

Supplemental data

Figure S1. Subgroup analysis data by the factor of control source under the T vs. C model.

Figure S2. Subgroup analysis data by the factor of country under the T vs. C model.

Figure S3. Subgroup analysis data by the factor of article quality under the T vs. C model.

Figure S4. Subgroup analysis data by the factor of genotyping assay under the T vs. C model.

Figure S5. Subgroup analysis data by the factor of cancer type under the TT vs. CC model.

Figure S6. Subgroup analysis data by the factor of cancer type under the CT vs. CC model.

Figure S7. Subgroup analysis data by the factor of cancer type under the CT+TT vs. CC model.

Figure S8. Subgroup analysis data by the factor of cancer type under the TT vs. CC+CT model.

Figure S9. Subgroup analysis data of different system cancers under the T vs. C model.

Figure S10. Trial sequential analysis for the association between *XPC* rs2228000 and the risk of gastric cancer under the CT+TT vs. CC model.

Figure S11. Trial sequential analysis for the association between *XPC* rs2228000 and the risk of bladder cancer under the TT vs. CC+CT model.

Table S1. Database search strategy in our study.

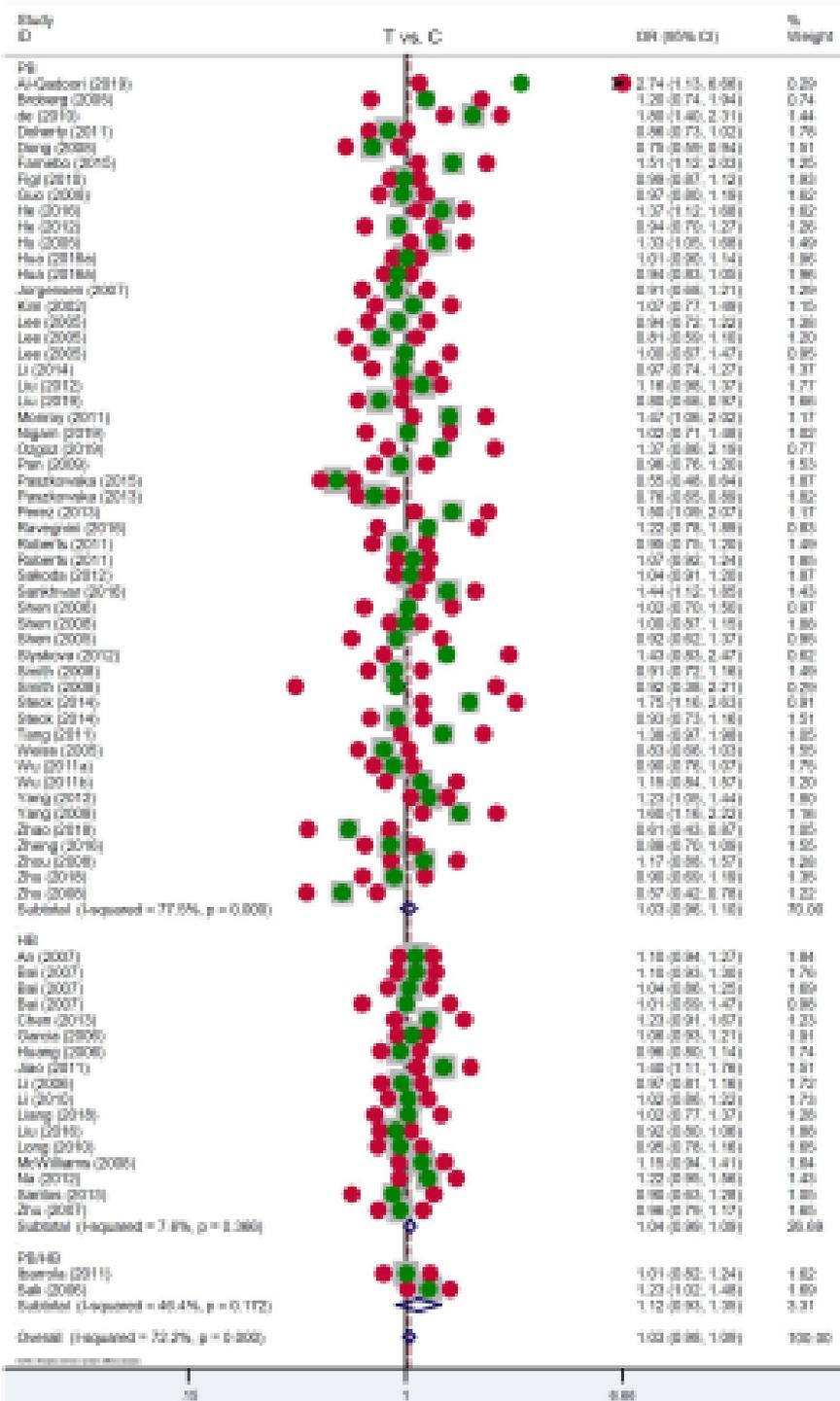
Table S2. Article quality assessment using the NOS system.

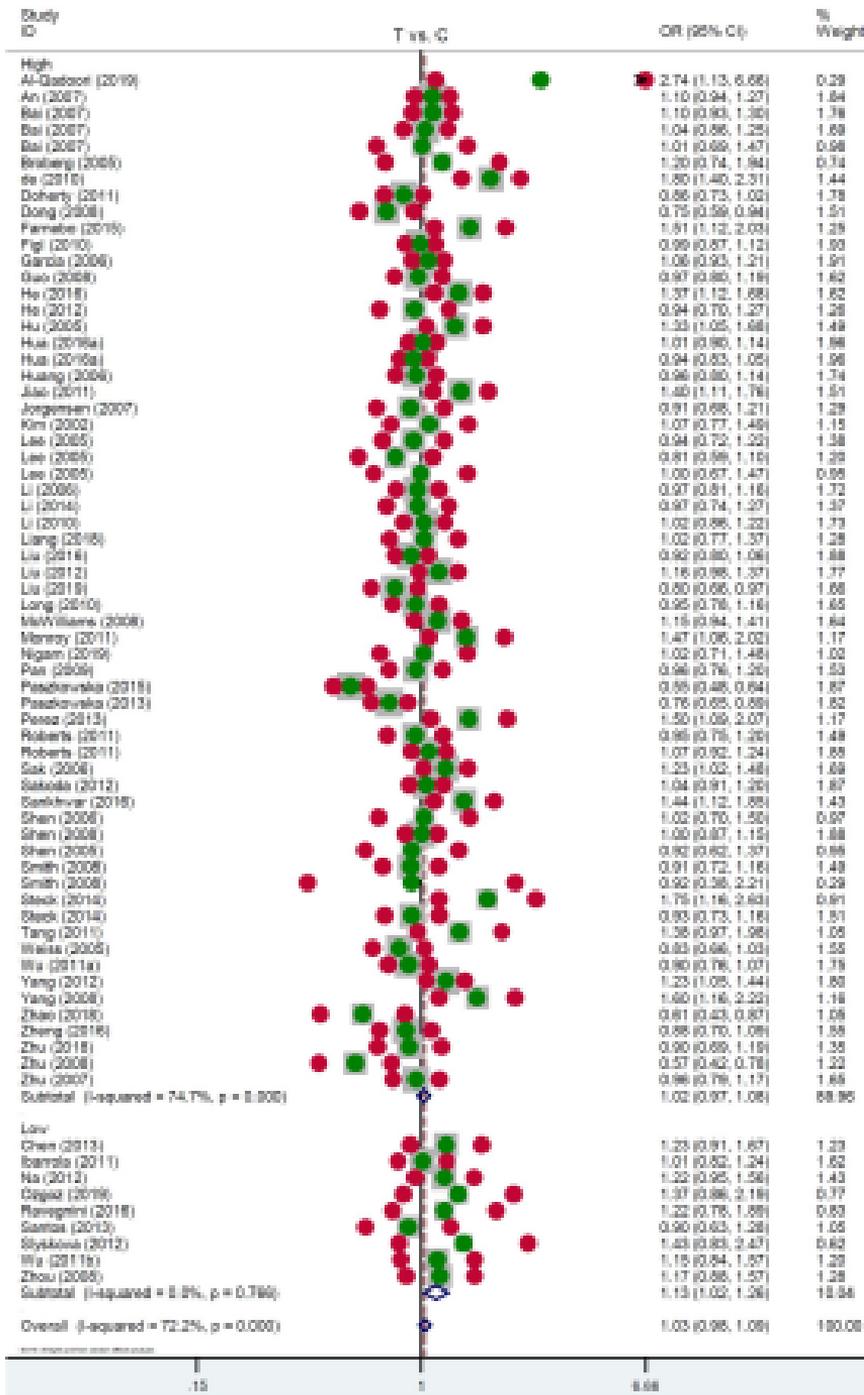
Table S3. Article quality assessment using the risk-of-bias score system.

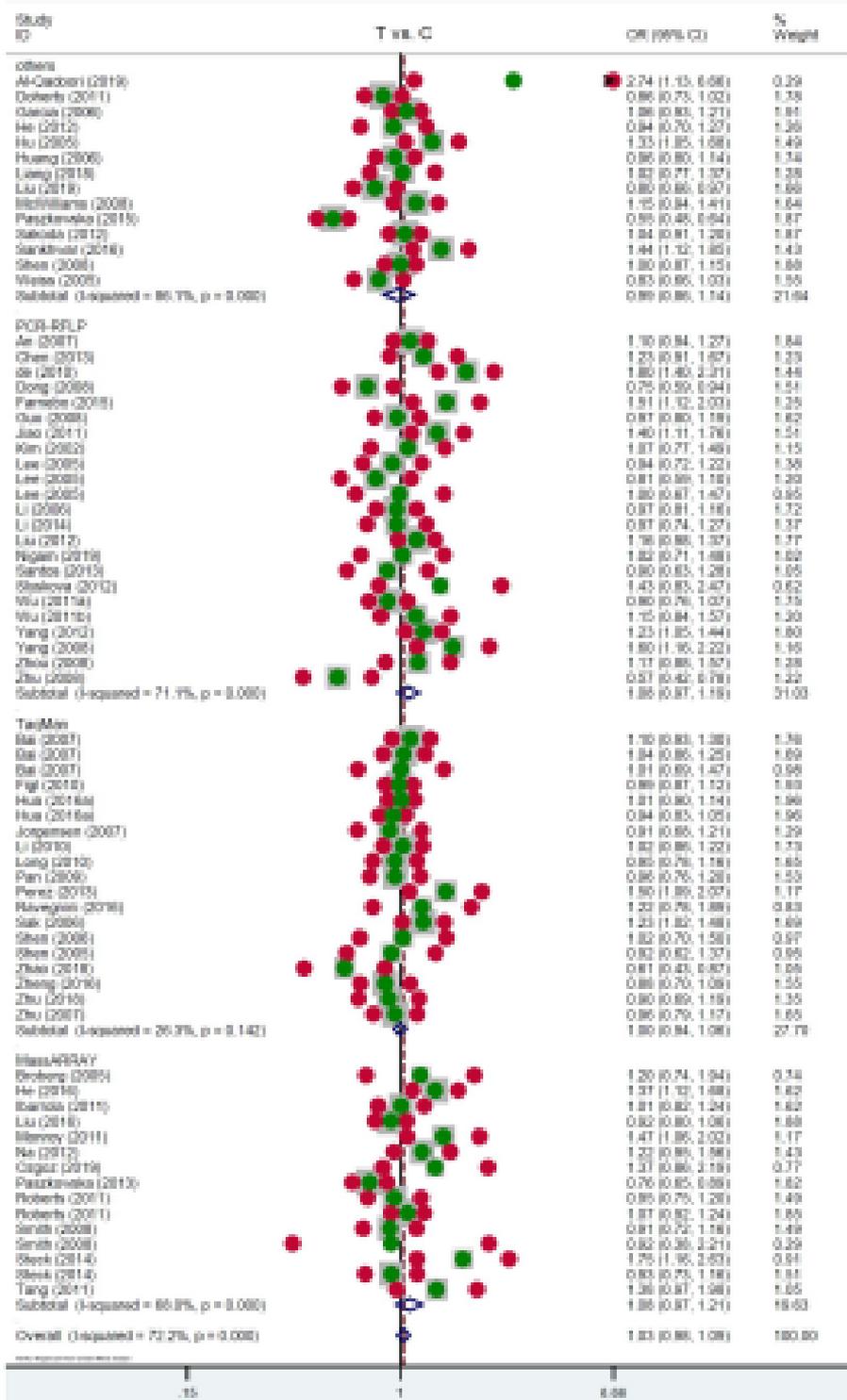
Table S4. Subgroup analysis data by the factors of country, genotyping assay and article quality.

Table S5. Subgroup analysis data of different system cancers.

Table S6. False-positive report probability values for the association between *XPC* rs2228000 and the risk of bladder, gastric and breast cancer.







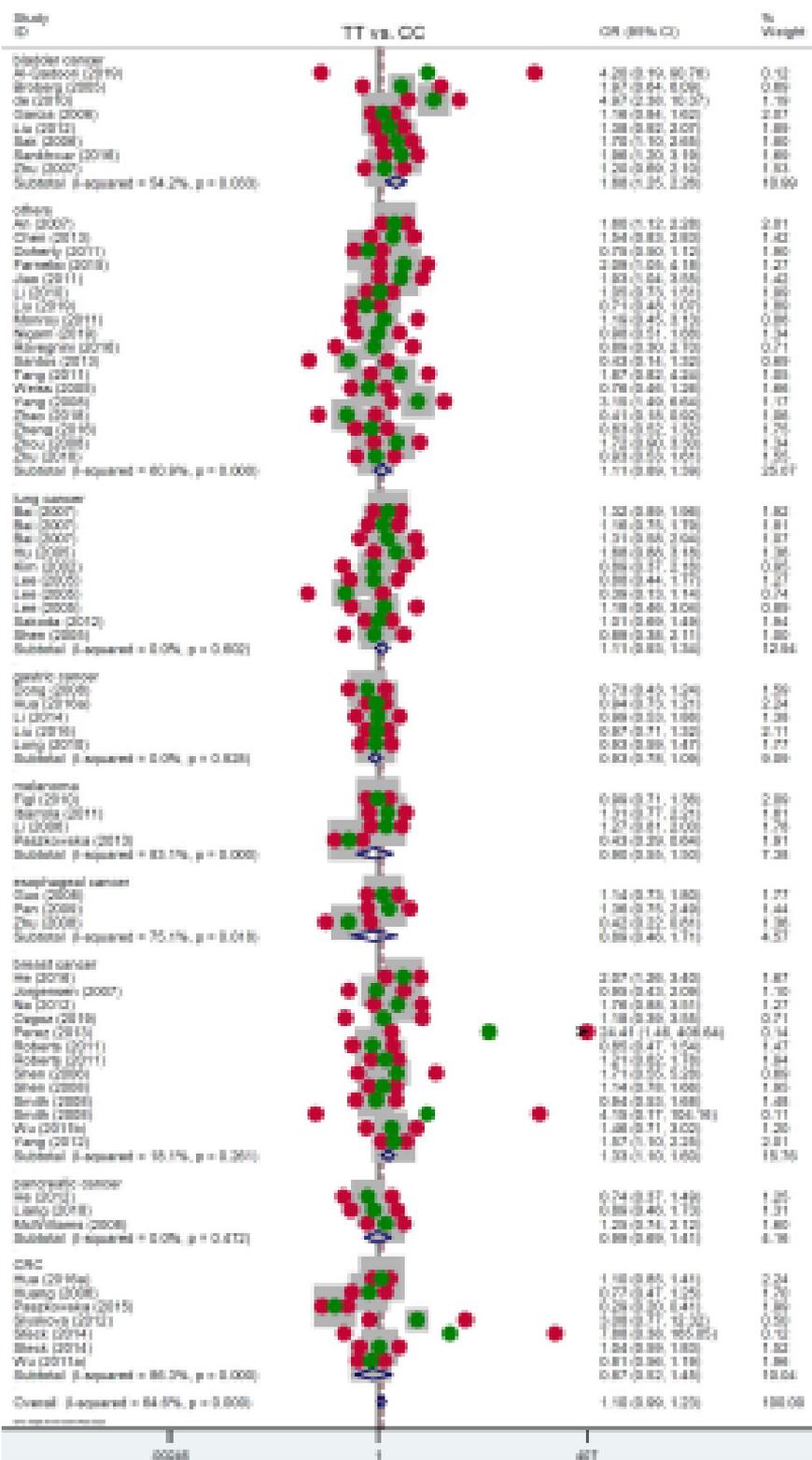
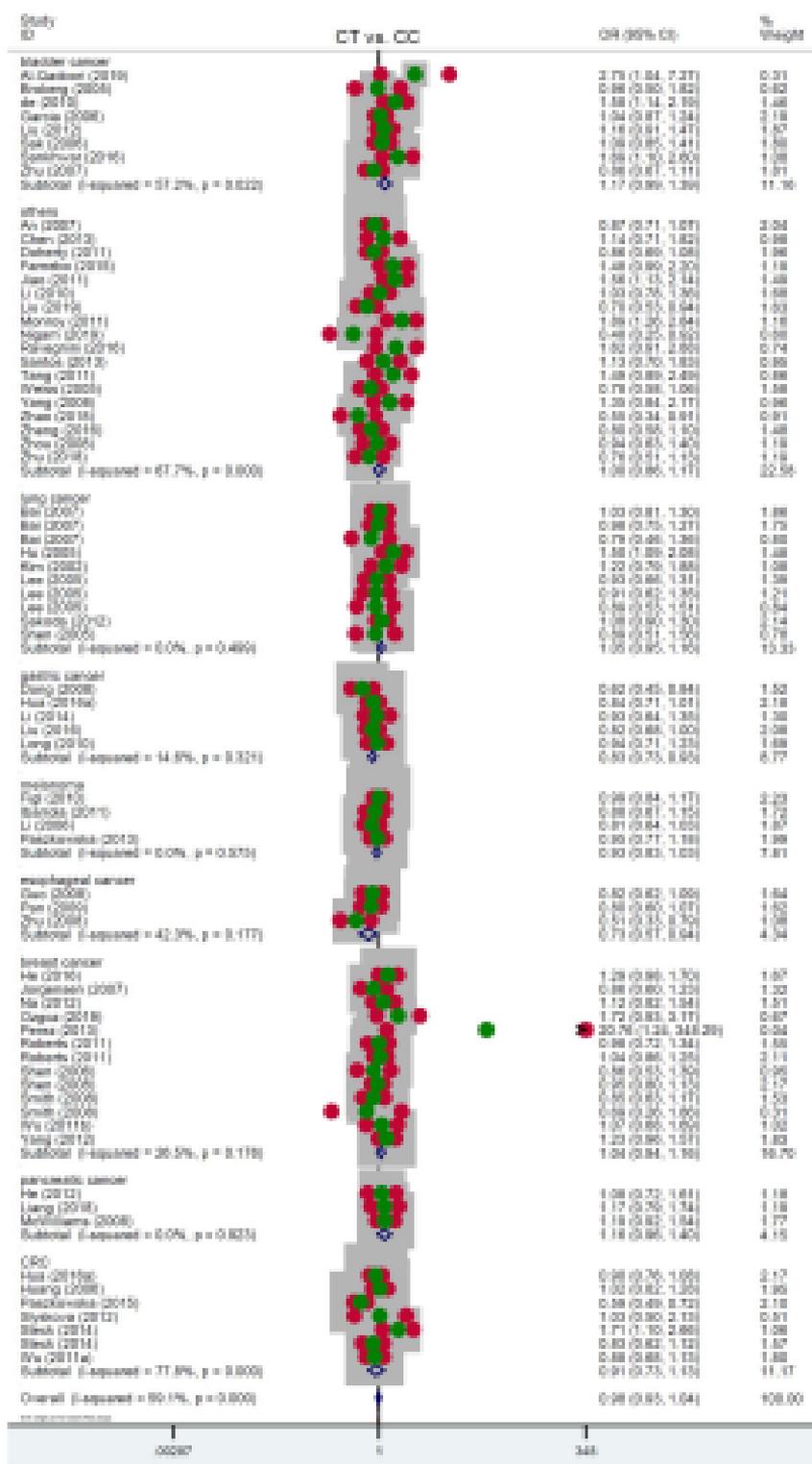


Figure S6



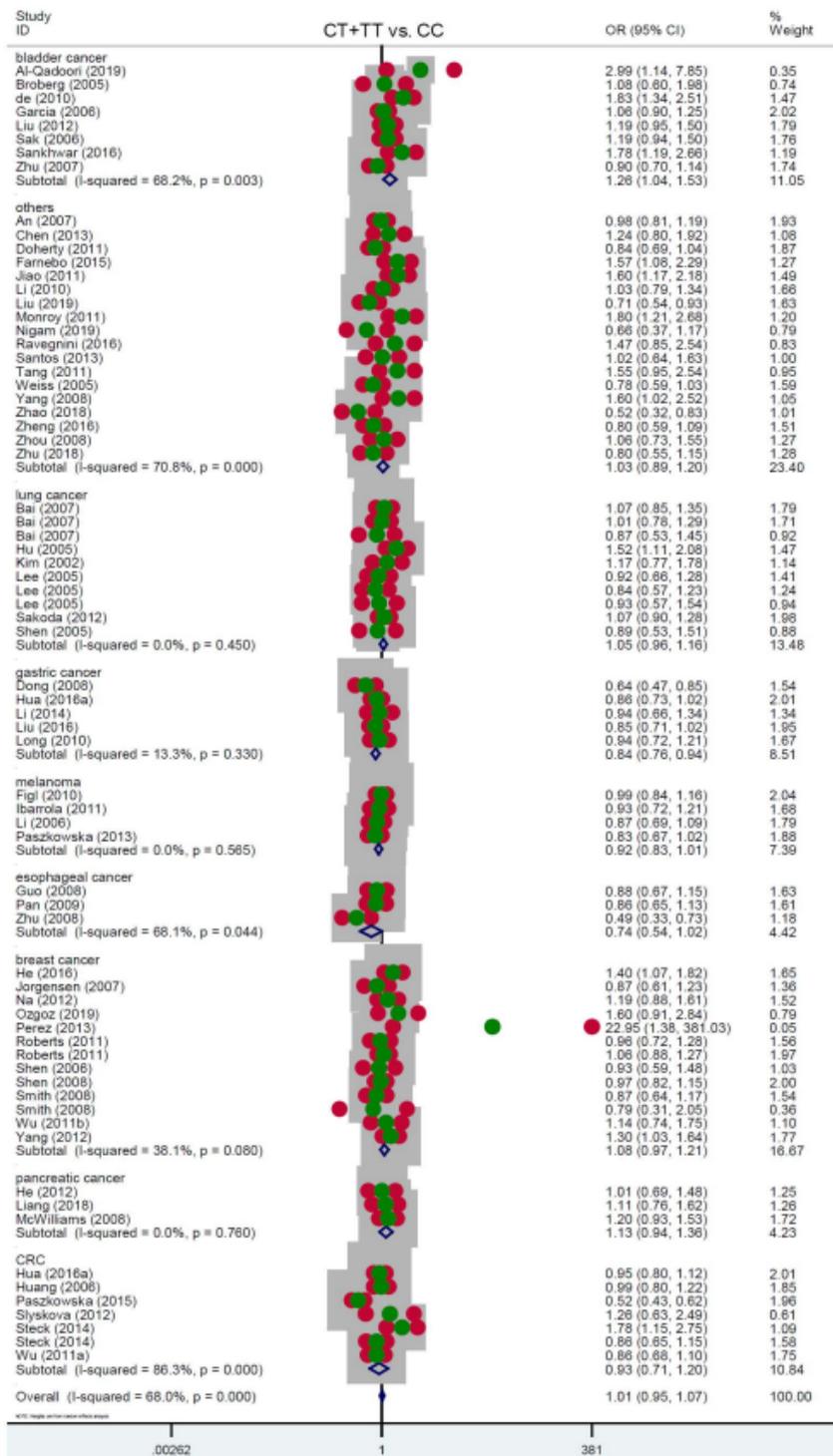
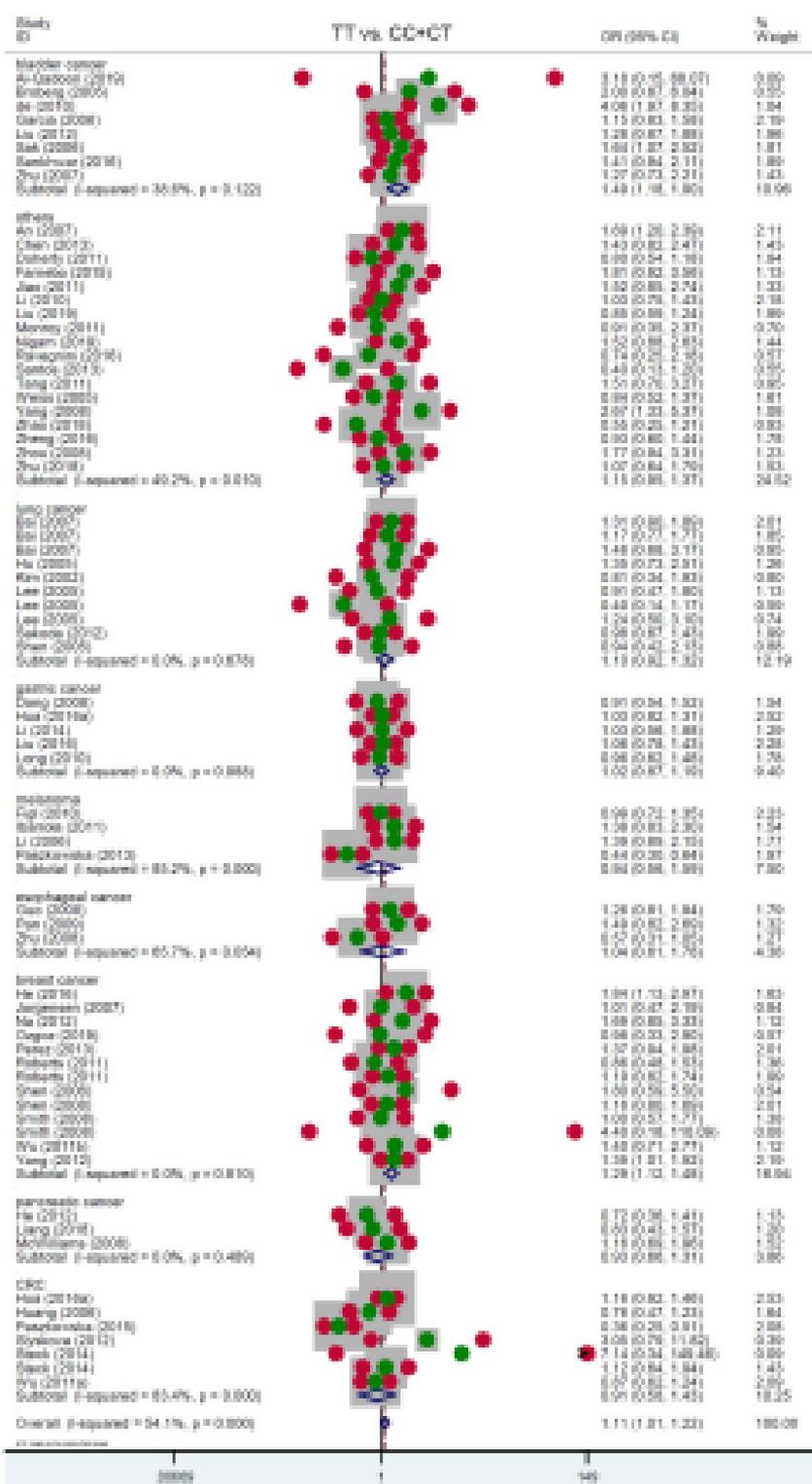


Figure S8



0.0005

145

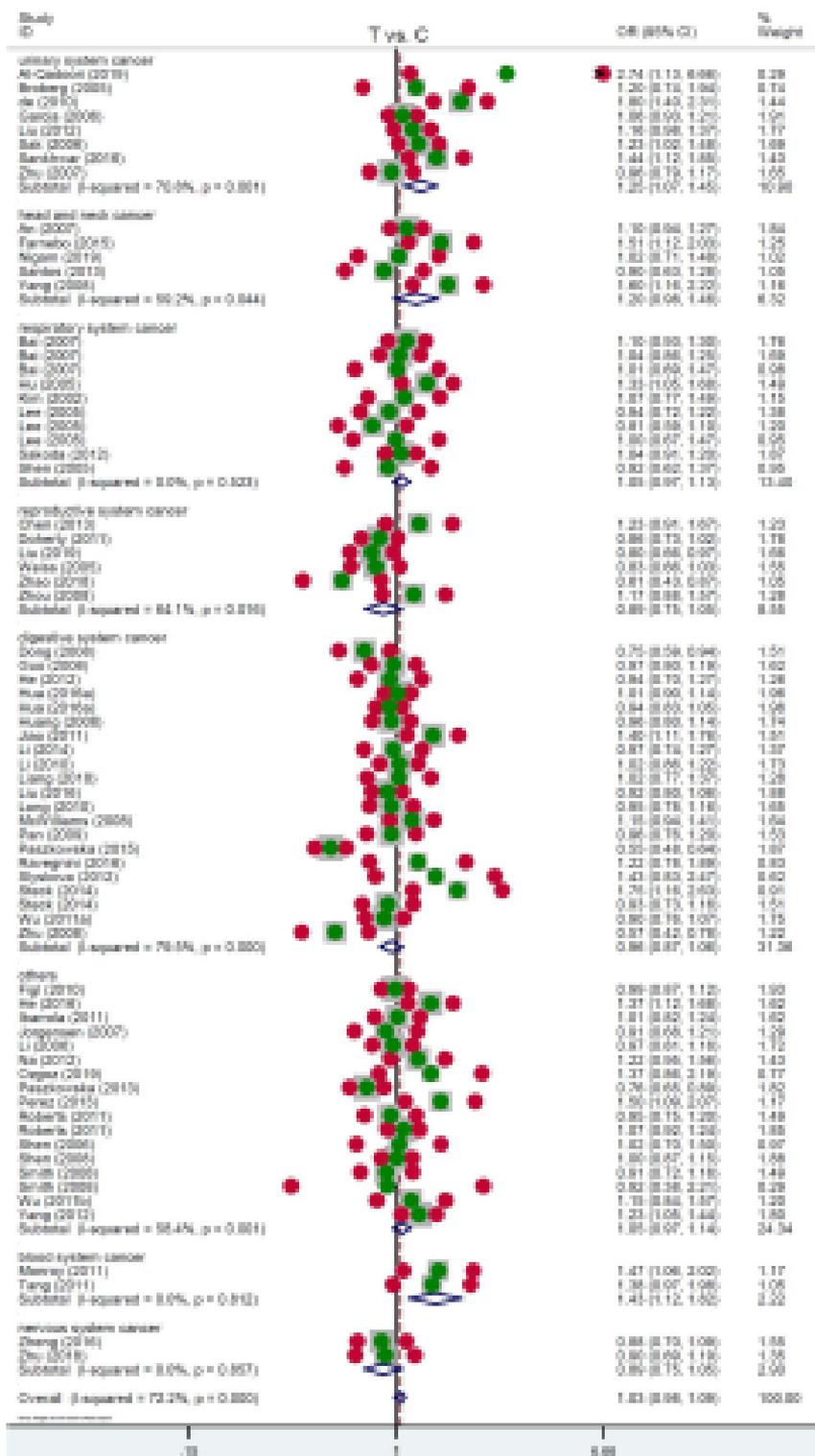


Figure S10

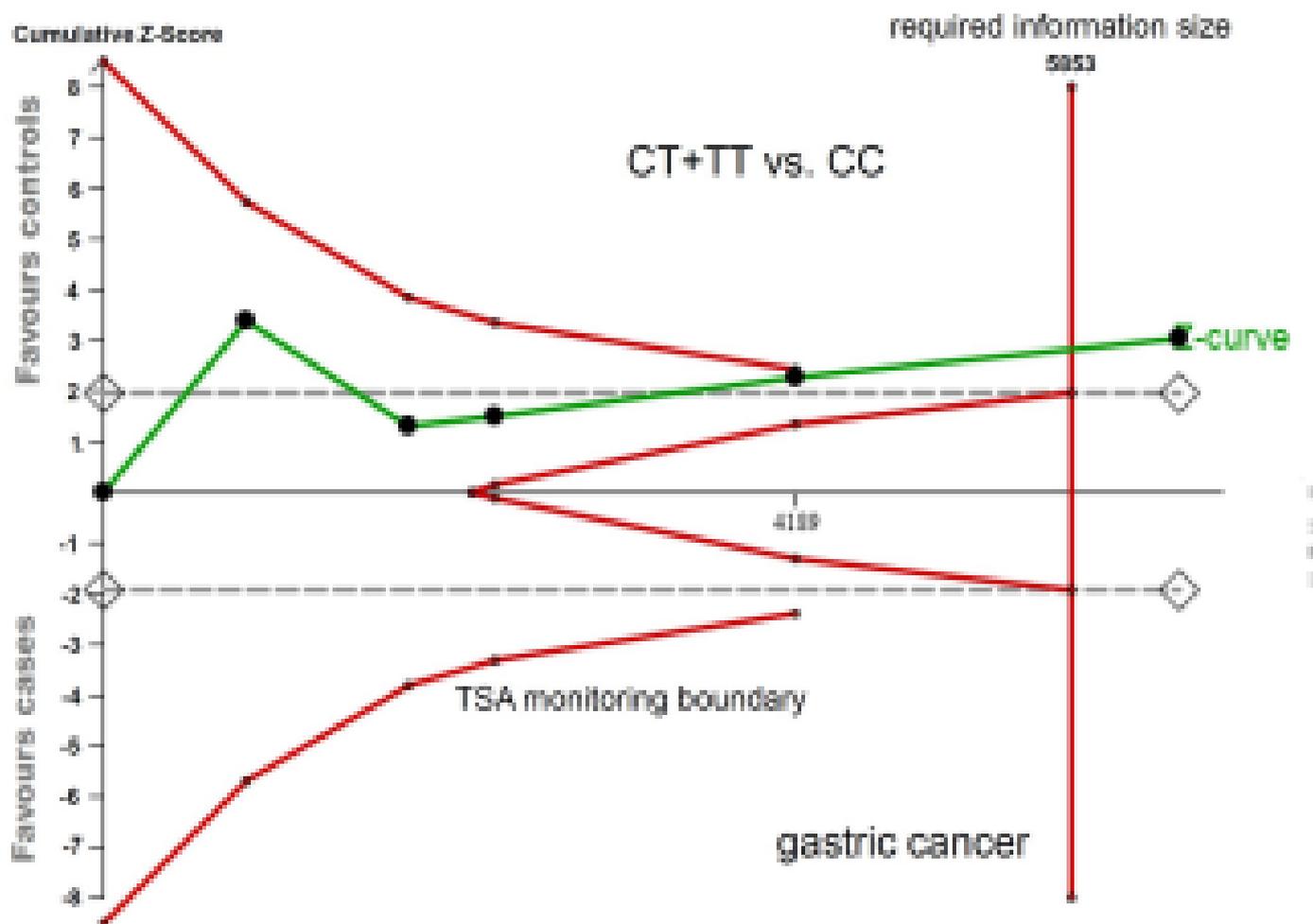


Table S1. Database search strategy in our study.

PubMed

#1 Search (((((((((((((((Neoplasms) OR Neoplasia) OR Neoplasias) OR Neoplasm) OR Tumors) OR Tumor) OR Cancer) OR Cancers) OR Malignancy) OR Malignancies) OR Malignant Neoplasms) OR Malignant Neoplasm) OR Neoplasm, Malignant) OR Neoplasms, Malignant) OR Benign Neoplasms) OR Neoplasms, Benign) OR Benign Neoplasm) OR Neoplasm, Benign **4,438,109**

#2 Search (((((((((((XPC) OR xeroderma pigmentosum complementation group C) OR Xeroderma Pigmentosum, Complementation Group C) OR (XPC Complex Subunit, DNA Damage Recognition And Repair Factor)) OR DNA Repair Protein Complementing XP-C Cells) OR XPCC) OR P125) OR Xeroderma Pigmentosum Group C-Complementing Protein) OR Mutant Xeroderma Pigmentosum Group C) OR RAD4) OR XP3 **1,662**

#3 #1 and #2

Search (((((((((((((((((((Neoplasms) OR Neoplasia) OR Neoplasias) OR Neoplasm) OR Tumors) OR Tumor) OR Cancer) OR Cancers) OR Malignancy) OR Malignancies) OR Malignant Neoplasms) OR Malignant Neoplasm) OR Neoplasm, Malignant) OR Neoplasms, Malignant) OR Benign Neoplasms) OR Neoplasms, Benign) OR Benign Neoplasm) OR Neoplasm, Benign)) AND (((((((((((XPC) OR xeroderma pigmentosum complementation group C) OR Xeroderma Pigmentosum, Complementation Group C) OR (XPC Complex Subunit, DNA Damage Recognition And Repair Factor)) OR DNA Repair Protein Complementing XP-C Cells) OR XPCC) OR P125) OR Xeroderma Pigmentosum Group C-Complementing Protein) OR Mutant Xeroderma Pigmentosum Group C) OR RAD4) OR XP3) **916**

#4 Search (((((Polymorphism, Genetic) OR Polymorphisms, Genetic) OR Genetic Polymorphisms) OR Genetic Polymorphism) OR Polymorphism (Genetics)) OR Polymorphisms (Genetics) **300,850**

#5 #3 and #4

Search (((((((((((((((((((((((Neoplasms) OR Neoplasia) OR Neoplasias) OR Neoplasm) OR Tumors) OR Tumor) OR Cancer) OR Cancers) OR Malignancy) OR Malignancies) OR Malignant Neoplasms) OR Malignant Neoplasm) OR Neoplasm, Malignant) OR Neoplasms, Malignant) OR Benign Neoplasms) OR Neoplasms, Benign) OR Benign Neoplasm) OR Neoplasm, Benign)) AND (((((((((((XPC) OR xeroderma pigmentosum complementation group C) OR Xeroderma Pigmentosum, Complementation Group C) OR (XPC Complex Subunit, DNA Damage Recognition And Repair Factor)) OR DNA Repair Protein Complementing XP-C Cells) OR XPCC) OR P125) OR Xeroderma Pigmentosum Group C-Complementing Protein) OR Mutant Xeroderma Pigmentosum

Group C) OR RAD4) OR XP3))) AND ((((((Polymorphism, Genetic) OR Polymorphisms, Genetic) OR Genetic Polymorphisms) OR Genetic Polymorphism) OR Polymorphism (Genetics)) OR Polymorphisms (Genetics)) **266**

Embase

#1 'xpc' OR 'xeroderma pigmentosum complementation group c' OR 'xeroderma pigmentosum, complementation group c' OR 'xpcc' OR 'p125' OR 'xeroderma pigmentosum group c-complementing protein'/exp OR 'xeroderma pigmentosum group c-complementing protein' OR 'mutant xeroderma pigmentosum group c' OR 'rad4' OR 'xp3' **3,077**

#2 'neoplasm'/exp OR 'neoplasm' OR 'acral tumor'/exp OR 'acral tumor' OR 'acral tumour'/exp OR 'acral tumour' OR 'neoplasia'/exp OR 'neoplasia' OR 'neoplasms'/exp OR 'neoplasms' OR 'neoplasms by histologic type'/exp OR 'neoplasms by histologic type' OR 'neoplasms, cystic, mucinous, and serous'/exp OR 'neoplasms, cystic, mucinous, and serous' OR 'neoplasms, embryonal and mixed'/exp OR 'neoplasms, embryonal and mixed' OR 'neoplasms, germ cell and embryonal'/exp OR 'neoplasms, germ cell and embryonal' OR 'neoplasms, glandular and epithelial'/exp OR 'neoplasms, glandular and epithelial' OR 'neoplasms, hormone-dependent'/exp OR 'neoplasms, hormone-dependent' OR 'neoplasms, post-traumatic'/exp OR 'neoplasms, post-traumatic' OR 'neoplastic disease'/exp OR 'neoplastic disease' OR 'tumor'/exp OR 'tumor' OR 'tumour'/exp OR 'tumour' **5,369,297**

#3 'genetic polymorphism'/exp OR 'genetic polymorphism' OR 'polymorphism (genetics)/exp OR 'polymorphism (genetics)' OR 'polymorphism, genetic'/exp OR 'polymorphism, genetic' OR 'polymorphism'/exp OR 'polymorphism' OR 'polymorphisms' OR 'mutations'/exp OR 'mutations' OR 'mutation'/exp OR 'mutation' **1,699,261**

#4 #1 and #2 and #3 **687**

CNKI

(keyword= Polymorphisms) And (keyword= XPC) **28**

WOS

#1 TOPIC: (Neoplasms) OR TOPIC: (Neoplasia) OR TOPIC: (Neoplasias) OR TOPIC: (Neoplasm) OR TOPIC: (Tumors) OR TOPIC: (Tumor) OR TOPIC: (Cancer) OR TOPIC: (Cancers) **3,784,624**

#2 TOPIC: (XPC) OR TOPIC: (xeroderma pigmentosum complementation group C) OR TOPIC: (XPC Complex Subunit, DNA Damage Recognition And Repair Factor) OR TOPIC: (XPCC) OR TOPIC: (P125) OR TOPIC: (Mutant Xeroderma Pigmentosum Group C) OR TOPIC: (RAD4) OR TOPIC: (XP3) **2,435**

#3 TOPIC: (Polymorphism, Genetic) OR TOPIC: (Polymorphisms, Genetic) OR TOPIC: (Genetic Polymorphisms) OR TOPIC: (Genetic Polymorphism) OR TOPIC: (Polymorphism (Genetics)) OR TOPIC: (Polymorphisms (Genetics)) **394,549**

#4 #1 and #2 and #3 **205**

CNKI, China National Knowledge Infrastructure; WOS, Web of Science.

Table S2. Article quality assessment using the NOS system.

First author	Year	Score	Case		Control		Comparability		Exposure	Method	Non-response
			Definition	Representativeness	Selection	Definition	Factor 1	Factor 1			
Al-Qadoori	2019	8	1	1	1	1	1	1	0	1	1
An	2007	8	1	1	0	1	1	1	1	1	1
Bai	2007	7	1	1	0	1	1	1	1	1	0
Broberg	2005	8	1	1	1	1	1	1	1	1	0
Chen	2013	7	1	1	0	0	1	1	1	1	1
de	2010	6	1	1	1	1	1	0	0	1	0
Doherty	2011	8	1	1	1	1	1	1	1	1	0
Dong	2008	9	1	1	1	1	1	1	1	1	1
Farnebo	2015	9	1	1	1	1	1	1	1	1	1
Figl	2010	6	1	1	1	1	0	1	0	1	0
Garcia	2006	6	1	1	0	0	1	1	1	1	0
Guo	2008	9	1	1	1	1	1	1	1	1	1
He	2016	9	1	1	1	1	1	1	1	1	1
He	2012	8	1	1	1	1	1	1	1	1	0
Hu	2005	8	1	1	1	1	1	1	1	1	0
Hua	2016a	9	1	1	1	1	1	1	1	1	1
Hua	2016b	9	1	1	1	1	1	1	1	1	1
Huang	2006	6	1	1	0	0	1	1	1	1	0
Ibarrola	2011	6	1	1	0	1	0	1	1	1	0
Jiao	2011	7	1	1	0	1	1	1	0	1	1

Jorgensen	2007	7	1	0	1	0						
Kim	2002	8	1	0								
Lee	2005	9	1									
Li	2006	6	1	1	0	0	1	1	0	0	1	1
Li	2014	8	1	0	1	1						
Li	2010	7	1	1	0	0	1	1	1	1	1	1
Liang	2018	7	1	1	0	0	1	1	1	1	1	1
Liu	2016	6	1	1	0	1	0	1	1	1	1	0
Liu	2012	9	1									
Liu	2019	8	1	1	1	1	1	1	0	1	1	1
Long	2010	7	1	1	0	0	1	1	1	1	1	1
McWilliams	2008	6	1	1	0	1	0	1	1	1	1	0
Monroy	2011	9	1									
Na	2012	7	1	1	0	0	1	1	1	1	1	1
Nigam	2019	7	1	0	1	0						
Ozgoz	2019	8	1	1	1	1	0	1	1	1	1	1
Pan	2009	8	1	0								
Paszkowski	2015	6	1	1	1	1	0	1	0	0	1	0
Paszkowski	2013	6	1	1	1	1	0	1	0	0	1	0
Perez	2013	8	1	0								
Ravegnini	2016	8	1	0	1	1						
Roberts	2011	8	1	0								
Sak	2006	6	1	1	0	1	1	0	1	1	1	0
Sakoda	2012	8	1	0								

Sankhwar	2016	8	1	1	1	1	0	1	1	1	1
Santos	2013	8	1	1	0	1	1	1	1	1	1
Shen	2006	7	1	1	1	1	0	1	1	1	0
Shen	2008	7	1	1	1	1	1	0	1	1	0
Shen	2005	8	1	0							
Slyskova	2012	8	1	0							
Smith	2008	8	1	0							
Steck	2014	8	1	0							
Tang	2011	7	1	1	1	1	1	1	0	1	0
Weiss	2005	9	1								
Wu	2011a	8	1	0							
Wu	2011b	8	1	0							
Yang	2012	8	1	1	1	1	1	1	0	1	1
Yang	2008	9	1								
Zhao	2018	8	1	1	1	1	1	1	0	1	1
Zheng	2016	7	1	1	1	1	1	1	0	1	0
Zhou	2008	8	1	1	1	1	1	1	0	1	1
Zhu	2018	8	1	1	1	1	1	1	0	1	1
Zhu	2008	8	1	1	1	1	1	1	0	1	1
Zhu	2007	6	1	1	0	0	1	1	1	1	0

NOS, Newcastle-Ottawa quality assessment Scale.

Table S3. Article quality assessment using the risk-of-bias score system.

First author	Year	Score	Representativeness of case ^a	Representativeness of control ^b	Ascertainment of case ^c	Control selection ^d	Genotyping examination ^e	HWE ^f	Total sample size ^g
Al-Qadoori	2019	10	1	3	2	2	1	1	0
An	2007	11	1	1	2	2	1	1	3
Bai	2007	11	1	1	2	2	2	1	2
Broberg	2005	11	1	3	2	2	1	1	1
Chen	2013	9	1	1	2	2	1	1	1
de	2010	10	2	3	1	1	0	1	2
Doherty	2011	13	2	3	1	1	2	1	3
Dong	2008	13	2	3	2	2	1	1	2
Farnebo	2015	10	1	3	0	2	1	1	2
Figl	2010	11	1	3	2	1	0	1	3
Garcia	2006	12	2	1	2	2	1	1	3
Guo	2008	10	2	3	1	1	0	1	2
He	2016	10	1	3	2	1	0	1	2
He	2012	10	1	3	2	2	0	1	1
Hu	2005	12	1	3	2	2	1	1	2
Hua	2016a	13	1	3	2	1	2	1	3
Hua	2016b	11	1	3	2	1	0	1	3
Huang	2006	10	2	1	0	1	2	1	3
Ibarrola	2011	8	1	3	0	0	1	1	2
Jiao	2011	10	1	1	2	2	1	1	2

Jorgensen	2007	11	2	3	1	2	0	1	2
Kim	2002	10	1	3	2	2	0	1	1
Lee	2005	12	1	3	2	2	1	1	2
Li	2006	12	2	1	2	2	1	1	3
Li	2014	12	1	3	2	2	1	1	2
Li	2010	12	1	1	2	2	2	1	3
Liang	2018	10	1	1	2	2	2	1	1
Liu	2016	10	2	1	2	0	1	1	3
Liu	2012	13	1	3	2	2	1	1	3
Liu	2019	11	1	3	2	1	1	1	2
Long	2010	10	1	1	2	2	1	1	2
McWilliams	2008	11	2	1	2	0	2	1	3
Monroy	2011	12	2	3	2	2	1	1	1
Na	2012	8	1	1	2	1	1	1	1
Nigam	2019	10	2	3	1	1	0	1	2
Ozgoz	2019	8	1	3	2	0	0	1	1
Pan	2009	13	2	3	1	2	2	1	2
Paszkowska	2015	10	2	3	1	0	0	1	3
Paszkowska	2013	10	2	3	1	0	0	1	3
Perez	2013	10	2	3	2	0	0	1	2
Ravegnini	2016	7	2	2	0	0	1	1	1
Roberts	2011	13	1	3	2	2	1	1	3
Sak	2006	10	1	0	2	2	1	1	3
Sakoda	2012	13	1	3	1	2	2	1	3
Sankhwar	2016	10	1	3	2	0	1	1	2
Santos	2013	9	1	1	2	2	1	1	1

Shen	2006	10	2	3	1	1	1	1	1	1
Shen	2008	13	2	3	1	1	2	1	1	3
Shen	2005	10	1	3	1	2	1	1	1	1
Slyskova	2012	9	1	3	2	1	1	1	1	0
Smith	2008	12	2	3	2	1	1	1	1	2
Steck	2014	10	2	1	1	2	1	1	1	2
Tang	2011	10	1	3	2	2	0	1	1	1
Weiss	2005	12	2	3	1	1	2	1	1	2
Wu	2011a	15	2	3	2	2	2	1	1	3
Wu	2011b	9	1	3	2	1	0	1	1	1
Yang	2012	12	1	3	2	1	1	1	1	3
Yang	2008	11	1	3	2	2	1	1	1	1
Zhao	2018	10	1	3	2	1	1	1	1	1
Zheng	2016	11	1	3	2	2	0	1	1	2
Zhou	2008	9	1	3	2	1	0	1	1	1
Zhu	2018	12	1	3	2	2	1	1	1	2
Zhu	2008	10	1	3	2	2	0	1	1	1
Zhu	2007	11	1	1	2	2	1	1	1	3

a, Selected from population cancer registry (2); Selected from hospital (1); No method of selection described (0).

b, Population-based (3); Blood donors (2); Hospital-based (1); Not described (0).

c, Histopathologic confirmation (2); by patient medical record (1); Not described (0).

d, Controls matched with cases by age and sex (2); Controls matched with cases only by age or by sex (1); Not matched or not described (0).

e, Genotyping performed blindly and quality control (2); only genotyping performed blindly or quality control (1); Unblinded and without quality control (0).

f, HWE in the control group (1); HWD in the control group or not mentioned (0).

g, > 1000 (3); 501~1000 (2); 201~500 (1); ≤ 200 (0).

Table S4. Subgroup analysis data by the factors of country, genotyping assay and article quality.

Genetic model	Subgroup	Sample size		Association	
		Study	Case/control	$P_{association}$	OR (95% CI)
T vs. C	USA	20	9,117/11,690	0.642	1.01 (0.95,1.08)
	China	32	11,180/16,386	0.497	1.02 (0.96,1.09)
	PCR-RFLP	23	6,404/9,124	0.147	1.08 (0.97,1.19)
	TaqMan	19	7,886/11,733	0.948	1.00 (0.94,1.06)
	MassARRAY	15	5,224/7,253	0.165	1.08 (0.97,1.21)
	High quality	62	25,006/35,149	0.473	1.02 (0.97,1.08)
TT vs. CC	USA	20	9,117/11,690	0.201	1.09 (0.95,1.25)
	China	32	11,180/16,386	0.109	1.11 (0.98,1.25)
	PCR-RFLP	23	6,404/9,124	0.033	1.26 (1.02,1.55)
	TaqMan	19	7,886/11,733	0.287	1.07 (0.95,1.20)
	MassARRAY	15	5,224/7,253	0.286	1.16 (0.98,1.25)
	High quality	62	25,006/35,149	0.221	1.08 (0.89,1.51)
CT vs. CC	USA	20	9,117/11,690	0.394	0.96 (0.88,1.05)

	China	32	11,180/16,386	0.299	0.95 (0.88,1.04)
	PCR-RFLP	23	6,404/9,124	0.862	0.99 (0.88,1.11)
	TaqMan	19	7,886/11,733	0.019	0.92 (0.85,0.99)
	MassARRAY	15	5,224/7,253	0.340	1.06 (0.94,1.21)
	High quality	62	25,006/35,149	0.381	0.97 (0.91,1.03)
<hr/>					
CT+TT vs. CC	USA	20	9,117/11,690	0.646	0.98 (0.90,1.06)
	China	32	11,180/16,386	0.738	0.98 (0.90,1.08)
	PCR-RFLP	23	6,404/9,124	0.557	1.04 (0.92,1.17)
	TaqMan	19	7,886/11,733	0.115	0.94 (0.88,1.01)
	MassARRAY	15	5,224/7,253	0.225	1.08 (0.95,1.24)
	High quality	62	25,006/35,149	0.853	0.99 (0.93,1.06)
<hr/>					
TT vs. CC+ CT	USA	20	9,117/11,690	0.031	1.04 (1.01,1.27)
	China	32	11,180/16,386	0.006	1.04 (1.04,1.24)
	PCR-RFLP	23	6,404/9,124	0.005	1.28 (1.08,1.52)
	TaqMan	19	7,886/11,733	0.018	1.12 (1.02,1.23)
	MassARRAY	15	5,224/7,253	0.337	1.13 (0.88,1.45)
	High quality	62	25,006/35,149	0.067	1.09 (0.99,1.20)

OR, odds ratio; CI, 95% confidence interval; $P_{association}$, P value in the association test; PCR, polymerase chain reaction;
RFLP, restriction fragment length polymorphism.

Table S5. Subgroup analysis data of different system cancers.

Genetic model	Subgroup	Sample size		Association	
		Study	Case/control	$P_{association}$	OR (95% CI)
T vs. C	urinary system cancer	8	3,460/3,613	0.004	1.25 (1.07,1.45)
	respiratory system cancer	10	2,642/6,319	0.222	1.05 (0.97,1.13)
	reproductive system cancer	6	1,907/2,480	0.166	0.89 (0.75,1.05)
	digestive system cancer	21	9,136/11,852	0.382	0.96 (0.87,1.06)
	head and neck cancer	5	1,327/1,875	0.078	1.20 (0.98,1.46)
TT vs. CC	urinary system cancer	8	3,460/3,613	0.001	1.68 (1.25,2.26)
	respiratory system cancer	10	2,642/6,319	0.252	1.11 (0.93,1.34)
	reproductive system cancer	6	1,907/2,480	0.442	0.87 (0.62,1.23)
	digestive system cancer	21	9,136/11,852	0.370	0.92 (0.75,1.11)
	head and neck cancer	5	1,327/1,875	0.119	1.48 (0.90,2.41)
CT vs. CC	urinary system cancer	8	3,460/3,613	0.069	1.17 (0.99,1.39)
	respiratory system cancer	10	2,642/6,319	0.368	1.05 (0.95,1.16)
	reproductive system cancer	6	1,907/2,480	0.006	0.81 (0.70,0.94)

	digestive system cancer	21	9,136/11,852	0.176	0.92 (0.83,1.04)
	head and neck cancer	5	1,327/1,875	0.883	1.02 (0.75,1.41)
CT+TT vs. CC	urinary system cancer	8	3,460/3,613	0.016	1.26 (1.04,1.53)
	respiratory system cancer	10	2,642/6,319	0.282	1.05 (0.96,1.16)
	reproductive system cancer	6	1,907/2,480	0.041	0.82 (0.68,0.99)
	digestive system cancer	21	9,136/11,852	0.255	0.93 (0.82,1.05)
	head and neck cancer	5	1,327/1,875	0.402	1.13 (0.85,1.49)
TT vs. CC+ CT	urinary system cancer	8	3,460/3,613	0.001	1.49 (1.18,1.90)
	respiratory system cancer	10	2,642/6,319	0.293	1.10 (0.92,1.32)
	reproductive system cancer	6	1,907/2,480	0.754	0.96 (0.72,1.26)
	digestive system cancer	21	9,136/11,852	0.601	0.96 (0.81,1.13)
	head and neck cancer	5	1,327/1,875	0.024	1.58 (1.06,2.34)

OR, odds ratio; CI, 95% confidence interval; $P_{association}$, P value in the association test.

Table S6. False-positive report probability values for the association between *XPC* rs2228000 and the risk of bladder, gastric and breast cancer.

Cancer type	Model	OR (95% CI)	P^{\S}	Statistical power	Prior probability				
					0.25	0.1	0.01	0.001	0.0001
bladder cancer	T vs. C	1.25 (1.07,1.45)	0.003	0.992	0.010	0.028	0.243	0.764	0.970
	TT vs. CC	1.68 (1.25,2.26)	<0.001	0.227	0.008	0.023	0.209	0.728	0.964
	CT+TT vs. CC	1.26 (1.04,1.53)	0.020	0.961	0.058	0.155	0.669	0.953	0.995
	TT vs. CC+ CT	1.49 (1.18,1.90)	0.001	0.522	0.007	0.022	0.198	0.714	0.961
breast cancer	T vs. C	1.11 (1.02,1.21)	0.018	1.000	0.050	0.138	0.637	0.947	0.994
	TT vs. CC	1.33 (1.10,1.60)	0.013	0.912	0.042	0.116	0.590	0.936	0.993
	TT vs. CC+ CT	1.29 (1.12,1.48)	<0.001	0.984	0.001	0.003	0.027	0.222	0.740
gastric cancer	T vs. C	0.92 (0.85,0.99)	0.026	1.000	0.072	0.189	0.719	0.963	0.996
	CT vs. CC	0.83 (0.73,0.93)	0.001	1.000	0.004	0.012	0.116	0.570	0.930
	CT+TT vs. CC	0.84 (0.76,0.94)	0.002	1.000	0.007	0.021	0.191	0.704	0.960

OR, odds ratio; CI, 95% confidence interval; P^{\S} , P value in Chi-square test for genotype frequency distributions;

FPRP value < 0.2 in bold.