

Supplementary materials

Table S1. SNPs ID, base change, position, and region

SNP ID ¹	Base change ²	Position on XDH ¹	Region ¹
rs207454	G<T	31,344,766	Intron
rs1884725	A<G	31,348,920	Exon, enhancer
rs17011368	C<T	31,368,051	Exon
rs494852	T<C	31,401,970	Intron, enhancer
rs206833	A<G	31,485,750	Intergenic variant/enhancer region

¹ Obtained from NCBI database (<http://www.ncbi.nlm.nih.gov/SNP>). ² The “<” sign means that left nucleotide is replaced by the right.

Table S2. Evaluation of the association between the five SNPs and BC under different genetic models

SNP	Model ¹	Genotype status	Control (n = 109) ¹	BC (n = 109) ¹	OR (95%CI)	p-value ²
rs207454	Codominant	T/T	84 (77.1%)	82 (75.2%)	1.00	0.45
		T/G	24 (22%)	27 (24.8%)	0.87 (0.46–1.63)	
		G/G	1 (0.9%)	0 (0%)	NA (0.00-NA)	
	Dominant	T/T T/G-G/G	84 (77.1%) 25 (22.9%)	82 (75.2%) 27 (24.8%)	1.00 0.90 (0.48–1.69)	0.75
	Recessive	T/T-T/G G/G	108 (99.1%) 1 (0.9%)	109 (100%) 0 (0%)	1.00 NA (0.00-NA)	0.24
rs1884725	Over-dominant	T/T-G/G T/G	85 (78%) 24 (22%)	82 (75.2%) 27 (24.8%)	1.00 0.86 (0.46–1.61)	0.63
	Additive	–	–	–	0.95 (0.52–1.74)	0.88
	Codominant	G/G	68 (62.4%)	74 (67.9%)	1.00	0.38
		G/A	34 (31.2%)	32 (29.4%)	1.16 (0.64–2.07)	
		A/A	7 (6.4%)	3 (2.8%)	2.54 (0.63–0.22)	
	Dominant	G/G G/A-A/A	68 (62.4%) 41 (37.6%)	74 (67.9%) 35 (32.1%)	1.00 1.27 (0.73–2.23)	0.39
	Recessive	G/G-G/A A/A	102 (93.6%) 7 (6.4%)	106 (97.2%) 3 (2.8%)	1.00 2.42 (0.61–9.63)	0.19

	Over-dominant	G/G-A/A G/A	75 (68.8%) 34 (31.2%)	77 (70.6%) 32 (29.4%)	1.00 1.09 (0.61–1.94)	0.77
	Additive	–	–	–	1.32 (0.83-2.11)	0.24
rs17011368	–	–	–	–	–	–
rs494852	Codominant	C/C	54 (49.5%)	52 (47.7%)	1.00	0.96
		C/T	42 (38.5%)	44 (40.4%)	0.92 (0.52–1.62)	
		T/T	13 (11.9%)	13 (11.9%)	0.96 (0.41–2.27)	
	Dominant	C/C	54 (49.5%)	52 (47.7%)	1.00	0.79
		C/T-C/C	55 (50.5%)	57 (52.3%)	0.93 (0.55–1.58)	
	Recessive	C/C-C/T	96 (88.1%)	96 (88.1%)	1.00	1.00
	T/T	13 (11.9%)	13 (11.9%)	1.00 (0.44–2.27)		
	Over-dominant	C/C-T/T	67 (61.5%)	65 (59.6%)	1.00	0.78
	C/T	42 (38.5%)	44 (40.4%)	0.93 (0.54–1.59)		
	Additive	–	–	–	0.96 (0.65–1.42)	0.84
rs206833	Codominant	G/G	72 (66.1%)	62 (56.9%)	1.00	0.37
		G/A	31 (28.4%)	40 (36.7%)	0.67 (0.37–1.19)	
		A/A	6 (5.5%)	7	0.74 (0.24–2.31)	
	Dominant	G/G	72 (66.1%)	62 (56.9%)	1.00	0.16
		G/A-A/A	37 (33.9%)	47 (43.1%)	0.68 (0.39–1.17)	
	Recessive	G/G-G/A	103 (94.5%)	102 (93.6%)	1.00	0.77
	A/A	6 (5.5%)	7 (6.4%)	0.85 (0.28–2.61)		
	Over-dominant	G/G-A/A	78 (71.6%)	69 (63.3%)	1.00	0.19
	G/A	31 (28.4%)	40 (36.7%)	0.69 (0.39–1.21)		
	Additive	–	–	–	0.76 (0.49–1.18)	0.22

Note: *n* (number of participants); OR (odd ratio); CI (confidence interval); NA (no association). ¹ Analysis was performed via SNPStats browser (<https://www.snpstats.net/analyzer.php>); ² *p*-values were calculated by Pearson’s chi-squared test: * indicates significant difference.