

SUPPLEMENTARY DATA

Table S1. Genetic polymorphisms in *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genes and quality control results.

Gene	TagSNP	Other SNPs on the block	Genotype call rate (%)	Genotype concordance rate	HWE	Passed quality check?
<i>PTGS2</i>	rs5275	Candidate SNP	100	1.00	1.00	Yes
	rs20417	Candidate SNP	100	1.00	1.00	Yes
	rs689466	Candidate SNP	100	1.00	0.52	Yes
<i>ABCC4</i>	rs12867485	rs9561811 rs17189481	0	-	-	No
	rs1611822	rs1751015	100	1.00	0.85	Yes
	rs1628382	rs4148527 rs8001657 rs12584534	27	-	-	No
	rs1678354	rs1751059 rs1729759	100	1.00	<0.0001	No
	rs1678374	rs1751025	100	1.00	0.78	Yes
	rs1678386	rs9516530	100	1.00	0.51	Yes
	rs1678396	singleton	100	1.00	0.26	Yes
	rs1678405	rs6492768	99	1.00	0.42	Yes
	rs17268122	rs1479389 rs17189376 rs17189446 rs17268163	99	1.00	0.014	No
	rs1751027	rs1564351 rs4148487 rs17189390 rs17268129 rs17268170	100	1.00	0.23	Yes
	rs1751031	rs931111 rs1189442 rs1189443 rs1189444 rs1189451 rs1189452 rs1612388 rs1630901 rs1729747 rs1751033 rs1751034 rs2619312	100	1.00	0.20	Yes
	rs1751051	rs1751050	100	1.00	1.00	Yes
	rs2127295	rs1564354 rs1564355 rs1617785 rs1630807 rs1638342 rs1678363 rs1678394 rs1729748 rs2698243 rs2766481 rs3825415 rs6650282	100	1.00	0.40	Yes
	rs2274403	rs3864997 rs4148481	100	1.00	0.52	Yes
	rs2892713	rs12865305	100	1.00	0.14	Yes
	rs2892715	rs9561814	100	1.00	0.26	Yes

SNP: Single Nucleotide Polymorphism; HWE: Hardy-Weinberg equilibrium.

Table S1 (cont.). Genetic polymorphisms in *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genes and quality control results.

Gene	TagSNP	Other SNPs on the block	Genotype call rate (%)	Genotype concordance rate	HWE	Passed quality check?
<i>ABCC4</i>	rs3742106	rs4148544 rs4148549 rs4148551 rs7330196 rs9302039 rs9524769	100	1.00	0.92	Yes
	rs3782958	rs4148515 rs7985457 rs10508023	100	1.00	0.74	Yes
	rs4148421	singleton	100	1.00	1.00	Yes
	rs4148422	rs17300935	100	1.00	0.0022	No
	rs4148437	rs2892716 rs4148436 rs4148446 rs9556466 rs10508018	100	1.00	0.38	Yes
	rs4148476	rs4773843 rs9524822	100	1.00	0.13	Yes
	rs4612933	rs899494 rs899495 rs899496 rs1678403 rs1824911 rs1824913 rs1926657 rs3782965 rs4148465 rs4148469 rs4303338 rs4334136 rs4505186 rs4773854 rs4773855 rs7325019 rs7333234 rs7335147 rs7983336 rs7987653 rs7988494 rs9524831 rs9524833 rs9524845 rs9524856 rs12870204	100	1.00	1.00	Yes
	rs4771912	rs7981095	100	1.00	0.70	Yes
	rs6492763	rs10508024	100	1.00	0.34	Yes
	rs7993878	rs9302040 rs9302042 rs9302043 rs9556455 rs9561768 rs9561769 rs9590168 rs10219913	100	1.00	0.25	Yes

SNP: Single Nucleotide Polymorphism; HWE: Hardy-Weinberg equilibrium.

Table S1 (cont.). Genetic polymorphisms in *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genes and quality control results.

Gene	TagSNP	Other SNPs on the block	Genotype call rate (%)	Genotype concordance rate	HWE	Passed quality check?
<i>ABCC4</i>	rs8002180	rs4148424 rs4771910 rs7317112 rs7322318 rs8001475 rs9584288 rs9590228	100	1.00	0.43	Yes
		rs869951	100	1.00	0.70	Yes
		rs9524821	100	1.00	0.42	Yes
		rs9590220	100	1.00	0.016	No
		rs9590222	64	-	-	No
<i>HPGD</i>	rs2612656	Candidate SNP	100	1.00	0.65	Yes
	rs2555639	Candidate SNP	100	1.00	1.00	Yes
	rs12500316	rs1863641 rs11722919	100	1.00	0.28	Yes
		singleton	100	1.00	0.065	Yes
	rs1426945	rs3756273	100	1.00	0.92	Yes
	rs1863642	rs2612659	100	1.00	0.23	Yes
	rs2303520	rs9312555 rs13106936 rs13127058 rs17060521	100	1.00	0.49	Yes
		rs2555632	100	1.00	0.43	Yes
	rs2612656	rs1816204 rs3846298 rs3857075 rs7685956 rs11133042	0	-	-	No
		rs8752	100	1.00	0.84	Yes
<i>SLCO2A1</i>	rs10935090	singleton	100	1.00	0.48	Yes
	rs1131598	singleton	100	1.00	0.26	Yes
	rs11915399	singleton	100	1.00	1.00	Yes
	rs4241362	rs4241361 rs4634113 rs6804798 rs9828294 rs9855403 rs9874493 rs9882333 rs11720811	100	1.00	0.42	Yes
		rs4241365	100	1.00	0.61	Yes
	rs4331673	rs4241361 rs6804798 rs9828294 rs9840711 rs9855403 rs9857498 rs9874493 rs11720811 rs11720843	100	1.00	0.87	Yes
		rs4854784	100	1.00	0.61	Yes
	rs4854784	singleton	100	1.00	0.61	Yes
	rs4854784	singleton	100	1.00	0.61	Yes

SNP: Single Nucleotide Polymorphism; HWE: Hardy-Weinberg equilibrium.

Table S1 (cont.). Genetic polymorphisms in *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genes and quality control results.

Gene	TagSNP	Other SNPs on the block	Genotype call rate (%)	Genotype concordance rate	HWE	Passed quality check?
<i>SLCO2A1</i>	rs6439448	rs2370512 rs3923835 rs34550074	100	1.00	0.88	Yes
	rs7340717	rs7340718	100	1.00	0.32	Yes
	rs7616492	rs10935089	100	1.00	0.69	Yes
	rs7625035	rs9822027	100	1.00	0.30	Yes
	rs7646392	rs4327389 rs7646298 rs7646473	100	1.00	0.29	Yes
	rs9820625	rs9836830 rs9917636 rs11709172 rs13083175	100	1.00	0.46	Yes
	rs9821091	rs6439450 rs7617777 rs9834727 rs9841380	100	1.00	0.44	Yes
	rs9834412	rs4854785 rs13067921	100	1.00	0.90	Yes

SNP: Single Nucleotide Polymorphism; HWE: Hardy-Weinberg equilibrium.

Table S2. Genotype risk estimates for the involvement of *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genetic variants in gastric cancer onset and estimated age at diagnosis.

SNP	Model	Genotype	Univariate analysis			Multivariate analysis*			Age at diagnosis			
			OR	95% CI	p value	aOR	95% CI	p value	Median (years)	95% CI	p value	
PTGS2												
rs5275	Codominant	TT	1.00	-	0.50	1.00	-	0.57	73.00	71.36-74.64	-	
		TC	1.20	0.85-1.71		1.27	0.81-1.99		73.00	70.58-75.42	0.18	
		CC	1.28	0.70-2.34		1.20	0.55-2.63		76.00	70.72-81.28	0.47	
	Dominant	TT	1.00	-	0.25	1.00	-	0.29	73.00	71.36-74.64	-	
		TC-CC	1.22	0.87-1.70		1.26	0.82-1.93		73.00	70.58-75.42	0.43	
	Recessive	TT-TC	1.00	-	0.59	1.00	-	0.85	73.00	71.62-74.38	-	
		CC	1.17	0.66-2.09		1.08	0.51-2.28		76.00	70.72-81.28	0.25	
	Overdominant	TT-CC	1.00	-	0.39	1.00	-	0.34	73.00	71.32-74.68	-	
		TC	1.16	0.83-1.62		1.24	0.80-1.90		73.00	71.58-75.42	0.12	
	Log-additive	-	1.16	0.90-1.50	0.26	1.16	0.84-1.62	0.37	-			
rs20417	Codominant	GG	1.00	-	0.76	1.00	-	0.65	73.00	71.60-74.40	-	
		GC	1.15	0.79-1.65		1.17	0.73-1.87		72.00	69.73-74.27	0.26	
		CC	1.15	0.43-3.10		1.61	0.46-5.57		77.00	57.75-96.25	0.53	
	Dominant	GG	1.00	-	0.45	1.00	-	0.42	73.00	71.60-74.40	-	
		GC-CC	1.15	0.80-1.63		1.20	0.76-1.89		72.00	68.91-75.09	0.43	
	Recessive	GG-GC	1.00	-	0.84	1.00	-	0.51	73.00	71.63-74.37	-	
		CC	1.11	1.41-2.96		1.53	0.44-5.26		77.00	57.75-96.25	0.44	
	Overdominant	GG-CC	1.00	-	0.49	1.00	-	0.56	73.00	71.58-74.42	-	
		GC	1.14	0.79-1.64		1.15	0.72-1.83		72.00	69.73-74.27	0.26	
	Log-additive	-	1.12	0.82-1.53	0.47	1.20	0.81-1.79	0.36	-			
rs689466	Codominant	AA	1.00	-	0.054	1.00	-	0.021	73.00	71.25-74.75	-	
		AG	1.29	0.89-1.86		1.50	0.93-2.42		73.00	68.89-77.11	0.21	
		GG	2.33	1.10-4.92		3.40	1.29-8.97		70.00	62.49-77.52	0.008	
	Dominant	AA	1.00	-	0.056	1.00	-	0.022	73.00	71.25-74.75	-	
		AG-GG	1.40	0.99-1.98		1.69	1.08-2.65		73.00	69.94-76.06	0.058	
	Recessive	AA-AG	1.00	-	0.046	1.00	-	0.027	73.00	71.48-74.52	-	
		GG	2.15	1.03-4.49		2.98	1.14-7.74		70.00	62.49-77.52	0.011	
	Overdominant	AA-GG	1.00	-	0.30	1.00	-	0.19	73.00	71.46-74.54	-	
		AG	1.21	0.85-1.74		1.37	0.86-2.19		73.00	68.89-77.11	0.38	
	Log-additive	-	1.40	1.06-1.86	0.021	1.66	1.15-2.40	0.007	-			

OR: odds ratio; aOR: odds ratio adjusted for age and gender; CI: confidence interval.

Values in **bold** are statistically significant (p < 0.05).

Table S2 (cont.). Genotype risk estimates for the involvement of *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genetic variants in gastric cancer onset and estimated age at diagnosis.

SNP	Model	Genotype	Univariate analysis			Multivariate analysis*			Age at diagnosis		
			OR	95% CI	p value	aOR	95% CI	p value	Median (years)	95% CI	p value
ABCC4											
rs1611822	Codominant	CC	1.00	-	0.20	1.00	-	0.53	72.00	70.49-73.51	-
		CT	1.24	0.87-1.78		1.22	0.77-1.93		72.00	70.01-73.99	0.95
		TT	1.52	0.95-2.43		1.37	0.75-2.47		72.00	66.99-77.01	0.42
	Dominant	CC	1.00	-	0.12	1.00	-	0.30	72.00	70.49-73.51	-
		CT-TT	1.31	0.93-1.83		1.26	0.82-1.93		72.00	70.24-73.76	0.75
	Recessive	CC-CT	1.00	-	0.18	1.00	-	0.46	72.00	70.80-73.20	-
		TT	1.34	0.88-2.04		1.22	0.72-2.08		72.00	66.99-77.01	0.45
	Overdominant	CC-TT	1.00	-	0.62	1.00	-	0.66	72.00	70.55-73.45	-
		CT	1.08	0.79-1.49		1.10	0.73-1.65		72.00	70.01-73.99	0.78
	Log-additive	-	1.23	0.98-1.55	0.072	1.18	0.88-1.57	0.27	-		
rs1678374	Codominant	TT	1.00	-	0.076	1.00	-	0.063	72.00	69.48-74.52	-
		TC	0.82	0.58-1.15		1.04	0.67-1.63		72.00	69.74-74.26	0.47
		CC	0.56	0.33-0.94		0.50	0.26-0.97		73.00	71.00-75.00	0.57
	Dominant	TT	1.00	-	0.09	1.00	-	0.55	72.00	69.48-74.52	-
		TC-CC	0.75	0.54-1.04		0.88	0.58-1.34		72.00	70.77-73.23	0.66
	Recessive	TT-TC	1.00	-	0.05	1.00	-	0.019	72.00	70.38-73.63	-
		CC	0.63	0.39-1.01		0.49	0.26-0.91		73.00	71.00-75.00	0.39
	Overdominant	TT-CC	1.00	-	0.30	1.00	-	0.28	72.00	70.46-73.54	-
		TC	1.21	0.85-1.74		1.25	0.83-1.89		72.00	69.74-74.26	0.31
	Log-additive	-	0.77	0.60-0.97	0.027	0.78	0.58-1.06	0.11	-		
rs1678386	Codominant	AA	1.00	-	0.82	1.00	-	0.34	72.00	70.04-73.96	-
		AC	0.90	0.64-1.26		0.75	0.49-1.16		72.00	70.48-73.52	0.80
		CC	0.98	0.56-1.72		1.13	0.55-2.33		71.00	58.59-83.41	0.87
	Dominant	AA	1.00	-	0.57	1.00	-	0.31	72.00	70.04-73.96	-
		AC-CC	0.91	0.66-1.26		0.81	0.54-1.22		72.00	70.06-73.94	0.89
	Recessive	AA-AC	1.00	-	0.93	1.00	-	0.50	72.00	70.91-73.09	-
		CC	1.03	0.59-1.77		1.28	0.63-2.58		71.00	58.59-83.41	0.75
	Overdominant	AA-CC	1.00	-	0.53	1.00	-	0.15	72.00	70.03-73.97	-
		AC	0.90	0.65-1.25		0.74	0.48-1.12		72.00	70.48-73.52	0.74
	Log-additive	-	0.95	0.75-1.22	0.70	0.92	0.67-1.27	0.63	-		

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Table S2 (cont.). Genotype risk estimates for the involvement of *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genetic variants in gastric cancer onset and estimated age at diagnosis.

SNP	Model	Genotype	Univariate analysis			Multivariate analysis*			Age at diagnosis		
			OR	95% CI	p value	aOR	95% CI	p value	Median (years)	95% CI	p value
rs1678396	Codominant	TT	1.00	-	0.74	1.00	-	0.77	70.00	68.08-71.92	-
		TC	0.91	0.63-1.30		0.88	0.55-1.40		74.00	71.50-76.50	0.39
		CC	1.06	0.67-1.69		0.82	0.45-1.47		72.00	69.70-74.30	0.58
	Dominant	TT	1.00	-	0.75	1.00	-	0.50	70.00	68.08-71.92	-
		TC-CC	0.94	0.67-1.33		0.86	0.56-1.33		73.00	71.65-74.35	0.39
	Recessive	TT-TC	1.00	-	0.57	1.00	-	0.63	72.00	70.67-73.33	-
		CC	1.13	0.75-1.70		0.88	0.52-1.48		72.00	69.70-74.30	0.92
	Overdominant	TT-CC	1.00	-	0.46	1.00	-	0.81	71.00	69.65-72.35	-
		TC	0.89	0.64-1.22		0.95	0.63-1.43		74.00	71.50-76.50	0.39
	Log-additive	-	1.01	0.80-1.28	0.92 0.052	0.90	0.67-1.20	0.48	-		
rs1678405	Codominant	TT	1.00	-		1.00	-	0.09	72.00	70.40-73.60	-
		TC	0.73	0.52-1.02		0.81	0.52-1.25		72.00	69.60-74.40	0.58
		CC	0.54	0.29-0.99		0.44	0.20-0.95		74.00	67.60-80.40	0.68
	Dominant	TT	1.00	-	0.027	1.00	-	0.13	72.00	70.40-73.60	-
		TC-CC	0.69	0.50-0.96		0.73	0.48-1.10		72.00	70.18-73.82	0.70
	Recessive	TT-TC	1.00	-	0.11	1.00	-	0.049	72.00	70.58-73.42	-
		CC	0.63	0.35-1.13		0.49	0.23-1.03		74.00	67.60-80.40	0.58
	Overdominant	TT-CC	1.00	-	0.21	1.00	-	0.76	72.00	70.46-73.54	-
		TC	0.81	0.59-1.12		0.94	0.62-1.42		72.00	69.60-74.40	0.48
	Log-additive	-	0.73	0.57-0.94	0.015	0.72	0.52-0.99	0.041	-		
rs1751027	Codominant	AA	1.00	-	0.096	1.00	-	0.66	72.00	70.19-73.81	-
		AG	1.30	0.86-1.96		1.27	0.73-2.20		72.00	71.05-72.95	0.51
		GG	6.82	0.70-66.05		1.64	0.12-22.90		73.00	66.60-79.40	0.96
	Dominant	AA	1.00	-	0.13	1.00	-	0.37	72.00	70.19-73.81	-
		AG-GG	1.37	0.92-2.05		1.28	0.75-2.20		72.00	71.00-73.00	0.52
	Recessive	AA-AG	1.00	-	0.076	1.00	-	0.73	72.00	70.58-73.42	-
		GG	6.51	0.67-62.91		1.57	0.11-22.03		73.00	66.60-79.40	1.00
	Overdominant	AA-GG	1.00	-	0.24	1.00	-	0.40	72.00	70.26-73.74	-
		AG	1.28	0.85-1.93		1.27	0.73-2.19		72.00	71.05-72.95	0.51
	Log-additive	-	1.42	0.97-2.08	0.074	1.27	0.76-2.12	0.36	-		

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Table S2 (cont.). Genotype risk estimates for the involvement of *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genetic variants in gastric cancer onset and estimated age at diagnosis.

SNP	Model	Genotype	Univariate analysis			Multivariate analysis*			Age at diagnosis		
			OR	95% CI	p value	aOR	95% CI	p value	Median (years)	95% CI	p value
rs1751031	Codominant	AA	1.00	-	0.10	1.00	-	0.073	72.00	70.25-73.75	-
		AG	0.69	0.48		0.61	0.39-0.95		72.00	69.72-74.28	0.66
		GG	1.15	0.49-2.70		0.57	0.17-1.92		78.00	69.81-86.19	0.29
	Dominant	AA	1.00	-	0.068	1.00	-	0.022	72.00	70.25-73.75	-
		AG-GG	0.73	0.52-1.03		0.60	0.39-0.94		72.00	70.08-73.93	0.46
	Recessive	AA-AG	1.00	-	0.55	1.00	-	0.52	72.00	70.61-73.39	-
		GG	1.30	0.56-3.01		0.68	0.21-2.24		78.00	69.81-86.19	0.31
	Overdominant	AA-GG	1.00	-	0.034	1.00	-	0.036	72.00	70.28-73.72	-
		AG	0.69	0.48-0.98		0.62	0.40-0.98		72.00	69.72-74.28	0.79
	Log-additive	-	0.81	0.61-1.09	0.17	0.65	0.44-0.96	0.028	-		
rs1751051	Codominant	TT	1.00	-	0.058	1.00	-	0.22	71.00	69.28-72.72	-
		TA	1.50	1.07-2.10		1.39	0.90-2.14		73.00	71.46-74.54	0.96
		AA	1.36	0.77-2.41		1.61	0.80-3.21		71.00	65.65-76.35	0.54
	Dominant	TT	1.00	-	0.018	1.00	-	0.09	73.00	71.45-74.55	-
		TA-AA	1.48	1.07-2.04		1.43	0.94-2.16		71.00	69.28-72.72	0.86
	Recessive	TT-TA	1.00	-	0.71	1.00	-	0.35	72.00	70.85-73.15	-
		AA	1.11	0.65-1.90		1.37	0.71-2.64		71.00	65.65-76.35	0.49
	Overdominant	TT-AA	1.00	-	0.032	1.00	-	0.26	71.00	69.38-72.62	-
		TA	1.42	1.03-1.95		1.27	0.84-1.92		73.00	71.46-74.54	0.83
	Log-additive	-	1.28	1.00-1.64	0.048	1.31	0.96-1.78	0.088	-		
rs2127295	Codominant	GG	1.00	-	0.39	1.00	-	0.30	73.00	71.01-74.99	-
		GA	0.94	0.64-1.36		1.10	0.67-1.81		71.00	69.16-72.84	0.61
		AA	1.24	0.79-1.95		1.55	0.86-2.79		72.00	69.64-74.36	0.50
	Dominant	GG	1.00	-	0.91	1.00	-	0.39	73.00	71.01-74.99	-
		GA-AA	1.02	0.72-1.45		1.22	0.77-1.95		72.00	70.40-73.60	0.52
	Recessive	GG-GA	1.00	-	0.18	1.00	-	0.14	72.00	70.51-73.49	-
		AA	1.30	0.89-1.90		1.46	0.89-2.37		72.00	69.64-74.36	0.49
	Overdominant	GG-AA	1.00	-	0.32	1.00	-	0.64	72.00	70.44-73.56	-
		GA	0.85	0.62-1.17		0.91	0.60-1.37		71.00	69.16-72.84	0.98
	Log-additive	-	1.10	0.88-1.39	0.39	1.24	0.92-1.67	0.15	-		

OR: odds ratio; aOR: odds ratio adjusted for age and gender; CI: confidence interval.

Values in **bold** are statistically significant (p < 0.05).

Table S2 (cont.). Genotype risk estimates for the involvement of *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genetic variants in gastric cancer onset and estimated age at diagnosis.

SNP	Model	Genotype	Univariate analysis			Multivariate analysis*			Age at diagnosis		
			OR	95% CI	p value	aOR	95% CI	p value	Median (years)	95% CI	p value
rs2274403	Codominant	AA	1.00	-	0.016	1.00	-	0.41	72.00	70.39-73.61	-
		AG	0.78	0.54-1.13		0.92	0.58-1.49		73.00	71.14-74.86	0.42
		GG	0.51	0.32-0.81		0.69	0.39-1.22		73.00	70.91-75.09	0.93
	Dominant	AA	1.00	-	0.035	1.00	-	0.44	72.00	70.39-73.61	-
		AG-GG	0.69	0.48-0.97		0.84	0.54-1.31		73.00	71.56-74.44	0.52
	Recessive	AA-AG	1.00	-	0.01	1.00	-	0.20	72.00	70.40-73.60	-
		GG	0.60	0.40-0.89		0.72	0.44-1.19		73.00	70.91-75.09	0.56
	Overdominant	AA-GG	1.00	-	0.80	1.00	-	0.70	72.00	70.75-73.25	-
		AG	1.04	0.76-1.43		1.08	0.72-1.63		73.00	71.14-74.86	0.31
	Log-additive	-	0.72	0.57-0.91	0.0046	0.84	0.63-1.11	0.22	-		
rs2892713	Codominant	CC	1.00	-	0.71	1.00	-	0.53	72.00	70.22-73.78	-
		CT	1.07	0.74-1.53		0.91	0.57-1.45		72.00	71.16-72.85	0.60
		TT	0.72	0.28-1.85		0.51	0.15-1.79		75.00	66.16-83.84	0.44
	Dominant	CC	1.00	-	0.89	1.00	-	0.50	72.00	70.22-73.78	-
		CT-TT	1.02	0.72-1.45		0.86	0.55-1.35		72.00	71.11-72.89	0.48
	Recessive	CC-CT	1.00	-	0.45	1.00	-	0.29	72.00	70.64-73.36	-
		TT	0.71	0.28-1.80		0.53	0.15-1.82		75.00	66.16-83.84	0.48
	Overdominant	CC-TT	1.00	-	0.66	1.00	-	0.79	72.00	70.17-73.83	-
		CT	1.08	0.76-1.55		0.94	0.59-1.49		72.00	71.16-72.85	0.66
	Log-additive	-	0.98	0.73-1.32	0.89	0.84	0.57-1.23	0.36	-		
rs2892715	Codominant	GG	1.00	-	0.52	1.00	-	0.73	72.00	70.56-73.44	-
		GA	1.07	0.75-1.53		1.18	0.75-1.85		73.00	71.20-74.80	0.56
		AA	0.82	0.51-1.33		0.99	0.54-1.81		72.00	69.81-74.19	0.76
	Dominant	GG	1.00	-	1.00	1.00	-	0.60	72.00	70.56-73.44	-
		GA-AA	1.00	0.72-1.40		1.12	0.73-1.72		73.00	71.58-74.42	0.67
	Recessive	GG-GA	1.00	-	0.28	1.00	-	0.71	72.00	70.42-73.58	-
		AA	0.79	0.51-1.22		0.90	0.52-1.56		72.00	69.81-74.19	0.56
	Overdominant	GG-AA	1.00	-	0.42	1.00	-	0.43	72.00	70.79-73.21	-
		GA	1.14	0.83-1.57		1.18	0.78-1.78		73.00	71.20-74.80	0.42
	Log-additive	-	0.94	0.75-1.18	0.57	1.02	0.77-1.37	0.87	-		

OR: odds ratio; aOR: odds ratio adjusted for age and gender; CI: confidence interval.

Values in **bold** are statistically significant (p < 0.05).

Table S2 (cont.). Genotype risk estimates for the involvement of *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genetic variants in gastric cancer onset and estimated age at diagnosis.

SNP	Model	Genotype	Univariate analysis			Multivariate analysis*			Age at diagnosis		
			OR	95% CI	p value	aOR	95% CI	p value	Median (years)	95% CI	p value
rs3742106	Codominant	AA	1.00	-	0.17	1.00	-	0.65	72.00	69.49-74.51	-
		AC	1.12	0.79-1.58		1.13	0.72-1.76		72.00	70.22-73.79	0.85
		CC	0.70	0.42-1.18		0.85	0.44-1.63		73.00	68.95-77.05	0.92
	Dominant	AA	1.00	-	0.95	1.00	-	0.80	72.00	69.49-74.51	-
		AC-CC	1.01	0.72-1.41		1.06	0.69-1.62		72.00	70.78-73.22	0.86
	Recessive	AA-AC	1.00	-	0.075	1.00	-	0.44	72.00	70.39-73.61	-
		CC	0.66	0.41-1.06		0.79	0.43-1.44		73.00	68.95-77.05	0.96
	Overdominant	AA-CC	1.00	-	0.19	1.00	-	0.43	72.00	69.82-74.18	-
		AC	1.24	0.90-1.70		1.18	0.78-1.78		72.00	70.22-73.79	0.89
	Log-additive	-	0.90	0.71-1.14	0.38	0.97	0.71-1.31	0.83	-		
rs3782958	Codominant	GG	1.00	-	0.20	1.00	-	0.14	72.00	70.29-73.71	-
		GC	0.80	0.55-1.16		0.72	0.45-1.16		72.00	69.75-74.25	0.71
		CC	0.43	0.12-1.50		0.32	0.07-1.44		74.00	-	0.92
	Dominant	GG	1.00	-	0.14	1.00	-	0.096	72.00	70.29-73.71	-
		GC-CC	0.76	0.53-1.10		0.68	0.43-1.08		72.00	69.73-74.29	0.72
rs3782958	Recessive	GG-GC	1.00	-	0.18	1.00	-	0.15	72.00	70.63-73.38	-
		CC	0.45	0.13-1.59		0.35	0.08-1.57		74.00	-	0.96
	Overdominant	GG-CC	1.00	-	0.29	1.00	-	0.23	72.00	70.28-73.72	-
		GC	0.82	0.57-1.19		0.75	0.47-1.20		72.00	69.75-74.25	0.70
	Log-additive	-	0.76	0.55-1.05	0.092	0.68	0.45-1.02	0.057	-		
rs4148421	Codominant	GG	1.00	-	0.66	1.00	-	0.27	71.00	67.11-74.89	-
		GA	0.90	0.61-1.31		0.69	0.43-1.12		72.00	70.81-73.19	0.81
		AA	1.07	0.69-1.66		0.92	0.52-1.63		72.00	69.24-74.76	0.62
	Dominant	GG	1.00	-	0.78	1.00	-	0.23	71.00	67.11-74.89	-
		GA-AA	0.95	0.67-1.35		0.76	0.48-1.19		72.00	70.84-73.16	0.71
	Recessive	GG-GA	1.00	-	0.47	1.00	-	0.55	72.00	70.54-73.46	-
		AA	1.15	0.79-1.67		1.16	0.71-1.89		72.00	69.24-74.76	0.63
	Overdominant	GG-AA	1.00	-	0.39	1.00	-	0.11	72.00	69.71-74.29	-
		GA	0.87	0.63-1.20		0.72	0.47-1.08		72.00	70.81-73.19	0.93
	Log-additive	-	1.03	0.82-1.29	0.81	0.94	0.70-1.26	0.68	-		

OR: odds ratio; aOR: odds ratio adjusted for age and gender; CI: confidence interval.

Values in **bold** are statistically significant (p < 0.05).

Table S2 (cont.). Genotype risk estimates for the involvement of *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genetic variants in gastric cancer onset and estimated age at diagnosis.

SNP	Model	Genotype	Univariate analysis			Multivariate analysis*			Age at diagnosis		
			OR	95% CI	p value	aOR	95% CI	p value	Median (years)	95% CI	p value
rs4148437	Codominant	TT	1.00	-	0.67	1.00	-	0.87	72.00	70.47-73.53	-
		TC	1.08	0.76-1.52		1.09	0.70-1.71		73.00	71.10-74.91	0.38
		CC	0.86	0.52-1.43		0.95	0.51-1.79		72.00	66.67-77.33	0.65
	Dominant	TT	1.00	-	0.90	1.00	-	0.79	72.00	70.47-73.53	-
		TC-CC	1.02	0.74-1.42		1.06	0.70-1.61		73.00	71.55-74.45	0.52
	Recessive	TT-TC	1.00	-	0.43	1.00	-	0.74	72.00	70.47-73.53	-
		CC	0.83	0.52-1.32		0.91	0.51-1.63		72.00	66.67-77.33	0.45
	Overdominant	TT-CC	1.00	-	0.50	1.00	-	0.62	72.00	70.67-73.33	-
		TC	1.12	0.81-1.54		1.11	0.73-1.67		73.00	71.10-74.91	0.27
	Log-additive	-	0.96	0.76-1.22	0.76	1.00	0.75-1.35	0.98	-		
rs4148476	Codominant	TT	1.00	-	0.81	1.00	-	0.44	72.00	70.67-73.34	-
		TG	1.12	0.78-1.61		1.27	0.79-2.05		74.00	70.85-77.15	0.57
		GG	0.98	0.42-2.31		1.66	0.58-4.77		71.00	55.55-86.46	0.61
	Dominant	TT	1.00	-	0.57	1.00	-	0.23	72.00	70.67-73.34	-
		TG-GG	1.11	0.78-1.56		1.32	0.84-2.07		73.00	69.73-76.27	0.69
	Recessive	TT-TG	1.00	-	0.91	1.00	-	0.42	72.00	70.88-73.12	-
		GG	0.95	0.41-2.22		1.56	0.55-4.42		71.00	55.55-86.46	0.57
	Overdominant	TT-GG	1.00	-	0.52	1.00	-	0.37	72.00	70.72-73.28	-
		TG	1.12	0.79-1.61		1.24	0.78-1.98		74.00	70.85-77.15	0.53
	Log-additive	-	1.07	0.80-1.42	0.66	1.28	0.88-1.86	0.20	-		
rs4612933	Codominant	CC	1.00	-	0.45	1.00	-	0.31	72.00	70.39-73.61	-
		CT	0.81	0.56-1.16		0.73	0.46-1.15		72.00	69.83-74.17	0.44
		TT	1.13	0.51-2.50		1.31	0.48-3.61		67.00	58.62-75.38	0.68
	Dominant	CC	1.00	-	0.32	1.00	-	0.27	72.00	70.39-73.61	-
		CT-TT	0.84	0.60-1.18		0.78	0.51-1.21		72.00	70.00-74.00	0.56
	Recessive	CC-CT	1.00	-	0.65	1.00	-	0.48	72.00	70.60-73.40	-
		TT	1.20	0.54-2.64		1.44	0.53-3.94		67.00	58.62-75.38	0.57
	Overdominant	CC-TT	1.00	-	0.22	1.00	-	0.15	72.00	70.42-73.58	-
		CT	0.80	0.56-0.14		0.72	0.45-1.13		72.00	69.83-74.17	0.40
	Log-additive	-	0.91	0.68-1.21	0.50	0.88	0.61-1.27	0.50	-		

OR: odds ratio; aOR: odds ratio adjusted for age and gender; CI: confidence interval.

Values in **bold** are statistically significant (p < 0.05).

Table S2 (cont.). Genotype risk estimates for the involvement of *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genetic variants in gastric cancer onset and estimated age at diagnosis.

SNP	Model	Genotype	Univariate analysis			Multivariate analysis*			Age at diagnosis		
			OR	95% CI	p value	aOR	95% CI	p value	Median (years)	95% CI	p value
rs4771912	Codominant	AA	1.00	-	0.52	1.00	-	0.20	72.00	70.79-73.21	-
		AG	0.84	0.57-1.24		0.64	0.38-1.08		72.00	69.45-74.55	0.19
		GG	0.61	0.17-2.26		0.58	0.14-2.46		70.00	-	0.71
	Dominant	AA	1.00	-	0.30	1.00	-	0.071	72.00	70.79-73.21	-
		AG-GG	0.82	0.56-1.20		0.64	0.39-1.05		72.00	70.49-73.51	0.24
	Recessive	AA-AG	1.00	-	0.48	1.00	-	0.53	72.00	70.87-73.13	-
		GG	0.64	0.17-2.34		0.64	0.15-2.70		70.00	-	0.58
	Overdominant	AA-GG	1.00	-	0.40	1.00	-	0.10	72.00	70.28-73.72	-
		AG	0.85	0.57-1.25		0.65	0.39-1.09		72.00	69.45-74.55	0.18
	Log-additive	-	0.82	0.58-1.16	0.26	0.68	0.44-1.05	0.077	-		
rs6492763	Codominant	TT	1.00	-	0.23	1.00	-	0.26	72.00	70.55-73.45	-
		TC	0.75	0.53-1.06		0.79	0.51-1.24		72.00	69.89-74.11	0.66
		CC	0.74	0.45-1.23		0.60	0.31-1.13		72.00	64.37-79.63	0.88
	Dominant	TT	1.00	-	0.084	1.00	-	0.17	72.00	70.55-73.45	-
		TC-CC	0.75	0.54-1.04		0.74	0.49-1.13		72.00	69.94-74.06	0.73
	Recessive	TT-TC	1.00	-	0.56	1.00	-	0.19	72.00	70.61-73.39	-
		CC	0.87	0.55-1.39		0.68	0.37-1.23		72.00	64.37-79.63	0.71
	Overdominant	TT-CC	1.00	-	0.20	1.00	-	0.68	72.00	70.48-73.52	-
		TC	0.81	0.59-1.12		0.92	0.61-1.38		72.00	69.89-74.11	0.55
	Log-additive	-	0.83	0.66-1.05	0.12	0.78	0.58-1.05	0.10	-		
rs7993878	Codominant	GG	1.00	-	0.40	1.00	-	0.18	72.00	70.54-73.46	-
		GA	0.84	0.57-1.25		0.67	0.40-1.13		76.00	73.59-78.42	0.29
		AA	0.51	0.14-1.83		0.42	0.09-1.97		68.00	51.28-84.72	0.84
	Dominant	GG	1.00	-	0.26	1.00	-	0.079	72.00	70.54-73.46	-
		GA-AA	0.81	0.55-1.18		0.64	0.39-1.06		76.00	73.52-78.48	0.29
	Recessive	GG-GA	1.00	-	0.30	1.00	-	0.29	72.00	70.63-73.37	-
		AA	0.53	0.15-1.90		0.46	0.10-2.14		68.00	51.28-84.72	0.90
	Overdominant	GG-AA	1.00	-	0.42	1.00	-	0.15	72.00	70.53-73.47	-
		GA	0.85	0.57-1.26		0.69	0.41-1.15		76.00	73.59-78.42	0.30
	Log-additive	-	0.80	0.57-1.13	0.20	0.66	0.42-1.04	0.064	-		

OR: odds ratio; aOR: odds ratio adjusted for age and gender; CI: confidence interval.

Values in **bold** are statistically significant (p < 0.05).

Table S2 (cont.). Genotype risk estimates for the involvement of *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genetic variants in gastric cancer onset and estimated age at diagnosis.

SNP	Model	Genotype	Univariate analysis			Multivariate analysis*			Age at diagnosis		
			OR	95% CI	p value	aOR	95% CI	p value	Median (years)	95% CI	p value
rs8002180	Codominant	TT	1.00	-	0.79	1.00	-	0.83	72.00	70.70-73.30	-
		TC	1.10	0.79-1.53		0.92	0.60-1.41		72.00	70.27-73.73	0.31
		CC	0.92	0.51-1.67		0.80	0.37-1.74		79.00	72.08-85.92	0.53
	Dominant	TT	1.00	-	0.70	1.00	-	0.60	72.00	70.70-73.30	-
		TC-CC	1.07	0.77-1.47		0.90	0.59-1.35		72.00	69.90-74.10	0.52
	Recessive	TT-TC	1.00	-	0.68	1.00	-	0.64	72.00	70.67-73.33	-
		CC	0.89	0.50-1.58		0.84	0.40-1.77		79.00	72.08-85.92	0.34
	Overdominant	TT-CC	1.00	-	0.53	1.00	-	0.79	72.00	70.62-73.38	-
		TC	1.11	0.80-1.54		0.95	0.62-1.43		72.00	70.27-73.73	0.21
	Log-additive	-	1.02	0.79-1.30	0.90	0.90	0.66-1.25	0.54	-		
rs869951	Codominant	GG	1.00	-	0.33	1.00	-	0.43	72.00	69.52-74.48	-
		GC	1.28	0.90-1.84		1.35	0.85-2.13		72.00	70.61-73.39	0.89
		CC	1.03	0.63-1.68		1.28	0.69-2.38		71.00	69.51-72.50	0.71
	Dominant	GG	1.00	-	0.26	1.00	-	0.20	72.00	69.52-74.48	-
		GC-CC	1.22	0.87-1.71		1.33	0.86-2.06		72.00	70.34-73.66	0.79
	Recessive	GG-GC	1.00	-	0.58	1.00	-	0.79	72.00	70.78-73.22	-
		CC	0.88	0.57-1.37		1.08	0.62-1.87		71.00	69.51-72.50	0.64
	Overdominant	GG-CC	1.00	-	0.14	1.00	-	0.30	72.00	70.39-73.61	-
		GC	1.27	0.92-1.75		1.24	0.82-1.87		72.00	70.61-73.39	0.94
	Log-additive	-	1.06	0.84-1.33	0.63	1.17	0.87-1.57	0.30	-		
rs9524821	Codominant	GG	1.00	-	0.15	1.00	-	0.33	72.00	70.08-73.92	-
		GA	1.05	0.74-1.49		1.22	0.78-1.92		72.00	70.15-73.85	0.48
		AA	1.56	0.98-2.49		1.57	0.85-2.89		71.00	67.01-74.99	0.86
	Dominant	GG	1.00	-	0.35	1.00	-	0.21	72.00	70.08-73.92	-
		GA-AA	1.17	0.84-1.62		1.31	0.86-1.99		72.00	70.29-73.71	0.63
	Recessive	GG-GA	1.00	-	0.056	1.00	-	0.23	72.00	70.88-73.13	-
		AA	1.53	0.99-2.34		1.42	0.81-2.48		71.00	67.01-74.99	0.62
	Overdominant	GG-AA	1.00	-	0.64	1.00	-	0.71	72.00	69.99-74.01	-
		GA	0.93	0.67-1.28		1.08	0.72-1.63		72.00	70.15-73.85	0.37
	Log-additive	-	1.21	0.96-1.51	0.10	1.25	0.93-1.67	0.14	-		

OR: odds ratio; aOR: odds ratio adjusted for age and gender; CI: confidence interval.

Values in **bold** are statistically significant (p < 0.05).

Table S2 (cont.). Genotype risk estimates for the involvement of *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genetic variants in gastric cancer onset and estimated age at diagnosis.

SNP	Model	Genotype	Univariate analysis			Multivariate analysis*			Age at diagnosis		
			OR	95% CI	p value	aOR	95% CI	p value	Median (years)	95% CI	p value
HPGD											
rs2612656	Codominant	AA	1.00	-	0.82	1.00	-	0.67	73.00	71.24-74.76	-
		AG	1.02	0.71-1.48		1.21	0.75-1.95		73.00	71.92-74.08	0.75
		GG	0.75	0.29-1.94		1.37	0.44-4.28		67.00	59.07-74.93	0.22
	Dominant	AA	1.00	-	0.97	1.00	-	0.39	73.00	71.24-74.76	-
		AG-GG	0.99	0.70-1.41		1.23	0.77-1.94		73.00	71.50-74.50	0.57
	Recessive	AA-AG	1.00	-	0.54	1.00	-	0.66	73.00	71.57-74.43	-
		GG	0.75	0.29-1.92		1.29	0.42-3.99		67.00	59.07-74.93	0.22
	Overdominant	AA-GG	1.00	-	0.84	1.00	-	0.47	73.00	71.32-74.68	-
		AG	1.04	0.72-1.49		1.19	0.74-1.91		73.00	71.92-74.08	0.84
	Log-additive	-	0.96	0.71-1.30	0.81	1.19	0.81-1.76	0.37	-		
rs2555639	Codominant	TT	1.00	-	0.23	1.00	-	0.42	73.00	70.49-75.51	-
		TC	0.97	0.68-1.39		1.08	0.68-1.73		73.00	71.28-74.72	0.75
		CC	1.52	0.91-2.55		1.55	0.81-2.96		72.00	67.67-76.33	0.54
	Dominant	TT	1.00	-	0.67	1.00	-	0.44	73.00	70.49-75.51	-
		TC-CC	1.08	0.77-1.50		1.19	0.77-1.83		73.00	71.26-74.74	0.63
	Recessive	TT-TC	1.00	-	0.086	1.00	-	0.20	73.00	71.47-74.53	-
		CC	1.54	0.95-2.52		1.49	0.81-2.74		72.00	67.67-76.33	0.61
	Overdominant	TT-CC	1.00	-	0.47	1.00	-	0.92	73.00	71.15-74.85	-
		TC	0.88	0.63-1.24		0.98	0.63-1.51		73.00	71.28-74.72	0.90
	Log-additive	-	1.15	0.90-1.47	0.25	1.20	0.89-1.63	0.24	-		
rs12500316	Codominant	CC	1.00	-	0.18	1.00	-	0.51	72.00	70.65-73.35	-
		CT	0.74	0.53-1.04		0.78	0.51-1.21		72.00	68.82-75.18	0.47
		TT	1.12	0.57-2.18		1.06	0.44-2.52		72.00	69.44-74.56	0.44
	Dominant	CC	1.00	-	0.15	1.00	-	0.34	72.00	70.65-73.35	-
		CT-TT	0.79	0.57-1.09		0.82	0.54-1.23		72.00	70.01-73.99	0.35
	Recessive	CC-CT	1.00	-	0.51	1.00	-	0.72	72.00	70.51-73.49	-
		TT	1.25	0.65-2.41		1.17	0.50-2.74		72.00	69.44-74.56	0.51
	Overdominant	CC-TT	1.00	-	0.069	1.00	-	0.25	72.00	70.81-73.19	-
		CT	0.73	0.53-1.03		0.78	0.51-1.19		72.00	68.82-75.18	0.53
	Log-additive	-	0.88	0.68-1.15	0.35	0.89	0.64-1.25	0.52	-		

OR: odds ratio; aOR: odds ratio adjusted for age and gender; CI: confidence interval.

Values in **bold** are statistically significant (p < 0.05).

Table S2 (cont.). Genotype risk estimates for the involvement of *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genetic variants in gastric cancer onset and estimated age at diagnosis.

SNP	Model	Genotype	Univariate analysis			Multivariate analysis*			Age at diagnosis		
			OR	95% CI	p value	aOR	95% CI	p value	Median (years)	95% CI	p value
rs1346271	Codominant	GG	1.00	-	0.035	1.00	-	0.30	73.00	70.85-75.15	-
		GC	0.68	0.48-0.96		0.71	0.45-1.11		72.00	70.06-73.94	0.48
		CC	1.12	0.69-1.82		0.93	0.50-1.74		71.00	68.85-73.15	0.77
	Dominant	GG	1.00	-	0.11	1.00	-	0.20	73.00	70.85-75.15	-
		GC-CC	0.77	0.55-1.06		0.76	0.50-1.15		72.00	70.63-73.37	0.54
	Recessive	GG-GC	1.00	-	0.16	1.00	-	0.69	72.00	70.83-73.17	-
		CC	1.38	0.88-2.17		1.12	0.63-2.01		71.00	68.85-73.15	0.92
	Overdominant	GG-CC	1.00	-	0.011	1.00	-	0.13	72.00	70.32-73.68	-
		GC	0.66	0.48-0.91		0.73	0.48-1.10		72.00	70.06-73.94	0.50
	Log-additive	-	0.95	0.75-1.20	0.66	0.90	0.66-1.21	0.48	-		
rs1426945	Codominant	GG	1.00	-	0.32	1.00	-	0.59	72.00	69.94-74.06	-
		GA	0.82	0.57-1.17		0.97	0.62-1.54		72.00	69.43-74.57	0.89
		AA	1.11	0.70-1.75		1.30	0.72-2.35		72.00	69.41-74.59	0.40
	Dominant	GG	1.00	-	0.49	1.00	-	0.80	72.00	69.94-74.06	-
		GA-AA	0.89	0.64-1.24		1.06	0.69-1.62		72.00	70.15-73.85	0.68
	Recessive	GG-GA	1.00	-	0.31	1.00	-	0.31	72.00	70.38-73.62	-
		AA	1.24	0.82-1.88		1.32	0.78-2.25		72.00	69.41-74.59	0.44
	Overdominant	GG-AA	1.00	-	0.15	1.00	-	0.59	72.00	70.38-73.62	-
		GA	0.79	0.57-1.09		0.89	0.59-1.35		72.00	69.43-74.57	0.85
	Log-additive	-	1.01	0.81-1.27	0.93	1.11	0.83-1.49	0.47	-		
rs1863642	Codominant	GG	1.00	-	0.18	1.00	-	0.56	73.00	71.38-74.62	-
		GT	0.74	0.53-1.03		0.87	0.57-1.34		72.00	69.75-74.25	0.15
		TT	1.03	0.57-1.85		1.31	0.62-2.77		70.00	67.19-72.81	0.10
	Dominant	GG	1.00	-	0.13	1.00	-	0.74	73.00	71.38-74.62	-
		GT-TT	0.78	0.57-1.08		0.93	0.62-1.40		72.00	70.22-73.78	0.07
	Recessive	GG-GT	1.00	-	0.58	1.00	-	0.38	72.00	70.74-73.26	-
		TT	1.17	0.67-2.08		1.39	0.67-2.87		70.00	67.19-72.81	0.16
	Overdominant	GG-TT	1.00	-	0.064	1.00	-	0.40	72.00	70.68-73.32	-
		GT	0.74	0.53-1.02		0.84	0.55-1.27		72.00	69.75-74.25	0.25
	Log-additive	-	0.88	0.69-1.14	0.34	1.02	0.74-1.41	0.90	-		

OR: odds ratio; aOR: odds ratio adjusted for age and gender; CI: confidence interval.

Values in **bold** are statistically significant (p < 0.05).

Table S2 (cont.). Genotype risk estimates for the involvement of *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genetic variants in gastric cancer onset and estimated age at diagnosis.

SNP	Model	Genotype	Univariate analysis			Multivariate analysis*			Age at diagnosis		
			OR	95% CI	p value	aOR	95% CI	p value	Median (years)	95% CI	p value
rs2303520	Codominant	GG	1.00	-	0.037	1.00	-	0.065	72.00	70.89-73.11	-
		GA	1.48	1.04-2.09		1.61	1.02-2.54		72.00	69.12-74.88	0.83
		AA	0.51	0.14-1.79		0.51	0.11-2.34		69.00	64.20-73.80	0.61
	Dominant	GG	1.00	-	0.066	1.00	-	0.086	72.00	70.89-73.11	-
		GA-AA	1.38	0.98-1.93		1.47	0.95-2.29		72.00	69.05-74.96	0.92
	Recessive	GG-GA	1.00	-	0.18	1.00	-	0.26	72.00	70.63-73.37	-
		AA	0.45	0.13-1.59		0.45	0.10-2.04		69.00	64.20-73.80	0.61
	Overdominant	GG-AA	1.00	-	0.021	1.00	-	0.031	72.00	70.87-73.13	-
		GA	1.51	1.07-2.13		1.65	1.05-2.59		72.00	69.12-74.88	0.81
	Log-additive	-	1.21	0.90-1.64	0.21	1.26	0.86-1.84	0.24	-		
rs2555632	Codominant	TT	1.00	-	0.45	1.00	-	0.16	73.00	71.62-74.38	-
		TC	1.00	0.71-1.41		1.29	0.83-2.00		72.00	69.22-74.78	0.58
		CC	1.57	0.78-3.14		2.19	0.90-5.30		70.00	66.67-73.33	0.019
	Dominant	TT	1.00	-	0.71	1.00	-	0.13	73.00	71.62-74.38	-
		TC-CC	1.06	0.77-1.47		1.39	0.91-2.10		71.00	68.72-73.28	0.26
	Recessive	TT-TC	1.00	-	0.20	1.00	-	0.12	72.00	70.73-73.27	-
		CC	1.57	0.79-3.10		1.99	0.84-4.73		70.00	66.67-73.33	0.027
	Overdominant	TT-CC	1.00	-	0.83	1.00	-	0.41	72.00	70.61-73.39	-
		TC	0.96	0.69-1.34		1.20	0.78-1.85		72.00	69.22-74.78	0.82
	Log-additive	-	1.11	0.85-1.45	0.43	1.38	0.98-1.94	0.066	-		
rs8752	Codominant	AA	1.00	-	0.32	1.00	-	0.30	72.00	70.13-73.87	-
		AG	1.28	0.90-1.80		1.39	0.90-2.17		72.00	70.32-73.68	0.60
		GG	0.99	0.59-1.68		1.39	0.71-2.72		72.00	66.96-77.04	0.31
	Dominant	AA	1.00	-	0.25	1.00	-	0.12	72.00	70.13-73.87	-
		AG-GG	1.21	0.87-1.68		1.39	0.91-2.12		72.00	70.45-73.55	0.46
	Recessive	AA-AG	1.00	-	0.56	1.00	-	0.64	72.00	70.53-73.47	-
		GG	0.87	0.53-1.41		1.16	0.62-2.16		72.00	66.96-77.04	0.41
	Overdominant	AA-GG	1.00	-	0.13	1.00	-	0.22	72.00	70.42-73.58	-
		AG	1.28	0.93-1.76		1.29	0.86-1.94		72.00	70.32-73.68	0.83
	Log-additive	-	1.07	0.84-1.35	0.58	1.24	0.91-1.68	0.17	-		

OR: odds ratio; aOR: odds ratio adjusted for age and gender; CI: confidence interval.

Values in **bold** are statistically significant (p < 0.05).

Table S2 (cont.). Genotype risk estimates for the involvement of *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genetic variants in gastric cancer onset and estimated age at diagnosis.

SNP	Model	Genotype	Univariate analysis			Multivariate analysis*			Age at diagnosis		
			OR	95% CI	p value	aOR	95% CI	p value	Median (years)	95% CI	p value
SLCO2A1											
rs10935090	Codominant	CC	1.00	-	0.13	1.00	-	0.026	73.00	71.81-74.19	-
		CT	1.40	0.95-2.06		1.46	0.90-2.39		70.00	67.56-72.44	0.034
		TT	2.00	0.66-6.04		4.68	1.32-16.61		62.00	59.61-64.39	<0.001
	Dominant	CC	1.00	-	0.054	1.00	-	0.038	73.00	71.81-74.19	-
		CT-TT	1.44	1.00-2.09		1.65	1.03-2.63		70.00	67.93-72.07	0.007
	Recessive	CC-CT	1.00	-	0.028	1.00	-	0.026	72.00	70.87-73.14	-
		TT	1.86	0.62-5.59		4.30	1.22-15.16		62.00	59.61-64.39	<0.001
	Overdominant	CC-TT	1.00	-	0.11	1.00	-	0.19	73.00	71.807-74.193	-
		CT	1.37	0.94-2.02		1.39	0.86-2.27		70.00	67.56-72.44	0.057
	Log-additive	-	1.40	1.01-1.95	0.044	1.69	1.12-2.53	0.012	-		
rs1131598	Codominant	AA	1.00	-	0.67	1.00	-	0.59	72.00	70.55-73.45	-
		AG	0.90	0.64-1.25		0.81	0.52-1.24		73.00	71.22-74.78	0.86
		GG	0.74	0.32-1.71		1.07	0.40-2.91		69.00	62.82-75.18	0.54
	Dominant	AA	1.00	-	0.44	1.00	-	0.38	72.00	70.55-73.45	-
		AG-GG	0.88	0.64-1.22		0.83	0.55-1.26		72.00	70.17-73.84	0.96
	Recessive	AA-AG	1.00	-	0.53	1.00	-	0.76	72.00	70.88-73.12	-
		GG	0.77	0.34-1.77		1.17	0.44-3.12		69.00	62.82-75.18	0.46
	Overdominant	AA-GG	1.00	-	0.59	1.00	-	0.31	72.00	70.39-73.61	-
		AG	0.91	0.66-1.27		0.80	0.52-1.22		73.00	71.22-74.78	0.77
	Log-additive	-	0.88	0.67-1.17	0.38	0.89	0.62-1.27	0.52	-		
rs11915399	Codominant	CC	1.00	-	0.72	1.00	-	0.12	72.00	70.27-73.73	-
		CT	0.87	0.60-1.24		0.61	0.38-0.99		73.00	71.47-74.53	0.13
		TT	0.88	0.33-2.33		0.75	0.22-2.63		74.00	59.93-88.07	0.52
	Dominant	CC	1.00	-	0.42	1.00	-	0.043	72.00	70.27-73.73	-
		CT-TT	0.87	0.61-1.23		0.62	0.39-0.99		73.00	71.53-74.47	0.11
	Recessive	CC-CT	1.00	-	0.86	1.00	-	0.81	72.00	70.64-73.37	-
		TT	0.91	0.35-2.41		0.86	0.25-2.96		74.00	59.93-88.07	0.59
	Overdominant	CC-TT	1.00	-	0.45	1.00	-	0.045	72.00	70.19-73.81	-
		CT	0.87	0.61-1.25		0.62	0.38-1.00		73.00	71.47-74.53	0.16
	Log-additive	-	0.89	0.65-1.21	0.45	0.69	0.46-1.03	0.065	-		

OR: odds ratio; aOR: odds ratio adjusted for age and gender; CI: confidence interval.

Values in **bold** are statistically significant (p < 0.05).

Table S2 (cont.). Genotype risk estimates for the involvement of *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genetic variants in gastric cancer onset and estimated age at diagnosis.

SNP	Model	Genotype	Univariate analysis			Multivariate analysis*			Age at diagnosis		
			OR	95% CI	p value	aOR	95% CI	p value	Median (years)	95% CI	p value
rs4241362	Codominant	TT	1.00	-	0.97	1.00	-	0.49	72.00	70.65-73.35	-
		TC	0.97	0.67-1.39		1.13	0.71-1.80		73.00	68.67-77.63	0.82
		CC	0.93	0.37-2.30		1.86	0.65-5.31		65.00	62.94-67.06	0.019
	Dominant	TT	1.00	-	0.83	1.00	-	0.42	72.00	70.65-73.35	-
		TC-CC	0.96	0.68-1.36		1.20	0.77-1.87		72.00	68.34-75.67	0.82
	Recessive	TT-TC	1.00	-	0.88	1.00	-	0.29	72.00	70.87-73.13	-
		CC	0.93	0.38-2.30		1.79	0.63-5.07		65.00	62.94-67.06	0.024
	Overdominant	TT-CC	1.00	-	0.87	1.00	-	0.70	72.00	70.64-73.36	-
		TC	0.97	0.68-1.39		1.10	0.69-1.74		73.00	68.67-77.63	0.70
	Log-additive	-	0.97	0.72-1.30	0.82	1.22	0.84-1.78	0.29	-		
rs4241365	Codominant	TT	1.00	-	0.89	1.00	-	0.53	72.00	70.71-73.30	-
		TC	1.08	0.77-1.51		1.10	0.71-1.71		72.00	69.77-74.23	0.58
		CC	1.11	0.56-2.17		1.65	0.68-3.99		74.00	67.61-80.39	0.61
	Dominant	TT	1.00	-	0.63	1.00	-	0.47	72.00	70.71-73.30	-
		TC-CC	1.08	0.78-1.50		1.17	0.77-1.77		72.00	69.67-74.33	0.71
	Recessive	TT-TC	1.00	-	0.83	1.00	-	0.30	72.00	70.65-73.35	-
		CC	1.07	0.55-2.08		1.59	0.67-3.78		74.00	67.61-80.39	0.56
	Overdominant	TT-CC	1.00	-	0.69	1.00	-	0.80	72.00	69.77-74.23	-
		TC	1.07	0.77-1.49		1.06	0.69-1.62		72.00	69.77-74.23	0.51
	Log-additive	-	1.07	0.82-1.38	0.63	1.19	0.84-1.67	0.32	-		
rs4331673	Codominant	CC	1.00	-	0.60	1.00	-	0.19	72.00	70.80-73.20	-
		CA	0.88	0.61-1.27		0.92	0.58-1.48		72.00	68.55-75.45	0.48
		AA	1.35	0.57-3.18		2.61	0.92-7.41		65.00	62.64-67.36	0.32
	Dominant	CC	1.00	-	0.67	1.00	-	0.84	72.00	70.80-73.20	-
		CA-AA	0.93	0.65-1.31		1.05	0.67-1.64		72.00	68.42-75.58	0.69
	Recessive	CC-CA	1.00	-	0.45	1.00	-	0.072	72.00	70.63-73.37	-
		AA	1.39	0.59-3.27		2.67	0.95-7.52		65.00	62.64-67.36	0.33
	Overdominant	CC-AA	1.00	-	0.45	1.00	-	0.59	72.00	70.53-73.48	-
		CA	0.87	0.61-1.25		0.88	0.55-1.40		72.00	68.55-75.45	0.44
	Log-additive	-	0.98	0.73-1.32	0.91	1.17	0.80-1.70	0.43	-		

OR: odds ratio; aOR: odds ratio adjusted for age and gender; CI: confidence interval.

Values in **bold** are statistically significant (p < 0.05).

Table S2 (cont.). Genotype risk estimates for the involvement of *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genetic variants in gastric cancer onset and estimated age at diagnosis.

SNP	Model	Genotype	Univariate analysis			Multivariate analysis*			Age at diagnosis		
			OR	95% CI	p value	aOR	95% CI	p value	Median (years)	95% CI	p value
rs4854784	Codominant	GG	1.00	-	0.58	1.00	-	0.73	72.00	70.10-73.90	-
		GA	0.98	0.70-1.37		1.06	0.69		72.00	70.64-73.36	0.27
		AA	0.75	0.43-1.31		1.32	0.67-2.62		67.00	65.21-68.80	0.10
	Dominant	GG	1.00	-	0.66	1.00	-	0.62	72.00	70.10-73.90	-
		GA-AA	0.93	0.68-1.28		1.11	0.74-1.68		72.00	70.26-73.74	0.59
	Recessive	GG-GA	1.00	-	0.30	1.00	-	0.46	72.00	70.84-73.16	-
		AA	0.76	0.44-1.30		1.28	0.67-2.46		67.00	65.21-68.80	0.071
	Overdominant	GG-AA	1.00	-	0.85	1.00	-	0.97	72.00	69.98-74.02	-
		GA	1.03	0.75-1.42		1.01	0.67-1.53		72.00	70.64-73.36	0.16
	Log-additive	-	0.91	0.71-1.15	0.42	1.12	0.82-1.52	0.47	-		
rs6439448	Codominant	CC	1.00	-	0.31	1.00	-	0.48	72.00	70.30-73.70	-
		CA	1.14	0.81-1.61		1.10	0.70-1.72		72.00	69.71-74.29	0.54
		AA	0.52	0.17-1.56		0.51	0.14-1.82		70.00	64.09-75.91	0.92
	Dominant	CC	1.00	-	0.67	1.00	-	0.91	72.00	70.30-73.70	-
		CA-AA	1.08	0.77-1.50		1.03	0.67-1.58		72.00	69.99-74.01	0.56
	Recessive	CC-CA	1.00	-	0.18	1.00	-	0.25	72.00	70.63-73.37	-
		AA	0.49	0.16-1.49		0.49	0.14-1.75		70.00	64.09-75.91	0.91
	Overdominant	CC-AA	1.00	-	0.36	1.00	-	0.58	72.00	70.28-73.73	-
		CA	1.17	0.83-1.65		1.13	0.73-1.76		72.00	69.71-74.29	0.53
	Log-additive	-	1.00	0.74-1.34	0.98	0.95	0.65-1.38	0.79	-		
rs7340717	Codominant	GG	1.00	-	0.30	1.00	-	0.37	72.00	70.34-73.66	-
		GT	1.15	0.82-1.62		1.23	0.79-1.91		72.00	69.69-74.31	0.53
		TT	0.77	0.45-1.32		0.80	0.41-1.56		74.00	70.51-77.49	0.63
	Dominant	GG	1.00	-	0.72	1.00	-	0.59	72.00	70.34-73.66	-
		GT-TT	1.06	0.77-1.47		1.12	0.74-1.69		72.00	70.18-73.82	0.49
	Recessive	GG-GT	1.00	-	0.19	1.00	-	0.29	72.00	70.62-73.38	-
		TT	0.72	0.43-1.19		0.72	0.38-1.34		74.00	70.51-77.49	0.80
	Overdominant	GG-TT	1.00	-	0.22	1.00	-	0.22	72.00	70.31-73.70	-
		GT	1.22	0.89-1.68		1.30	0.86-1.96		72.00	69.69-74.31	0.60
	Log-additive	-	0.96	0.76-1.21	0.71	0.98	0.73-1.32	0.90	-		

OR: odds ratio; aOR: odds ratio adjusted for age and gender; CI: confidence interval.

Values in **bold** are statistically significant ($p < 0.05$).

Table S2 (cont.). Genotype risk estimates for the involvement of *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genetic variants in gastric cancer onset and estimated age at diagnosis.

SNP	Model	Genotype	Univariate analysis			Multivariate analysis*			Age at diagnosis		
			OR	95% CI	p value	aOR	95% CI	p value	Median (years)	95% CI	p value
rs7616492	Codominant	GG	1.00	-	0.83	1.00	-	0.74	72.00	69.60-74.40	-
		GA	1.08	0.77-1.52		1.06	0.69-1.65		72.00	69.76-74.24	0.94
		AA	1.15	0.70-1.89		0.82	0.43-1.59		72.00	69.58-74.42	0.34
	Dominant	GG	1.00	-	0.58	1.00	-	0.98	72.00	69.60-74.40	-
		GA-AA	1.10	0.79-1.52		1.01	0.67-1.52		72.00	70.73-73.27	0.63
	Recessive	GG-GA	1.00	-	0.68	1.00	-	0.47	72.00	69.58-74.42	-
		AA	1.10	0.69-1.75		0.80	0.43-1.48		72.00	69.58-74.42	0.36
	Overdominant	GG-AA	1.00	-	0.79	1.00	-	0.61	72.00	70.26-73.74	-
		GA	1.05	0.76-1.44		1.11	0.74-1.68		72.00	69.76-74.24	0.85
	Log-additive	-	1.07	0.85-1.35	0.55	0.95	0.70-1.28	0.74	-		
rs7625035	Codominant	AA	1.00	-	0.29	1.00	-	0.48	72.00	70.10-73.90	-
		AG	0.85	0.61-1.20		0.91	0.59-1.40		72.00	70.08-73.92	0.66
		GG	1.49	0.74-2.98		1.57	0.67-3.71		72.00	66.87-77.13	0.19
	Dominant	AA	1.00	-	0.62	1.00	-	0.94	72.00	70.10-73.90	-
		AG-GG	0.92	0.67-1.27		0.98	0.65-1.49		72.00	70.40-73.60	0.43
	Recessive	AA-AG	1.00	-	0.20	1.00	-	0.26	72.00	70.55-73.45	-
		GG	1.58	0.80-3.12		1.63	0.70-3.79		72.00	66.87-77.13	0.20
	Overdominant	AA-GG	1.00	-	0.26	1.00	-	0.52	72.00	70.08-73.92	-
		AG	0.83	0.59-1.16		0.87	0.57-1.33		72.00	70.08-73.92	0.83
	Log-additive	-	1.01	0.77-1.32	0.94	1.07	0.76-1.49	0.70	-		
rs7646392	Codominant	CC	1.00	-	0.63	1.00	-	0.90	72.00	69.68-74.32	-
		CT	0.87	0.61-1.23		0.90	0.57-1.41		72.00	70.42-73.58	0.64
		TT	0.82	0.51-1.31		0.94	0.52-1.71		72.00	67.51-76.50	0.87
	Dominant	CC	1.00	-	0.35	1.00	-	0.66	72.00	69.68-74.32	-
		CT-TT	0.86	0.62-1.19		0.91	0.60-1.38		72.00	70.69-73.31	0.65
	Recessive	CC-CT	1.00	-	0.57	1.00	-	1.00	72.00	70.70-73.30	-
		TT	0.88	0.57-1.36		1.00	0.58-1.73		72.00	67.51-76.50	0.93
	Overdominant	CC-TT	1.00	-	0.62	1.00	-	0.67	72.00	70.08-73.92	-
		CT	0.92	0.67-1.27		0.91	0.60-1.38		72.00	70.42-73.58	0.61
	Log-additive	-	0.90	0.72-1.13	0.35	0.96	0.72-1.28	0.76	-		

OR: odds ratio; aOR: odds ratio adjusted for age and gender; CI: confidence interval.

Values in **bold** are statistically significant (p < 0.05).

Table S2 (cont.). Genotype risk estimates for the involvement of *PTGS2*, *ABCC4*, *HPGD*, and *SLCO2A1* genetic variants in gastric cancer onset and estimated age at diagnosis.

SNP	Model	Genotype	Univariate analysis			Multivariate analysis*			Age at diagnosis		
			OR	95% CI	p value	aOR	95% CI	p value	Median (years)	95% CI	p value
rs9820625	Codominant	AA	1.00	-	1.00	1.00	-	0.84	72.00	69.85-74.15	-
		AC	0.99	0.68-1.43		1.06	0.66-1.71		72.00	70.12-73.88	0.80
		CC	0.99	0.63-1.55		1.19	0.67-2.09		72.00	68.89-75.11	0.31
	Dominant	AA	1.00	-	0.94	1.00	-	0.68	72.00	69.85-74.15	-
		AC-CC	0.99	0.70-1.40		1.10	0.70-1.72		72.00	70.32-73.68	0.86
	Recessive	AA-AC	1.00	-	1.00	1.00	-	0.58	72.00	70.58-73.42	-
		CC	1.00	0.68-1.46		1.15	0.71-1.87		72.00	68.89-75.11	0.23
	Overdominant	AA-CC	1.00	-	0.95	1.00	-	0.94	72.00	70.19-73.81	-
		AC	0.99	0.72-1.36		0.98	0.64-1.48		72.00	70.12-73.88	0.43
	Log-additive	-	0.99	0.80-1.24	0.96	1.09	0.82-1.44	0.56	-		
rs9821091	Codominant	GG	1.00	-	0.32	1.00	-	0.045	72.00	69.77-74.23	-
		GA	0.86	0.61-1.22		0.81	0.52-1.28		73.00	71.43-74.57	0.11
		AA	1.22	0.76-1.97		1.75	0.95-3.20		71.00	68.17-73.83	0.16
	Dominant	GG	1.00	-	0.70	1.00	-	0.96	72.00	69.77-74.23	-
		GA-AA	0.94	0.68-1.30		0.99	0.65-1.50		72.00	70.56-73.44	0.42
	Recessive	GG-GA	1.00	-	0.21	1.00	-	0.02	72.00	70.76-73.24	-
		AA	1.33	0.86-1.12		1.95	1.12-3.40		71.00	68.17-73.83	0.017
	Overdominant	GG-AA	1.00	-	0.20	1.00	-	0.085	71.00	69.06-72.94	-
		GA	0.81	0.59-1.12		0.70	0.46-1.05		73.00	71.43-74.57	0.018
	Log-additive	-	1.05	0.83-1.32	0.70	1.19	0.89-1.61	0.24	-		
rs9834412	Codominant	CC	1.00	-	0.94	1.00	-	0.94	73.00	71.02-74.98	-
		CA	0.94	0.67-1.32		1.00	0.65-1.55		72.00	71.10-72.90	0.78
		AA	1.02	0.53-1.95		1.15	0.52-2.55		72.00	64.23-79.77	0.36
	Dominant	CC	1.00	-	0.78	1.00	-	0.91	73.00	71.02-74.98	-
		CA-AA	0.96	0.69-1.32		1.02	0.68-1.55		72.00	71.15-72.86	0.59
	Recessive	CC-CA	1.00	-	0.90	1.00	-	0.72	72.00	70.54-73.46	-
		AA	1.04	0.55-1.97		1.15	0.53-2.50		72.00	64.23-79.77	0.34
	Overdominant	CC-AA	1.00	-	0.73	1.00	-	0.94	72.00	70.22-73.78	-
		CA	0.94	0.68-1.31		0.98	0.64-1.50		72.00	71.10-72.90	0.92
	Log-additive	-	0.98	0.75-1.27	0.86	1.04	0.75-1.44	0.81	-		

OR: odds ratio; aOR: odds ratio adjusted for age and gender; CI: confidence interval.

Values in **bold** are statistically significant (p < 0.05)

Table S3. Raw quantification data from the real-time polymerase chain reaction.

	C_T Mean				
	Target genes				Reference genes
	<i>PTGS2</i>	<i>ABCC4</i>	<i>HPGD</i>	<i>SLCO2A1</i>	<i>IPO8</i> and <i>HPRT1</i>
GN1		34,44	32,02	34,58	36,17
GN2	36,16	33,43	31,30	32,78	35,47
GN3		33,91	31,44	34,81	36,34
GN4	37,73	31,83	28,93	31,88	33,30
GN5	37,52	33,38	29,71	33,71	34,66
GN6	34,11	33,70	33,41	33,93	33,57
GN7	37,27	33,03	29,46	32,67	34,11
GN8	34,57	31,82	28,35	31,76	33,34
GN9		34,28	31,52	34,28	35,79
GN10	36,38	32,33	29,76	32,86	33,64
GN11	34,17	32,46	29,46	32,23	34,11
GN12		33,08	29,58	32,04	33,44
GN13	34,70	31,97	28,45	31,96	33,06
GN14	35,89	32,12	27,55	31,69	33,13
GN15	35,59	32,66	30,27	32,76	33,89
GN16	37,76	33,41	30,45	33,83	34,29
GN17	36,51	33,26	30,59	33,62	34,68
GN18	34,35	31,45	27,46	31,35	32,84
GN19	37,31	33,62	30,85	34,01	35,25
GN20	36,27	32,16	28,77	31,78	33,34
GN21		33,14	29,86	34,14	35,45
GN22		34,26	30,89	34,78	37,34
GN23		35,76	31,26	35,13	37,09
GN24	35,48	32,17	28,62	31,66	34,08
GN25	35,34	33,41	31,19	32,98	34,95
GN26		34,83	30,62	34,58	35,38
GN27		32,51	28,45	33,39	34,78
GN33	35,65	32,33	29,92	32,68	34,08
GN34	37,78	32,71	29,38	33,42	35,06
GN35	35,79	34,47	31,79	34,14	35,15
GN36		33,13	29,69	33,03	33,89
GN37		33,43	29,13	33,54	34,82
GN38	36,67	33,41	31,10	33,44	35,51
GN39	36,75	33,52	31,18	32,98	33,90
GN40		33,73	31,02	34,46	34,36
GN41	35,44	31,58	28,67	31,49	33,37
GN42	37,60	33,87	30,64	34,18	36,39
GN43	35,80	32,13	29,97	32,75	33,12
GN44	33,96	31,85	29,15	32,07	33,67
GN45		32,58	29,54	31,76	33,06
GN46	35,13	31,50	28,20	31,20	33,24
GN47	36,05	31,89	28,20	32,37	33,45
GN49	37,90	33,29	31,60	34,39	33,00
GN50	36,79	33,06	30,24	33,85	35,23
GN51	35,89	33,39	29,92	33,20	34,14

C_T: cycle threshold.

Table S3 (cont.). Raw quantification data from the real-time polymerase chain reaction.

	C_T Mean				
	Target genes				Reference genes
	<i>PTGS2</i>	<i>ABCC4</i>	<i>HPGD</i>	<i>SLCO2A1</i>	<i>IPO8</i> and <i>HPRT1</i>
GN52		35,89	33,51	36,04	37,60
GN53	37,21	33,85	30,99	33,93	34,70
GN54	36,17	34,24	32,78	33,80	34,79
GN55		33,39	30,24	33,38	33,86
GN56		33,88	31,43	34,85	36,63
GN57	38,28	34,12	32,36	34,84	35,95
GN58	38,05	35,08	32,38	35,33	36,78
GN59		34,17	31,20	34,61	36,00
GN61	37,72	35,29	32,95	35,16	36,24
GN62		35,40	31,76		37,51
GN63	37,00	36,43	33,91	35,55	36,55
GN64	35,45	32,28	29,66	32,17	33,86
GN65	36,67	33,41	32,29	33,78	35,02
GN67		36,15	33,15	36,80	37,91
GN68		34,75	33,56	34,86	36,39
GN69		35,04	33,04	35,31	35,81
GN70	36,91	34,36	32,14	34,19	35,67
GN71	36,80	32,48	29,89	32,86	34,17
GN72		32,65	30,19	32,40	34,15
GN73		33,02	31,29	33,05	33,68
GN74		32,75	29,32	33,21	34,67
GN103	38,35	34,77	32,55	35,73	36,47
GN105		33,89	31,23	35,32	36,12
GN106	38,44	33,71	29,91	34,34	35,63
GN107	37,93	33,64	31,62	34,04	35,93
GN108		34,86	31,71	35,44	37,45
GN110		33,98	31,80	34,88	35,31
GN111	36,71	33,25	29,77	33,39	34,84
GN113	37,16	33,56	31,48	33,60	35,61
GN114		32,93	29,26	33,32	35,35
GN115	38,14	34,33	31,53	33,74	35,97
GN119		33,93	31,09	34,37	36,55
GN120		34,19	31,39	34,77	38,03
GN121		34,57	33,02	36,20	37,95
GN122		36,05	36,41	35,28	37,94
GN123		34,43	31,37	34,08	35,01
GN124	38,21	33,86	31,26	33,97	34,20
GN125		32,38	28,52	31,65	34,24
GN127	37,72	32,68	29,60	32,23	33,90
GN128	38,40	34,44	32,58	35,07	36,93
GN129		33,73	32,38	33,71	35,42
GN131		36,05	35,16	36,85	37,70
GN132		37,81	35,32	33,04	37,42
GN133		33,86	31,25	33,90	35,54
GN134		33,58	31,02	34,30	35,46

C_T: cycle threshold.

Table S3 (cont.). Raw quantification data from the real-time polymerase chain reaction.

	C_T Mean				
	Target genes				Reference genes
	<i>PTGS2</i>	<i>ABCC4</i>	<i>HPGD</i>	<i>SLCO2A1</i>	<i>IPO8</i> and <i>HPRT1</i>
GN135	38,60	33,83	30,31	33,97	35,08
GN136		32,85	30,05	33,65	35,31
GN137		34,01	30,44	34,16	35,49
GN138	36,61	33,38	31,39	33,34	35,19
GN139		34,42	33,30	36,01	37,30
GN140	38,40	34,93	33,50	35,99	37,17
GN141	37,96	34,21	32,70	35,56	36,30
GN143		35,31	33,05	35,71	38,09
GN144	37,05	34,86	32,89	35,99	37,23
GT1	34,99	33,61	34,29	36,01	33,72
GT2	31,37	30,42	31,74	33,84	32,40
GT3	35,13	32,97	32,83	34,96	33,45
GT4	32,40	31,71	32,22	32,59	33,15
GT5	33,05	32,07	32,78	32,27	33,31
GT6	34,34	33,92	30,71	33,64	34,67
GT7	35,13	31,44	33,70	32,88	32,86
GT8	35,40	32,73	33,46	33,69	32,89
GT9	37,06	33,06	31,57	34,55	35,09
GT10	35,28	31,40	30,90	31,66	32,66
GT11	29,65	32,87	31,85	31,38	31,88
GT12	30,44	31,46	30,25	31,54	31,87
GT13	32,21	32,29	31,56	31,01	32,76
GT14	33,90	31,90	32,41	33,13	33,77
GT15	32,79	31,45	32,52	31,71	32,27
GT16	34,52	33,13	34,07	35,00	33,56
GT17	32,15	33,82	35,23	33,67	33,01
GT18	31,26	31,50	32,98	31,11	32,11
GT19	32,46	31,45	28,87	32,47	33,64
GT20	33,84	29,95	31,92	32,40	31,84
GT21	32,51	32,93	29,62	33,01	32,89
GT22	35,20	35,22	33,80		36,82
GT23	36,00	32,44	32,99	35,35	34,86
GT24		34,97	31,35	36,63	33,90
GT25	35,27	31,07	29,42	33,23	32,59
GT26	35,04	33,25	32,26	34,11	34,21
GT27	35,53	32,57	30,27	32,89	33,31
GT32	33,50	32,51	30,74	34,72	33,46
GT33		34,64	36,48		39,07
GT34		33,18	33,34	34,88	35,10
GT35	34,75	34,54	35,21	36,53	35,39
GT36	36,35	33,98	32,59	34,91	35,89
GT38	36,46	35,11			35,87
GT47	37,18	33,25	32,01	34,68	35,82
GT48	35,46	34,87	34,71	38,01	36,26
GT51	38,80	35,57	32,17		35,78

C_T: cycle threshold.

Table S3 (cont.). Raw quantification data from the real-time polymerase chain reaction.

	C_T Mean				
	Target genes				Reference genes
	<i>PTGS2</i>	<i>ABCC4</i>	<i>HPGD</i>	<i>SLCO2A1</i>	<i>IPO8</i> and <i>HPRT1</i>
GT52	38,10	32,97	33,77	33,09	35,79
GT57		36,50	35,95	35,94	35,91
GT62		35,78	35,74	39,29	35,78
GT64	35,49	32,31	35,29	33,55	34,74
GT65		34,91	35,25	34,69	36,05
GT69		37,76		39,27	38,66
GT73		33,05	35,90	34,75	34,66
GT102	38,75	36,00	36,89	35,57	38,54
GT103		33,54		37,04	36,16
GT105		35,07	33,95	35,74	36,81
GT106	37,07	35,20	35,74	37,62	36,22
GT107	35,79	34,35	34,83	36,32	36,04
GT108		32,49	34,25	34,23	35,65
GT109		31,24	32,86	35,04	34,60
GT110	37,48	34,90	35,65	35,45	36,45
GT111	35,86	32,82	33,70	36,01	35,46
GT113	33,45	34,01	36,50	37,20	35,40
GT114	35,10	32,39	32,77	35,13	35,35
GT116		34,02	36,18	33,82	36,19
GT117	33,87	33,63	31,94	34,76	33,48
GT118		34,92	37,05		37,41
GT119	37,69	36,09	34,38	38,95	35,98
GT120	37,84	34,04		37,88	38,30
GT122	35,64	33,53	36,40	34,72	34,76
GT123	36,76	33,81	33,90	35,22	34,21
GT124		33,62	33,84	34,05	34,74
GT128		34,84		37,11	37,40
GT129	37,43	32,77	34,23	35,01	34,79
GT131		34,18	35,64	35,65	37,86
GT132		35,99	37,19		37,86
GT133		34,11	35,61	33,68	36,08
GT134	35,00	30,82	34,71	34,33	33,75
GT135	31,82	32,42	33,58	36,87	34,09
GT138	36,55	34,50	33,97	34,00	35,49
GT139	36,69	34,12	36,01	35,36	36,21
GT141		36,50		38,78	37,25
GT142	36,47	33,40	34,06	37,79	35,33
GT143	36,94	35,66	34,37	37,74	36,61
GT145	37,92	37,32	35,21	37,73	36,19
GT147		33,52	33,20	35,17	36,06
GT148		34,55	35,07	35,93	35,54
GT149	36,92	33,44	35,25	33,62	37,07
GT150		33,65		34,22	34,62
GT151	35,96	33,88	34,07	36,51	35,54
GT152	34,70	32,72	35,85	37,07	34,18

C_T: cycle threshold.

Table S3 (cont.). Raw quantification data from the real-time polymerase chain reaction.

	C_T Mean				
	Target genes				Reference genes
	<i>PTGS2</i>	<i>ABCC4</i>	<i>HPGD</i>	<i>SLCO2A1</i>	<i>IPO8</i> and <i>HPRT1</i>
GT153	35,62	33,23	33,42	34,61	35,87
GT154		33,74	33,32	35,56	36,02
GT155	37,64	32,72	33,14	33,32	35,36
GT156	37,31	32,91	36,33	33,88	37,14
GT157	37,87	34,22	34,75	36,47	35,91
GT158	38,06	34,18	35,66		36,89
GT159	33,61	32,97	34,73	36,24	34,65
GT160	37,41	33,32	33,57	34,43	34,50
GT162		35,68	35,35	36,36	36,67
GT163	34,49	35,83		36,31	35,87
GT164		36,08	37,32	36,77	37,43
GT165	38,32	35,89	35,26		36,75
GT166		35,41	35,87	36,33	35,94
GT167	36,90	34,87	36,85		37,29
GT168		34,58	34,88	36,06	36,31

C_T: cycle threshold.