Supplementary Information

Supplementary Methods

Patient cohort

In total, we analyzed 77 samples from 30 patients (18 with large adenomas and 12 with colorectal adenocarcinomas). In the adenoma cohort, additional biopsies from rectal mucosa were obtained if the lesion was located in the colon (see Figure 1A). Fourteen neoplastic lesions were located at the right side of the colon (coecum through transverse colon), and 16 at the left side or in the rectum. The majority of adenomas (Supplementary Table 1) were either of tubular or tubulovillous histology and there were three cases of serrated lesions (sessile or traditional serrated adenomas). Twelve patients with adenomas had previous or synchronous adenomas. Regarding CRC patients (Supplementary Table 2), our cohort included tumors with all T stages (T1 = 1, T2 = 2, T3 = 5, T4 = 4), node positive (N = 8) and negative (N = 4), and metastasized (N = 5) and non-metastasized (N = 7) disease. For two patients with large exulcerated tumors (G025 and G029) the histologic examination of endoscopic biopsies revealed adenomas with high-grade dysplasia without evidence of invasive growth (subgroup 4.1, Vienna classification). As both patients had synchronous, histologically proven metastases of CRC, we assumed endoscopic sampling error and assigned both cases into the adenocarcinoma group. None of the included patients had a known hereditary cancer predisposition.

Sample storage and DNA isolation

All samples from the adenoma cohort (adenoma, surrounding tissue and rectum) were immediately fixed with the PAXgene Tissue System (Qiagen) and stored at -80°C. Samples from the adenocarcinoma cohort (tumor and surrounding tissue) were snap-frozen and stored in liquid nitrogen. No dissection of tumor and non-tumor within biopsies was performed on adenoma or adenocarcinoma samples prior to DNA isolation and sequencing. DNA from tissue samples were isolated using PAXgene Tissue DNA Kit (Qiagen) or with the

DNA blood and tissue kit (Qiagen), according to the manufacturer's recommendations. DNA concentration was measured using a NanoDrop 1000.

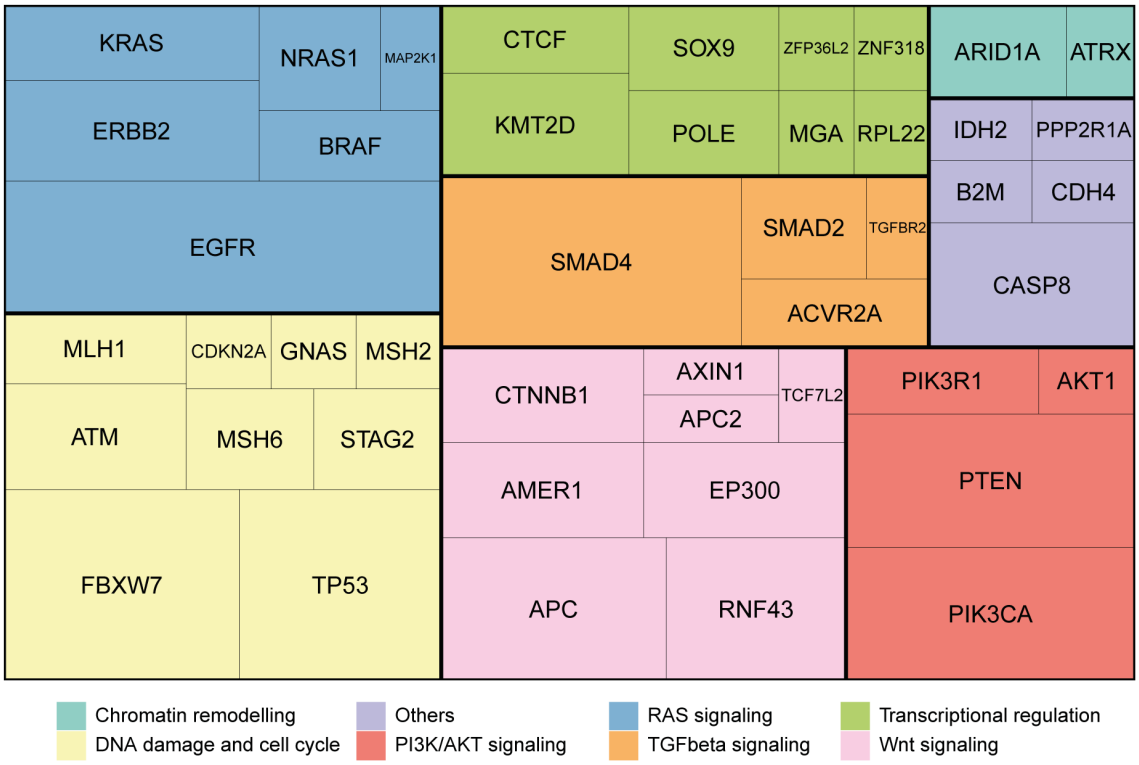
Amplicon panel

A total of 46 genetic loci were captured with 157 amplicons of approximately 250 bp length. A list of targeted hot-spots and corresponding primer pairs can be found in Supplementary Table 3. Several amplicons covered overlapping genetic regions and were therefore merged in subsequent analyses, resulting in a total of 119 unique amplicon regions.

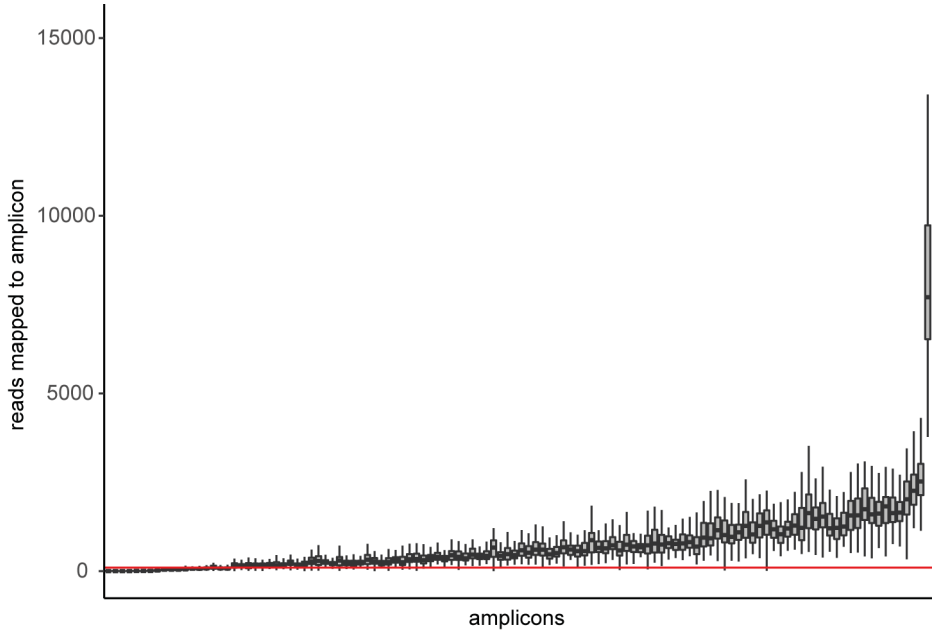
Bioinformatic analysis and variant calling

Raw sequencing reads were pre-processed using fastqc[21] to evaluate the quality and Cutadapt[22] for trimming. After mapping the reads to GRC38 reference genome using BWA[23], the data was analyzed using GATK[24,25]. Base recalibration was performed and variants were called using the MuTect2 pipeline of GATK with a panel of normal samples as reference for variant detection, consisting of 50 randomly selected individuals from 1000 Genomes project. Bedtools[26] was used to evaluate the number of reads aligned to each amplicon. Amplicons with less than 100 reads aligned were excluded from further analysis. Variants were annotated with ENSEMBL Variant Effect Predictor[27] and manually checked. The variants that VEP assigned to have HIGH or MODERATE impact were kept, as well as non-synonymous variants present in COSMIC[20], variants with an allele frequency between 5% and 90%, with more than 9 as alternative allele depth, with low strand bias (FS < 60) and, whenever the information was available, with a frequency in the general population as determined by a GnomAD[28] below 0.0003.

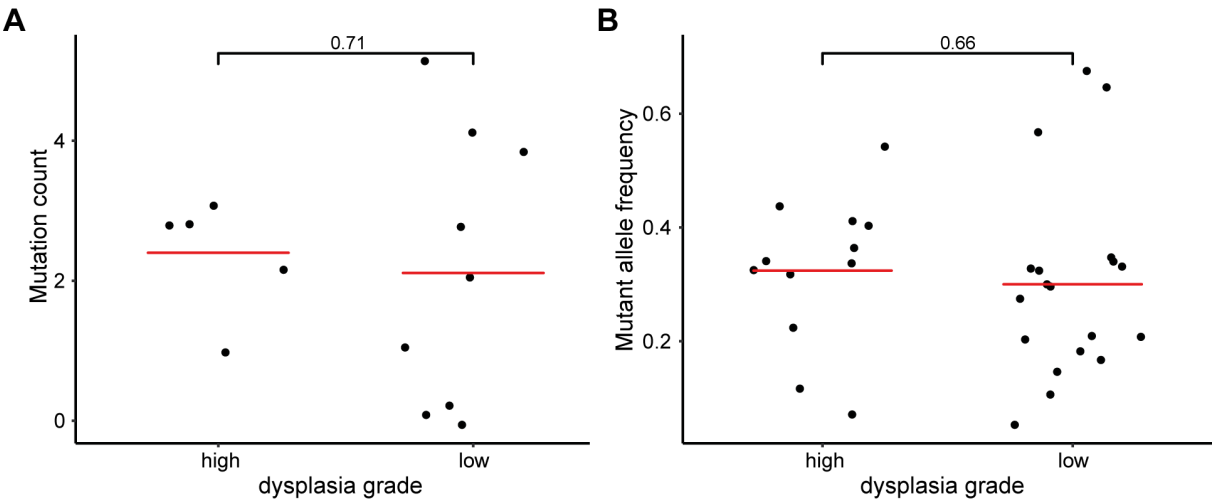
Supplementary Figures



Supplementary Figure 1: Overview of genes included in the custom amplicon panel. A total number of 157 amplicons were designed to cover 119 hot spots in genes associated with major cellular processes and signaling pathways altered in colorectal cancer.



Supplementary Figure 2: Distribution of sequencing reads over the 119 genomic regions. 102 of 119 genomic regions covering mutational hot-spots could be sequenced with sufficient depth (>100 mapped aligned reads per amplicon and sample).



Supplementary Figure 3: Mutations identified in large colorectal adenomas, surrounding normal mucosa and rectal mucosa, related to Figure 1. (A) Mutation count in adenomas with high-grade vs. low-grade dysplasia. **(B)** Fraction of mutated alleles detected in adenomas with high-grade vs. low-grade dysplasia.

Supplementary Tables

Supplementary Table 1: Characteristics of patients with adenomas

ID	Age	Sex	Lokalisation	Histology	Grading	Vienna classification	Size (cm)	Previous or synchronous polyps	No. of additional synchronous polyps
F001	55	f	asc	tubulo-villous	high-grade	4.1	4.5 x 3 x 1.5	adenomas	2
F003	80	f	sigmoid	tubulo-villous	high-grade	4.1	2 x 2 x 1	NA	0
F004	63	m	coecum	tubulo-villous	low-grade	3	2.5 x 2.5 x 1	NA	0
F013	70	m	des	tubulo-villous	high-grade	4.1	1.5 x 1.5 x 1.5	adenoma	0
F017	71	m	asc	tubulo-villous	low-grade	3	2 x 1 x 1	adenomas	4
F025	80	m	asc	TSA	low-grade	3	1.7 x 1.5 x 1	carcinoma	0
F026	72	m	coecum	tubulo-villous	low-grade	3	1.5 x 1 x 0.5	adenoma	0
F028	67	m	transv	tubulo-villous	low-grade	3	1.5 x 1 x 1	no	0
F033	66	m	transv	tubulo-villous	low-grade	3	1.4 x 1.1 x 0.7	carcinoma	4
F035	62	m	sigmoid	tubular	low-grade	3	2 x 1.5 x 1	adenoma	2
F043	55	f	asc	tubular	low-grade	3	0.4 x 0.3 x 0.3	adenoma	1
F044	80	m	rectum	tubulo-villous	high-grade	4.1	7 x 6 x 2	no	0
F045	55	m	sigmoid	tubular	low-grade	3	0.6 x 0.6 x 0,3	adenomas	2
F048	76	m	asc	tubulo-villous	low-grade	3	2 x 1 x 1	adenomas	1
F049	55	f	asc	SSA	low-grade	3	1.5 x 1.5 x 0.3	adenomas	3
F051	63	m	rectum	tubulo-villous	high-grade	4.1	4.5 x 3 x 1.5	no	0
F055	74	m	transv	tubulo-villous	low-grade	3	NA	adenoma	1
F0X0	53	f	asc	SSA	NA	0	NA	no	0

Abbreviations: m, male; f, female; asc, ascending colon; des, descending colon; transv, transverse colon; NA, not available; TSA, traditional serrated adenoma; SSA, sessile serrated adenoma.

Supplementary Table 2: Characteristics of patients with colorectal cancers

ID	Age	Sex	No. of additional polyps	T	N	M	G	Location	Tumor size (cm)	MMR deficiency	RAS (sanger)
G0X3	69	f	0	2	1	0	2	rectum	11	NA	NA
G050	84	f	0	1	0	0	2	rectum	4	NA	NA
G005	88	m	2	3	2	0	2	rectum	6	neg	neg
G008	51	f	3	3	1	0	2	asc	4	neg	KRAS G12D
G009	72	m	3	2	0	0	2	rectum	2	neg	neg
G011	74	m	3	4	2	1 (hep, pulm)	2	rectum	NA	NA	neg
G012	70	m	0	3	0	0	3	asc	7	pos	neg
G016	49	m	0	3	1	1 (hep, pulm)	2	rectum	3	neg	KRAS G12C
G017	63	m	1	4	2	0	1	rectum	NA	NA	neg
G023	82	m	0	4	2	1 (pulm)	2	rectum	NA	neg	KRAS G12A
G025	69	m	0	4	2	1 (hep)	2	rectum	NA	NA	neg
G029	72	m	1	3	0	1 (pulm)	2	sigmoid	5	neg	NA

Abbreviations: m, male; f, female; asc, ascending colon; NA, not available; pos, positive; neg, negative

Supplementary Table 3: Amplicon regions used for target enrichment

Target Region	Build ID	Chromosome	Start Position	End Position	Expected Amplifed Region Size
RPL22	hg19	chr1	6257700	6257810	225
ARID1A	hg19	chr1	27100154	27100202	259
ARID1A	hg19	chr1	27105906	27105963	265
NRAS	hg19	chr1	115256420	115256605	260
NRAS	hg19	chr1	115258670	115258844	261
PTEN	hg19	chr10	89624209	89624393	259
PTEN	hg19	chr10	89685270	89685464	263
PTEN	hg19	chr10	89685270	89685464	260
PTEN	hg19	chr10	89692883	89692995	235
PTEN	hg19	chr10	89711865	89712039	249
PTEN	hg19	chr10	89711865	89712039	259
PTEN	hg19	chr10	89717489	89717801	273
PTEN	hg19	chr10	89717489	89717801	242
PTEN	hg19	chr10	89720684	89720991	247
PTEN	hg19	chr10	89720684	89720991	250
TCF7L2	hg19	chr10	114925292	114925355	253
ATM	hg19	chr11	108117772	108117820	249
ATM	hg19	chr11	108216455	108216504	249
ATM	hg19	chr11	108236056	108236113	225
KRAS	hg19	chr12	25378532	25378717	271
KRAS	hg19	chr12	25380245	25380427	267
KRAS	hg19	chr12	25398225	25398414	272
KRAS	hg19	chr12	25398225	25398414	225
KMT2D	hg19	chr12	49416390	49416438	267
KMT2D	hg19	chr12	49434465	49434517	271
KMT2D	hg19	chr12	49443641	49443698	265
POLE	hg19	chr12	133249816	133249873	225
POLE	hg19	chr12	133253153	133253210	273
AKT1	hg19	chr14	105246520	105246577	244
MGA	hg19	chr15	42052601	42052658	267
B2M	hg19	chr15	45003756	45003813	231
MAP2K1	hg19	chr15	66727420	66727477	269
IDH2	hg19	chr15	90631806	90631863	265
AXIN1	hg19	chr16	347957	348014	242
CTCF	hg19	chr16	67645310	67645367	261
CTCF	hg19	chr16	67660439	67660496	225
TP53	hg19	chr17	7572930	7573008	239
TP53	hg19	chr17	7573927	7574033	251
TP53	hg19	chr17	7576530	7577165	272
TP53	hg19	chr17	7576530	7577165	265
TP53	hg19	chr17	7576530	7577165	270
TP53	hg19	chr17	7576530	7577165	259
TP53	hg19	chr17	7577499	7577608	226
TP53	hg19	chr17	7578167	7578564	246
TP53	hg19	chr17	7578167	7578564	275
TP53	hg19	chr17	7579302	7579922	270
TP53	hg19	chr17	7579302	7579922	269
TP53	hg19	chr17	7579302	7579922	269
ERBB2	hg19	chr17	37868165	37868222	262
ERBB2	hg19	chr17	37879627	37879684	271
ERBB2	hg19	chr17	37880191	37880361	266
ERBB2	hg19	chr17	37880191	37880361	231
ERBB2	hg19	chr17	37880963	37881482	267
ERBB2	hg19	chr17	37880963	37881482	258
ERBB2	hg19	chr17	37880963	37881482	259
RNF43	hg19	chr17	56435140	56435188	249

RNF43	hg19	chr17	56435789	56435840	257
RNF43	hg19	chr17	56439892	56439944	253
RNF43	hg19	chr17	56448271	56448324	257
SOX9	hg19	chr17	70119763	70119925	227
SOX9	hg19	chr17	70120248	70120305	230
SMAD2	hg19	chr18	45368180	45368237	247
SMAD2	hg19	chr18	45374855	45374956	228
SMAD4	hg19	chr18	48575126	48575306	251
SMAD4	hg19	chr18	48581085	48581351	231
SMAD4	hg19	chr18	48581085	48581351	246
SMAD4	hg19	chr18	48584523	48584719	252
SMAD4	hg19	chr18	48584523	48584719	258
SMAD4	hg19	chr18	48586229	48586421	275
SMAD4	hg19	chr18	48586229	48586421	231
SMAD4	hg19	chr18	48591796	48591982	227
SMAD4	hg19	chr18	48591796	48591982	231
SMAD4	hg19	chr18	48593372	48593552	235
SMAD4	hg19	chr18	48593372	48593552	229
SMAD4	hg19	chr18	48602993	48603173	261
SMAD4	hg19	chr18	48602993	48603173	226
SMAD4	hg19	chr18	48604638	48604808	235
PPP2R1A	hg19	chr19	52715951	52716008	245
ZFP36L2	hg19	chr2	43452490	43452633	262
MSH2	hg19	chr2	47698149	47698206	272
MSH6	hg19	chr2	48026173	48026230	241
MSH6	hg19	chr2	48030613	48030665	247
ACVR2A	hg19	chr2	148657018	148657075	225
ACVR2A	hg19	chr2	148683660	148683713	253
CASP8	hg19	chr2	202131215	202131395	243
CASP8	hg19	chr2	202141564	202141621	259
CASP8	hg19	chr2	202149767	202149824	233
CASP8	hg19	chr2	202151110	202151297	253
GNAS	hg19	chr20	57484394	57484442	273
CDH4	hg19	chr20	60503304	60503361	268
EP300	hg19	chr22	41536167	41536215	273
EP300	hg19	chr22	41572324	41572372	243
EP300	hg19	chr22	41574650	41574707	227
TGFBR2	hg19	chr3	30691840	30691897	269
MLH1	hg19	chr3	37067207	37067399	263
MLH1	hg19	chr3	37070324	37070375	271
CTNNB1	hg19	chr3	41266010	41266180	241
CTNNB1	hg19	chr3	41274866	41274923	255
CTNNB1	hg19	chr3	41277249	41277297	273
PIK3CA	hg19	chr3	178916836	178917024	259
PIK3CA	hg19	chr3	178921520	178921714	229
PIK3CA	hg19	chr3	178921520	178921714	257
PIK3CA	hg19	chr3	178927906	178928082	269
PIK3CA	hg19	chr3	178927906	178928082	265
PIK3CA	hg19	chr3	178936044	178936214	275
PIK3CA	hg19	chr3	178938827	178939009	245
PIK3CA	hg19	chr3	178951881	178952184	227
PIK3CA	hg19	chr3	178951881	178952184	245
FBXW7	hg19	chr4	153244124	153244181	229
FBXW7	hg19	chr4	153245416	153245604	249
FBXW7	hg19	chr4	153247167	153247417	267
FBXW7	hg19	chr4	153247167	153247417	234
FBXW7	hg19	chr4	153249338	153249520	247
FBXW7	hg19	chr4	153250848	153251036	273
FBXW7	hg19	chr4	153251876	153251933	273

FBXW7	hg19	chr4	153258948	153259147	275
PIK3R1	hg19	chr5	67588920	67588977	257
PIK3R1	hg19	chr5	67591066	67591123	231
APC	hg19	chr5	112128112	112128169	231
APC	hg19	chr5	112151173	112151230	239
APC	hg19	chr5	112162860	112162917	261
APC	hg19	chr5	112164585	112164642	226
APC	hg19	chr5	112173703	112174071	247
APC	hg19	chr5	112173703	112174071	230
APC	hg19	chr5	112173703	112174071	255
APC	hg19	chr5	112174603	112176042	225
APC	hg19	chr5	112174603	112176042	226
APC	hg19	chr5	112174603	112176042	225
APC	hg19	chr5	112174603	112176042	265
APC	hg19	chr5	112174603	112176042	249
APC	hg19	chr5	112174603	112176042	227
APC	hg19	chr5	112174603	112176042	225
APC	hg19	chr5	112174603	112176042	226
APC	hg19	chr5	112174603	112176042	226
APC	hg19	chr5	112174603	112176042	264
ZNF318	hg19	chr6	43308078	43308135	275
EGFR	hg19	chr7	55211047	55211243	275
EGFR	hg19	chr7	55221787	55221969	268
EGFR	hg19	chr7	55229242	55229299	229
EGFR	hg19	chr7	55233014	55233208	257
EGFR	hg19	chr7	55240650	55240843	250
EGFR	hg19	chr7	55241600	55241805	225
EGFR	hg19	chr7	55241600	55241805	244
EGFR	hg19	chr7	55242383	55242581	257
EGFR	hg19	chr7	55248879	55249178	251
EGFR	hg19	chr7	55248879	55249178	260
EGFR	hg19	chr7	55259401	55259585	269
EGFR	hg19	chr7	55259401	55259585	229
BRAF	hg19	chr7	140453053	140453217	227
BRAF	hg19	chr7	140481364	140481550	253
CDKN2A	hg19	chr9	21970993	21971050	259
AMER1	hg19	chrX	63411647	63411704	235
AMER1	hg19	chrX	63412064	63412121	251
AMER1	hg19	chrX	63412619	63412674	261
ATRX	hg19	chrX	76854917	76854974	275
STAG2	hg19	chrX	123191778	123191830	225
STAG2	hg19	chrX	123220513	123220565	275

Supplementary Table 4: Mutations found in adenomas, colorectal cancers, surrounding normal mucosa and normal rectum mucosa

Patient	Sample	CHROM	POS	REF	ALT	SYMBOL	Protein_position	Amino_acids	Consequence	AF
F001	Adenoma	chr12	25245350	C	T	KRAS	12	G/D	missense_variant	0,542
F001	Adenoma	chr17	39723405	G	A	ERBB2	678	R/Q	missense_variant	0,364
F001	Adenoma	chr5	112840074	GA	G	APC	1494	E/X	frameshift_variant	0,337
F003	Adenoma	chr12	25245350	C	A	KRAS	12	G/V	missense_variant	0,071
F003	Adenoma	chr5	112792446	C	T	APC	216	R/*	stop_gained	0,117
F003	Normal rectum	chr5	112840131	G	T	APC	1513	E/*	stop_gained	0,051
F004	Adenoma	chr12	25245350	C	A	KRAS	12	G/V	missense_variant	0,324
F004	Adenoma	chrX	64192215	G	A	AMER1	358	R/*	stop_gained	0,675
F004	Adenoma	chr10	87933156	G	T	PTEN	133	V/L	missense_variant	0,146
F004	Adenoma	chr5	112828889	C	T	APC	554	R/*	stop_gained	0,296
F013	Adenoma	chr17	7673802	C	T	TP53	273	R/H	missense_variant	0,325
F017	Adenoma	chr12	25245350	C	A	KRAS	12	G/V	missense_variant	0,347
F017	Adenoma	chr15	41760405	G	A	MGA	2425	R/H	missense_variant	0,208
F017	Adenoma	chr7	55143444	C	T	EGFR	127	A/V	missense_variant	0,053
F017	Adenoma	chrX	64191798	G	A	AMER1	497	R/*	stop_gained	0,331
F017	Normal rectum	chr7	55181407	G	T	EGFR	800	D/Y	missense_variant	0,086
F017	Normal surrounding	chr17	7676026	G	T	TP53	115	H/N	missense_variant	0,054
F025	Adenoma	chr12	25245351	C	A	KRAS	12	G/C	missense_variant	0,408
F025	Adenoma	chr5	112839826	GT	G	APC	1411	S/X	frameshift_variant	0,713
F025	Normal surrounding	chr5	112839953	TA	T	APC	1454	K/X	frameshift_variant	0,064
F026	Adenoma	chr12	25245347	C	T	KRAS	13	G/D	missense_variant	0,34
F026	Adenoma	chr10	87933189	A	T	PTEN	144	K/*	stop_gained	0,167
F026	Adenoma	chr5	112838220	C	T	APC	876	R/*	stop_gained	0,3
F026	Adenoma	chr5	112839978	AAG	A	APC	1462	K/X	frameshift_variant	0,328
F026	Adenoma	chr2	147926116	TAA	T	ACVR2A	435	K/X	frameshift_variant	0,646
F028	Adenoma	chr12	25245350	C	T	KRAS	12	G/D	missense_variant	0,209
F033	Adenoma	chr17	39723405	G	A	ERBB2	678	R/Q	missense_variant	0,203
F033	Adenoma	chr5	112839495	AC	A	APC	1301	T/X	frameshift_variant	0,567
F033	Adenoma	chr1	114716123	C	T	NRAS	13	G/D	missense_variant	0,275
F033	Normal rectum	chr7	55174033	C	T	EGFR	725	T/M	missense_variant	0,055
F033	Normal surrounding	chr17	7676531	G	T	TP53	22	L/I	missense_variant	0,061
F033	Normal surrounding	chrX	64192203	G	T	AMER1	362	L/M	missense_variant	0,171
F033	Normal surrounding	chr5	112840131	G	T	APC	1513	E/*	stop_gained	0,054
F043	Adenoma	chr12	25225628	C	T	KRAS	146	A/T	missense_variant	0,182
F043	Adenoma	chr5	112839942	C	T	APC	1450	R/*	stop_gained	0,106
F043	Normal surrounding	chr5	112839953	TA	T	APC	1454	K/X	frameshift_variant	0,063
F044	Adenoma	chr12	25245350	C	A	KRAS	12	G/V	missense_variant	0,437
F044	Adenoma	chr20	58909366	G	A	GNAS	201	R/H	missense_variant	0,411
F044	Adenoma	chr5	112839882	AC	A	APC	1430	T/X	frameshift_variant	0,224
F045	Adenoma	chr5	112792446	C	T	APC	216	R/*	stop_gained	0,388
F045	Adenoma	chr5	112839551	TG	T	APC	1320	V/X	frameshift_variant	0,384
F045	Adenoma	chr1	114716126	C	A	NRAS	12	G/V	missense_variant	0,262
F048	Normal surrounding	chr12	25245350	C	T	KRAS	12	G/D	missense_variant	0,433
F048	Normal surrounding	chr18	51078285	G	T	SMAD4	493	D/Y	missense_variant	0,604
F049	Adenoma	chr2	47471041	G	T	MSH2	580	E/*	stop_gained	0,064
F049	Adenoma	chr7	140753336	A	T	BRAF	600	V/E	missense_variant	0,098
F051	Adenoma	chr12	25245350	C	T	KRAS	12	G/D	missense_variant	0,341
F051	Adenoma	chr20	58909366	G	A	GNAS	201	R/H	missense_variant	0,403
F051	Adenoma	chr5	112839942	C	T	APC	1450	R/*	stop_gained	0,318
FX	Adenoma	chr7	140753336	A	T	BRAF	600	V/E	missense_variant	0,283
G005	Colorectal cancer	chr7	140753336	A	T	BRAF	600	V/E	missense_variant	0,251
G008	Colorectal cancer	chr12	25245350	C	T	KRAS	12	G/D	missense_variant	0,384
G008	Colorectal cancer	chr5	112792446	C	T	APC	216	R/*	stop_gained	0,32
G008	Colorectal cancer	chr5	112839953	TA	T	APC	1454	K/X	frameshift_variant	0,07
G009	Colorectal cancer	chr17	7674250	C	T	TP53	238	C/Y	missense_variant	0,411
G009	Normal surrounding	chr5	112839953	TA	T	APC	1454	K/X	frameshift_variant	0,091
G012	Colorectal cancer	chr16	297982	AC	A	AXIN1	508	G/X	frameshift_variant	0,146
G016	Colorectal cancer	chr1	114716127	C	A	NRAS	12	G/C	missense_variant	0,597
G016	Colorectal cancer	chr17	7675131	C	T	TP53	161	A/T	missense_variant	0,56
G016	Colorectal cancer	chr5	112839606	C	T	APC	1338	Q/*	stop_gained	0,105
G017	Colorectal cancer	chr4	152328232	C	T	FBXW7	465	R/H	missense_variant	0,096
G017	Colorectal cancer	chr5	112839953	TA	T	APC	1454	K/X	frameshift_variant	0,058
G023	Colorectal cancer	chr12	25245350	C	G	KRAS	12	G/A	missense_variant	0,163
G023	Colorectal cancer	chr17	7674230	C	T	TP53	245	G/S	missense_variant	0,196
G023	Colorectal cancer	chr4	152326055	G	C	FBXW7	452	T/S	missense_variant	0,064
G023	Colorectal cancer	chr4	152326214	C	T	FBXW7	479	R/Q	missense_variant	0,058
G023	Colorectal cancer	chr4	152329731	G	A	FBXW7	393	R/*	stop_gained	0,057
G023	Colorectal cancer	chr7	55181471	T	A	EGFR	821	I/N	missense_variant	0,086

G023	Normal surrounding	chr18	51078373	C	T	SMAD4	522	P/L	missense_variant	0,076
G025	Colorectal cancer	chr3	179218294	G	A	PIK3CA	542	E/K	missense_variant	0,158
G025	Colorectal cancer	chr5	112839913	C	T	APC	1440	P/L	missense_variant	0,061
G025	Colorectal cancer	chr5	112839953	TA	T	APC	1454	K/X	frameshift_variant	0,052
G025	Normal surrounding	chr5	112839953	TA	T	APC	1454	K/X	frameshift_variant	0,055
G029	Colorectal cancer	chr17	7676051	G	C	TP53	106	S/R	missense_variant	0,378
G029	Normal surrounding	chr17	7676167	C	T	TP53	68	E/K	missense_variant	0,058
G029	Normal surrounding	chr7	55181384	TC	T	EGFR	792	L/X	frameshift_variant	0,071
G050	Colorectal cancer	chr17	39711955	C	T	ERBB2	310	S/F	missense_variant	0,406
G050	Colorectal cancer	chr17	39724008	G	T	ERBB2	769	D/Y	missense_variant	0,413
G050	Colorectal cancer	chr17	72123667	C	A	SOX9	270	F/L	missense_variant	0,149
G050	Colorectal cancer	chr3	179234169	G	A	PIK3CA	1004	M/I	missense_variant	0,202
G050	Colorectal cancer	chr4	152328233	G	A	FBXW7	465	R/C	missense_variant	0,083
G050	Colorectal cancer	chr5	112838220	C	T	APC	876	R/*	stop_gained	0,352
G050	Colorectal cancer	chr5	112839942	C	T	APC	1450	R/*	stop_gained	0,212
G050	Normal surrounding	chr18	51054873	C	A	SMAD4	183	Q/K	missense_variant	0,057
G0X3	Colorectal cancer	chr12	25225713	T	A	KRAS	117	K/N	missense_variant	0,614
G0X3	Colorectal cancer	chr20	58909365	C	T	GNAS	201	R/C	missense_variant	0,143
G0X3	Colorectal cancer	chr5	112838220	C	T	APC	876	R/*	stop_gained	0,378
G0X3	Colorectal cancer	chrX	64192215	G	A	AMER1	358	R/*	stop_gained	0,484