Supplementary Materials

Association of *FADS1* (rs174537), *BDNF* (rs6265), and *NPY* (rs16147) Polymorphisms with Colorectal Cancer Risk in a Turkish Population

Table S1. Firth's bias-reduced logistic regression analysis of the association between the studied polymorphisms and colorectal cancer, adjusted for age and sex.

Polymorphism / model	Term	*n*	OR (95% CI)	*p* value
***BDNF* rs6265**				
Codominant	GA vs. GG	155	0.871 (0.186–3.780)	0.852
	AA vs. GG		1.542 (0.185–14.141)	0.687
	Age (per year)		0.985 (0.957–1.012)	0.277
	Female vs. male		1.152 (0.609–2.187)	0.664
Additive	Per A allele	155	1.220 (0.418–3.667)	0.713
	Age (per year)		0.983 (0.956–1.010)	0.228
	Female vs. male		1.149 (0.607–2.184)	0.669
***FADS1* rs174537**				
Codominant	GT vs. TT	140	0.615 (0.134–2.489)	0.496
	GG vs. TT		0.065 (0.005–0.476)	0.006
	Age (per year)		0.974 (0.944–1.004)	0.088
	Female vs. male		1.334 (0.663–2.712)	0.420
Additive	Per G allele	140	0.239 (0.074–0.622)	0.002
	Age (per year)		0.974 (0.944–1.004)	0.087
	Female vs. male		1.249 (0.625–2.513)	0.529
***NPY* rs16147**				
Codominant	AG vs. AA	157	2.269 (0.607–10.003)	0.225
	GG vs. AA		0.702 (0.087–5.059)	0.724
	Age (per year)		0.979 (0.952–1.007)	0.141
	Female vs. male		1.126 (0.596–2.139)	0.715
Additive	Per G allele	157	0.892 (0.343–2.281)	0.809
	Age (per year)		0.982 (0.955–1.008)	0.180
	Female vs. male		1.051 (0.561–1.972)	0.876

Firth's penalized-likelihood logistic regression; 95% CIs are profile penalized-likelihood intervals and *p* values are from penalized likelihood-ratio tests. Each polymorphism was analyzed in a separate model including genotype, age (continuous), and sex. In the codominant model, homozygotes for the first listed allele are the reference; in the additive model, genotype was entered as the number of copies of the second listed allele. OR, odds ratio; CI, confidence interval.

Table S2. Sex-stratified genotype and allele distributions of the studied polymorphisms in patients with colorectal cancer and controls.

Sex	Controls *n*	Patients *n*	Controls, genotype n (%)	Patients, genotype n (%)	Genotype *p*	Second allele, % (controls / patients)	Allele OR (95% CI)	Allele *p*
***BDNF* rs6265 (genotype × sex interaction, $p = 0.870$)**								
Men	40	39	GG 1 (2.5); GA 37 (92.5); AA 2 (5.0)	GG 1 (2.6); GA 35 (89.7); AA 3 (7.7)	0.835	51.3 / 52.6	1.054 (0.539–2.063)	0.875
Women	37	39	GG 2 (5.4); GA 35 (94.6); AA 0 (0.0)	GG 3 (7.7); GA 35 (89.7); AA 1 (2.6)	1.000	47.3 / 47.4	1.006 (0.506–1.997)	1.000
***FADS1* rs174537 (genotype × sex interaction, $p = 0.623$)**								
Men	40	31	TT 0 (0.0); GT 35 (87.5); GG 5 (12.5)	TT 2 (6.5); GT 28 (90.3); GG 1 (3.2)	0.138	56.3 / 48.4	0.731 (0.355–1.496)	0.399
Women	36	33	TT 3 (8.3); GT 25 (69.4); GG 8 (22.2)	TT 3 (9.1); GT 30 (90.9); GG 0 (0.0)	0.008	56.9 / 45.5	0.632 (0.304–1.302)	0.233
***NPY* rs16147 (genotype × sex interaction, $p = 0.519$)**								
Men	38	39	AA 1 (2.6); AG 34 (89.5); GG 3 (7.9)	AA 1 (2.6); AG 37 (94.9); GG 1 (2.6)	0.675	52.6 / 50.0	0.901 (0.456–1.777)	0.750
Women	39	41	AA 5 (12.8); AG 31 (79.5); GG 3 (7.7)	AA 2 (4.9); AG 38 (92.7); GG 1 (2.4)	0.244	47.4 / 48.8	1.055 (0.542–2.057)	0.876

Genotype *p* values were obtained using Fisher's exact test (2 × 3) and allele *p* values using Fisher's exact test (2 × 2); allele ORs (conditional maximum-likelihood estimates with exact 95% CIs) refer to the second listed allele (*BDNF* A, *FADS1* G, *NPY* G) in patients relative to controls. Interaction *p* values are from likelihood-ratio tests comparing logistic regression models (additive genotype, age, and sex) with and without a genotype × sex interaction term. OR, odds ratio; CI, confidence interval.