Appendix Table 1. Single nucleotide polymorphisms (SNPs) considered to generate the polygenic risk score (PRS), adapted from Thomas et al. [15]

Locus	rsID lead variant	Variant	Chr.	Position (Build 37)	Risk allele
1p34.3	rs4360494	1:38455891_G/C	1	38455891	G
1p32.3	rs12144319	1:55246035_T/C	1	55246035	C
1p36.12	rs72647484	1:22587728_T/C	1	22587728	T
1p31.3	rs7542665	1:62673037_T/C	1	62673037	C
1q25.3	rs6678517	1:183002639_A/G	1	183002639	A
1q41	rs17011141	1:222112634_A/G	1	222112634	G
2q24.2	rs448513	2:159964552_T/C	2	159964552	C
2q33.1	rs11884596	2:199612407_T/C	2	199612407	C
2q33.1	rs983402	2:199781586_T/C	2	199781586	T
2p16.3	rs7606562	2:48686695_T/A	2	48686695	T
2q11.2	rs11692435	2:98275354_G/A	2	98275354	G
2q35	rs3731861	2:219191256_T/C	2	219191256	T
3q22.2	rs10049390	3:133701119_G/A	3	133701119	A
3q13.2	rs13086367	3:112903888_A/G	3	112903888	A
3q13.2	rs72942485	3:112999560_G/A	3	112999560	G
3p21.1	rs9831861	3:53088285_T/G	3	53088285	G
3p22.1	rs35470271	3:40915239_A/G	3	40915239	G
3q13.2	rs12635946	3:112916918_C/T	3	112916918	C
3q22.2	rs113569514	3:133748789_T/C	3	133748789	T
3q26.2	rs9876206	3:169517436_C/T	3	169517436	C
3p14.1	rs6781752	3:66365163_G/A	3	66365163	A
4q31.21	rs11727676	4:145659064_T/C	4	145659064	C
4q24	rs1391441	4:106128760_G/A	4	106128760	A
4q22.2	rs13149359	4:94938618_C/A	4	94938618	A
5p13.1	rs7708610	5:40102443_G/A	5	40102443	A
5p15.33	rs78368589	5:1240204_C/T	5	1240204	T
5q21.1	rs145364999	5:98206082_T/A	5	98206082	T
5p15.33	rs2735940	5:1296486_A/G	5	1296486	G
5p13.1	rs12514517	5:40280076_G/A	5	40280076	A
5q22.2	rs755229494	5:112097351_A/G	5	112097351	G
5q23.2	rs12659017	5:125988175_G/A	5	125988175	G
5q31.1	rs4976270	5:134467220_C/T	5	134467220	C
6p12.1	rs13204733	6:55566108_A/G	6	55566108	G
6p21.33	rs116685461	6:31315512_G/A	6	31315512	G
6p21.32	rs9271695	6:32593080_A/G	6	32593080	G
6p21.33	rs2516420	6:31449620_C/T	6	31449620	C
6p21.33	rs116353863	6:31010185_T/C	6	31010185	C
6p21.31	rs16878812	6:35569562_A/G	6	35569562	A

Appendix Table 1, continued.

Locus	rsID lead variant	Variant	Chr.	Position (Build 37)	Risk allele
6p21.2	rs9470361	6:36623379_G/A	6	36623379	A
6p12.1	rs62404966	6:55712124_C/T	6	55712124	C
6p21.33	rs3131043	6:30758466_A/G	6	30758466	G
6p24.1	rs2070699	6:12292772_G/T	6	12292772	T
6p22.1	rs1476570	6:29809860_G/A	6	29809860	A
6p21.32	rs3830041	6:32191339_C/T	6	32191339	T
6q21	**rs6928864[a]**	**6:105966894_C/A**	**6**	**105966894**	**C**
6p21.1	rs62396735	6:41702582_C/T	6	41702582	C
7p13	rs12672022	7:45136423_T/C	7	45136423	T
7p12.3	rs80077929	7:46094089_C/T	7	46094089	T
7p12.3	rs10951878	7:46926695_C/T	7	46926695	C
7p12.3	rs3801081	7:47511161_A/G	7	47511161	G
8q24.21	rs7013278	8:128414892_T/C	8	128414892	T
8q24.21	rs4313119	8:128571855_G/T	8	128571855	G
8q23.3	rs16892766	8:117630683_A/C	8	117630683	C
8q23.3	rs6469654	8:117632965_G/C	8	117632965	G
8q24.11	rs117079142	8:117790914_C/A	8	117790914	A
8q24.21	rs6983267	8:128413305_G/T	8	128413305	G
9q22.33	rs34405347	9:101679752_T/G	9	101679752	T
9p21.3	rs1537372	9:22103183_G/T	9	22103183	G
9q31.3	rs10980628	9:113671403_T/C	9	113671403	C
10p14	rs12217641	10:8663875_C/T	10	8663875	C
10q24.2	rs10786560	10:101315166_G/A	10	101315166	G
10q22.3	rs1250567	10:81046265_T/C	10	81046265	C
10p14	rs11255841	10:8739580_T/A	10	8739580	T
10q11.23	rs10821907	10:52648454_C/T	10	52648454	C
10q22.3	rs704017	10:80819132_A/G	10	80819132	G
10q24.2	rs11190164	10:101351704_A/G	10	101351704	G
10q25.2	rs12246635	10:114288619_T/C	10	114288619	C
10q25.2	rs11196170	10:114722621_G/A	10	114722621	A
11q13.4	rs7946853	11:74409077_T/C	11	74409077	C
11q22.1	rs55864876	11:100717136_G/A	11	100717136	G
11q22.1	rs2186607	11:101656397_T/A	11	101656397	T
11q13.4	rs61389091	11:74427921_C/T	11	74427921	C
11p15.4	rs4450168	11:10286755_A/C	11	10286755	C
11q12.2	rs174533	11:61549025_G/A	11	61549025	G
11q13.4	rs7121958	11:74280012_T/G	11	74280012	G
11q23.1	rs3087967	11:111156836_T/C	11	111156836	T
12q13.3	rs4759277	12:57533690_C/A	12	57533690	A

Appendix Table 1, continued.

Locus	rsID lead variant	Variant	Chr.	Position (Build 37)	Risk allele
12q24.21	rs1427760	12:115100714_T/C	12	115100714	C
12p13.32	rs3217874	12:4400808_C/T	12	4400808	T
12p13.31	rs10849433	12:6406904_T/C	12	6406904	C
12q12	rs11610543	12:43134191_A/G	12	43134191	G
12p13.32	rs35808169	12:4368607_T/C	12	4368607	C
12p13.32	rs3217810	12:4388271_C/T	12	4388271	T
12p13.31	rs2250430	12:6421174_A/T	12	6421174	T
12p11.21	rs77969132	12:31594813_C/T	12	31594813	T
12q13.12	rs12372718	12:51171090_A/G	12	51171090	G
12q24.12	rs597808	12:111973358_A/G	12	111973358	G
12q24.21	rs7300312	12:115890922_T/C	12	115890922	C
12p13.2	rs2710310	12:12035649_C/T	12	12035649	C
13q22.1	rs78341008	13:73791554_T/C	13	73791554	C
13q34	rs8000189	13:111075881_C/T	13	111075881	T
13q22.1	rs45597035	13:73649152_A/G	13	73649152	A
13q22.1	rs1924816	13:73997961_A/G	13	73997961	A
13q13.3	rs7333607	13:37462010_A/G	13	37462010	G
13q22.3	rs1330889	13:78609615_T/C	13	78609615	C
13q13.2	rs377429877	13:34092164_C/T	13	34092164	C
14q22.2	rs1951864	14:54369299_G/A	14	54369299	A
14q23.1	rs17094983	14:59189361_G/A	14	59189361	G
14q23.1	rs8020436	14:59208437_G/A	14	59208437	A
14q22.2	rs35107139	14:54419106_A/C	14	54419106	C
14q22.2	rs4901473	14:54445157_G/A	14	54445157	G
15q23	rs745213	15:68060389_T/G	15	68060389	G
15q22.31	rs12594720	15:67007018_C/G	15	67007018	C
15q22.33	rs56324967	15:67402824_T/C	15	67402824	C
15q13.3	rs17816465	15:33156386_G/A	15	33156386	A
15q13.3	rs12708491	15:32992836_G/A	15	32992836	G
15q13.3	rs2293581	15:33010736_G/A	15	33010736	A
15q26.1	rs7495132	15:91172901_C/T	15	91172901	T
16q23.2	rs9930005	16:80043258_C/A	16	80043258	C
16q24.1	rs12447408	16:86252544_G/A	16	86252544	A
16q22.1	rs9924886	16:68743939_A/C	16	68743939	A
16q24.1	rs12149163	16:86339315_T/C	16	86339315	T
16q24.1	rs62042090	16:86703949_C/T	16	86703949	T
17q24.3	rs983318	17:70413253_G/A	17	70413253	A
17p13.3	rs73975586	17:814243_A/T	17	814243	A
17p12	rs1078643	17:10707241_G/A	17	10707241	A
17q25.3	rs75954926	17:81061048_A/G	17	81061048	G

Appendix Table 1, continued.

Locus	rsID lead variant	Variant	Chr.	Position (Build 37)	Risk allele
17q25.3	rs373585858	17:80394556_G/A	17	80394556	A
17p13.3	rs4968127	17:809643_G/A	17	809643	G
18q21.1	rs11874392	18:46453156_A/T	18	46453156	A
19q13.43	rs73068325	19:59079096_C/T	19	59079096	T
19p13.11	rs34797592	19:16417198_C/T	19	16417198	T
19q13.11	rs28840750	19:33519927_T/G	19	33519927	T
19q13.2	rs1963413	19:41871573_G/A	19	41871573	A
19q13.33	rs12979278	19:49218602_C/T	19	49218602	T
20q13.33	rs2738783	20:62308612_T/G	20	62308612	T
20q13.13	rs6067417	20:48983697_C/T	20	48983697	C
20q13.12	rs6031311	20:42666475_C/T	20	42666475	T
20q13.13	rs6091189	20:49256285_C/T	20	49256285	T
20p12.3	rs994308	20:6603622_C/T	20	6603622	C
20p12.3	rs28488	20:6762221_C/T	20	6762221	T
20p12.3	rs556532366	20:8568071_C/T	20	8568071	T
20p12.3	rs189583	20:6376457_G/C	20	6376457	G
20p12.3	rs4813802	20:6699595_T/G	20	6699595	G
20p12.3	rs11087784	20:7740976_A/G	20	7740976	G
20q13.13	rs6066825	20:47340117_A/G	20	47340117	A
20q13.13	rs6063514	20:49055318_C/T	20	49055318	C
20q13.32	rs13831	20:57475191_A/G	20	57475191	G
20q13.33	rs1741640	20:60932414_T/C	20	60932414	C
20q11.22	rs6058093	20:33213196_A/C	20	33213196	C

[a] The missing reference SNP was replaced by rs6904092 (linkage disequilibrium, D'=1 and r2=1).

Appendix Table 2. Comparison of PPVs for detecting advanced neoplasia of both FITs achieved at different PRS categories and specificities, using the weighted PRS

		Positive predictive value for advanced neoplasia [%] (95% CI)			Difference in positive predictive value for advanced neoplasia [%] (95% CI)[2]		
FIT	Cutoff[1]	Low PRS	Medium PRS	High PRS	Medium vs. low	High vs. medium	High vs. low
Ridascreen hemoglobin	Low	18 (15-22)	25 (21-29)	32 (28-37)	**7** (3-10)	**7** (3-13)	**14** (10-19)
	Intermediate	23 (19-27)	30 (25-36)	38 (33-44)	**8** (3-12)	**8** (3-14)	**16** (11-21)
	High	33 (26-40)	42 (34-50)	51 (42-59)	**9** (4-14)	**9** (3-14)	**18** (13-24)
FOB Gold	Low	20 (18-22)	27 (25-29)	34 (32-37)	**7** (3-11)	**7** (3-13)	**14** (11-20)
	Intermediate	24 (21-26)	32 (29-35)	40 (36-43)	**8** (3-12)	**8** (3-14)	**16** (11-22)
	High	32 (28-36)	41 (37-46)	50 (45-54)	**9** (4-14)	**9** (3-14)	**18** (13-24)

Abbreviations: CI, confidence interval; FIT, fecal immunochemical test; PRS, polygenic risk score. Cutoffs measured in µg hemoglobin per gram of stool. Ridascreen cutoffs: 1.7 µg/g (low specificity), 4.0 µg/g (medium specificity), 12.0 µg/g (high specificity); FOB Gold cutoffs: 8.5 µg/g (low specificity), 11.6 µg/g (medium specificity), 22.7 µg/g (high specificity).