Web Appendix

Search strategies

MEDLINE

(tp53[All Fields] OR p53[All Fields] OR p-53[All Fields] OR tp-53[All Fields]) AND ("neoplasms"[MeSH Terms] OR "neoplasms"[All Fields] OR "cancer"[All Fields] OR carcinoma* OR cancer OR cancer? OR neoplasm* OR adenocarcinoma*)
AND (("polymorphism, genetic"[MeSH Terms] OR ("polymorphism"[All Fields] AND "genetic"[All Fields]) OR "genetic polymorphism"[All Fields] OR "polymorphism"[All Fields]) OR arg72pro[All Fields] OR arg72[All Fields] OR pro72[All Fields] OR pro72arg[All Fields] OR rs1042522[All Fields] OR variant* OR variati* OR "haplotypes"[MeSH Terms] OR "haplotypes"[All Fields] OR "haplotype"[All Fields] OR polymorph*)

Human Genome Epidemiology Literature Finder

Database: www.hugenavigator.net
Search criteria: All publications>>TP53, TP53I3, TP53BP2, TP53RK, TP53INP1, TP53AIP1[Gene]>>Mammary Neoplasms, Invasive Ductal Breast Carcinoma, Carcinoma, Endometrioid, Noninfiltrating Intraductal Carcinoma, Carcinoma, Non-Small-Cell Lung, Colonic Neoplasms, Colorectal Neoplasms, Hereditary Nonpolyposis Colorectal Neoplasms, Endometrial Neoplasms, Neoplasm of lung (disorder), Neoplasms, Hormone-Dependent, ovarian neoplasm, Rectal Neoplasms, Small cell carcinoma of lung[Mesh]

Note: In addition to *TP53*, we searched for genes belonging to the p53 pathway to increase the sensitivity of the search (in studies of these genes *TP53* polymorphisms are also often investigated).

Other databases (*International Agency for Research on Cancer TP53 database, the p53 Website, Genetic Association Database*)

These databases provide annotated bibliography lists; as such, no specific search strategy was constructed.

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Model specification for Bayesian and maximum likelihood analyses

We wanted to examine the effect of using DNA isolated from tumor tissue vs. normal tissue on the association of the Arg72Pro polymorphism with five common epithelial cancers (lung, breast, colorectal, ovarian, endometrial). Because of loss-of-heterozygosity (LOH), associations in tumor tissue are spurious (biased). We assumed that LOH has the same effect (biases the association by a similar amount) across the five cancer topics; however, we allowed the genetic effect to be different for each cancer subtype.

We specified a two level model: the first level was the patient; the second level was the study. At the second level we have parameters that are common across all five cancer topics. Subscript $i = [1,2,\ldots,N]$ denotes the study. N is the number of published studies.

Level one (within studies)

For the cases and controls in the i-th study we assume that the number of Pro-encoding alleles, r, follows a binomial distribution with probability p (i.e., the true frequency of the minor allele in cases, p^{case}, and controls, p^{con}) out of a sample of size n (the total number of alleles in each group):

$$r_i^{case} \sim Bin(p_i^{case}, n_i^{case}) \text{ and } r_i^{con} \sim Bin(p_i^{con}, n_i^{con})$$

We assume that the log-transformed odds ratios, d_i, of each study

$$d_i = \log \frac{p_i^{case}}{1 - p_i^{case}} - \log \frac{p_i^{con}}{1 - p_i^{con}}$$

are random effects that vary by function of a study specific genetic effect, d_i^*, and its modification by explanatory variables x_i (an indicator of the use of tumor or normal tissue for genotyping), w_i (an indicator of whether the study investigated lung cancer), z_i (an indicator of whether the study investigated colorectal cancer), v_i (an indicator of whether the study investigated ovarian cancer) and g_i (an indicator of whether the study investigated endometrial cancer); breast cancer is not encoded by an indicator variable because it serves as the baseline cancer type in this analysis

$$d_i = d_i^* + b_{tissue} \cdot x_i + b_{lung,i} \cdot w_i + b_{colorectal,i} \cdot z_i + b_{ovarian,i} \cdot v_i + b_{endometrial,i} \cdot g_i$$

Here b_{tissue}, b_{lung}, $b_{colorectal}$, $b_{ovarian}$ and $b_{endometrial}$ are the regression coefficients for the indicator variables for use of tumor tissue, lung cancer, colorectal cancer, ovarian cancer and endometrial cancer, respectively. d^* is technically the log odds ratio for breast cancer studies.

Level two (study level)

We assume that $d^* \sim N(\bar{\delta}, \tau^2)$, $b_{lung,i} \sim N(\overline{\beta_{lung}}, \tau^2)$, $b_{colorectal,i} \sim N(\overline{\beta_{colorectal}}, \tau^2)$, $b_{ovarian,i} \sim N(\overline{\beta_{ovarian}}, \tau^2)$, $b_{endometrial,i} \sim N(\overline{\beta_{endometrial}}, \tau^2)$and $\log \frac{p_i^{con}}{1-p_i^{con}} \sim N(\bar{\mu}, \upsilon^2)$, where $\bar{\delta}$ is the log-transformed "overall" summary effect in breast cancer and $\bar{\delta}+\overline{\beta_{lung}}$, $\bar{\delta}+\overline{\beta_{colorectal}}$, $\bar{\delta}+\overline{\beta_{ovarian}}$, $\bar{\delta}+\overline{\beta_{endometrial}}$ are the summary log-transformed effect sizes for lung, colorectal, ovarian and endometrial cancer, respectively. $\bar{\mu}$ is the summary logit-transformed frequency of the minor allele in controls (a nuisance parameter).

In our main analysis the bias effect was treated as a fixed effect across studies with an informative prior distribution. This distribution was based on the results of an individual-patient data meta-analysis of the association between rs1042522 and cervical cancer (Klug, Lancet Oncology, 2009). Specifically, under a dominant genetic model the study reported that the Pro-encoding allele had an odds ratio (OR) of 0.935 (standard error for the log-OR, SE_{wbc} = 0.095) among studies using white blood cells for obtaining genotyping material for cases. The corresponding OR for studies using tumor tissue as the source of genotyping material was 0.719 (SE_{tissue} = 0.103). Assuming that log-ORs are normally distributed, and because studies used to obtain the aforementioned estimates were independent, the relative log-odds ratio is -0.263 with variance = $SE_{tissue}^2 + SE_{wbc}^2 = 0.020$. Thus, we used $b_{tissue} \sim N(-0.263, 0.020)$ as an informative prior distribution for the bias parameter.

In sensitivity analyses we also used a non-informative prior distribution for the bias effect: $b_{tissue} \sim N(0, 10^6)$. Analyses where the bias effect was treated as a random effect across studies produced similar results to the main analyses (not shown).

For all other model parameters (and all analyses performed) we used non-informative priors: $\bar{\delta} \sim N(0, 10^6)$, $\overline{\beta_{lung}} \sim N(0, 10^6)$, $\overline{\beta_{colorectal}} \sim N(0, 10^6)$, $\overline{\beta_{ovarian}} \sim N(0, 10^6)$, $\overline{\beta_{endometrial}} \sim N(0, 10^6)$, $\bar{\mu} \sim N(0, 10^6)$, $\tau \sim U(0, 10)$ and $\upsilon \sim U(0, 10)$.

Model estimation

For Bayesian analyses, the model was fit using Markov Chain Monte Carlo (MCMC). For each model we ran 3 MCMC chains for a total of 100,000 iterations, using a burn in of 10,000. Convergence of the MCMC chains was checked by Brooks-Gelman-Rubin criteria and by inspection of trace plots (Brooks SP and Gelman A, Journal of Computational and Graphical Statistics, 1997). We evaluated the fit of the Bayesian models based on the summary Deviance Information Criterion (DIC) as well as inspection of shrinkage plots (graphs of posterior estimates for model parameters plotted along with the prior study estimates). DIC is a deviance measure of goodness of fit equal to the posterior mean of minus twice the log likelihood, penalized by an estimate of the effective number of parameters in the model. DIC is a Bayesian measure analogous to the Akaike Information Criterion used in non-Bayesian analysis, but which can also be applied to hierarchical models. It penalizes the likelihood for addition of parameters so

that models of different complexity can be appropriately compared (Spiegelhalter DJ, et al. Journal of the Royal Statistical Society, Series B, 2002).

For maximum likelihood analyses we used mixed effects logistic regression with normal likelihood for the random effects. We used adaptive quadrature to maximize the marginal likelihood over studies (Rabe-Hesketh S, et al. The Stata Journal, 2002). These analyses were performed using the `xtmelogit` command in Stata version 11.1/SE (StataCorp, College Station, TX).

Web Tables

Web Table 1: Meta-analysis results for breast, lung, colorectal, ovarian, and endometrial cancer using a 2-level mixed effects logistic regression (Bayesian implementation) model (informative prior).

Cancer	Studies using appropriate DNA sources OR (95% CrI)	Studies using tumor tissue OR (95% CrI)
Breast cancer	0.99 (0.94-1.03)	0.77 (0.69-0.87)
Lung cancer	1.09 (1.01-1.16)	0.85 (0.74-0.97)
Colorectal cancer	1.09 (0.99-1.20)	0.85 (0.75-0.98)
Ovarian cancer	1.05 (0.91-1.19)	0.82 (0.69-0.97)
Endometrial cancer	1.08 (0.88-1.32)	0.84 (0.68-1.05)
Bias effect (across cancers)	0.78 (0.70-0.88)	
*Probability bias <0	>0.999	

CrI = credibility interval; OR = odds ratio.

*This effectively expresses the probability that use of tumor tissue as the source of genotyping material for cases leads to underestimation.

Web Table 2: Meta-analysis results for breast, lung, colorectal, ovarian, and endometrial cancer using a 2-level mixed effects logistic regression (Bayesian implementation) model (non-informative prior).

Cancer	Studies using appropriate DNA sources OR (95% CrI)	Studies using tumor tissue OR (95% CrI)
Breast cancer	0.99 (0.94-1.03)	0.78 (0.68-0.88)
Lung cancer	1.09 (1.01-1.16)	0.85 (0.74-0.98)
Colorectal cancer	1.09 (0.99-1.20)	0.86 (0.75-0.99)
Ovarian cancer	1.05 (0.92-1.19)	0.83 (0.69-0.99)
Endometrial cancer	1.08 (0.89-1.32)	0.85 (0.68-1.06)
Bias effect (across cancers)	0.79 (0.69-0.89)	
*Probability bias <0	>0.999	

CrI = credibility interval; OR = odds ratio.

*This effectively expresses the probability that use of tumor tissue as the source of genotyping material for cases leads to underestimation of the genetic effect of the Pro-allele.

Web Table 3: Meta-analysis results for breast, lung, colorectal, ovarian, and endometrial cancer using a 2-level mixed effects logistic regression (maximum likelihood) model.

Cancer	Studies using appropriate DNA sources OR (95% CI)	p-value	Studies using tumor tissue OR (95% CI)	p-value
Breast cancer	0.98 (0.94-1.04)	0.552	0.74 (0.66-0.85)	<0.001
Lung cancer	1.08 (1.02-1.15)	0.014	0.82 (0.71-0.94)	0.005
Colorectal cancer	1.09 (1.00-1.19)	0.042	0.83 (0.72-0.95)	0.006
Ovarian cancer	1.05 (0.94-1.18)	0.397	0.80 (0.67-0.94)	0.008
Endometrial cancer	1.09 (0.91-1.32)	0.350	0.83 (0.67-1.02)	0.082
Bias effect (across cancers)	0.75 (0.67-0.86), p<0.001			

CI = confidence interval; OR = odds ratio

Web Table 4: Meta-analysis results for breast cancer, excluding studies using tumor tissue as the source of genotyping material for cases

Characteristic		Studies (cases, controls)	Heterogeneity (pQ; I^2)	OR (95% CI); p-value
All studies		59 (29801, 35436)	<0.001; 53%	0.99 (0.94-1.03); 0.532
Ethnicity	Whites	40 (25469, 29930)	<0.001; 53%	1.01 (0.96-1.06); 0.609
	East Asians	7 (2859, 2880)	0.055; 51%	1.04 (0.92-1.16); 0.525
Control selection	Disease controls	4 (933, 1050)	0.131; 47%	1.13 (0.93-1.33); 0.239
	Healthy controls	55 (28868, 34386)	<0.001; 53%	0.98 (0.93-1.02); 0.334
Matching	No/NR	33 (17420, 17988)	0.012; 39%	0.97 (0.91-1.02); 0.215
	Yes	26 (12381, 17448)	<0.001; 62%	1.01 (0.94-1.08); 0.814
Genotyping QC	No/NR	36 (7577, 10814)	<0.001; 52%	0.95 (0.87-1.02); 0.162
	Yes	23 (22224, 24622)	0.001; 53%	1.02 (0.96-1.07); 0.560
Blinding	No	54 (26232, 31253)	<0.001; 55%	0.98 (0.93-1.03); 0.376
	Yes	5 (3569, 4183)	0.249; 26%	1.04 (0.95-1.12); 0.415
Genotyping method	Non-RFLP	30 (20889, 22928)	0.001; 52%	0.98 (0.93-1.03); 0.484
	RFLP	29 (8912, 12508)	<0.001; 56%	1.00 (0.91-1.08); 0.913
HWE	Compliant	47 (28149, 32483)	<0.001; 48%	1.01 (0.97-1.05); 0.698
	In violation	12 (1652, 2953)	0.003; 61%	0.84 (0.68-1.00); 0.033

CI = confidence interval; HWE = Hardy-Weinberg equilibrium; OR = odds ratio; p_Q = p-value from Cochran's Q statistic; QC = quality control; RFLP = restriction fragment length polymorphism.

Web Table 5: Meta-analysis results for lung cancer, excluding studies using tumor tissue as the source of genotyping material for cases

Characteristic		Studies (cases, controls)	Heterogeneity (pQ; I^2)	OR (95% CI); p-value
All studies		39 (16522, 16235)	<0.001; 54%	1.09 (1.03-1.15); 0.003
Ethnicity	Whites	15 (7121, 8596)	<0.001; 68%	1.04 (0.93-1.14); 0.521
	East Asians	12 (8028, 5877)	0.067; 41%	1.13 (1.05-1.21); 0.002
Control selection	Disease controls	17 (6041, 6216)	0.234; 19%	1.14 (1.07-1.21); <0.001
	Healthy controls	22 (10481, 10019)	<0.001; 67%	1.04 (0.95-1.13); 0.356
Matching	No/NR	19 (11163, 9215)	0.005; 51%	1.10 (1.03-1.18); 0.010
	Yes	20 (5359, 7020)	0.001; 57%	1.08 (0.99-1.18); 0.105
Genotyping QC	No/NR	22 (7488, 5545)	<0.001; 59%	1.07 (0.97-1.17); 0.178
	Yes	17 (9034, 10690)	0.018; 47%	1.10 (1.03-1.17); 0.006
Blinding	No	30 (12125, 11457)	<0.001; 55%	1.09 (1.02-1.16); 0.020
	Yes	9 (4397, 4778)	0.037; 51%	1.09 (0.99-1.19); 0.098
Genotyping method	Non-RFLP	16 (10801, 9502)	<0.001; 65%	1.09 (1.00-1.18); 0.064
	RFLP	23 (5721, 6733)	0.011; 45%	1.09 (1.01-1.18); 0.032
HWE	Compliant	34 (16034, 15519)	0.003; 45%	1.10 (1.04-1.15); 0.001
	In violation	5 (488, 716)	<0.001; 82%	0.95 (0.52-1.38); 0.810

CI = confidence interval; HWE = Hardy-Weinberg equilibrium; OR = odds ratio; p_Q = p-value from Cochran's Q statistic; QC = quality control; RFLP = restriction fragment length polymorphism.

Web Table 6: Meta-analysis results for colorectal cancer, excluding studies using tumor tissue as the source of genotyping material for cases

Characteristic		Studies (cases, controls)	Heterogeneity (pQ; I^2)	OR (95% CI); p-value
All studies		20 (6951, 9275)	<0.001; 75%	1.09 (0.98-1.20); 0.136
Ethnicity	Whites	12 (5273, 6446)	0.358; 9%	0.97 (0.90-1.04); 0.351
	East Asians	7 (1592, 2669)	0.005; 67%	1.18 (1.00-1.35); 0.074
Control selection	Disease controls	7 (1537, 1935)	0.218; 28%	1.05 (0.91-1.18); 0.501
	Healthy controls	13 (5414, 7340)	<0.001; 83%	1.11 (0.96-1.26); 0.183
Matching	No/NR	13 (3962, 5272)	0.156; 29%	0.98 (0.88-1.08); 0.721
	Yes	7 (2989, 4003)	<0.001; 86%	1.25 (1.05-1.46); 0.033
Genotyping QC	No/NR	10 (1620, 2527)	0.002; 65%	1.07 (0.89-1.24); 0.456
	Yes	10 (5331, 6748)	<0.001; 81%	1.11 (0.95-1.26); 0.196
Blinding	No	17 (5886, 7515)	<0.001; 77%	1.10 (0.96-1.23); 0.171
	Yes	3 (1065, 1760)	0.033; 71%	1.06 (0.82-1.30); 0.633
Genotyping method	Non-RFLP	10 (4559, 5788)	0.266; 19%	0.95 (0.87-1.04); 0.252
	RFLP	10 (2392, 3487)	<0.001; 78%	1.25 (1.07-1.44); 0.016
HWE	Compliant	19 (6865, 9115)	<0.001; 62%	1.05 (0.95-1.14); 0.344
	In violation	1 (86, 160)	NA	3.07 (2.68-3.45); <0.001

CI = confidence interval; HWE = Hardy-Weinberg equilibrium; NA = not applicable; OR = odds ratio; p_Q = p-value from Cochran's Q statistic; QC = quality control; RFLP = restriction fragment length polymorphism.

Web Table 7: Meta-analysis results for ovarian cancer, excluding studies using tumor tissue as the source of genotyping material for cases

Characteristic		Studies (cases, controls)	Heterogeneity (pQ; I^2)	OR (95% CI); p-value
All studies		14 (1892, 5146)	0.534; 0%	1.10 (1.01-1.19); 0.031
Ethnicity	Whites	12 (1779, 4711)	0.567; 0%	1.11 (1.02-1.21); 0.019
	East Asians	1 (68, 95)	NA	1.15 (0.69-1.60); 0.558
Control selection	Disease controls	1 (45, 340)	NA	0.78 (0.32-1.24); 0.281
	Healthy controls	13 (1847, 4806)	0.650; 0%	1.12 (1.03-1.21); 0.016
Matching	No/NR	9 (1091, 2934)	0.674; 0%	1.12 (1.01-1.24); 0.050
	Yes	5 (801, 2212)	0.208; 32%	1.07 (0.90-1.23); 0.437
Genotyping QC	No/NR	6 (484, 910)	0.385; 5%	1.19 (0.99-1.39); 0.086
	Yes	8 (1408, 4236)	0.560; 0%	1.08 (0.98-1.18); 0.131
Blinding	No	13 (1700, 4691)	0.476; 0%	1.09 (1.00-1.18); 0.063
	Yes	1 (192, 455)	NA	1.18 (0.91-1.45); 0.224
Genotyping method	Non-RFLP	12 (1755, 4829)	0.463; 0%	1.09 (1.00-1.18); 0.071
	RFLP	2 (137, 317)	0.575; 0%	1.26 (0.96-1.57); 0.135
HWE	Compliant	11 (1512, 4071)	0.574; 0%	1.10 (1.00-1.20); 0.065
	In violation	3 (380, 1075)	0.190; 40%	1.12 (0.87-1.38); 0.372

CI = confidence interval; HWE = Hardy-Weinberg equilibrium; NA = not applicable; OR = odds ratio; p_Q = p-value from Cochran's Q statistic; QC = quality control; RFLP = restriction fragment length polymorphism.

Web Table 8: Meta-analysis results for endometrial cancer, excluding studies using tumor tissue as the source of genotyping material for cases

Characteristic		Studies (cases, controls)	Heterogeneity (pQ; I^2)	OR (95% CI); p-value
All studies		6 (590, 1202)	0.265; 22%	1.10 (0.91-1.29); 0.338
Ethnicity	Whites	4 (368, 665)	0.739; 0%	1.22 (1.01-1.43); 0.068
	East Asians	2 (222, 537)	0.080; 67%	0.91 (0.46-1.36); 0.682
Control selection	Disease controls	2 (305, 732)	0.803; 0%	1.15 (0.94-1.36); 0.193
	Healthy controls	4 (285, 470)	0.114; 50%	1.08 (0.69-1.47); 0.697
Matching	No/NR	4 (278, 582)	0.119; 49%	1.07 (0.69-1.44); 0.735
	Yes	2 (312, 620)	0.912; 0%	1.17 (0.94-1.39); 0.175
Genotyping QC	No/NR	4 (278, 582)	0.119; 49%	1.07 (0.69-1.44); 0.735
	Yes	2 (312, 620)	0.912; 0%	1.17 (0.94-1.39); 0.175
Blinding	No	6 (590, 1202)	0.265; 22%	1.10 (0.91-1.29); 0.338
	Yes	none	NA	NA
Genotyping method	Non-RFLP	4 (361, 777)	0.700; 0%	1.19 (1.00-1.39); 0.080
	RFLP	2 (229, 425)	0.078; 68%	0.92 (0.44-1.39); 0.716
HWE	Compliant	5 (482, 1107)	0.834; 0%	1.18 (1.01-1.36); 0.055
	In violation	1 (108, 95)	NA	0.71 (0.29-1.13); 0.104

CI = confidence interval; HWE = Hardy-Weinberg equilibrium; NA = not applicable; OR = odds ratio; p_Q = p-value from Cochran's Q statistic; QC = quality control; RFLP = restriction fragment length polymorphism.

Web Table 9: Meta-regression results for breast, lung and colorectal cancer, excluding studies using tumor tissue as the source of genotyping material for cases.

Cancer	*Contrast*	*rOR (95% CI)*	*p-value*
Breast cancer	East Asians vs. Whites	1.02 (0.88-1.17)	0.798
	Disease vs. healthy controls	0.87 (0.70-1.08)	0.209
	Matching vs. no matching	1.05 (0.95-1.16)	0.360
	Genotyping QC vs. no/NR	1.06 (0.96-1.18)	0.249
	Blinding vs. no/NR	1.05 (0.90-1.23)	0.506
	RFLP vs. non-RFLP method	1.02 (0.91-1.14)	0.723
	Violations vs. compliance with HWE	**0.86 (0.74-0.99)**	**0.038**
	Year of publication (continuous)	1.07 (0.91-1.25)	0.415
Lung cancer	East Asians vs. Whites	0.92 (0.81-1.05)	0.199
	Disease vs. healthy controls	0.99 (0.87-1.13)	0.880
	Matching vs. no matching	1.02 (0.89-1.16)	0.807
	Genotyping QC vs. no/NR	1.00 (0.86-1.16)	0.977
	Blinding vs. no/NR	1.00 (0.88-1.15)	0.955
	RFLP vs. non-RFLP method	0.97 (0.76-1.24)	0.818
	Violations vs. compliance with HWE	1.01 (0.99-1.02)	0.303
	Year of publication (continuous)	1.07 (0.91-1.25)	0.415
Colorectal cancer	East Asians vs. Whites	**1.21 (1.03-1.44)**	**0.023**
	Disease vs. healthy controls	1.05 (0.80-1.40)	0.711
	Matching vs. no matching	1.25 (0.98-1.61)	0.077
	Genotyping QC vs. no/NR	1.04 (0.80-1.36)	0.754
	Blinding vs. no/NR	0.97 (0.68-1.39)	0.869
	RFLP vs. non-RFLP method	**1.31 (1.04-1.65)**	**0.023**
	Violations vs. compliance with HWE	**2.93 (1.79-4.80)**	**<0.001**
	Year of publication (continuous)	1.01 (0.99-1.04)	0.215
Ovarian cancer	East Asians vs. Whites	1.03 (0.65-1.63)	0.908
	Disease vs. healthy controls	1.44 (0.90-2.29)	0.129
	Matching vs. no matching	0.95 (0.80-1.14)	0.607
	Genotyping QC vs. no/NR	0.90 (0.73-1.12)	0.363
	Blinding vs. no/NR	1.08 (0.81-1.43)	0.591
	RFLP vs. non-RFLP method	1.16 (0.84-1.59)	0.361
	Violations vs. compliance with HWE	1.02 (0.82-1.26)	0.864
	Year of publication (continuous)	1.00 (0.96-1.03)	0.814
Endometrial cancer	East Asians vs. Whites	0.76 (0.52-1.12)	0.164
	Disease vs. healthy controls	0.91 (0.59-1.42)	0.678
	Matching vs. no matching	1.12 (0.73-1.73)	0.593
	Genotyping QC vs. no/NR	1.12 (0.73-1.73)	0.593
	Blinding vs. no/NR	1.10 (0.91-1.32)	0.321
	RFLP vs. non-RFLP method	0.77 (0.53-1.13)	0.189
	Violations vs. compliance with HWE	**0.60 (0.38-0.94)**	**0.026**
	Year of publication (continuous)	1.03 (0.94-1.12)	0.539

CI = confidence interval; HWE = Hardy-Weinberg equilibrium; NR = not reported; RFLP = restriction fragment length polymorphism; QC = quality control; rOR = relative odds ratio. Significant results are shown in bold type.