Table S1. Articles included in meta-analysis of association between *GSTM1-null* and cervical cancer risk.

Autors	Study region	Mean age (cases/controls)	Type of sample	Methode	Cases/ Controls	*GSTM1-present* cases/controls	*GSTM1-null* cases/controls	All Sample
Ângela Inácio *et al*. 2023 [50]	Portugual	NA	Blood cells	PCR	308/552	46/93	53/73	860
Ahlem Helaoui *et al.* 2023 [51]	Tunisia	45.26 ± 10.12 / 45 ± 11.34	Blood cells	PCR	71/100	66/94	5/6	171
T. Clarisse Ouedraogo *et al*. 2020 [8]	Burkina Faso, Mali	41.42 ± 13.51	Cervical cell and tissues	PCR	209/100	42/75	167/25	309
Kailas D. Datkhile *et al.* 2019 [7]	India	48.67 ± 13.78 / 46.37 ± 13.90	Blood cells	PCR	350/400	223/284	127 /116	750
A.L.M. Tacca *et al*. 2019 [52]	Brezil	49.6 ± 14.3 / 54.3 ± 15.1	Blood cells	PCR	135/100	105/55	30/45	235
K. Satinder *et al*. 2017 [53]	North-Indian	48.5 ± 9.4 / 46.1 ± 11.2	Blood cells	PCR	150/150	87/98	63 /52	300
Tulsi Rani Thakre *et al*. 2016 [54]	India	47.49 ± 10.95 / 47.6 ± 10.98	Blood cells	PCR	230/230	195/215	35/15	460
Anita Sharma *et al*. 2015 [42]	India	40.7 ± 9.5 ; 42.1 ± 11.7 / 41.1 ± 8.9	Tissue	PCR	160/457	71/297	89/160	617
Osamu Nunobiki *et al*. 2015 [41]	Japan	NA	Blood cells	PCR	140/52	66/24	76/28	192
Sitakan Natphopsuk *et al*. 2015 [55]	Thailand	NA	Blood cells	PCR	198/198	68/73	130/125	396
Sarah Hasan *et al.* 2015 [56]	Pakistan	NA	Blood cells	PCR	50/50	13/33	37/17	100
Ivana Stosic *et al.* 2014 [49]	Serbia	44.54 ± 12.19 / 42.98 ± 8.26	Blood cells	PCR	97/50	25/22	72 /28	147
A. J. de Oliveira Soares *et al*. 2013 [48]	Brazil	NA	Blood cells	PCR	100/120	10/50	7/ 33	220
Leyla B. Djansugurova *et al.* 2013 [57]	Kazakhstan	NA	Blood cells	PCR	207/160	186/156	31/4	367
József Cseh *et al*. 2011 [40]	Hungary	NA	Cervical cells	PCR	117/136	54/83	63/53	253
Osamu Nunobiki *et al.* 2011 [58]	Japan	NA	Cervical cells	PCR	54/144	69/26	75/28	198
Antonella Agodi *et al*. 2010 [59]	Sicily	NA	Cervical cells	PCR	27/162	11/70	16/92	189
Masatsugu Ueda *et al*. 2010 [60]	Japan	NA	Blood cells	PCR	299/158	148/86	151/72	457
Beray Kiran *et al*. 2010 [61]	Turkish	53.73 ± 10.35 / 51.32 ± 8.86	Blood cells	PCR	46/52	21/22	25/30	98
Selena Palma *et al*. 2010 [47]	Italy	41.7 ± 12.3 / 36.3 ± 10.1	Blood cells	PCR	81/111	32/53	49/58	192
W. Settheetham-Ishida *et al.* 2009 [46]	Thailand	NA	Blood cells	PCR	90/94	36/38	54 /56	184
Hariom Singh *et al*. 2008 [62]	India	45.2 ± 8.8 / 50.3 ± 8.3	Blood cells	PCR	150/168	86/122	64 /46	318
Koji Nishino *et al*. 2008 [45]	Japan	41.6 ± 8 / 40.6 ± 10.5	Blood cells	PCR + sequence	124/125	47/66	77 /59	249
C. H. Sierra-Torres *et al.* 2006 [63]	Colombia	44.53 ± 14.62 / 42.34 ± 10.56	Blood cells	PCR	91/92	55/54	36 /38	183
Thomas Joseph *et al.* 2006 [39]	India	46 ± 10.3 / 47 ± 9.2	Blood cells	PCR	147/165	68/111	79/54	312
Theodoros Agorastos *et al*. 2007 [44]	Greece	NA	cervical cells	PCR	166/114	60/39	88/60	280
R.C. Sobti *et al.* 2006 [21]	India	48.6 ± 6 9.9; 48.0 ± 6 11.3	Blood cells	PCR	103/103	61/65	42/38	206
Yoshimitsu Niwa *et al.* 2005 [64]	Japan	47.2 ± 12.2 / 56.2 ± 11.8	Blood cells	PCR	131/320	61/136	70 /184	451
Masatsugu Ueda *et al.* 2005 [65]	Japan	NA	cervical cells	PCR	144/54	69/26	75/28	198
A.Sharma *et al.* 2004 [66]	India	49.2 ± 8.8 / 41.4 ± 8.4	Blood cells	PCR	142/96	61/63	81/33	238
Sang-Ah Lee *et al*. 2004 [20]	Korean	NA	Blood cells	PCR	81/86	39/44	42/42	167
Carlos H. Sierra-Torres *et al.* 2003 [38]	Texas	38.3 ± 13.4 /34.8 ± 11.0	Blood cells	PCR	69/72	34/43	35 /29	141
Marc T. Goodman *et al.* 2001 [23]	Hawaii	32.3/39.1	Blood cells	PCR	131/180	57/82	74/98	311

Jin W. Kim *et al.* 2000 [67]	Korea	46.5 ± 10.1 / 46.5 ± 10.1	Blood cells	PCR	181/181	86/85	95 /96	362
Chu Chen *et al.* 1999 [22]	Washington State	NA	Blood cells	PCR	190/206	89/88	101 /118	396
A.P. Warwick *et al.* 1994 [43]	United Kingdom	NA	Blood cells	PCR	255/178	122/74	133/104	433

Legend: NA= not available, PCR= Polymerase Chain Reaction, *GSTM1*= Glutathione S-Transferase Mu1.

Table S2. Summary of the Mix statistic results in the meta-analysis

Studies (cases/controls)	Articles (n)	OR (95%CI)	Z_{test}	p-value	Q	Heterogeneity		τ^2	$P_{egger's\ test}$	$P_{Begg\ \&\ Mazumdar\ test}$	$P_{hi\text{-}square\ test}$
						P_Q	I^2				
GSTM1-null											
Mix (CC and SIL)	36	1.41 (1.14-1.75) [R]	3.31	0.001**	160.51	0.000	78.20%	0.25	0.340	0.205	0.000
***GSTM1-null* and histological status**											
CC	24	1.47 (1.07-2.03) [R]	2.53	0.011**	129.98	0.000	82.31%	0.34	0.247	0.150	0.000
SCC	12	1.52 (1.02-2.26) [R]	2.33	0.020*	46.39	0.000	76.29%	0.20	0.224	0.583	0.000
AC	02	1.39 (0.01-201.21) [F]	0.84	0.399	0.00	0.961	0.00%	0.00	---	0.317	0.199
Unknow_CC	11	1.43 (0.77-2.65) [R]	1.29	0.197	82.65	0.000	87.90%	0.68	0.510	0.186	0.000
SIL	15	1.42 (0.99-2.04) [R]	2.10	0.035	57.27	0.000	75.56%	0.28	0.285	0.138	0.000
SIL	14	1.50 (1.03-2.18) [R]	2.33	0.020*	50.09	0.000	74.04%	0.28	0. 528	0.155	0.000
LSIL	09	1.21 (0.94-1.56) [F]	1.75	0.081	4.01	0.856	0.00%	0.00	0.171	0.118	0.079
HSIL	12	1.48 (0.86-2.55) [R]	1.57	0.116	62.06	0.000	82.28%	0.60	0.462	0.064	0.000
***GSTM1-null* and source of controls**											
Hospital-based											
Mix (**CC** and **SIL**)	27	1.35 (1.04-1.76) [R]	2.39	**0.017***	134.26	0.000	80.63%	0.31	0,819	0.559	0.000
CC	15	1.45 (0.90-2.35) [R]	1.66	0.098	105.15	0.000	86.69%	0.54	0.579	0.299	0.000
Population-based											
Mix (**CC** and **SIL**)	04	1.22 (0.66-2.26) [R]	1.04	0.299	8.85	0.031	66.10%	0.10	0.141	0.174	0.003
CC	04	1.15 (0.63-2.09) [R]	0.73	0.463	7.94	0.047	62.23%	0.09	0.594	0.174	0.015
Unclarified											
Mix (CC and SIL)	04	1.88 (0.65-5.43) [R]	1.89	0.058	9.43	0.024	68.18%	0.19	0.223	0.042	0.000
CC	04	1.76 (0.61-5.11) [R]	1.69	0.091	8.33	0.040	63.99%	0.17	0.340	0.174	0.000
***GSTM1-null* and Geographic region**											
Africa											
Mix_Africa	01	1.19 (0.34-4.09)	---	---	---	---	---	---	---	---	---
America											
Mix_America	06	0.87 (0.51-1.46) [R]	-0.71	0.477	13.84	0.017	63.88%	0.14	0.865	0.348	0.002
CC_America	02	0.56 (0.00-152.96) [R]	-1.32	0.185	6.31	0.012	84.15%	0.33	---	0.317	0.000
SIL_America	02	1.08 (0.07-16.13) [F]	0.37	0.710	0.00	0.968	0.00%	0.00	---	0.317	0.406
SCC_America	01	0.85 (0.57-1.26)	---	---	---	---	---	---	---	---	0.135
AC_America	00	---	---	---	---	---	---	---	---	---	---
HSIL_America	00	---	---	---	---	---	---	---	---	---	---
LSIL_America	00	---	---	---	---	---	---	---	---	---	---

Asia											
Mix_Asia	21	1.49 (1.18-1.86) [R]	3.64	0.000**	58.49	0.000	65.81%	0.12	0.331	0.740	0.000
CC_Asia	16	1.54 (1.15-2.06) [R]	3.13	0.002**	51.13	0.000	70.67%	0.16	0.179	0.280	0.000
SCC_Asia	10	1.74 (1.13-2.66) [R]	2.94	0.003**	32.51	0.000	72.32%	0.17	0.197	0.531	0.000
AC_Asia	02	1.39 (0.01-201.21) [F]	0.84	0.399	0.00	0.961	0.00%	0.00	---	0.317	0.199
SIL_Asia	05	1.11 (0.77-1.60) [F]	0.78	0.437	0.72	0.949	0.00%	0.00	0.380	0.462	0.358
HSIL_Asia	04	0.95 (0.51-1.76) [F]	-0.26	0.798	0.51	0.916	0.00%	0.00	0.028*	0.734	0.342
LSIL_Asia	04	1.14 (0.72-1.82) [F]	0.90	0.365	0.44	0.931	0.00%	0.00	0.048*	0.089	0.342
Europe											
Mix_Europe	07	1.28 (0.90-1.81) [R]	1.71	0.087	12.24	0.057	50.97%	0.08	0.193	0.453	0.001
CC_Europe	04	1.05 (0.61-1.82) [F]	0.29	0.774	2.77	0.428	0.00%	0.00	0.102	0.042*	0.112
SCC_Europe	01	0.77 (0.45-1.32)	---	---	---	---	---	---	---	---	0.135
AC_Europe	00	---	---	---	---	---	---	---	---	---	---
SIL_Europe	07	1.37 (0.90-2.09) [R]	1.83	0.067	14.24	0.027	57.86%	0.13	0.120	0.176	0.000
HSIL_Europe	07	1.34 (0.72-2.51) [R]	1.16	0.246	18.36	0.005	67.31%	0.26	0.142	0.099	0.000
LSIL_Europe	05	1.31 (0.82-2.07) [F]	1.61	0.107	3.20	0.526	0.00%	0.00	0.066	0.050*	0.055
***GSTM1-null* and DNA source**											
Blood cell											
Mix_Blood cell	29	1.31 (1.07-1.61) [R]	2.77	0.006**	87.62	0.000	68.04%	0.15	0.139	0.115	0.000
CC_Blood cell	22	1.27 (0.98-1.65) [R]	1.94	0.052	69.76	0.000	69.90%	0.17	0.193	0.067	0.000
SCC_Blood cell	11	1.42 (0.94-2.16) [R]	1.89	0.059	35.52	0.000	71.84%	0.17	0.086	0.312	0.000
AC_Blood cell	02	1.39 (0.01-201.21) [F]	0.84	0.399	0.00	0.961	0.00%	0.00	---	0.317	0.199
SIL_Blood cell	08	1.17 (0.92-1.49) [F]	1.58	0.115	11.65	0.113	39.93%	0.06	0.161	0.138	0.003
HSIL_Blood cell	06	1.30 (0.61-2.81) [R]	0.89	0.374	14.02	0.016	64.33%	0.28	0.008*	0.015*	0.001
LSIL_Blood cell	06	1.26 (0.89-1.76) [F]	1.72	0.085	3.72	0.590	0.00%	0.00	0.236	0.188	0.038
Cervical cell											
CC_Cervical cell	00	---	---	---	---	---	---	---	---	---	---
SIL_Cervical cell	05	1.19 (0.82-1.73) [F]	1.27	0.203	4.06	0.398	1.47%	0.00	0.539	0.806	0.074
HSIL_Cervical cell	05	1.14 (0.75-1.73) [F]	0.87	0.382	5.49	0.240	27.16%	0.04	0.253	0.806	0.055
LSIL_Cervical cell	03	1.12 (0.48-2.63) [F]	0.56	0.574	0.05	0.977	0.00%	0.00	0.000*	0.296	0.423
Tissue											
Mix_Tissue	01	2.33 (1.61-3.36)	---	---	---	---	---	---	---	---	0.000
CC_Tissue	01	2.62 (1.77-3.88)	---	---	---	---	---	---	---	---	0.000
SIL_Tissue	01	1.24 (0.54-2.82)	---	---	---	---	---	---	---	---	0.223
***GSTM1-null* and HPV infection status**											
HPV-positive											
Mix_HPV +	08	2.40 (1.20-4.82) [R]	2.97	0.003**	23.87	0.001	70.67%	0.41	0.545	0.621	0.000

CC_HPV+	03	4.88 (0.43-55.92) [R]	2.79	…	8.58	0.014	76.69%	0.69	0.558	0.602	0.000
CC_HPV+	03	3.96 (1.41-11.14) [F]	5.73	0.000	8.58	0.014	76.69%	0.69	0.558	0.602	0.000
SCC_HPV+	01	2.72 (1.48-4.98)	---	---	---	---	---	---	---	---	0.001
AC_HPV+	00	---	---	---	---	---	---	---	---	---	---
SIL_HPV+	06	1.93 (0.67-5.52) [R]	1.60	0.109	18.46	0.002	72.91%	0.61	0.818	0.851	0.000
HSIL_HPV+	04	2.12 (0.32-13.99) [R]	1.27	0.205	17.49	0.001	82.84%	0.91	0.731	1	0.000
LSIL_HPV+	01	2.18 (0.47-10.10)	---	---	---	---	---	---	---	---	0.135
HPV-negative											
Mix_HPV -	07	1.74 (0.65-4.68) [R]	1.37	0.170	41.61	0.000	85.58%	0.88	0.983	0.881	0.000
CC_HPV-	03	2.77 (0.05-168.38) [R]	1.07	0.287	23.93	0.000	91.64%	1.79	0.531	0.602	0.000
SCC_HPV-	01	1.93 (1.04-3.58)	---	---	---	---	---	---	---	---	0.018
AC_HPV-	00	---	---	---	---	---	---	---	---	---	
SIL_HPV-	05	1.83 (0.43-7.84) [R]	1.15	0.249	25.64	0.000	84.40%	1.15	0.765	0.624	0.000
HSIL_HPV-	03	2.23 (0.03-145.59) [R]	0.83	0.409	17.24	0.000	88.40%	3.06	0.246	0.602	0.000
LSIL_HPV-	01	0.79 (0.37-1.72)	---	---	---	---	---	---	---	---	0.223
***GSTM1-null* and Smoking status**											
Smoking											
Mix_Smoking	11	1.23 (0.96-1.58) [F]	1.88	0.060	10.76	0.376	7.09%	0.01	0.428	0.815	0.006
CC_ Smoking	05	1.30 (0.87-1.93) [F]	1.80	0.072	4.67	0.323	14.32%	0.02	0.963	0.624	0.02
SCC_ Smoking	04	1.12 (0.64-1.94) [F]	0.62	0.532	2.54	0.468	0.00%	0.00	0.039*	0.042*	0.151
AC_ Smoking	00	---	---	---	---	---	---	---	---	---	---
SIL_ Smoking	04	0.84 (0.43-1.63) [F]	-0.84	0.401	0.54	0.910	0.00%	0.00	0.410	0.497	0.265
HSIL_ Smoking	02	0.68 (0.03-14.97) [F]	-1.56	0.119	0.04	0.842	0.00%	0.00	---	0.317	0.061
LSIL_ Smoking	02	1.11 (0.03-48.95) [F]	0.36	0.719	0.13	0.720	0.00%	0.00	---	0.317	0.406
Non-smoking											
Mix_Non-Smoking	11	1.31 (0.94-1.83) [R]	1.84	0.065	22.68	0.012	55.91%	0.14	0.211	0.697	0.000
CC_ Non-Smoking	06	1.11 (0.53-2.35) [R]	0.36	0.720	25.03	0.000	80.02%	0.38	0.093	0.348	0.000
SCC_ Non-Smoking	04	0.95 (0.24-3.81) [R]	-0.11	0.914	23.01	0.000	86.96%	0.85	0.271	0.497	0.000
AC_ Non-Smoking	00	---	---	---	---	---	---	---	---	---	---
SIL_ Non-Smoking	04	1.06 (0.53-2.11) [F]	0.25	0.805	1.45	0.694	0.00%	0.00	0.636	1	0.202
HSIL_ Non-Smoking	02	0.82 (0.00-816.94) [R]	-0.37	0.711	2.51	0.113	60.09%	0.36	---	0.317	0.061
LSIL_ Non-Smoking	02	1.16 (0.02-72.62) [F]	0.45	0.650	0.44	0.507	0.00%	0.00	---	0.317	0.287
***GSTM1-null*_Smoking status_ HPV infection**	01	---	---	---	---	---	---	---	---	---	---

Legend: CC = all **C**ervical **C**ancer; SIL= all **S**quamous **I**ntraepithelial **L**esions; LSIL= **L**ow-grade **S**quamous **I**ntraepithelial **L**esions; HSIL= **H**igh-grade **S**quamous **I**ntraepithelial **L**esions; SCC= **S**quamous **C**ell **C**arcinoma; AC= **A**denocarcinoma; ASC= **A**denosquamous **C**arcinoma; HPV+ = positive infection of human papillomavirus; HPV- = negative infection of human papillomavirus, Mix= group composed of cases with a mixture of lesions and cancer, * = statistical significant result, ** = highly significant, R=Random effect model, F=fixed effect model