Table S1. Genetic variation in *PGES*, *EP2*, *EP4*, and *PGDH* and results of quality control

Gene	SNP[a]	dbSNP identifier	Location	Tag or Candidate	Converted to Illumina?	Quality control measures: Genotype Call Rate	Non-blinded Duplicate Concordance	Blinded Duplicate Concordance	HWE p-value[b]	Passed QC?	MAF[b]
PGES	1152G>A	rs4837408	intron 1	bin 1	yes	0.98	1.00	0.97	0.78	yes	0.07
	-664A>T	rs7873087	5'UTR	bin 2	yes	0.98	1.00	0.97	0.50	yes	0.10
	-1254T>C	rs45566632	5'UTR	bin 3	no[d]	0.98	1.00	0.97	0.50	yes	0.04
	-1129G>C	rs35549539	5'UTR	singleton	no	—	—	—	—	—	—
	-1314C>T	rs35450091	5'UTR	singleton	no	—	—	—	—	—	—
	211A>G	rs2241271	intron 1	singleton	yes	0.96	1.00	0.97	0.33	yes	0.19
	3006G>A	rs45509796	intron 1	singleton	yes	0.98	1.00	1.00	0.47	yes	0.03
	5164T>C	rs35618739	intron 2	singleton	no	—	—	—	—	—	—
	13425A>C	rs2302821	3'UTR	singleton	yes	0.98	1.00	1.00	0.78	yes	0.09
	14326C>T	rs45544737	3'UTR	singleton	yes	**0.01**	—	—	—	no	NA
EP2	-616G>C	rs2075797	5'UTR	bin 1	yes	0.97	1.00	1.00	1.00	yes	0.12
	1690G>A	rs11851457	intron 1	bin 2	yes	0.98	1.00	1.00	0.19	yes	0.04
	-967G>A	rs45487500	5'UTR	bin 3	yes	0.98	1.00	1.00	1.00	yes	0.05
	-1722A>G	rs1254601	5'UTR	bin 4	yes	0.97	1.00	0.97	0.54	yes	0.39
	9814C>A	rs1254585	intron 1	bin 5	yes	0.97	1.00	1.00	0.41	yes	0.23
	15674G>A	rs34337770	3'UTR	bin 6	yes	0.98	1.00	0.97	0.89	yes	0.19
	-166G>A	rs1353411	5'UTR	singleton	yes	**0.01**	—	—	—	no	NA
	3096A/-	rs1692043	intron 1	singleton	no	—	—	—	—	—	—
	4950G>A	rs33993630	intron 1	singleton	yes	0.98	1.00	1.00	0.69	yes	0.12
	12010G>A	rs708499	intron 1	singleton	yes	0.98	1.00	0.97	0.55	yes	0.17
	12741A>G Leu304Leu	rs2229187	exon 2	singleton	yes	0.98	1.00	1.00	—*	no	NA
EP4[c]	1455A>G	rs4546432	intron 2	bin 1	yes	0.94	1.00	1.00	0.24	yes	0.38
	13877A>C	rs7730368	3'UTR	bin 2	yes	0.98	1.00	1.00	0.75	yes	0.27
	-1307G>A	rs10039983	5'UTR	bin 3	yes	0.97	1.00	1.00	0.68	yes	0.45
	2472A>G	rs11957406	intron 2	bin 4	yes	0.97	1.00	1.00	0.55	yes	0.45
	-132C>G	rs45480797	intron 1	bin 5	yes	0.98	1.00	1.00	0.63	yes	0.09
	6374G>A	rs28540420	intron 2	bin 6	yes	0.97	1.00	1.00	0.72	yes	0.23
	-1529G>A	rs4133101	intron 1	singleton	yes	0.98	1.00	1.00	0.65	yes	0.36
	-1408G>A	rs13186505	intron 1	singleton	yes	0.97	1.00	1.00	0.44	yes	0.24
	8907G>A	rs10060234	intron 2	singleton	yes	0.98	1.00	1.00	0.30	yes	0.32
	11851G>A	rs16870224	3'UTR	singleton	yes	0.98	1.00	0.97	1.00	yes	0.11
	13981A>G	rs4957343	3'UTR	singleton	yes	0.98	1.00	1.00	0.61	yes	0.42
	Thr176Ile	NA	exon 2	candidate	no[d]	0.97	1.00	1.00	—*	no	NA
	Val294Ile	NA	exon 3	candidate	no[d]	0.97	1.00	1.00	0.31	yes	0.02
PGDH	31659A>G	rs9312555	3'UTR	bin 1	yes	0.97	1.00	0.97	0.26	yes	0.15
	343C>A	rs45567139	intron 1	bin 2	yes	0.97	1.00	1.00	0.69	yes	0.06
	16362G>A	rs11133042	intron 4	bin 3	yes	0.98	1.00	1.00	0.07	yes	0.23
	-1868G>A	rs45535235	5'UTR	bin 4	yes	0.98	1.00	0.97	0.66	yes	0.13
	782A>G	rs1365613	intron 2	bin 5	yes	0.98	1.00	1.00	0.03	yes	0.19
	20518A>G	rs11724251	intron 4	bin 6	yes	0.98	1.00	0.92	0.22	yes	0.42
	3580G>A	rs12500316	intron 2	bin 7	yes	0.98	1.00	0.97	0.16	yes	0.23
	26646G>A	rs2303520	intron 4	bin 8	yes	0.98	1.00	0.95	0.46	yes	0.20
	9691C>A	rs1863642	intron 3	bin 9	yes	0.98	1.00	0.97	0.45	yes	0.29
	12184A/-	rs3839192	intron 3	bin 10	no[d]	0.99	1.00	1.00	0.83	yes	0.12
	-1635G>A	rs3756273	5'UTR	bin 11	yes	0.97	1.00	1.00	1.00	yes	0.47
	19433G>A	rs7349744	intron 4	bin 12	yes	0.97	1.00	0.97	0.25	yes	0.30
	18349G>A	rs45593131	intron 4	bin 13	yes	0.98	1.00	1.00	0.14	yes	0.11

[a] Counting begins at the start codon. Variants located 5' of the start codon are counted backwards from the base preceding the start codon and begin with a "-" sign.
[b] Among controls only
[c] The start codon for *EP4* is in exon 2.
[d] This SNP was genotyped in the Molecular Epidemiology Laboratory at Fred Hutchinson Cancer Research Center
* This locus was monomorphic in our study population.

Table S1. Continued

Gene	SNP[a]	dbSNP identifier	Location	Tag or Candidate	Converted to Illumina?	Quality control measures: Genotype Call Rate	Non-blinded Duplicate Concordance	Blinded Duplicate Concordance	HWE p-value[b]	Passed QC?	MAF[b]
PGDH	19979A>T	rs12640361	intron 4	bin 14	no[d]	0.99	1.00	1.00	0.72	yes	0.18
	-1162T>G	rs2612672	5'UTR	singleton	no	—	—	—	—	—	—
	-404G>C	rs1346271	5'UTR	singleton	yes	0.97	1.00	0.95	<.0001	no	0.02
	179A/-	rs11433148	intron 1	singleton	no	—	—	—	—	—	—
	448G>A										
	Gln52Gln	rs1050145	exon 2	singleton	yes	0.97	1.00	1.00	0.98	yes	0.42
	1113G>A	rs34449204	intron 2	singleton	yes	0.98	1.00	0.97	0.84	yes	0.10
	1543G>A	rs45545934	intron 2	singleton	yes	0.97	1.00	0.97	0.75	yes	0.49
	9442A>G	rs2555632	intron 3	singleton	yes	0.97	1.00	0.97	0.01	yes	0.30
	13316A>C	rs2555629	intron 3	singleton	yes	0.98	1.00	0.97	0.82	yes	0.33
	13796C>T	rs3775977	intron 4	singleton	yes	0.98	1.00	0.97	0.37	yes	0.26
	14233A/-	rs5864277	intron 4	singleton	no	—	—	—	—	—	—
	14872T>G	rs7673685	intron 4	singleton	yes	0.97	1.00	0.97	<.0001	no	0.37
	17450A>G	rs45462895	intron 4	singleton	yes	0.97	1.00	0.97	0.19	yes	0.12
	19850A>C	rs2555649	intron 4	singleton	no	—	—	—	—	—	—
	20605T>G	rs17360144	intron 4	singleton	yes	0.98	1.00	1.00	<.0001	no	NA
	20750A>G	rs45482095	intron 4	singleton	yes	0.98	1.00	1.00	0.98	yes	0.01
	20855T/-	rs45612543	intron 4	singleton	no	—	—	—	—	—	—
	22496GTC/-	rs10659517	intron 4	singleton	no	—	—	—	—	—	—
	23196A>G	rs6828850	intron 4	singleton	yes	0.97	1.00	0.97	0.07	yes	0.27

[a] Counting begins at the start codon in exon 1. Variants located 5' of the start codon are counted backwards from the base preceding the start codon and begin with a "-" sign.

[b] Among controls only

[c] The start codon for *EP4* is in exon 2.

[d] This SNP was genotyped in the Molecular Epidemiology Laboratory at Fred Hutchinson Cancer Research Center

* This locus was monomorphic in our study population.

Table S2. Genetic variation in *EP2* and *PGDH*, NSAID use, and risk of adenoma[a]

			NSAID Use							
			No				Yes			
Gene	**SNP**	**Genotype**	**Cases**	**Controls**	**OR**	**95% CI**	**Cases**	**Controls**	**OR**	**95% CI**
EP2	**9814C>A**	CC	192	193	**1.00**	—	96	156	**0.49**	0.34-.714
		CA or AA	117	130	**0.83**	0.58-1.18	78	102	**0.71**	0.48-1.07
						global p-interaction=0.05				
PGDH	**343C>A**	CC	259	289	**1.00**	—	153	222	**0.71**	0.52-0.95
		CA or AA	49	35	**1.98**	1.18-3.33	21	36	**0.56**	0.29-1.08
						global p-interaction=0.03				

[a] Regular NSAID use is defined as at least once a week for at least one month
[b] Adjusted for age, BMI, total intakes of energy, alcohol, and fiber, sex, post-menopausal hormone use (women only), and smoking (pack-years)
[c] Test for differences in genotype trend among strata of NSAID use

Table S3. Haplotypes in *PGES*, *EP2*, *EP4*, and *PGDH* and risk of colorectal adenoma[a]

Gene	Haplotype	Cases %	Controls %	OR	95% CI
***PGES*[b]**	AA	80.2	81.0	**1.00**	—
	TG	9.6	10.1	**1.01**	0.75-1.37
	AG	10.2	8.8	**1.18**	0.87-1.60
	<5%	0	0.1	—	—
					global p=0.37
***EP2*[c]**	GGCG	66.6	64.6	**1.00**	—
	CGAA	13.1	12.2	**1.01**	0.77-1.33
	GACG	8.9	12.1	**0.70**	0.52-0.96
	GGAG	7.5	6.2	**1.09**	0.76-1.55
	<5%	3.9	4.9	**0.81**	0.51-1.28
					global p=0.18
***EP4* (Block 1)[d]**	GGACAA	42.6	45.5	**1.00**	—
	AAGCGG	26.9	24.4	**1.14**	0.91-1.43
	AGGCGG	12.0	11.6	**1.13**	0.84-1.51
	GGGGAA	8.7	9.3	**0.96**	0.69-1.34
	GGGCAG	7.4	6.6	**1.20**	0.84-1.71
	<5%	2.4	2.6	**1.01**	0.51-2.02
					global p=0.76
***EP4* (Block 2)[e]**	GGAG	40.2	41.7	**1.00**	—
	AGAA	33.0	31.6	**1.08**	0.89-1.31
	GGCA	15.0	15.0	**1.03**	0.80-1.34
	GACA	11.4	11.6	**1.02**	0.77-1.36
	<5%	0.4	0.1	—	—
					global p=0.56
***PGDH* (Block 1)[f]**	GC	49.9	53.1	**1.00**	—
	AC	42.3	40.6	**1.11**	0.92-1.34
	AA	7.8	6.4	**1.39**	0.98-1.99
	<5%	0	0	—	—
					global p=0.16
***PGDH* (Block 2)[g]**	AGGGAC	22.2	22.6	**1.00**	—
	AGGAAA	20.4	21.6	**0.94**	0.71-1.24
	AGAGGC	20.1	18.6	**1.00**	0.77-1.31
	GGAGAC	16.1	17.3	**0.89**	0.67-1.19
	AAAGGC	11.6	10.4	**1.12**	0.80-1.57
	AGGGAA	7.7	6.3	**1.29**	0.88-1.89
	<5%	1.9	3.2	**0.65**	0.35-1.23
					global p=0.39
***PGDH* (Block 3)[h]**	AAGGGGA	21.7	24.0	**1.00**	—
	GAGAGGA	19.1	17.2	**0.87**	0.66-1.14
	GAGGAGA	15.7	18.2	**1.05**	0.79-1.40
	GAGGGAG	15.5	14.5	**0.88**	0.66-1.18
	GAAAGGA	11.4	11.3	**0.93**	0.67-1.29
	GGGGAGA	10.7	8.6	**0.81**	0.57-1.15
	<5%	5.9	6.2	**1.04**	0.69-1.55
					global p=0.75

[a] Adjusted for age and sex.
[b] Order of SNPs in haplotype: -664A>T, 211A>G
[c] Order of SNPs in haplotype: -616C>G, 4950G>A, 9814C>A, 12010G>A
[d] Order of SNPs in haplotype: -1529G>A, -1408G>A, -1307G>A, -132C>G, 1455A>G, 2472A>G
[e] Order of SNPs in haplotype: 8907G>A, 11851G>A, 13877A>C, 13981A>G
[f] Order of SNPs in haplotype: -1635G>A, 343C>A
[g] Order of SNPs in haplotype: 782A>G. 1113G>A, 1543G>A, 3580G>A, 9442A>G, 9691C>A
[h] Order of SNPs in haplotype: 16362G>A, 17450A>G, 18349G>A, 19433G>A, 23196A>G, 26646G>A, 31659A>G

Table S4. Results of Principal Components Analysis[a]

Gene	Number of SNPs	Number of principal components[b]	p-value[c]
EP2	8	3	0.67
EP4	11	2	0.46
PGDH	21	7	0.70
PGES	5	3	0.85

[a] Adjusted for age and sex.
[b] Number of principal components that explain ≥80% of the variance in polyp risk
[c] Likelihood ratio test comparing a model with principle components + age and sex to a model containing only age and sex. DF=the number of principal components.

Table S5. Results of Chatterjee testing

Gene1	Gene2	Permutation P-value	Asymptotic P-value
EP2	EP4	0.30	0.32
EP2	PGDH	0.49	0.45
EP2	PGES	0.21	0.21
EP4	PGDH	0.98	0.96
EP4	PGES	0.64	0.53
PGDH	PGES	0.34	0.27

Table S6. Best models for logic regression models of size 1-15[a]

Model size	Number of Trees	Score	β Estimates[b]
1	1	1396.1	-0.336 * dEP4 -1307G>A
2	1	1389.9	+1.78 * ((not dEP4 13981A>G) and rEP2 15674G>A)
3	2	1385.3	-0.722 * rEP2 9814C>A -2.48 * ((not rEP2 15674G>A) or dEP4 13981A>G)
4	1	1374.6	+1.66 * ((dEP4 8907G>A and dEP4 6374G>A) and (rEP2 -1722G>A or dPGDH 1113G>A))
5	3	1372.5	+1.51 * rEP2 9814C>A +2.46 * ((not rEP2 9814C>A) or (not dEP4 13981A>G)) -1.19 * (dPGDH 17450A>G and (not dPGDH 9691C>A))
6	3	1369.9	-2.52 * ((not rEP2 15674G>A) or dEP4 13981A>G) +0.788 * (not rEP2 9814C>A) +1.04 * ((not dPGDH 17450A>G) or (rPGDH 13316A>C or dEP4 8907G>A))
7	2	1361.6	-1.75 * ((not dEP4 8907G>A) or (((not rEP2 -1722G>A) or (not dEP4 6374G>A)) and (not rPGDH 782A>G))) -0.799 * ((dPGDH 1543G>A and (not dPGDH 9442A>G)) and dEP4 -1307G>A)
8	4	1359.0	-0.713 * rEP2 -1722G>A +0.762 * ((not dPGDH 17450A>G) or dEP4 8907G>A) -2 * ((not dEP4 13877A>C) or (((not dPGES 211A>G) and (not dEP4 1455A>G)) or (not rEP2 -1722G>A))) -0.374 * dEP2 4950G>A
9	5	1354.9	-17.2 * rEP2 9814C>A +2.86 * ((not rEP2 9814C>A) or (not dEP4 13981A>G)) +2.34 * (dEP2 -1722G>A or ((not rPGDH 1543G>A) or (not rEP4 1455A>G))) +19 * (rEP2 9814C>A and (not rEP4 6374G>A)) -0.384 * dPGDH 17450A>G
10	4	1352.0	-2.55 * (rEP4 1455A>G and ((dEP2 4950G>A or (not dPGDH Gln52Gln)) and ((not dEP2 -1722G>A) and (not dPGES -664A>T)))) -0.367 * dPGDH 17450A>G +0.629 * ((not rPGDH 19433G>A) and (not dEP4 -1307G>A)) -1.54 * (rEP4 13877A>C and dPGDH 782A>G)
11	5	1341.411	+0.596 * (not dEP4 -1307G>A) +2.61 * ((dEP2 -1722G>A or (not rEP4 1455A>G)) or ((dPGDH Gln52Gln and (not dPGDH 1113G>A)) and (not rPGDH 13796C>T))) -0.356 * dPGDH 3580G>A -1.15 * ((not dPGDH 9691C>A) and dPGDH 17450A>G) +1.6 * ((not dPGDH 782A>G) or (not rEP4 13877A>C))
12	2	1334.0	-20 * (((dPGDH 17450A>G and (not rPGDH 23196A>G)) or rEP4 11851G>A) and ((not dPGDH 9691C>A) and ((not dEP4 8907G>A) or dPGDH 31659A>G))) -2.64 * ((dEP4 13981A>G or ((not dEP4 6374G>A) or dPGDH 13796C>T)) or (((not dPGDH 1113G>A) or (not dPGDH 23196A>G)) and (not rEP2 -1722G>A)))
13	4	1341.2	-3.81 * ((not dPGDH 782A>G) or (rEP4 13877A>C and (dPGDH -1635G>A or (not dEP2 9814C>A)))) +2.2 * (((not dPGDH 17450A>G) or dEP4 8907G>A) or dPGDH 3580G>A) -0.907 * (dEP4 -1307G>A or (rEP4 8907G>A or (not dEP2 -1722G>A))) -3.94 * ((dEP4 8907G>A or (not rPGDH 23196A>G)) and dPGDH 782A>G)
14	4	1333.8	-0.739 * (dPGDH 3580G>A and ((not dPGDH -1635G>A) or dEP2 -616C>G)) +1.71 * (((not dEP4 -1307G>A) and dEP2 -1722G>A) and ((not dPGDH -1635G>A) or rEP2 9814C>A)) -0.963 * ((not rPGDH 782A>G) and (not rEP4 11851G>A)) -2.28 * (((dPGDH 17450A>G and (not dPGDH 9691C>A)) or (rEP4 13877A>C and (not rPGDH 23196A>G))) and dPGDH 782A>G)
15	2	1337.4	-0.767 * (((dPGDH 31659A>G or dEP2 -967G>A) or ((not rPGDH 1543G>A) and (not dEP2 1690G>A))) and ((dEP4 -1307G>A and dPGDH 1543G>A) or ((not dPGDH 16362G>A) and dEP2 4950G>A))) +3.46 * ((dPGDH 3580G>A and (dEP4 -1529G>A or (not dPGDH 18349G>A))) or (((not dPGDH 17450A>G) or dEP4 8907G>A) or (rPGDH 23196A>G and (not rPGDH 343C>A))))

[a] Adjusted for age and sex

[b] d=dominant, r=recessive. Any dominant genotype preceded by "not" indicates that the wildtype genotype is predictive of adenoma risk. Any recessive genotype preceded by "not" indicates that the wildtype and heterozygous genotypes are predictive of risk

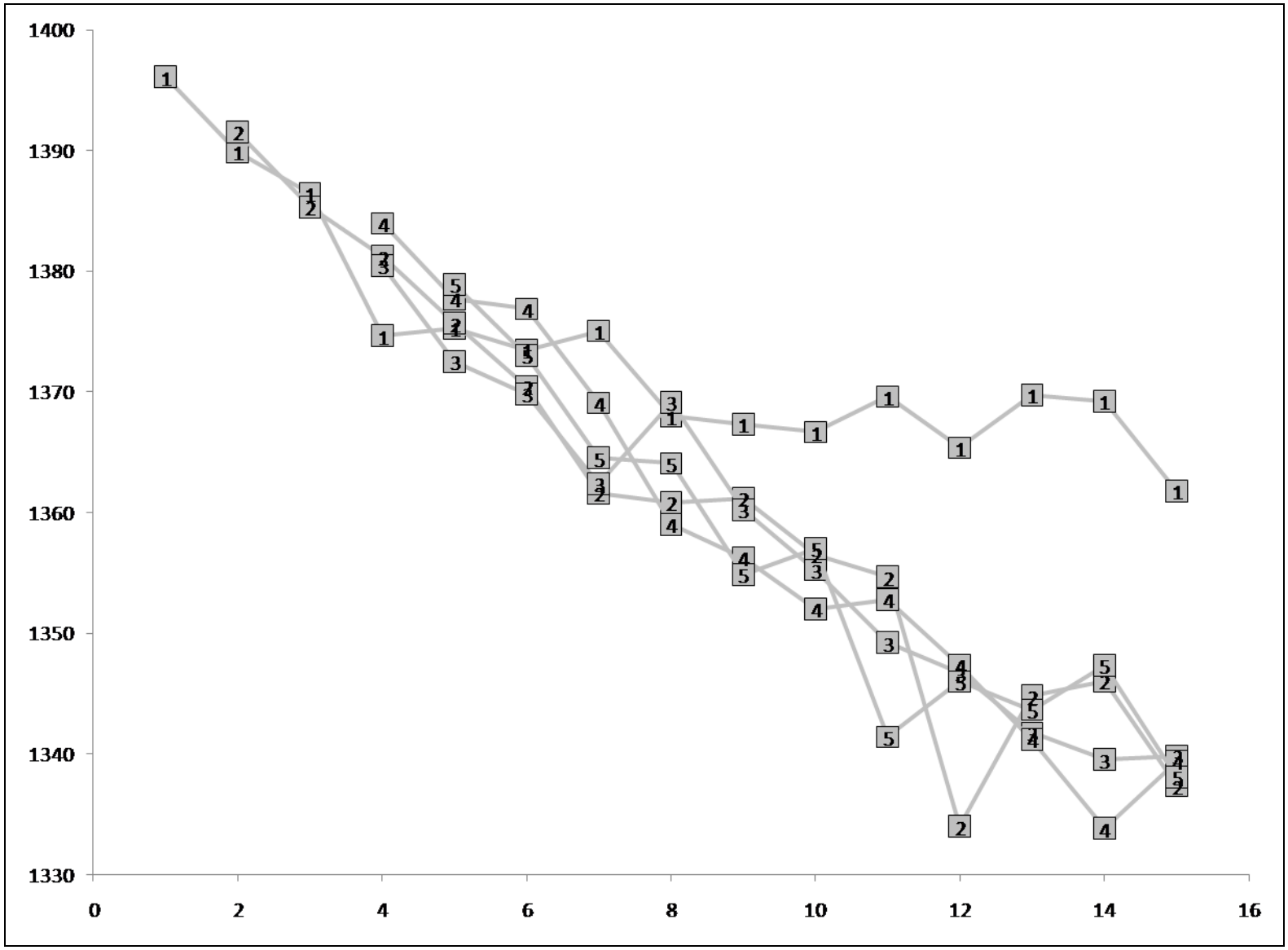

Figure S1. Plot of model size (i.e. number of leaves or variables) against the scores (i.e. fit) of each model.
The numbers in the boxes are the numbers of trees. A smaller score indicates a better fit.

Table S7. The twenty most commonly occurring SNP pairs in Monte Carlo logic regression[a]

SNP1	SNP2	Frequency[b] (%)
rPGDH 1543G>A	dEP4 -1307G>A	0.4%
dPGDH -1868G>A	dEP4 -1307G>A	0.3%
dEP4 13981A>G	rEP2 -1722G>A	0.3%
rEP4 -1408G>A	dEP4 -1307G>A	0.3%
dEP4 -1307G>A	dEP2 -616C>G	0.3%
dPGDH -1635G>A	dEP2 4950G>A	0.3%
dEP4 13981A>G	rEP2 9814C>A	0.3%
dEP4 -1307G>A	rEP2 -1722G>A	0.3%
dPGDH -1868G>A	rEP2 -1722G>A	0.3%
rPGDH 1543G>A	dEP2 -616C>G	0.3%
dPGDH 17450A>G	dPGDH 782A>G	0.3%
dPGDH 17450A>G	dEP4 2472A>G	0.3%
rEP4 13877A>C	dEP4 -1307G>A	0.2%
rPGDH -1635G>A	dEP4 -1307G>A	0.2%
rEP4 13981A>G	dEP4 -1307G>A	0.2%
dPGDH 1543G>A	dEP4 -1307G>A	0.2%
rPGDH 13796C>T	dPGDH 782A>G	0.2%
dPGES 3006G>A	dEP4 -1307G>A	0.2%
dPGDH 13316A>C	dEP4 -1307G>A	0.2%
dEP4 -1307G>A	dEP2 -1722G>A	0.2%

[a] Adjusted for age and sex; d=dominant, r=recessive. Any dominant genotype preceded by "not" indicates that the wildtype genotype is predictive of adenoma risk. Any recessive genotype preceded by "not" indicates that the wildtype and heterozygous genotypes are predictive of risk

[b] out of 100,000 iterations

Table S8. The twenty most commonly occurring single SNPs in Monte Carlo estimation[a]

SNP	Frequency[b] (%)
dEP4 -1307G>A	13.3%
dEP2 4950G>A	7.3%
dPGDH 17450A>G	5.1%
dEP4 13981A>G	4.3%
dPGDH 782A>G	3.5%
dPGDH 3580G>A	3.0%
rPGDH 23196A>G	2.9%
dPGDH 1543G>A	2.7%
rEP4 2472A>G	2.6%
dPGDH -1635G>A	2.4%
rEP4 13877A>C	2.4%
rPGDH 1543G>A	2.1%
rPGDH 9691C>A	2.1%
dPGDH 343C>A	2.1%
dPGDH 13316A>C	2.1%
dPGDH 9442A>G	2.0%
dEP2 -1722G>A	1.9%
rEP2 -1722G>A	1.9%
rPGDH 782A>G	1.9%
dEP4 -1408G>A	1.9%

[a] Adjusted for age and sex; d=dominant, r=recessive. Any dominant genotype preceded by "not" indicates that the wildtype genotype is predictive of adenoma risk. Any recessive genotype preceded by "not" indicates that the wildtype and heterozygous genotypes are predictive of risk

[b] out of 100,000 iterations

Table S9. Potential functionally relevant SNPs in LD with adenoma-associated SNPs

Gene	SNP of interest	Linked SNP	r^2	Conservation score[a]	Location	Potential functional consequences[b]
PGES	rs7873087 (-664A>T)	rs7859349	1	0	intergenic	
	rs7873087	rs7872802	1	0	near 5' utr	could be in regulatory region, in structural variant
	rs7873087	rs45487392	0.3	0.095	intron	1 bp indel
EP2[c]	rs1254585 (9814C>A)	rs1353411	0.643	0	near 5' utr	could be in a regulatory region
	rs1254585	rs1254598	0.625	0	5' utr	could be in a regulatory region
	rs1254585	rs2075797	0.571	0	near 5' utr	could be in a regulatory region
	rs1254585	rs1658086	0.537	0.159	near 5' utr	could be in a regulatory region
	rs1254585	rs45460603	0.436	0	3' utr	4 bp indel
	rs1254585	rs17197	0.436	0	3' utr	
	rs1254585	rs708502	0.436	0.053	3' utr	
	rs1254585	rs1042618	0.386	0	3' utr	
	rs1254585	rs1254599	0.33	0	near 5' utr	could be in a regulatory region
	rs1254585	rs1254601	0.33	0.058	near 5' utr	
EP4	rs10039983 (-1307G>A)	rs45437592	1	0	near 5' utr	could be in regulatory region
	rs10039983	rs45613037	0.714	0	near 5' utr	could be in regulatory region
	rs10039983	rs13186505	0.388	0	near 5' utr	could be in regulatory region
	rs10039983	rs4133101	0.358	0	near 5' utr	could be in regulatory region
PGDH	rs45567139 (343C>A)	rs10520285	0.318	0.002	near 3' utr	
	rs45567139	rs17060524	0.318	0.004	near 3' utr	
	rs45567139	rs45522334	0.318	0.923	3' utr	
	rs12640361 (19979A>T)	rs1365613	0.342	0.96	intron	close to transcription factor binding site
	rs9312555 (31659T>C)	rs17060521	1	0.011	near 3' utr	
	rs9312555	rs45486497	0.779	0.007	intron	3 bp indel
	rs9312555	rs45552837	0.779	0	near 3' utr	1 bp indel

[a]Conservation score of the linked SNP from the Genome Variation Server.[1]

[b]Information about regulatory regions and transcription factor binding sites is from the UCSC Genome Browser.[2]

[c]*EP2* 4950G>A had no SNPs with r2>0.30.

[1] http://gvs.gs.washington.edu/GVS/
[2] http://genome.ucsc.edu/