a lower prevalence of MMR deficiency (4.4%). To the best of our knowledge, this is the first study to systematically screen a large, consecutive group of small bowel adenocarcinomas for the prevalence of MMR deficiency. Previous studies were either smaller and/or used selected cases with a higher a priori chance of being related to Lynch syndrome. Furthermore, many of these studies did not include molecular analysis to verify whether MMR deficiency was Lynch syndrome-related or sporadic.[2,15,23]
A recently published French study by Aparicio *et al.*[24] reported a Lynch syndrome prevalence of 6.9% in a large cohort of small bowel adenocarcinomas, in line with a prevalence of at least 6.2% in our cohort. MMR deficiency prevalence could not be compared because this French cohort was not systematically screened for MMR deficiency.

Of particular note, the prevalence of MMR deficiency in our study differed considerably between the resected and biopsied specimens. A higher prevalence of MMR deficiency in resected versus biopsied samples might be related to the association of MMR deficiency with a better prognosis in other cancers,[25] so resections may represent cancer patients with a relatively good prognosis, whereas biopsies may represent patients with a poor prognosis who are less likely to undergo resection. Interestingly, the prevalence of MMR deficiency identified in biopsied samples, 4.4%, is close to the 5.0% prevalence identified in a metastatic colorectal cancer cohort.[26] However, as no further clinical data were available to verify that a biopsied sample was a confirmed primary small bowel cancer, our cohort may also have included cancers with a different primary location (where MMR deficiency prevalence is lower). Further validation of

the prevalence of MMR deficiency in a cohort of small bowel cancers that were not resected is therefore required.
The relevance of subclonal loss of MMR protein expression is still poorly understood. While it seems unlikely that these patients have Lynch syndrome, the relevance of subclonal loss for prognosis and/or therapy will require further investigation.[18,27]

A significant overrepresentation of patients with coeliac disease was noted amongst cases with sporadic MMR deficiency. An association of coeliac disease with sporadic MMR deficiency (particularly with *MLH1* promoter hypermethylation) has been described previously,[28,29] and two out of three MMR-deficient cases from our cohort also showed *MLH1* promoter hypermethylation. A limitation of our study was the lack of accompanying clinical data, which meant that we had no information on treatment/diet and could not verify whether the pathological signs of coeliac disease correlated with patient symptoms. These results should therefore be interpreted with caution, because there are other conditions that mimic the histological signs of coeliac disease.[30] Another drawback of anonymous data is that it precludes verification of the number of Lynch syndrome cases, knowledge that might otherwise be used to establish how many patients are missed using current practices. Nevertheless, from pathology reports we could deduce that thirteen out of twenty Lynch patients were likely already identified, either because MSI and/or immunohistochemical testing was described (in the small bowel tumour or a previous tumour) or a previous diagnosis of Lynch syndrome was mentioned (Supplemental Table 3).

There is an ongoing discussion whether a two-antibody panel for immunohistochemical staining of the MMR proteins has sufficient sensitivity to detect MMR deficient cases. Although a small number of MMR deficient cases may be missed with a two-antibody panel, it is not expected that the results of a four-antibody approach would alter our conclusions.

A molecular cause of MMR deficiency could not always be identified (*n*=12). This is likely partly explained by the fact that we did not perform multiplex ligation-dependent probe amplification (MPLA) analysis to screen samples for deletions and/or insertions (germline or somatic) of the MMR genes or *EPCAM* (Table 2 and Supplemental Table 2). Nonetheless, NGS data was manually checked using the Integrative Genomics Viewer (IGV) for evidence suggesting a deletion, which led to the identification of deletions in three samples (Supplemental Table 2, e.g. study ID 33). Although this approach lowers the risk of missing copy number variants, not all deletions/insertions

will be identified. As *EPCAM* was not sequenced, deletions of this gene will have been missed by definition. However, as only 1-3% of all Lynch syndrome families carry an *EPCAM* deletion and deletions/insertions of the MMR genes explain a minority of Lynch syndrome families,[4,31] MLPA analysis is unlikely to have altered our conclusions and recommendations. Another possible explanation for the failure of NGS results to resolve all MMR deficiency cases is that some cases lacked the informative single nucleotide polymorphisms (SNPs) required to determine whether loss of heterozygosity has occurred.

The analysis of *PMS2* is complicated by the presence of pseudogenes. Nevertheless, researchers from our group have shown that it is possible to reliably detect variants in *PMS2*, even when using DNA isolated from FFPE material, as long as the correct amplicons are selected.[32] Exceptions include variants in exon 12-15 due to gene conversion. The two germline variants identified in our cohort are found in exons 1-11. In our cohort, the prevalence of MMR deficiency in resected cases (22.3%) was higher than the reported prevalence of MMR deficiency in colorectal cancer (15%).[33] This finding has implications for daily clinical practice in relation to three important issues: prognosis, treatment and surveillance. In (early-stage) colorectal cancer, MMR deficiency has been linked to a better prognosis,[25,34,35] an association that may also hold true for MMR-deficient small bowel cancers. Indeed, the aforementioned study by Aparicio *et al*. reported a trend towards better prognosis for Lynch-associated small bowel adenocarcinomas versus those related to Crohn's disease.[24] Furthermore, with the advent of immunoblockade therapy and its proven efficacy in MMR-deficient cancers,[36] MMR status is relevant when formulating treatment strategies regardless of germline or sporadic status. Finally, due to the high prevalence of Lynch syndrome, small bowel cancer as an entity may facilitate the identification of new Lynch syndrome families and consequently allow surveillance measures to be offered.

In light of the high prevalence of MMR deficiency and Lynch syndrome, together with associated relevance and benefits, we recommend the implementation of universal screening of all primary small bowel adenocarcinomas for the presence of MMR deficiency. An age limit of 70 years is often used in the universal screening of colorectal cancers for mismatch repair deficiency. However, as the Lynch syndrome-associated cases included in our study showed a very broad age range (35-77 years, table 3) at diagnosis, we suggest that age limits on universal screening for small bowel cancer may be detrimental.

ACKNOWLEDGMENTS

This work was supported by a grant from the Dutch Cancer Society (KWF UL 2012–5155).

We thank Medactie.com for assistance with the editing of this manuscript.

We thank our PALGA-group collaborators for providing patient samples: dr. E.J.M. Ahsmann, Klinische pathologie Groene Hart Ziekenhuis; dr. C. Jansen, Laboratorium Pathologie Oost-Nederland; R.S. van der Post, Radboud UMC Nijmegen; C. Wauters, CWZ Nijmegen; dr. C.Y. Yick, Amphia Ziekenhuis Breda.

REFERENCES

1. Pan SY, Morrison H. Epidemiology of cancer of the small intestine. *World Journal of Gastrointestinal Oncology.* 2011;3(3):33-42.
2. Aparicio T, Zaanan A, Mary F, Afchain P, Manfredi S, Evans TR. Small Bowel Adenocarcinoma. *Gastroenterology Clinics of North America.* 2016;45(3):447-457.
3. Jasperson KW, Patel SG, Ahnen DJ. APC-Associated Polyposis Conditions. In: Adam MP, Ardinger HH, Pagon RA, et al., eds. *GeneReviews((R)).* Seattle (WA)1993.
4. Kohlmann W, Gruber SB. Lynch Syndrome. In: Adam MP, Ardinger HH, Pagon RA, et al., eds. *GeneReviews((R)).* Seattle (WA)1993.
5. Giardiello FM, Allen JI, Axilbund JE, Boland CR, Burke CA, Burt RW, Church JM, Dominitz JA, Johnson DA, Kaltenbach T, Levin TR, Lieberman DA, Robertson DJ, Syngal S, Rex DK, Cancer USM-STFoC. Guidelines on genetic evaluation and management of Lynch syndrome: a consensus statement by the US Multi-Society Task Force on colorectal cancer. *Gastroenterology.* 2014;147(2):502-526.
6. Koornstra JJ, Kleibeuker JH, Vasen HF. Small-bowel cancer in Lynch syndrome: is it time for surveillance? *Lancet Oncology.* 2008;9(9):901-905.
7. Vasen HF, Abdirahman M, Brohet R, Langers AM, Kleibeuker JH, van Kouwen M, Koornstra JJ, Boot H, Cats A, Dekker E, Sanduleanu S, Poley JW, Hardwick JC, de Vos Tot Nederveen Cappel WH, van der Meulen-de Jong AE, Tan TG, Jacobs MA, Mohamed FL, de Boer SY, van de Meeberg PC, Verhulst ML, Salemans JM, van Bentem N, Westerveld BD, Vecht J, Nagengast FM. One to 2-year surveillance intervals reduce risk of colorectal cancer in families with Lynch syndrome. *Gastroenterology.* 2010;138(7):2300-2306.
8. de Vos tot Nederveen Cappel WH, Jarvinen HJ, Lynch PM, Engel C, Mecklin JP, Vasen HF. Colorectal surveillance in Lynch syndrome families. *Familial Cancer.* 2013;12(2):261-265.
9. Yoon YS, Yu CS, Kim TW, Kim JH, Jang SJ, Cho DH, Roh SA, Kim JC. Mismatch repair status in sporadic colorectal cancer: immunohistochemistry and microsatellite instability analyses. *Journal of Gastroenterology and Hepatology.* 2011;*26*(12):1733-1739.
10. Cerretelli G, Ager A, Arends MJ, Frayling IM. Molecular pathology of Lynch syndrome. *Journal of Pathology.* 2020;250(5):518-531.
11. Battaglin F, Naseem M, Lenz HJ, Salem ME. Microsatellite instability in colorectal cancer: overview of its clinical significance and novel perspectives. *Clinical Advances in Hematology & Oncology.* 2018;16(11):735-745.
12. Le DT, Durham JN, Smith KN, Wang H, Bartlett BR, Aulakh LK, Lu S, Kemberling H, Wilt C, Luber BS, Wong F, Azad NS, Rucki AA, Laheru D, Donehower R, Zaheer A, Fisher GA, Crocenzi TS, Lee JJ, Greten TF, Duffy AG, Ciombor KK, Eyring AD, Lam BH, Joe A, Kang SP, Holdhoff M, Danilova L, Cope L, Meyer C, Zhou S, Goldberg RM, Armstrong DK, Bever KM, Fader AN, Taube J, Housseau F, Spetzler D, Xiao N, Pardoll DM, Papadopoulos N, Kinzler KW, Eshleman JR, Vogelstein B, Anders RA, Diaz LA, Jr. Mismatch repair deficiency predicts response of solid tumors to PD-1 blockade. *Science.* 2017;357(6349):409-413.
13. Vindigni SM, Kaz AM. Universal Screening of Colorectal Cancers for Lynch Syndrome: Challenges and Opportunities. *Digestive Diseases and Sciences.* 2016;61(4):969-976.
14. Dillon JL, Gonzalez JL, DeMars L, Bloch KJ, Tafe LJ. Universal screening for Lynch syndrome in endometrial cancers: frequency of germline mutations and identification of patients with Lynch-like syndrome. *Human Pathology.* 2017;70:121-128.
15. Jun SY, Lee EJ, Kim MJ, Chun SM, Bae YK, Hong SU, Choi J, Kim JM, Jang KT, Kim JY, Kim GI, Jung SJ, Yoon G, Hong SM. Lynch syndrome-related small intestinal adenocarcinomas. *Oncotarget.* 2017;8(13):21483-21500.
16. Casparie M, Tiebosch AT, Burger G, Blauwgeers H, van de Pol A, van Krieken JH, Meijer GA. Pathology databanking and biobanking in The Netherlands, a central role for PALGA, the nationwide histopathology and cytopathology data network and archive. *Cellular Oncology.* 2007;29(1):19-24.

17. Mojtahed A, Schrijver I, Ford JM, Longacre TA, Pai RK. A two-antibody mismatch repair protein immunohistochemistry screening approach for colorectal carcinomas, skin sebaceous tumors, and gynecologic tract carcinomas. *Modern Pathology.* 2011;24(7):1004-1014.
18. Stelloo E, Jansen AML, Osse EM, Nout RA, Creutzberg CL, Ruano D, Church DN, Morreau H, Smit V, van Wezel T, Bosse T. Practical guidance for mismatch repair-deficiency testing in endometrial cancer. *Annals of Oncology.* 2017;28(1):96-102.
19. van Eijk R, Stevens L, Morreau H, van Wezel T. Assessment of a fully automated high-throughput DNA extraction method from formalin-fixed, paraffin-embedded tissue for KRAS, and BRAF somatic mutation analysis. *Experimental and Molecular Pathology.* 2013;94(1):121-125.
20. van Roon EH, Boot A, Dihal AA, Ernst RF, van Wezel T, Morreau H, Boer JM. BRAF mutation-specific promoter methylation of FOX genes in colorectal cancer. *Clinical Epigenetics.* 2013;5(1):2.
21. Perez-Carbonell L, Alenda C, Paya A, Castillejo A, Barbera VM, Guillen C, Rojas E, Acame N, Gutierrez-Avino FJ, Castells A, Llor X, Andreu M, Soto JL, Jover R. Methylation analysis of MLH1 improves the selection of patients for genetic testing in Lynch syndrome. *Journal of Molecular Diagnostics.* 2010;12(4):498-504.
22. Moller P, Seppala TT, Bernstein I, Holinski-Feder E, Sala P, Gareth Evans D, Lindblom A, Macrae F, Blanco I, Sijmons RH, Jeffries J, Vasen HFA, Burn J, Nakken S, Hovig E, Rodland EA, Tharmaratnam K, de Vos Tot Nederveen Cappel WH, Hill J, Wijnen JT, Jenkins MA, Green K, Lalloo F, Sunde L, Mints M, Bertario L, Pineda M, Navarro M, Morak M, Renkonen-Sinisalo L, Valentin MD, Frayling IM, Plazzer JP, Pylvanainen K, Genuardi M, Mecklin JP, Moeslein G, Sampson JR, Capella G, Mallorca G. Cancer risk and survival in path_MMR carriers by gene and gender up to 75 years of age: a report from the Prospective Lynch Syndrome Database. *Gut.* 2018;67(7):1306-1316.
23. Latham A, Srinivasan P, Kemel Y, Shia J, Bandlamudi C, Mandelker D, Middha S, Hechtman J, Zehir A, Dubard-Gault M, Tran C, Stewart C, Sheehan M, Penson A, DeLair D, Yaeger R, Vijai J, Mukherjee S, Galle J, Dickson MA, Janjigian Y, O'Reilly EM, Segal N, Saltz LB, Reidy-Lagunes D, Varghese AM, Bajorin D, Carlo MI, Cadoo K, Walsh MF, Weiser M, Aguilar JG, Klimstra DS, Diaz LA, Jr., Baselga J, Zhang L, Ladanyi M, Hyman DM, Solit DB, Robson ME, Taylor BS, Offit K, Berger MF, Stadler ZK. Microsatellite Instability Is Associated With the Presence of Lynch Syndrome Pan-Cancer. *Journal of Clinical Oncology.* 2019;37(4):286-295.
24. Aparicio T, Henriques J, Manfredi S, Tougeron D, Bouche O, Pezet D, Piessen G, Coriat R, Zaanan A, Legoux JL, Terrebone E, Pocard M, Gornet JM, Lecomte T, Lombard-Bohas C, Perrier H, Lecaille C, Lavau-Denes S, Vernerey D, Afchain P, Investigators N. Small bowel adenocarcinoma: Results from a nationwide prospective ARCAD-NADEGE cohort study of 347 patients. *International Journal of Cancer.* 2020.
25. Deng Z, Qin Y, Wang J, Wang G, Lang X, Jiang J, Xie K, Zhang W, Xu H, Shu Y, Zhang Y. Prognostic and predictive role of DNA mismatch repair status in stage II-III colorectal cancer: A systematic review and meta-analysis. *Clinical Genetics.* 2020;97(1):25-38.
26. Venderbosch S, Nagtegaal ID, Maughan TS, Smith CG, Cheadle JP, Fisher D, Kaplan R, Quirke P, Seymour MT, Richman SD, Meijer GA, Ylstra B, Heideman DA, de Haan AF, Punt CJ, Koopman M. Mismatch repair status and BRAF mutation status in metastatic colorectal cancer patients: a pooled analysis of the CAIRO, CAIRO2, COIN, and FOCUS studies. *Clinical Cancer Research.* 2014;20(20):5322-5330.
27. Chen W, Pearlman R, Hampel H, Pritchard CC, Markow M, Arnold C, Knight D, Frankel WL. MSH6 immunohistochemical heterogeneity in colorectal cancer: comparative sequencing from different tumor areas. *Human Pathology.* 2020;96:104-111.
28. Vanoli A, Di Sabatino A, Furlan D, Klersy C, Grillo F, Fiocca R, Mescoli C, Rugge M, Nesi G, Fociani P, Sampietro G, Ardizzone S, Luinetti O, Calabro A, Tonelli F, Volta U, Santini D, Caio G, Giuffrida P, Elli L, Ferrero S, Latella G, Ciardi A, Caronna R, Solina G, Rizzo A, Ciacci C, D'Armiento FP, Salemme M, Villanacci V, Cannizzaro R, Canzonieri V, Reggiani Bonetti L, Biancone L, Monteleone G, Orlandi A, Santeusanio G, Macciomei MC, D'Inca R, Perfetti

V, Sandri G, Silano M, Florena AM, Giannone AG, Papi C, Coppola L, Usai P, Maccioni A, Astegiano M, Migliora P, Manca R, Martino M, Trapani D, Cerutti R, Alberizzi P, Riboni R, Sessa F, Paulli M, Solcia E, Corazza GR. Small Bowel Carcinomas in Coeliac or Crohn's Disease: Clinico-pathological, Molecular, and Prognostic Features. A Study From the Small Bowel Cancer Italian Consortium. *Journal of Crohn's & Colitis.* 2017;11(8):942-953.

29. Rizzo F, Vanoli A, Sahnane N, Cerutti R, Trapani D, Rinaldi A, Sellitto A, Ciacci C, Volta U, Villanacci V, Calabro A, Arpa G, Luinetti O, Paulli M, Solcia E, Di Sabatino A, Sessa F, Weisz A, Furlan D. Small-bowel carcinomas associated with celiac disease: transcriptomic profiling shows predominance of microsatellite instability-immune and mesenchymal subtypes. *Virchows Archiv.* 2019.
30. Kamboj AK, Oxentenko AS. Clinical and Histologic Mimickers of Celiac Disease. *Clin Transl Gastroenterol.* 2017;8(8):e114.
31. Kuiper RP, Vissers LE, Venkatachalam R, Bodmer D, Hoenselaar E, Goossens M, Haufe A, Kamping E, Niessen RC, Hogervorst FB, Gille JJ, Redeker B, Tops CM, van Gijn ME, van den Ouweland AM, Rahner N, Steinke V, Kahl P, Holinski-Feder E, Morak M, Kloor M, Stemmler S, Betz B, Hutter P, Bunyan DJ, Syngal S, Culver JO, Graham T, Chan TL, Nagtegaal ID, van Krieken JH, Schackert HK, Hoogerbrugge N, van Kessel AG, Ligtenberg MJ. Recurrence and variability of germline EPCAM deletions in Lynch syndrome. *Human Mutation.* 2011;32(4):407-414.
32. Jansen AML, Tops CMJ, Ruano D, van Eijk R, Wijnen JT, Ten Broeke S, Nielsen M, Hes FJ, van Wezel T, Morreau H. The complexity of screening PMS2 in DNA isolated from formalin-fixed paraffin-embedded material. *European Journal of Human Genetics.* 2020;28(3):333-338.
33. Vilar E, Gruber SB. Microsatellite instability in colorectal cancer-the stable evidence. *Nature Reviews: Clinical Oncology.* 2010;7(3):153-162.
34. Benson AB, 3rd, Venook AP, Cederquist L, Chan E, Chen YJ, Cooper HS, Deming D, Engstrom PF, Enzinger PC, Fichera A, Grem JL, Grothey A, Hochster HS, Hoffe S, Hunt S, Kamel A, Kirilcuk N, Krishnamurthi S, Messersmith WA, Mulcahy MF, Murphy JD, Nurkin S, Saltz L, Sharma S, Shibata D, Skibber JM, Sofocleous CT, Stoffel EM, Stotsky-Himelfarb E, Willett CG, Wu CS, Gregory KM, Freedman-Cass D. Colon Cancer, Version 1.2017, NCCN Clinical Practice Guidelines in Oncology. *Journal of the National Comprehensive Cancer Network.* 2017;15(3):370-398.
35. Wang B, Li F, Zhou X, Ma Y, Fu W. Is microsatellite instability-high really a favorable prognostic factor for advanced colorectal cancer? A meta-analysis. *World Journal of Surgical Oncology.* 2019;17(1):169.
36. Zhao P, Li L, Jiang X, Li Q. Mismatch repair deficiency/microsatellite instability-high as a predictor for anti-PD-1/PD-L1 immunotherapy efficacy. *Journal of Hematology & Oncology.* 2019;12(1):54.

SUPPLEMENTAL METHODS + SUPPLEMENTAL TABLE 1 - 3

Immunohistochemical staining

4µm FFPE sections were deparaffinized with xylene and rehydrated in ethanol. A 0.3% H2O2-solution was used to block endogenous peroxidase, and microwave-mediated antigen retrieval was performed in Tris-EDTA, pH 9.0. Sections were incubated overnight with primary antibodies against MLH1 (clone ES05, 1:50; Agilent, USA), MSH2 (clone FE11, 1:200, Agilent, USA), MSH6 (clone EPR3945, 1:200, Genetex, USA) or PMS2 (clone EP51, 1:40, Agilent, USA) at 4°C. After washing, they were then incubated for 30 minutes with poly-HRP (VWRKDPVM110HRP, ImmunoLogic), visualised using a DAB+ substrate chromogen system (K3468; Agilent) and counterstained with haematoxylin. Finally, the sections were dehydrated and mounted with coverslips.

Targeted Next Generation Sequencing (NGS)

Sequencing was performed using the Ion Torrent platform according to the manufacturer's recommendations. In brief, 21 ng/14 µl isolated DNA was used to prepare two primer pools. After the first PCR, the pools were combined and a new PCR run was performed to digest the primers. A third PCR was then performed to add barcodes to the samples. After purification using AMPureXP beads (A63882; Beckman Coulter), the NGS libraries were pooled, diluted to 60 pmol/L and loaded on a chip using the Ion Chef. Sequencing was subsequently performed in an Ion GeneStudio S5 Series sequencer.

Supplemental table 1 – msCRC panel genes and coverage

Name	Chromosome	Exons	Coverage (%)
APC	5	16	100
BMPR1A	10	11	94.3
BRCA1	17	23	100
BRCA2	13	26	100
ENG	9	15	100
MLH1	3	21	100
MSH2	2	17	100
MSH3	5	24	99.8
MSH6	2	12	100
MUTYH	1	16	100
NTHL1	16	6	100
PALB2	16	42	100
PMS2	7	15	96.8
POLD1	19	26	100
POLE	12	40	100
PTEN	10	10	98.9
RNF43	17	9	99.9
SMAD4	18	11	98.5
STK11	19	9	100
TP53	17	12	100
KRAS	12	2,3,4	Hotspots
HRAS	11	2,3	Hotspots
NRAS	1	2,3,4	Hotspots
BRAF	7	11,15	Hotspots
CTNNB1	3	8	Hotspots
MYC	8	CNV	Hotspots

4

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 frequency. Immunohistochemistry results: + = normal nuclear staining. - = loss of staining in neoplastic cells with positive internal controls. +/++ = weak staining in neoplastic cells compared to internal controls.
* 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 anonymity

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
						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 syndrome patient
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 suggestive	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 LOH probable	Not performed

335	Resection	+	np	-	-	MSH2	Missense variant classified as likely pathogenic by InSiGHT*	0.520:1997	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
									Possibly	

558	Resection	-	+	Subclonal -	+/++	PMS2	NM_000535.5:c.638del	0.378:1995	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 variant	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

Supplemental Table 3 - clinical details of Lynch syndrome patients
Abbreviations: n.o.s. = not otherwise specified

Study ID	Gene	Sex	Age decade at small bowel cancer diagnosis (years)	Location of tumour	Differentiation grade as reported in PA-report	Aberrent IHC, MSI or Lynch diagnosis in pathology report	History of Lynch-associated malignancy	Number of Lynch-associated malignancies (excluding small bowel)	History of other malignancy (non-Lynch associated)	Number of other malignancies (non-Lynch associated)
3	MSH2	m	40-49	small bowel n.o.s.	moderate	yes	yes	1	no	-
85	MLH1	m	30-39	ileum	moderate	yes	yes	1	no	-
98	MSH6	m	70-79	duodenum	moderate	no	no	-	yes	1
119	PMS2	m	70-79	duodenum	moderate	yes	no	-	no	-
124	MSH2	v	60-69	jejunum	moderate	yes	yes	4	no	-
206	MLH1	f	30-39	duodenum	moderate	no	no	-	no	-
236	MSH6	m	40-49	duodenum	moderate	yes	yes	1	no	-
316	MSH2	f	50-59	jejunum	could not be assessed	yes	yes	2	no	-
335	MSH2	f	60-69	ileum	moderate	yes	yes	1	yes	1

363	MSH2	m	40-49	duodenum	moderate to high	yes	no	-	no	-	
379	PMS2	m	50-59	duodenum	moderate	no	no	-	no	-	
414	MSH6	f	50-59	duodenum	moderate	yes	yes	1	yes	1	
426	MLH1	m	40-49	duodenum	poorly/high grade	yes	no	-	no	-	
474	MSH2	f	50-59	duodenum	moderate	no	yes	1	no	-	
480	MLH1	m	60-69	duodenum	moderate	yes	yes	2	no	-	
595	MSH6	m	50-59	jejunum	poorly/high grade	no	no	-	no	-	
720	MSH2	m	50-59	duodenum	moderate	no	yes	1	no	-	
722	MSH6	f	50-59	ileum	could not be assessed	no	yes	2	yes	1	
723	MLH1	m	50-59	small bowel n.o.s.	moderate	yes	yes	1	yes	1	
746	MLH1	m	50-59	duodenum	moderate	yes	yes	3	yes	1	