Supplementary Table 1. Sequences of primers employed for PCR amplification and for primer extension

Templates for primer extension were generated as previously described (26) using PCR-primers listed below. Primer extension assays were performed using PCR-amplified gDNA or cDNA templates treated with Exonuclease I and Shrimp Alkaline Phosphatase (USB, Cleveland, OH, USA) for 20 min at 37°C, followed by enzyme inactivation for 20 min at 80°C. The reactions were performed in a total volume of 20 µl containing 1x Thermosequenase Reaction Buffer, 0.5U of Thermosequenase (Amersham Biosciences Inc., Piscataway, NJ, USA), 40 ng of treated PCR product annealed with 25 pmoles of the HPLC-purified primer (Sigma Genosys Ltd. Cambridge, UK) listed below, in the presence of 0.05 mM of the ddCTP specific for the primer extension assay (Roche Diagnostics, Mannheim, Germany), and 0.05 mM of the other three dNTPs. Ten µl of primer extension reaction product were resolved on a denaturing high performance liquid chromatography (DHPLC) Wave 1100 instrument (Transgenomic Inc., Omaha, NE, USA) held at constant oven temperature of 80°C using a linear acetonitrile gradient obtained as previously described (26). Primer extension peaks were detected with a UV-detector at 260 nm and the data analyzed by the Wave System's WAVEMAKER Software.

***APC* Variant**	**PCR-Primers for gDNA (5'>3')**	**PCR-Primers for cDNA (5'>3')†**	**Primer for Primer extension (5'>3')**	**ddNTP**
c.1458C>T	f: ttagatgattgtctttttcctcttgc* r: tgagctatcttaagaaatacatgttataaaaaca*	1st round f: gaagagcatagacatgcaatg r: aatactgtagtggtcattag	f: gcaagtggactgtgaaat	ddCTP
		2nd round f:gagcatagacatgcaatgaatg r: actgtagtggtcattagtaag		

*Primers for gDNA amplification derive from ref. 27; f (forward); r (reverse).

† To eliminate residual genomic DNA, RNA preparations were treated with DNase I (Invitrogen, Carlsbad, CA). In addition, for cDNA amplification, primers employed for 1st round PCR lie in contiguous exons to avoid amplification of contaminating gDNA that might be present despite DNAse treatment.

Supplementary Table 2. Allelic ratios of gDNA from 70 controls and 57 cases heterozygous at allelic marker rs2229992

Individual code	Allelic ratio	CV%*
CTRL 1	0.85	2.62
CTRL 2	0.93	5.41
CTRL 3	0.82	1.90
CTRL 4	0.85	2.65
CTRL 5	0.83	1.33
CTRL 6	0.97	7.63
CTRL 7	0.91	8.19
CTRL 8	0.83	5.58
CTRL 9	0.84	3.14
CTRL 10	0.93	3.18
CTRL 11	0.83	3.63
CTRL 12	0.86	7.81
CTRL 13	0.80	7.70
CTRL 14	0.81	6.90
CTRL 15	0.90	13.93
CTRL 16	0.82	1.40
CTRL 17	0.92	12.72
CTRL 18	0.92	5.22
CTRL 19	0.83	4.32
CTRL 20	0.85	3.21
CTRL 21	0.86	2.87
CTRL 22	0.90	6.85
CTRL 23	0.95	8.09
CTRL 24	0.95	12.18
CTRL 25	0.86	0.85
CTRL 26	0.87	2.77
CTRL 27	0.81	6.82
CTRL 28	0.87	1.40
CTRL 29	0.87	1.93
CTRL 30	0.92	3.06
CTRL 31	0.94	10.68
CTRL 32	0.84	7.74
CTRL 33	0.87	2.72
CTRL 34	0.89	3.67
CTRL 35	0.80	5.09
CTRL 36	0.84	0.12
CTRL 37	0.87	0.83
CTRL 38	0.88	2.22
CTRL 39	0.87	8.88
CTRL 40	0.90	8.51
CTRL 41	0.92	6.45
CTRL 42	0.87	1.09
CTRL 43	0.99	13.64
CTRL 44	0.84	1.43
CTRL 45	0.87	4.70
CTRL 46	0.88	0.65
CTRL 47	0.82	12.39
CTRL 48	0.84	2.98
CTRL 49	0.87	1.67
CTRL 50	0.97	11.46
CTRL 51	0.85	15.02
CTRL 52	0.86	8.24
CTRL 53	0.92	7.25
CTRL 54	0.89	5.95
CTRL 55	0.90	5.31
CTRL 56	0.85	8.22
CTRL 57	0.85	3.41
CTRL 58	0.86	1.16
CTRL 59	0.90	5.86
CTRL 60	0.86	2.40
CTRL 61	0.86	3.57

CTRL 62	0.84	1.95
CTRL 63	0.85	5.66
CTRL 64	0.85	2.22
CTRL 65	0.89	11.05
CTRL 66	0.93	3.44
CTRL 67	0.96	12.93
CTRL 68	0.85	8.94
CTRL 69	0.90	8.55
CTRL 70	0.95	5.84
CASE 1	0.88	7.77
CASE 2	0.87	0.27
CASE 3	0.88	15.06
CASE 4	0.85	2.50
CASE 5	0.89	1.73
CASE 6	0.89	5.38
CASE 7	0.88	3.51
CASE 8	0.90	11.90
CASE 9	0.95	10.02
CASE 10	0.91	4.35
CASE 11	0.93	6.60
CASE 12	0.90	2.47
CASE 13	0.88	10.52
CASE 14	0.84	2.98
CASE 15	0.88	6.51
CASE 16	0.86	2.93
CASE 17	0.84	5.31
CASE 18	0.85	9.23
CASE 19	0.83	2.70
CASE 20	0.86	16.38
CASE 21	0.93	12.27
CASE 22	0.89	3.72
CASE 23	0.86	5.37
CASE 24	0.87	4.83
CASE 25	0.83	3.35
CASE 26	0.82	4.72
CASE 27	0.88	3.18
CASE 28	0.87	9.70
CASE 29	0.97	12.74
CASE 30	0.95	5.34
CASE 31	0.87	17.22
CASE 32	1.00	7.95
CASE 33	0.87	0.75
CASE 34	0.93	13.26
CASE 35	0.87	7.58
CASE 36	0.88	4.47
CASE 37	0.86	14.49
CASE 38	0.87	1.85
CASE 39	0.87	2.83
CASE 40	0.91	10.98
CASE 41	0.93	8.44
CASE 42	0.95	11.90
CASE 43	0.94	10.15
CASE 44	0.84	2.67
CASE 45	0.95	14.93
CASE 46	0.85	9.32
CASE 47	0.93	5.21
CASE 48	0.85	3.43
CASE 49	0.80	3.11
CASE 50	0.92	9.85
CASE 51	0.97	13.16
CASE 52	0.89	2.57
CASE 53	0.90	4.77
CASE 54	0.83	5.44
CASE 55	0.85	6.92
CASE 56	0.83	6.14
CASE 57	0.94	9.31

*coefficient of variation

Supplementary Table 3. Clinical and demographic data

	N	Age * mean (SD)	P value selected vs. unselected cases	Gender M/F	P value selected vs. unselected cases	BMI* mean (SD)	P value selected vs. unselected cases
Selected cases	53	62.24 (11.53)	0.12	31/22	0.59	25.04 ^ (3.96)	0.92
Unselected cases	281	64.99 (10.18)		153/128		24.96 + (4.70)	
Controls	68	59.78 (17.00)		44/24		27.73 § (3.81)	

*Age and BMI at diagnosis for cases and at recruitment for controls
^ : available for 43 individuals.
+ : available for 135 individuals.
§ : available for 61 individuals.

Supplementary Table 4. Allele-specific expression of *APC* in the 121 individuals analyzed (68 controls and 53 cases).

Individual code	ASE value	CV%*
CTRL 1	1.92	5.34
CTRL 2	1.41	14.81
CTRL 3	1.51	3.58
CTRL 4	1.38	2.71
CTRL 5	0.90	8.47
CTRL 6	1.48	8.27
CTRL 7	1.58	4.77
CTRL 8	1.11	16.08
CTRL 9	1.03	9.25
CTRL 10	1.60	7.18
CTRL 11	1.35	13.32
CTRL 12	1.48	5.25
CTRL 13	1.21	16.80
CTRL 14	1.30	12.56
CTRL 15	1.39	0.93
CTRL 16	1.02	16.22
CTRL 17	1.67	7.37
CTRL 18	1.28	15.60
CTRL 19	1.03	9.92
CTRL 20	1.18	5.86
CTRL 21	1.55	6.50
CTRL 22	1.07	13.88
CTRL 23	0.99	10.00
CTRL 24	1.14	5.39
CTRL 25	1.16	3.63
CTRL 26	1.12	6.46
CTRL 27	1.19	4.64
CTRL 28	1.20	0.90
CTRL 29	1.12	0.02
CTRL 30	1.06	8.34
CTRL 31	1.16	1.58
CTRL 32	1.45	7.35
CTRL 33	1.47	2.91
CTRL 34	1.08	1.01
CTRL 35	1.03	9.67
CTRL 36	1.11	1.98
CTRL 37	1.27	10.65
CTRL 38	1.30	7.98
CTRL 39	1.02	12.96
CTRL 40	1.52	7.29
CTRL 41	1.19	4.08
CTRL 42	1.49	15.52
CTRL 43	1.22	8.64
CTRL 44	1.15	16.69
CTRL 45	1.12	5.32
CTRL 46	1.49	0.19
CTRL 47	1.23	8.51
CTRL 48	0.98	15.99
CTRL 49	0.89	9.26
CTRL 50	1.26	2.23
CTRL 51	1.29	2.15
CTRL 52	1.32	9.26
CTRL 53	1.16	0.39
CTRL 54	1.01	3.00
CTRL 55	1.15	1.75
CTRL 56	1.45	4.85
CTRL 57	1.11	15.80
CTRL 58	1.14	0.63
CTRL 59	1.25	5.75
CTRL 60	0.99	0.63
CTRL 61	1.43	6.75

CTRL 62	1.17	7.58
CTRL 63	1.11	11.49
CTRL 64	1.47	2.69
CTRL 65	1.62	8.98
CTRL 66	1.04	7.43
CTRL 67	1.47	5.48
CTRL 68	1.07	15.18
CASE 1	0.81	14.41
CASE 2	1.58	3.37
CASE 3	0.75	9.51
CASE 4	1.31	10.14
CASE 5	1.26	0.96
CASE 6	1.07	4.95
CASE 7	1.59	6.85
CASE 8	1.42	8.36
CASE 9	1.19	7.60
CASE 10	1.38	6.64
CASE 11	1.10	17.52
CASE 12	0.93	13.61
CASE 13	1.28	16.49
CASE 14	1.30	11.89
CASE 15	1.29	4.85
CASE 16	1.57	13.87
CASE 17	1.44	15.69
CASE 18	1.78	5.67
CASE 19	0.43	2.69
CASE 20	1.27	9.36
CASE 21	1.21	15.62
CASE 22	1.64	2.56
CASE 23	2.46	6.83
CASE 24	1.18	13.05
CASE 25	1.72	9.34
CASE 26	1.26	1.11
CASE 27	1.43	5.48
CASE 28	1.76	0.63
CASE 29	0.98	2.52
CASE 30	1.18	3.09
CASE 31	0.68	10.88
CASE 32	0.95	5.14
CASE 33	0.94	3.91
CASE 34	1.70	17.15
CASE 35	1.08	6.75
CASE 36	1.08	12.27
CASE 37	1.78	7.41
CASE 38	1.19	6.69
CASE 39	1.31	7.68
CASE 40	1.00	13.91
CASE 41	1.24	9.92
CASE 42	1.43	15.85
CASE 43	1.39	14.71
CASE 44	1.55	15.80
CASE 45	1.35	14.80
CASE 46	1.20	13.81
CASE 47	1.32	16.21
CASE 48	1.21	14.71
CASE 49	1.59	2.76
CASE 50	1.58	3.17
CASE 51	0.94	7.93
CASE 52	1.11	9.24
CASE 53	0.96	14.53

*coefficient of variation

Supplementary Table 5. Markers used for SNP genotyping* of cases and controls

SNP code	Location in APC	Genomic location (NCBI Build 36/hg18)	Function (if known)	MAF† Cases	MAF† Controls	HWE‡ Cases	HWE‡ Controls
rs10428710	upstream	112035150	–	0.27	0.31	**0.0057**	**0.0014**
rs13358140	upstream	112044477	–	0.15	0.11	0.3335	0.1664
rs971517	upstream	112050154	–	0.46	0.52	0.385	**0.0011**
rs467033	intron 5	112141426	–	0.45	0.41	**3.93E-08**	**1.41E-08**
rs35790168§	exon 6	112144392	frameshift	0.00	0.00	1.000	1.000
rs2431238	intron 6	112152268	–	0.29	0.38	**0.0012**	**4.41E-06**
rs62619935§	exon 7	112156042	nonsense	0.01	0.00	1.000	1.000
rs2431507	intron 8	112174080	–	0.06	0.09	1.000	1.000
rs66650735§	exon10	112182769	frameshift	0.00	0.00	1.000	1.000
rs1801166§	exon 16	112203139	missense	0.02	0.01	1.000	1.000
rs377860§	exon 16	112203298	missense	0.00	0.00	1.000	1.000
rs67622085§	exon 16	112203516	synonymous	0.02	0.00	1.000	1.000
rs73220015§	exon 16	112203808	missense	0.00	0.00	1.000	1.000
rs459552	exon 16	112204655	missense	0.19	0.27	0.180	0.002
rs41115	exon 16	112203669	synonymous	0.40	0.46	**7.82E-06**	**1.36E-10**
rs34157245§	exon 16	112204835	missense	0.00	0.00	1.000	1.000
rs72541814§	exon 16	112204892	missense	0.00	0.00	1.000	1.000
rs35817266§	exon 16	112205993	frameshift	0.00	0.00	1.000	1.000
rs34919187§	exon 16	112206011	missense	0.00	0.00	1.000	1.000
rs33941929§	exon 16	112206685	missense	0.00	0.00	1.000	1.000
rs4705693§	exon 16	112206757	missense	0.00	0.00	1.000	1.000
rs35043160§	exon 16	112206894	synonymous	0.00	0.00	1.000	1.000
rs72541816§	exon 16	112207052	missense	0.00	0.01	1.000	1.000

*A total of 23 SNPs were selected to test for association of genetic variation with ASE, using two criteria. The first was to select tagSNPs from HapMap CEU data, using the following criteria: MAF of 0.10 and an r^2 cutoff of 0.8. We also included approximately 40 kilobases of sequence upstream of the APC gene. Eight SNPs were selected using these criteria and ability to design assays into our genotyping platform. In addition, putative functional SNPs that included frameshift, nonsense and missense mutations were selected.

†MAF: minor allele frequency.

‡ HWE: Hardy Weinberg Equilibrium. Some SNPs deviated from HWE in either cases, controls, or both. Large deviations from HWE were not unexpected because all of the samples were chosen *a priori* to be heterozygous for the ASE marker, rs2229992. Thus, SNPs deviating from HWE were left in the analyses of associations between SNPs and ASE outcome (see Table 4).

§These SNPs were excluded from further analyses because they are monomorphic or have a MAF <0.03 for both cases and controls.

Supplementary Table 6. Mean and median ASE values for cases and controls excluding the patient with polyposis (case 19)

	N	Mean (±SD)	Median	Min	Max	Shapiro-Wilk normality*	T-test with unequal variance	Bartlett's test
Case	52	1.30 (0.32)	1.28	0.68	2.46	0.0138	0.5238**	0.003**
Control	68	1.25 (0.21)	1.20	0.89	1.92	0.0468		
Total	120	1.27 (0.26)	1.24	0.68	2.46	0.0007		

* Not from log transformed data
**These p values were obtained using log transformed ASE because transformations successfully normalized the data (not shown).

Supplementary Table 7. Distribution of cases and controls at increasing distance from the overall mean ASE excluding the patient with polyposis (case 19)

More than 1.645 standard deviations from the overall mean (<0.844 and >1.703)					
Status	Within 1.645 SD	Out of 1.645 SD	Total	Chi-square p-Value	Fisher's Exact p-value
Cases	44	8	52	**0.004**	**0.01**
Controls	67	1	68		
Total	111	9	120		
More than 1.0 standard deviation from the overall mean (<1.013 and >1.534)					
Status	Within 1 SD	Out of 1 SD	Total	Chi-square p-Value	Fisher's Exact p-value
Cases	29	23	52	**0.001**	**0.002**
Controls	56	12	68		
Total	85	35	120		

Supplementary Table 8. **Association of SNPs in *APC* with ASE outcome**

a. Cases and controls combined

SNP	genotypes	N	ASE						
			Mean	St Dev	Median	Min	Max	Anova p-value	Bartlett's test p-value
rs41115								**0.0091**	0.066
	C/C	2	1.38	0.13	1.38	1.28	1.47		
	C/T	97	1.22	0.24	1.20	0.43	1.92		
	T/T	19	1.43	0.36	1.35	0.96	2.46		
rs41115 (C as dominant model)**								**0.0268#**	**0.015**
	C/T&C/C	99	1.23	0.24	1.21	0.43	1.92		
	T/T	19	1.43	0.36	1.35	0.96	2.46		
rs459552								0.8310#	**0.013**
	A/A	-	-	-	-	-	-		
	A/T	64	1.27	0.31	1.22	0.43	2.46		
	T/T	54	1.26	0.22	1.23	0.89	1.92		
rs467033								0.1060^	0.212
	T/T	1	1.26	-	1.26	1.26	1.26		
	T/A	98	1.29	0.28	1.25	0.43	2.46		
	A/A	20	1.15	0.22	1.12	0.68	1.60		
rs467033 (T as dominant model)**								**0.0342^**	0.222
	T/T&A/T	99	1.29	0.28	1.25	0.43	2.46		
	A/A	20	1.15	0.22	1.12	0.68	1.60		
rs971517								**0.0010**	0.084
	G/G	22	1.16	0.21	1.12	0.68	1.60		
	G/C	73	1.24	0.24	1.20	0.43	1.92		
	C/C	24	1.43	0.33	1.43	0.94	2.46		
rs2431238								0.7139^	0.097
	T/T	2	1.26	0.32	1.26	1.03	1.48		
	T/C	78	1.24	0.24	1.22	0.43	1.92		
	C/C	38	1.31	0.33	1.27	0.75	2.46		
rs2431238 (T as dominant model)**								0.4118#^	**0.019**
	T/C&T/T	80	1.24	0.24	1.22	0.43	1.92		
	C/C	38	1.31	0.33	1.27	0.75	2.46		
rs2431507								**0.0168^**	0.190
	G/G	-	-	-	-	-	-		
	G/A	19	1.14	0.21	1.11	0.68	1.60		
	A/A	100	1.29	0.28	1.26	0.43	2.46		
rs10428710								0.8598^	0.063
	T/T	2	1.18	0.14	1.18	1.08	1.28		
	T/C	68	1.28	0.31	1.22	0.43	2.46		
	C/C	49	1.25	0.22	1.23	0.68	1.78		
rs10428710 (T as dominant model)**								0.7851#	**0.019**
	T/C&T/T	70	1.27	0.30	1.22	0.43	2.46		
	C/C	49	1.25	0.22	1.23	0.68	1.78		
rs13358140								0.1509^	0.178
	C/C	2	1.49	0.08	1.49	1.43	1.55		
	C/T	24	1.31	0.21	1.33	0.94	1.78		
	T/T	93	1.25	0.28	1.20	0.43	2.46		

b. Controls only

SNP	genotypes	N	ASE						
			Mean	St Dev	Median	Min	Max	Anova p-value	Bartlett's test p-value
rs41115	C/C	1	1.47	-	1.47	1.47	1.47	0.5907^	0.803
	C/T	58	1.25	0.21	1.20	0.89	1.92		
	T/T	7	1.24	0.20	1.16	1.03	1.58		
rs41115 (C as dominant model)**								0.9088^	0.802
	C/T&CC	59	1.25	0.21	1.20	0.89	1.92		
	T/T	7	1.24	0.20	1.16	1.03	1.58		
rs459552								0.9640^	0.653
	A/A	30	1.25	0.20	1.18	0.99	1.67		
	A/T	36	1.25	0.22	1.21	0.89	1.92		
	T/T	-	-	-	-	-	-		
rs467033								0.1752^	0.989
	T/T	-	-	-	-	-	-		
	T/A	54	1.26	0.21	1.22	0.89	1.92		
	A/A	13	1.18	0.21	1.12	0.90	1.60		
rs467033 (T as dominant model)**								0.1752^	0.989
	T/A&T/T	54	1.26	0.21	1.22	0.89	1.92		
	A/A	13	1.19	0.21	1.12	0.90	1.60		
rs971517								0.1641^	0.935
	G/G	12	1.19	0.22	1.12	0.90	1.60		
	G/C	46	1.25	0.21	1.20	0.89	1.92		
	C/C	9	1.34	0.19	1.43	1.08	1.58		
rs2431238								0.9929	0.671
	T/T	2	1.26	0.32	1.26	1.03	1.48		
	T/C	47	1.25	0.22	1.19	0.89	1.92		
	C/C	17	1.25	0.19	1.20	0.99	1.58		
rs2431238 (T as dominant model)**								0.9049	0.470
	T/C&T/T	49	1.25	0.22	1.19	0.89	1.92		
	C/C	17	1.25	0.19	1.20	0.99	1.58		
rs2431507								0.0920^	0.887
	G/G	-	-	-	-	-	-		
	G/A	12	1.17	0.20	1.12	0.90	1.60		
	A/A	55	1.27	0.21	1.22	0.89	1.92		
rs10428710								0.9337^	0.840
	T/T	2	1.18	0.14	1.18	1.08	1.28		
	T/C	40	1.25	0.22	1.19	0.89	1.92		
	C/C	25	1.25	0.21	1.21	0.90	1.60		
rs10428710 (T as dominant model)**								0.9898^	0.775
	T/C&T/T	42	1.25	0.22	1.19	0.89	1.92		
	C/C	25	1.25	0.21	1.21	0.90	1.60		
rs13358140								0.1336^	0.591
	C/C	2	1.49	0.08	1.49	1.43	1.55		
	C/T	9	1.30	0.18	1.30	1.02	1.52		
	T/T	56	1.23	0.21	1.17	0.89	1.92		

c. Cases only

SNP	Genotypes	N	ASE						
			Mean	St Dev	Median	Min	Max	Anova p-value	Bartlett's test p-value
rs41115								**0.0058**	0.131
	C/C	1	1.28	-	1.28	1.28	1.28		
	C/T	39	1.20	0.28	1.21	0.43	1.70		
	T/T	12	1.54	0.39	1.50	0.96	2.46		
rs41115 (C as dominant model)								**0.0013**	0.116
	C/T&CC	40	1.20	0.27	1.23	0.43	1.70		
	T/T	12	1.54	0.39	1.50	0.96	2.46		
rs459552								0.7220#	**0.025**
	A/A	34	1.29	0.38	1.29	0.43	2.46		
	A/T	18	1.27	0.23	1.25	0.93	1.70		
	T/T	-	-	-	-	-	-		
rs467033								0.2535	0.289
	T/T	1	1.26	-	1.26	1.26	1.26		
	T/A	44	1.31	0.34	1.28	0.43	2.46		
	A/A	7	1.08	0.24	1.07	0.68	1.32		
rs467033 (T as dominant model)								0.0973	0.302
	T/A&T/T	45	1.31	0.34	1.27	0.43	2.46		
	A/A	7	1.08	0.24	1.07	0.68	1.32		
rs971517								**0.0103**	0.148
	G/G	10	1.11	0.20	1.15	0.68	1.32		
	G/C	27	1.23	0.30	1.24	0.43	1.70		
	C/C	15	1.48	0.38	1.43	0.94	2.46		
rs2431238								0.2476#	**0.041**
	T/T	-	-	-	-	-	-		
	T/C	31	1.22	0.27	1.24	0.43	1.70		
	C/C	21	1.36	0.41	1.31	0.75	2.46		
rs2431238 (T as dominant model)								0.2476#	**0.041**
	T/C	31	1.22	0.27	1.24	0.43	1.70		
	C/C	21	1.37	0.41	1.31	0.75	2.46		
rs2431507								0.0973	0.302
	G/G	-	-	-	-	-	-		
	G/A	7	1.08	0.24	1.07	0.68	1.32		
	A/A	45	1.31	0.34	1.27	0.43	2.46		
rs10428710								0.5819#	**0.013**
	T/T	-	-	-	-	-	-		
	T/C	28	1.31	0.40	1.28	0.43	2.46		
	C/C	24	1.25	0.24	1.26	0.68	1.78		
rs10428710 (T as dominant model)								0.5819#	**0.013**
	T/C&T/T	28	1.31	0.40	1.28	0.43	2.46		
	C/C	24	1.25	0.24	1.26	0.68	1.78		
rs13358140								0.6526	0.066
	C/C	-	-	-	-	-	-		
	C/T	15	1.31	0.24	1.35	0.94	1.78		
	T/T	37	1.27	0.37	1.26	0.43	2.46		

*Analyses were done on untransformed data using either ANOVA, where appropriate, or Kruskal Wallis (as noted). This was because transformation failed to normalize data that deviated from normality.
**In situations where there were few homozygotes of one class, analyses were performed using all three genotypes, as well as on heterozygotes pooled with the rare homozygotes (dominant model).
Kruskal-Wallis test used because of deviations from equal variance
^ Kruskal-Wallis used because of deviation from normality

Supplementary Table 9. Association of SNPs in *APC* with ASE outcome excluding the patient with polyposis (case 19) *

	Cases and controls combined		Controls only		Cases only	
SNP	**Anova p-value**	**Bartlett's test p-value**	**Anova p-value**	**Bartlett's test p-value**	**Anova p-value**	**Bartlett's test p-value**
rs41115	**0.0195**	0.376	0.5737	0.776	**0.0132**	0.574
rs41115 (dominant)**	**0.0074**	0.190	0.9323	0.774	**0.0033**	0.538
rs459552	0.7460	0.064	0.7161^	0.643	0.8194	0.078
rs467033	0.0606	0.990	0.2071	0.806	0.1198	0.941
rs467033 (dominant)**	**0.0177**	0.967	0.2071	0.806	**0.0387**	0.911
rs971517	**0.0012**	0.534	0.2088	0.841	**0.0128**	0.750
rs2431238	0.6538	0.155	0.9993	0.673	0.3060	0.050
rs2431238 (dominant)**	0.4723#	**0.037**	0.9704	0.509	0.3060	0.050
rs2431507	**0.0088**	0.962	0.1051	0.919	**0.0387**	0.911
rs10428710	0.7230	0.454	0.9144	0.925	0.4006	0.157
rs10428710 (dominant)**	0.5160	0.260	0.9611	1.000	0.4006	0.157
rs13358140	0.2527	0.239	0.1684	0.548	0.6254	0.120

*Analyses were done on transformed data using either ANOVA, where appropriate, or Kruskal Wallis (as noted).

**In situations where there were few homozygotes of one class, analyses were performed using all three genotypes, as well as on heterozygotes pooled with the rare homozygotes (dominant model).

#Kruskal-Wallis test used because of deviations from equal variance

^ Kruskal-Wallis used because of deviation from normality

Supplementary Table 10. **Association of SNPs in *APC* with ASE outcome excluding the patient with polyposis (case 19)**

a. Cases and controls combined

SNP	Genotypes	N	ASE						
			Mean	St Dev	Median	Min	Max	Anova p-value	Bartlett's test p-value
rs41115								**0.0195**	0.376
	C/C	2	1.375	0.13	1.38	1.28	1.47		
	C/T	96	1.24	0.23	1.21	0.68	1.92		
	T/T	19	1.43	0.36	1.35	0.96	2.46		
rs41115 (C as dominant model)								**0.0074**	0.190
	C/T&C/C	98	1.24	0.23	1.22	0.68	1.92		
	T/T	19	1.43	0.36	1.35	0.96	2.46		
rs459552								0.7460	0.064
	A/A	-	-	-	-	-	-		
	A/T	63	1.28	0.29	1.23	0.68	2.46		
	T/T	54	1.26	0.22	1.23	0.89	1.92		
rs467033								0.0606	0.990
	T/T	1	1.26	-	1.26	1.26	1.26		
	T/A	97	1.29	0.26	1.25	0.75	2.46		
	A/A	20	1.15	0.22	1.12	0.68	1.60		
rs467033 (T as dominant model)								**0.0177**	0.967
	T/T&A/T	98	1.29	0.26	1.26	0.75	2.46		
	A/A	20	1.15	0.22	1.12	0.68	1.60		
rs971517								**0.0012**	0.534
	G/G	22	1.16	0.21	1.12	0.68	1.60		
	G/C	72	1.25	0.23	1.21	0.75	1.92		
	C/C	24	1.43	0.33	1.43	0.94	2.46		
rs2431238								0.6538	0.155
	T/T	2	1.26	0.32	1.26	1.03	1.48		
	T/C	77	1.25	0.22	1.22	0.68	1.92		
	C/C	38	1.31	0.33	1.27	0.75	2.46		
rs2431238 (T as dominant model)								0.4723*	**0.037**
	T/C&T/T	79	1.25	0.22	1.22	0.68	1.92		
	C/C	38	1.31	0.33	1.27	0.75	2.46		
rs2431507								**0.0088**	0.962
	G/G	-	-	-	-	-	-		
	G/A	19	1.14	0.21	1.11	0.68	1.60		
	A/A	99	1.30	0.26	1.26	0.75	2.46		
rs10428710								0.7230	0.454
	T/T	2	1.18	0.14	1.18	1.08	1.28		
	T/C	67	1.29	0.29	1.22	0.75	2.46		
	C/C	49	1.25	0.22	1.23	0.68	1.78		
rs10428710 (T as dominant model)								0.5160	0.260
	T/C&T/T	69	1.29	0.29	1.22	0.75	2.46		
	C/C	49	1.25	0.22	1.23	0.68	1.78		
rs13358140								0.2527	0.239
	C/C	2	1.49	0.08	1.49	1.43	1.55		
	C/T	24	1.31	0.21	1.33	0.94	1.78		
	T/T	92	1.26	0.27	1.20	0.68	2.46		

b. Controls only

SNP	Genotypes	N	ASE						
			Mean	St Dev	Median	Min	Max	Anova p-value	Bartlett's test p-value
rs41115								0.5737	0.776
	C/C	1	1.47	-	1.47	1.47	1.47		
	C/T	58	1.25	0.21	1.20	0.89	1.92		
	T/T	7	1.24	0.20	1.16	1.03	1.58		
rs41115 (C as dominant model)								0.9323	0.774
	C/T&C/C	59	1.25	0.21	1.20	0.89	1.92		
	T/T	7	1.24	0.20	1.16	1.03	1.58		
rs459552								0.7161^	0.643
	A/A	30	1.25	0.20	1.18	0.99	1.67		
	A/T	36	1.25	0.22	1.21	0.89	1.92		
	T/T	-	-	-	-	-	-		
rs467033								0.2071	0.806
	T/T	-	-	-	-	-	-		
	T/A	54	1.26	0.21	1.22	0.89	1.92		
	A/A	13	1.18	0.21	1.12	0.90	1.60		
rs467033 (T as dominant model)								0.2071	0.806
	T/A&T/T	54	1.26	0.21	1.22	0.89	1.92		
	A/A	13	1.19	0.21	1.12	0.90	1.60		
rs971517								0.2088	0.841
	G/G	12	1.19	0.22	1.12	0.90	1.60		
	G/C	46	1.25	0.21	1.20	0.89	1.92		
	C/C	9	1.34	0.19	1.43	1.08	1.58		
rs2431238								0.9993	0.673
	T/T	2	1.26	0.32	1.26	1.03	1.48		
	T/C	47	1.25	0.22	1.19	0.89	1.92		
	C/C	17	1.25	0.19	1.20	0.99	1.58		
rs2431238 (T as dominant model)								0.9704	0.509
	T/C&T/T	49	1.25	0.22	1.19	0.89	1.92		
	C/C	17	1.25	0.19	1.20	0.99	1.58		
rs2431507								0.1051	0.919
	G/G	-	-	-	-	-	-		
	G/A	12	1.17	0.20	1.12	0.90	1.60		
	A/A	55	1.27	0.21	1.22	0.89	1.92		
rs10428710								0.9144	0.925
	T/T	2	1.18	0.14	1.18	1.08	1.28		
	T/C	40	1.25	0.22	1.19	0.89	1.92		
	C/C	25	1.25	0.21	1.21	0.90	1.60		
rs10428710 (T as dominant model)								0.9611	1.000
	T/C&T/T	42	1.25	0.22	1.19	0.89	1.92		
	C/C	25	1.25	0.21	1.21	0.90	1.60		
rs13358140								0.1684	0.548
	C/C	2	1.49	0.08	1.49	1.43	1.55		
	C/T	9	1.30	0.18	1.30	1.02	1.52		
	T/T	56	1.23	0.21	1.17	0.89	1.92		

c. Cases only

SNP	Genotypes	N	ASE						
			Mean	St Dev	Median	Min	Max	Anova p-value	Bartlett's test p-value
rs41115								**0.0132**	0.574
	C/C	1	1.28	-	1.28	1.28	1.28		
	C/T	38	1.22	0.25	1.23	0.68	1.70		
	T/T	12	1.54	0.39	1.50	0.96	2.46		
rs41115 (C as dominant model)								**0.0033**	0.538
	C/T&C/C	39	1.22	0.25	1.24	0.68	1.70		
	T/T	12	1.54	0.39	1.50	0.96	2.46		
rs459552								0.8194	0.078
	A/A	33	1.31	0.36	1.29	0.68	2.46		
	A/T	18	1.27	0.23	1.25	0.93	1.70		
	T/T	-	-	-	-	-	-		
rs467033								0.1198	0.941
	T/T	1	1.26	-	1.26	1.26	1.26		
	T/A	43	1.33	0.32	1.29	0.75	2.46		
	A/A	7	1.08	0.24	1.07	0.68	1.32		
rs467033 (T as dominant model)								**0.0387**	0.911
	T/A&T/T	44	1.33	0.32	1.28	0.75	2.46		
	A/A	7	1.08	0.24	1.07	0.68	1.32		
rs971517								**0.0128**	0.750
	G/G	10	1.11	0.20	1.15	0.68	1.32		
	G/C	26	1.26	0.26	1.25	0.75	1.70		
	C/C	15	1.48	0.38	1.43	0.94	2.46		
rs2431238								0.3060	0.050
	T/T	-	-	-	-	-	-		
	T/C	30	1.25	0.23	1.25	0.68	1.70		
	C/C	21	1.36	0.41	1.31	0.75	2.46		
rs2431238 (T as dominant model)								0.3060	0.050
	T/C	30	1.25	0.23	1.25	0.68	1.70		
	C/C	21	1.37	0.41	1.31	0.75	2.46		
rs2431507								**0.0387**	0.911
	G/G	-	-	-	-	-	-		
	G/A	7	1.08	0.24	1.07	0.68	1.32		
	A/A	44	1.33	0.32	1.28	0.75	2.46		
rs10428710								0.4006	0.157
	T/T	-	-	-	-	-	-		
	T/C	27	1.31	0.37	1.29	0.75	2.46		
	C/C	24	1.25	0.24	1.26	0.68	1.78		
rs10428710 (T as dominant model)								0.4006	0.157
	T/C&T/T	27	1.37	0.37	1.29	0.75	2.46		
	C/C	24	1.25	0.24	1.26	0.68	1.78		
rs13358140								0.6254	0.120
	C/C	-	-	-	-	-	-		
	C/T	15	1.31	0.24	1.35	0.94	1.78		
	T/T	36	1.29	0.35	1.27	0.68	2.46		

* Kruskal-Wallis test used because of deviations from equal variance

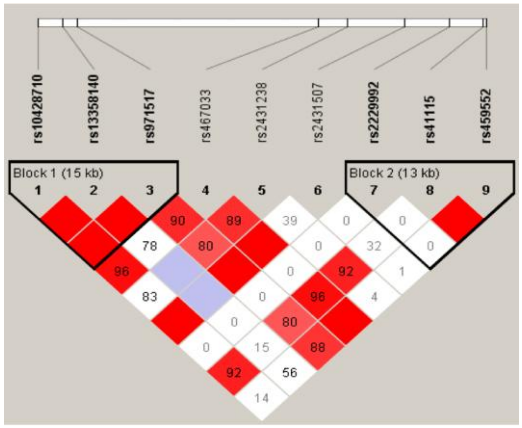
^ Kruskal-Wallis test used because of deviation from normality

n.a.: unable to calculate probability of deviation from normality due to low cell count

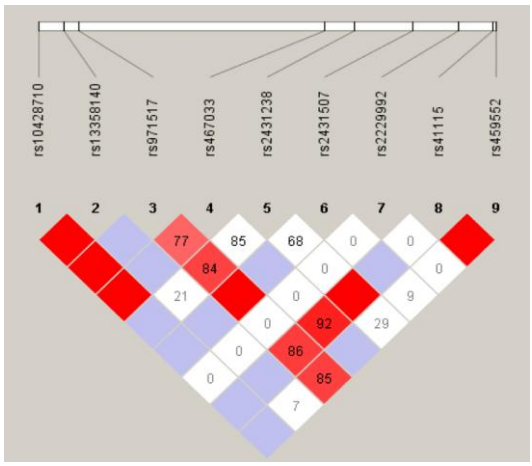
Supplementary Figure 1

Linkage disequilibrium patterns (D') among SNPs analyzed for association with ASE.

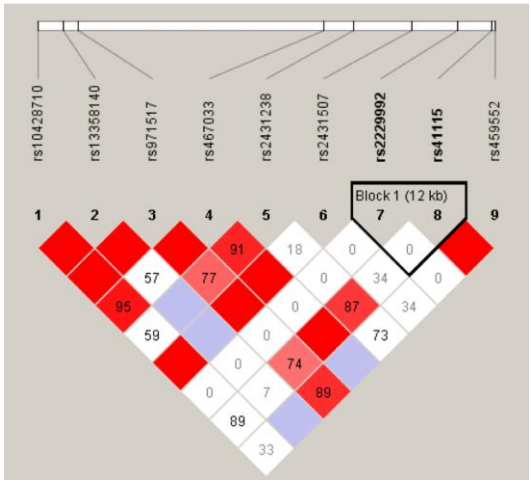
Cases and controls combined



Cases only



Controls only



Legend to supplementary figure

Supplementary Figure 1 Linkage disequilibrium plots

Plots show linkage disequilibrium patterns (D') among SNPs analyzed for association with ASE. Red diamonds denote SNPs showing evidence of linkage disequilibrium, white no evidence of LD and blue for D'=1 but LOD values below 2 and hence not having high likelihood of providing reliable measures of LD. LD values are shown in the diamonds. Topmost panel is the entire data set, middle panel is for the cases only and the lowest panel is for controls only.