

Supplementary Table 1: Complete list of genes sequenced

<u>Gene</u>	<u>N. of patients tested</u>	<u>%</u>
<i>APC</i>	70	100
<i>MUTYH (full seq.)</i>	53	75.7
<i>MLH1</i>	43	61.4
<i>MSH2</i>	43	61.4
<i>MSH6</i>	42	60.0
<i>PMS2</i>	42	60.0
<i>EPCAM</i>	41	58.5
<i>CHEK2</i>	39	55.7
<i>TP53</i>	39	55.7
<i>BMPR1A</i>	38	54.2
<i>CDH1</i>	38	54.2
<i>PTEN</i>	38	54.2
<i>SMAD4</i>	38	54.2
<i>STK11</i>	38	54.2
<i>GREM1</i>	36	51.4
<i>POLD1</i>	36	51.4
<i>POLE</i>	36	51.4
<i>ATM</i>	33	47.1
<i>AXIN2</i>	28	40.0
<i>BRCA1</i>	23	32.8
<i>BRCA2</i>	23	32.8
<i>NBN</i>	21	30.0
<i>PALB2</i>	21	30.0
<i>RAD51D</i>	21	30.0
<i>BARD1</i>	19	27.1
<i>CDKN2A</i>	19	27.1
<i>RAD51C</i>	19	27.1
<i>BRIP1</i>	18	25.7

NF1	17	24.2
MUTYH (Y179C and G396D mutations only)	17	24.2
CDK4	16	22.8
SMARCA4	16	22.8
NTHL1	15	21.4
RAD50	15	21.4
DICER1	14	20.0
HOXB13	14	20.0
MSH3	13	18.5
VHL	13	18.5
MEN1	12	17.1
SDHA	12	17.1
SDHB	12	17.1
SDHC	12	17.1
SDHD	12	17.1
TSC1	12	17.1
TSC2	12	17.1
KIT	10	14.2
FLCN	9	12.8
PDGFRA	9	12.8
CTNNA1	8	11.4
BAP1	7	10.0
BLM	7	10.0
FH	7	10.0
MAX	7	10.0
MITF	7	10.0
RET	7	10.0
SDHAF2	7	10.0

<i>TMEM127</i>	7	10.0
<i>MRE11A</i>	7	10.0
<i>GALNT12</i>	7	10.0
<i>ALK</i>	6	8.5
<i>CDC73</i>	6	8.5
<i>MET</i>	6	8.5
<i>NF2</i>	6	8.5
<i>PHOX2B</i>	6	8.5
<i>PRKAR1A</i>	6	8.5
<i>PTCH1</i>	6	8.5
<i>RB1</i>	6	8.5
<i>SMARCB1</i>	6	8.5
<i>SUFU</i>	6	8.5
<i>AIP</i>	5	7.1
<i>CDKN1B</i>	5	7.1
<i>EGFR</i>	5	7.1
<i>POT1</i>	5	7.1
<i>RECQL4</i>	5	7.1
<i>SMARCE1</i>	5	7.1
<i>FANCC</i>	5	7.1
<i>TERT</i>	4	5.7
<i>RPS20</i>	4	5.7
<i>CASR</i>	3	4.2
<i>WT1</i>	3	4.2
<i>MLH3</i>	3	4.2
<i>CDKN1C</i>	2	2.8
<i>CEBPA</i>	2	2.8
<i>DIS3L2</i>	2	2.8
<i>GATA2</i>	2	2.8
<i>GPC3</i>	2	2.8

<i>HRAS</i>	2	2.8
<i>RUNX1</i>	2	2.8
<i>TERC</i>	2	2.8
<i>WRN</i>	2	2.8
<i>XRCC2</i>	2	2.8
<i>KIF1B</i>	2	2.8
<i>LZTR1</i>	2	2.8
<i>EGLN1</i>	2	2.8
<i>FAM175A</i>	2	2.8
<i>PALLD</i>	2	2.8
<i>RINT1</i>	2	2.8
<i>BUB1B</i>	2	2.8
<i>ENG</i>	2	2.8
<i>XRCC2</i>	2	2.8
<i>CTRC</i>	1	1.4
<i>FANCA</i>	1	1.4
<i>RNF43</i>	1	1.4
<i>CFTR</i>	1	1.4
<i>CPA1</i>	1	1.4
<i>PRSS1</i>	1	1.4
<i>SPINK1</i>	1	1.4
<i>CEP57</i>	1	1.4

Supplementary Table 2. Adenomatous polyp histology in patients with CPUE

<u>Histology</u>	<u>Total adenomas</u> (N=348)	<u>%</u>
Tubular adenoma- low-grade dysplasia	313	89.9
Tubular adenoma- high-grade dysplasia	7	2.0
Tubulovillous adenoma- low-grade dysplasia	23	6.6
Tubulovillous adenoma- high-grade dysplasia	4	1.1
Villous adenoma- low-grade dysplasia	1	0.3

Supplementary Table 2. Adenomatous polyp histology type distribution calculated from 348 colonoscopy reports, excluding cases in which intramucosal carcinoma or colorectal cancer were diagnosed.

Supplementary Table 3. Clinical correlations for patients with a significant clinical outcome (Intramucosal cancer, invasive cancer, or colectomy)

<u>Clinical characteristics</u>	<u>Significant clinical outcome group (N=11)</u>	<u>Patients without cancer or colectomy (N=59)</u>	<u>^aP-value</u>
Males	7 (63.6%)	41 (69.5%)	0.73
Smokers	6 (54.5%)	35 (60.3%)	0.74
Metabolic comorbidities	3 (27.3%)	26 (44.1%)	0.34
Presence of FDR with malignancy	7 (63.6%)	46 (78.0%)	0.44
Presence of FDR with CRC	(27.3%) 17	17 (28.8%)	1
Cumulative adenoma burden (Mean rank)	42.91	34.12	^b 0.18
Number of FDR with any malignancy (Mean rank)	29.68	36.58	^b 0.27
Number of FDR with CRC (Mean rank)	35.69	34.50	^b 0.82

Number of colonoscopies (Mean rank)	34.82	35.63	^b 0.80
Number of different extra colonic malignancy (Mean rank)	35.09	35.58	^b 0.93
Colonoscopy surveillance period (months) (Mean+-SD)	140.1250+-87.10	148.3818+-73.44	^c 0.80

Supplementary Table 3. Comparison between the patients with significant outcome (N=11) to the rest of the cohort (N=59). No significant difference in any of the parameters examined was found. ^a Fisher's Exact Test - Exact ^b Mann-Whitney U test. ^c 2-sided t-test for Equality of Means Significance

**Supplementary Table 4. Extra colonic malignancies and potential clinical predictors-
Univariable logistic regression.**

	<u>Odds ratio (OR)</u>	<u>95% C.I. for OR</u>		<u>P value</u>
		<u>Lower</u>	<u>Upper</u>	
<u>Any ECM (N=35)</u>				
Cumulative adenoma burden	0.998	0.973	1.024	0.885
Gender	1.000	0.364	2.744	1.000
<u>Breast cancer (N=4)</u>				
Cumulative adenoma burden	1.016	0.972	1.063	0.483
Age	0.889	0.811	0.976	0.013
<u>Prostate cancer (N=6)</u>				
Cumulative adenoma burden	0.976	0.915	1.042	0.471
Age	0.957	0.884	1.036	0.281
<u>Melanoma (N=5)</u>				
Cumulative adenoma burden	0.995	0.943	1.050	0.858
Age	0.906	0.840	0.977	0.010
Gender	0.667	0.103	4.304	0.670
<u>Non-melanoma skin cancer (N=25)</u>				
Cumulative adenoma burden	1.006	0.979	1.034	0.655
Age	0.951	0.903	1.002	0.057
Gender	1.865	0.585	5.944	0.292

Supplementary Table 4. Univariable logistic regression analysis was used to estimate the relationship between categorical dependent variables (extra colonic malignancies) and different independent variables and their prediction potential.