

Supplementary Materials

Genome-Wide Association Study Identifies Novel Candidate Variants Associated with Postoperative Nausea and Vomiting

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Table S1. Demographic and clinical data of patient subjects for the replication study.

Demographic data:	<i>n</i>	Minimum	Maximum	Mean	SD	Median
Gender						
male	0					
female	333					
Age [years]	333	21	69	39.20	8.60	40.00
Height [cm]	333	141.3	174.5	159.82	5.57	160.00
Weight [kg]	333	37.45	82.9	54.55	8.22	53.55
Body mass index (BMI) [kg/m ²]	333	15.10	29.70	21.36	3.09	20.90
Duration of surgery [min]	333	26	303	128.90	45.20	124.00
Duration of anaesthesia [min]	333	69	328	175.10	48.20	171.00
Total dose of propofol [mg]	333	0	1850	854.10	302.20	800.00
Average remifentanyl infusion rate [µg/kg/min]	333	0.022	0.713	0.30	0.07	0.30
Frequency of acetaminophen administration	333	1	4	2.9	0.6	3
PCA fentanyl consumption (µg/kg)	333	0	20.88	5.53	4.44	4.54
Total postoperative fentanyl administration (µg/kg)	333	3.92	25.39	9.73	4.51	8.79
Incidence of PONV						
absence	289					
presence	44					
Administration of rescue analgesic						
absence	306					
presence	27					
Average pain score of numerical rating scale	333	0	6	1.83	1.15	1.70

Table S2. Top 20 candidate SNPs selected from the GWAS for nausea in all patients.

Model	Rank	CH R	SNP	Posi- tion	<i>p</i>	Related gene	Genotype (Nau- sea +)			Genotype (Nau- sea -)		
							A/ A	A/B	B/B	A/ A	A/B	B/B
Trend	1	21	rs283650 5	3991855 3	0.000004 044	<i>ERG</i>	16	91	158	57	258	226
Trend	2	16	rs992593 4	1702824 7	0.000005 621		1	65	199	3	60	478
Trend	3	20	rs602169 3	5069428 7	0.000006 882		42	154	69	59	247	235
Trend	4	16	rs649864 3	1705087 4	0.000008 058		2	71	192	5	68	467
Trend	5	5	rs771972 3		0.000011 76		27	126	112	122	250	169
Trend	6	20	rs601722 7	4259322 0	0.000012 31	<i>TOX2</i>	0	39	226	0	30	511
Trend	7	5	rs156063 9	1736092 74	0.000013 24		11	81	173	11	99	431
Trend	8	17	rs197813 6	3237769 8	0.000014 58		57	138	70	68	258	215
Trend	9	17	exm1284 008		0.000022 98	<i>LOC728392</i>	8	78	179	5	101	435
Trend	10	13	rs954976 3	1140524 70	0.000024 32		0	50	215	22	146	373
Trend	11	7	rs198243 6	1344706 32	0.000026 39		9	98	158	9	131	401
Trend	12	10	rs707377 0	1541753 7	0.000026 81	<i>CALD1</i>	1	12	252	1	84	456
Trend	13	13		4872425	0.000028		0	29	236	0	19	522
Trend	14	23	rs645833 rs787922	6 9572143	15 0.000028		0	12	127	0	1	234
Trend	15	17	rs116559 26	3524337 0	0.000028 33		24	118	123	29	176	336
Trend	16	12	rs648851 9	1253298 4	0.000031 17		6	43	216	1	49	491
Trend	17	1	exm2250 857	2304695 05	0.000032 32	<i>PGBD5</i>	80	140	45	113	268	160

			rs803290	3976787	0.000032								
Trend	18	15	0	8	74			6	76	183	7	88	446
				1033475	0.000034								
Trend	19	13	rs612938	91	82			2	57	205	0	63	477
			rs109310	1832389	0.000035								
Trend	20	2	08	19	32	PDE1A		38	131	96	132	276	133
Domi-			rs602169	5069428	0.000001								
nant	1	20	3	7	494			42	154	69	59	247	235
Domi-			rs283650	3991855	0.000002								
nant	2	21	5	3	134	ERG		16	91	158	57	258	226
Domi-			rs649864	1705087	0.000002								
nant	3	16	3	4	438			2	71	192	5	68	467
Domi-			rs172966	1252968	0.000002								
nant	4	8	67	72	821			2	85	178	9	87	445
Domi-			rs992593	1702824	0.000003								
nant	5	16	4	7	257			1	65	199	3	60	478
Domi-			rs707377	1541753	0.000003								
nant	6	10	0	7	458			1	12	252	1	84	456
Domi-			rs171028	1237285	0.000004								
nant	7	10	09	23	27	NSMCE4A		19	136	110	43	179	318
Domi-			rs156063	1736092	0.000014								
nant	8	5	9	74	2			11	81	173	11	99	431
Domi-			rs109005	2041081	0.000015								
nant	9	1	53	63	72	ETNK2		32	118	115	87	303	151
Domi-			rs297058	2120975	0.000017								
nant	10	1	0	21	62			5	39	221	12	154	375
Domi-			rs605764	2996045	0.000018								
nant	11	20	9	8	29	DEFB118		20	137	108	37	196	308
Domi-			rs608744	2999025	0.000018								
nant	11	20	5	2	29			21	136	108	38	195	308
Domi-			rs237685	3000335	0.000018								
nant	11	20	8	0	29			21	136	108	38	195	308
Domi-			rs218056	3001885	0.000018								
nant	11	20	6	4	29			21	136	108	39	194	308
Domi-			rs608821	3002178	0.000018								
nant	11	20	5	9	29			21	136	108	38	195	308
Domi-			rs168396	2404383	0.000024								
nant	16	1	92	07	74	FMN2		68	145	52	107	251	183
Domi-			rs601722	4259322	0.000025								
nant	17	20	7	0	06	TOX2		0	39	226	0	30	511
Domi-				2996501	0.000026								
nant	18	20	rs709045	4	22	DEFB119		20	136	109	37	196	308

Domi-			exm2272	2996886	0.000026							
nant	18	20	889	3	22	DEFB119	20	136	109	37	196	308
Domi-			rs491127	2996886	0.000026							
nant	18	20	4	3	22	DEFB119	20	136	109	37	196	308
Domi-			rs220638	2997821	0.000026							
nant	18	20	1	6	22	DEFB119	20	136	109	37	196	308
Domi-				2998190	0.000026							
nant	18	20	rs765736	7	22		20	136	109	37	196	308
Reces-			rs940352	1439941	0.000002							
sive	1	6	1	99	564	PHACTR2	11	138	116	80	241	220
Reces-			rs482337	4517172	0.000002	PRR5-						
sive	2	22	6	9	832	ARHGAP8,ARHGAP8	9	117	139	72	191	278
Reces-			rs940352	1440049	0.000003							
sive	3	6	3	81	427	PHACTR2	13	139	113	86	241	214
Reces-			rs178280	4094699	0.000009							
sive	4	13	5	3	06	TTL	19	84	162	6	182	353
Reces-			rs771972		0.000012							
sive	5	5	3	2137758	46		27	126	112	122	250	169
Reces-			rs112552	1230196	0.000017							
sive	6	10	7	16	14		78	122	65	87	282	172
Reces-			rs153920	2125809	0.000032							
sive	7	1	6	22	9	TMEM206	79	114	72	91	267	183
Reces-			rs712260	1096416	0.000034							
sive	8	11	7	52	87		2	86	177	37	176	328
Reces-				1096409	0.000035							
sive	9	11	rs989695	72	42		2	83	179	37	175	329
Reces-			rs414127	2907987	0.000038							
sive	10	7	5	0	35	CPVL	81	124	60	94	289	158
Reces-				4591667	0.000038							
sive	11	22	rs136723	9	52	FBLN1	29	95	141	18	206	316
Reces-				2908439	0.000057							
sive	12	7	rs505532	2	47	CPVL	80	122	61	95	284	160
Reces-			rs721949	6472214	0.000060							
sive	13	17	5	5	64	PRKCA	60	116	89	62	261	218
Reces-			rs173008	9588252	0.000061							
sive	14	13	65	4	64	ABCC4	1	97	167	31	160	350
Reces-			rs707650	1230217	0.000061							
sive	15	10	0	31	72		51	120	94	49	265	227
Reces-			rs107850	7400640	0.000061							
sive	16	12	56	1	94		16	137	112	85	247	209
Reces-			rs297658	1343349	0.000063							
sive	17	8	9	04	01		20	89	156	9	186	346

Reces-			1580893	0.000063								
sive	18	2	rs876718	5	61		8	112	144	59	201	279
Reces-			rs104969	1426650	0.000064							
sive	19	2	07	64	43	<i>LRP1B</i>	6	130	129	52	207	281
Reces-			rs183257	2014905	0.000068							
sive	20	1	4	8	67		20	130	115	96	235	210

B/B, homozygote for the major allele for each SNP

Model, the genetic model in which candidate SNPs were selected by the GWAS; CHR, chromosome number; Position, chromosomal position (bp); Related gene, the nearest gene from the SNP site; A/A, homozygote for the minor allele for each SNP; A/B, heterozygote for each SNP; B/B, homozygote for the major allele for each SNP.

Table S3. Top 20 candidate SNPs selected from the GWAS for vomiting in all patients.

Model	Rank	CH R	SNP	Position	p	Related gene	Genotype (Nausea +)			Genotype (Nausea -)		
							A/A	A/B	B/B	A/A	A/B	B/B
Trend	1	2	rs13420654	79560656	0.00000209 5		0	29	120	1	43	613
Trend	2	18	exm1387565	50866195	0.00000221 7	<i>DCC</i>	1	28	120	1	45	611
Trend	3	5	rs4518389	12432786 2	0.00000240 4		16	77	56	163	346	146
Trend	4	5	rs1421691	16454146 6	0.00000336 0.00000406		6	51	92	9	127	520
Trend	5	2	exm185124	32641040	6	<i>BIRC6</i>	0	7	142	0	2	655
Trend	5	3	exm2047963	19597424 6	0.00000406 6	<i>PCYT1A</i>	0	7	142	0	2	655
Trend	5	12	rs1805772	9087081	0.00000406 6	<i>PHC1</i>	0	7	142	0	2	655
Trend	8	20	rs6013869	52619796	0.00000921 6	<i>BCAS1</i>	24	60	65	179	312	166
Trend	9	20	rs12624524	46557322	0.00000975 9		3	35	111	6	67	584
Trend	10	20	rs2299723	52622783	0.00001035	<i>BCAS1</i>	58	66	25	146	321	190
Trend	11	5	rs10440778	12432930 6	0.00001216		16	78	55	161	343	153
Trend	12	9	rs306772	12409235 5	0.00001335	<i>GSN</i>	3	46	100	4	110	543
Trend	13	2	rs2216322	56374910	0.00001457		11	58	80	21	167	469
Trend	14	20	rs6118234	8509458	0.00001568	<i>PLCB1</i>	29	66	54	40	303	314

Trend	15	20	rs7270072	57998583	0.00001769		25	88	36	68	304	285
				16616488								
Trend	16	2	rs1965757	7	0.00001807	SCN2A	53	74	22	142	329	186
				16755910								
Trend	17	4	rs28391069	6	0.00002093		1	9	139	0	8	649
Trend	18	15	rs10520799	96201031	0.00002426		0	15	134	0	17	640
Trend	19	19	rs751792	35157254	0.00002445		46	61	42	94	308	255
Trend	20	7	rs12704714	93930713	0.00002464		41	67	41	86	309	261
				10995506		TMEM23						
Dominant	1	5	rs10064687	2	0.00000906	2	28	62	59	171	343	141
Dominant	2	2	rs13420654	79560656	0.00000937		0	29	120	1	43	613
Dominant	3	20	rs7270072	57998583	0.00001178		25	88	36	68	304	285
Dominant	4	18	exm1387565	50866195	0.00001421	DCC	1	28	120	1	45	611
Dominant	5	20	rs6013869	52619796	0.00001427	BCAS1	24	60	65	179	312	166
				10991006		TMEM23						
Dominant	6	5	rs4317370	7	0.00001449	2	28	62	59	173	341	143
				16454146								
Dominant	7	5	rs1421691	6	0.00001715		6	51	92	9	127	520
Dominant	8	20	rs12624524	46557322	0.00001763		3	35	111	6	67	584
						CCDC88						
Dominant	9	2	rs12991861	55585915	0.0000206	A	39	82	28	121	296	240
Dominant	10	12	rs4761419	76712538	0.00002599		17	81	50	45	264	348
Dominant	11	16	rs12595990	12471112	0.00002909	SNX29	22	56	71	131	333	193
				10805871								
Dominant	12	10	rs10748915	6	0.00003335		11	86	48	47	266	341
Dominant	13	9	rs13296679	71347988	0.00004011	PIP5K1B	17	86	46	78	254	323
				18775399								
Dominant	14	3	rs11710227	5	0.00004041		21	76	52	70	234	352
				18775388								
Dominant	15	3	exm2255887	9	0.00004112		21	76	52	70	235	352
				18775388								
Dominant	15	3	rs16862908	9	0.00004112		21	76	52	70	235	352
Dominant	17	19	rs11668036	35186128	0.00004865		13	48	87	81	312	263
						CCDC88						
Dominant	18	2	rs1045613	55516090	0.00005243	A	39	80	30	120	292	245
						CCDC88						
Dominant	19	2	rs13019339	55589364	0.00005317	A	48	78	23	149	301	207
Dominant	20	9	rs4743505	98827451	0.00005637		15	44	90	70	311	276

					0.00000194							
Recessive	1	20	rs6118234	8509458	9	<i>PLCB1</i>	29	66	54	40	303	314
					0.00000620							
Recessive	2	5	rs9292416	31021518	8		58	58	33	135	341	181
					0.00000650							
Recessive	3	19	rs751792	35157254	4		46	61	42	94	308	255
Recessive	4	9	rs7027092	95812707	0.00001309		55	59	33	129	324	194
Recessive	5	5	rs6869417	31020501	0.00001545		56	61	32	133	333	191
Recessive	6	19	rs1985840	54880076	0.00001764		18	49	82	19	247	391
Recessive	7	4	rs6448841	11861566	0.00001953		17	49	83	17	249	391
Recessive	7	4	rs12645979	11868097	0.00001953		17	50	82	17	251	389
Recessive	9	9	exm2266850	95812707	0.0000209		55	61	33	129	327	195
Recessive	10	3	rs9809465	16674026	0.00002504		25	55	69	37	308	312
				10624712								
Recessive	11	13	rs10508158	4	0.00003162		28	57	64	46	288	323
Recessive	12	19	rs8109293	21009270	0.00003279		57	55	37	140	354	162
Recessive	13	5	rs40654	9371411	0.00003672	<i>SEMA5A</i>	6	27	116	0	118	539
Recessive	14	17	rs7219495	64722145	0.00003791	<i>PRKCA</i>	40	61	48	82	316	259
Recessive	15	13	rs2028809	44523136	0.00004081		3	84	62	81	281	295
Recessive	16	20	rs2299723	52622783	0.00004292	<i>BCAS1</i>	58	66	25	146	321	190
Recessive	17	1	rs12045323	11764281	0.00004639	<i>C1orf187</i>	9	69	71	124	307	226
				12214653								
Recessive	18	11	rs1025139	3	0.00004693		20	44	85	26	247	384
Recessive	19	7	rs12704714	93930713	0.00005179		41	67	41	86	309	261
Recessive	20	11	rs10830263	89100329	0.00005396	<i>NOX4</i>	6	74	69	104	292	261

B/B, homozygote for the major allele for each

SNP

Model, the genetic model in which candidate SNPs were selected by the GWAS; CHR, chromosome number; Position, chromosomal position (bp); Related gene, the nearest gene from the SNP site; A/A, homozygote for the minor allele for each SNP; A/B, heterozygote for each SNP; B/B, homozygote for the major allele for each SNP.

Table S4. Top 20 candidate SNPs selected from the GWAS for PONV in all patients.

Model	Rank	CH R	SNP	Posi- tion	<i>p</i>	Related gene	Genotype (Nau- sea +)			Genotype (Nau- sea -)		
							A/ A	A/B	B/B	A/ A	A/B	B/B
Trend	1	20	rs6021693	5069428 7	0.0000020 62	<i>TACC2</i>	48	156	76	53	245	228
Trend	2	10	rs7097450	1238780 29	0.0000073 02		3	16	260	0	6	518
Trend	3	13	rs645833	4872425 6	0.0000075 39		0	31	249	0	17	509
Trend	4	16	rs9925934	1702824 7	0.0000114 4		1	67	212	3	58	465
Trend	5	10	rs7073770	1541753 7	0.0000147 9		1	13	266	1	83	442
Trend	6	20	rs743093	5069584 9	0.0000157 6	<i>ACCN1</i>	35	146	95	34	235	254
Trend	7	8	rs17296667	1252968 72	0.0000175 2		2	90	188	9	82	435
Trend	8	17	rs1978136	3237769 8	0.0000191 5		60	144	76	65	252	209
Trend	9	16	rs6498643	1705087 4	0.0000212 0.0000216		2	73	205	5	66	454
Trend	10	17	rs886359	3239997 4	0.0000216 2		38	141	101	128	267	131
Trend	11	20	rs6013382	5070263 3	0.0000224 2	<i>ZFP64</i>	35	148	97	35	235	256
Trend	11	20	rs6013382	5070263 3	0.0000224 2		35	148	97	35	235	256
Trend	13	21	rs2836505	3991855 3	0.0000235 3	<i>ERG</i>	17	101	162	56	248	222
Trend	14	1	rs11582464	3074526 8	0.0000255 3		8	87	185	5	105	416
Trend	15	17	rs12602886	3239234 6	0.0000259 7	<i>ACCN1</i>	38	141	101	128	266	132
Trend	16	18	rs1944967	3953113 9	0.0000260 9		61	136	82	70	231	225
Trend	17	20	rs2273382	5070521 1	0.0000266 1	<i>ZFP64</i>	35	148	97	35	236	255
Trend	18	10	rs7911912	1543908 0	0.0000298 9		1	41	238	7	140	378

					0.0000301								
Trend	19	5	rs7719723	2137758	9			30	134	116	119	242	165
				6882034	0.0000306								
Trend	20	5	rs28558979	8	4	OCLN		13	92	175	54	218	254
Domi-				1252968	0.0000009								
nant	1	8	rs17296667	72	951			2	90	188	9	82	435
Domi-				1541753	0.0000024								
nant	2	10	rs7073770	7	25			1	13	266	1	83	442
Domi-				1702824	0.0000048								
nant	3	16	rs9925934	7	67			1	67	212	3	58	465
Domi-				1705087	0.0000055								
nant	4	16	rs6498643	4	39			2	73	205	5	66	454
Domi-				5069428	0.0000062								
nant	5	20	rs6021693	7	86			48	156	76	53	245	228
Domi-				9820680	0.0000099								
nant	6	6	rs600613	5	47			52	157	71	77	233	216
Domi-					0.0000139								
nant	7	4	rs4689343	6136653	2	JAKMIP1		0	3	277	0	41	485
Domi-				4872425	0.0000155								
nant	8	13	rs645833	6	7			0	31	249	0	17	509
Domi-					0.0000158								
nant	9	9	rs7869201	5551261	5	PDCD1LG2		40	142	98	61	197	268
Domi-				9825098	0.0000188								
nant	10	3	exm333077	6	6	GPR15		31	101	148	67	264	194
Domi-				9825098	0.0000193								
nant	11	3	rs2230344	6	6	GPR15		31	101	148	67	264	195
Domi-				2836610	0.0000197								
nant	12	7	rs17156585	0	6	CREB5		4	84	192	7	87	431
Domi-				2041081	0.0000203								
nant	13	1	rs10900553	63	3	ETNK2		33	127	120	86	294	146
Domi-				2837005	0.0000224								
nant	14	7	rs6978238	8	4	CREB5		2	83	195	7	83	436
Domi-				1237285	0.0000227								
nant	15	10	rs17102809	23	8	NSMCE4A		20	140	120	42	175	308
Domi-				2120975	0.0000231								
nant	16	1	rs2970580	21	7			5	43	232	12	150	364
Domi-				5527463	0.0000240								
nant	17	17	rs7212872	0	1			13	119	148	20	147	359
Domi-				3991855	0.0000240								
nant	18	21	rs2836505	3	9	ERG		17	101	162	56	248	222

Domi-				1192271	0.0000256							
nant	19	4	rs2171726	2	6		10	68	201	24	202	299
Domi-				1543908	0.0000261							
nant	20	10	rs7911912	0	2		1	41	238	7	140	378
Reces-				1440049	0.0000051							
sive	1	6	rs9403523	81	61	<i>PHACTR2</i>	15	146	119	84	234	208
Reces-				1439941	0.0000064							
sive	2	6	rs9403521	99	21	<i>PHACTR2</i>	13	145	122	78	234	214
Reces-				4517172	0.0000118	<i>PRR5-</i>						
sive	3	22	rs4823376	9	6	<i>ARHGAP8,ARHGAP8</i>	11	125	144	70	183	273
Reces-				6472214	0.0000129							
sive	4	17	rs7219495	5	80	<i>PRKCA</i>	64	126	90	58	251	217
Reces-				1218901	0.0000180							
sive	5	11	rs10831744	3	1	<i>MICAL2</i>	15	148	117	80	238	208
Reces-				2908439	0.0000216							
sive	6	7	rs505532	2	2	<i>CPVL</i>	85	129	64	90	277	157
Reces-				2907987	0.0000224							
sive	7	7	rs4141275	0	4	<i>CPVL</i>	85	132	63	90	281	155
Reces-					0.0000244							
sive	8	5	rs7719723	2137758	5		30	134	116	119	242	165
Reces-				9588252	0.0000298							
sive	9	13	rs17300865	4	3	<i>ABCC4</i>	1	100	179	31	157	338
Reces-				7400640	0.0000301							
sive	10	12	rs10785056	1	5		17	141	122	84	243	199
Reces-				1553828	0.0000339							
sive	11	6	rs9322497	07	3		52	108	120	44	253	229
Reces-				4554367	0.0000350							
sive	12	20	rs6122536	6	50	<i>EYA2</i>	30	136	108	119	234	169
Reces-			exm105207	1323252	0.0000387							
sive	13	12	4	39	30	<i>MMP17</i>	78	123	79	81	288	157
Reces-				1323252	0.0000391							
sive	14	12	rs6598163	39	70	<i>MMP17</i>	78	123	79	81	287	157
Reces-				1311914	0.0000392							
sive	15	9	rs2270202	03	1	<i>CERCAM</i>	26	156	98	107	256	163
Reces-					0.0000425							
sive	16	8	rs7816614	5344373	1		19	75	185	6	156	358
Reces-				5488007	0.0000527							
sive	17	19	rs1985840	6	4		25	95	160	12	201	313
Reces-				1421657	0.0000614							
sive	18	4	rs7672861	41	5		32	106	142	20	209	296

Reces-				1857768	0.0000707								
sive	19	4	rs12650715	50	9			21	127	132	92	203	231
Reces-				6473117	0.0000718								
sive	20	17	rs8067877	8	80	PRKCA		62	126	92	59	249	218
Reces-				6473140	0.0000718								
sive	20	17	rs6504452	2	80	PRKCA		62	126	92	59	249	218

B/B, homozygote for the major allele for each SNP

Model, the genetic model in which candidate SNPs were selected by the GWAS; CHR, chromosome number; Position, chromosomal position (bp); Related gene, the nearest gene from the SNP site; A/A, homozygote for the minor allele for each SNP; A/B, heterozygote for each SNP; B/B, homozygote for the major allele for each SNP.

Table S5. Top 20 candidate SNPs selected from the GWAS for nausea in patients who received propofol.

Model	Rank	CHR	SNP	Position	p	Related gene	Genotype (Nausea +)			Genotype (Nausea -)		
							A/A	A/B	B/B	A/A	A/B	B/B
Trend	1	17	rs11079308	55604585	0.0000015 44	MSI2	9	54	86	1	67	225
Trend	2	9	rs4977887	23718520	0.0000015 99	ELAVL2	10	57	82	50	148	95
Trend	3	6	rs7356878	40494855	0.0000019 69	LRFN2	52	77	20	56	145	92
Trend	4	6	rs1433742	40503796	0.0000035 73	LRFN2	26	75	48	23	112	158
Trend	5	5	rs7719723	2137758	0.0000041 31		11	71	67	73	134	86
Trend	6	6	rs382023	40491240	0.0000058 78	LRFN2	15	76	58	75	151	67
Trend	7	15	rs11072390	73136716	0.0000062 07		42	72	35	39	134	120
Trend	8	7	rs1982436	13447063	0.0000070 65	CALD1	5	63	81	5	65	223
Trend	9	6	rs403606	40493903	0.0000072 95	LRFN2	15	73	61	76	144	73
Trend	10	10	rs10901376	12708581	0.0000124 9		0	9	140	4	62	227
Trend	11	17	rs11655926	35243370	0.0000136 6		15	68	66	11	93	189
Trend	12	6	rs909988	40489573	0.0000198 2	LRFN2	35	85	29	35	151	107

					0.0000214							
Trend	13	15	rs12439063	73150166	1		22	80	47	24	113	156
					0.0000261							
Trend	14	23	rs7879223	95721436	6		0	12	126	0	1	234
					0.0000270							
Trend	15	6	rs2235705	40486159	6	LRFN2	25	83	41	19	145	129
					0.0000283							
Trend	16	18	rs540291	77585900	4		31	78	40	35	119	139
			exm-		0.0000321							
Trend	17	3	rs2286720	42448471	3	LYZL4	3	58	88	27	147	119
					0.0000321							
Trend	17	3	rs2286720	42448471	3	LYZL4	3	58	88	27	147	119
					0.0000365							
Trend	19	10	rs10828239	21679527	2		31	86	32	38	130	123
					0.0000397							
Trend	20	3	rs1529047	98252027	8		16	63	70	11	91	191
				13447063	0.0000046							
Dominant	1	7	rs1982436	2	2	CALD1	5	63	81	5	65	223
					0.0000058							
Dominant	2	9	rs4977887	23718520	09	ELAVL2	10	57	82	50	148	95
				12708581	0.0000065							
Dominant	3	10	rs10901376	8	65		0	9	140	4	62	227
					0.0000066	PDCD1L						
Dominant	4	9	rs4143813	5534243	94	G2	9	63	77	14	63	216
					0.0000087	CCDC102						
Dominant	5	18	rs1942295	66544809	6	B	10	39	100	21	141	131
Dominant	6	10	rs10828239	21679527	0.0000139		31	86	32	38	130	123
					0.0000141							
Dominant	7	15	rs12439063	73150166	2		22	80	47	24	113	156
					0.0000144							
Dominant	8	6	rs1433742	40503796	2	LRFN2	26	75	48	23	112	158
					0.0000167							
Dominant	9	5	rs11749532	55002265	2	SLC38A9	28	87	34	46	119	128
Dominant	10	6	rs7356878	40494855	0.0000279	LRFN2	52	77	20	56	145	92
					0.0000279							
Dominant	11	8	rs12550470	55344415	5		15	58	76	43	162	88
					0.0000298							
Dominant	12	11	rs7933966	32875597	8	PRRG4	30	58	61	64	166	63
			exm-		0.0000298							
Dominant	12	11	rs10767971	32895664	8		30	58	61	64	166	63

					0.0000298							
Dominant	12	11	rs10767971	32895664	8		30	58	61	64	166	63
					0.0000327							
Dominant	15	8	rs13258851	55330814	8		11	48	90	30	148	115
					0.0000328							
Dominant	16	10	rs511991	29449129	4		24	67	58	58	177	58
				24051196	0.0000342							
Dominant	17	1	rs6658239	5	9	FMN2	15	82	52	27	102	164
					0.0000378							
Dominant	18	18	rs540291	77585900	6		31	78	40	35	119	139
Dominant	19	10	rs2781256	25616473	0.000038	GPR158	5	62	82	8	66	219
					0.0000383							
Dominant	20	8	rs10099341	55368646	6		17	59	73	46	162	84
					0.0000050							
Recessive	1	5	rs7719723	2137758	31		11	71	67	73	134	86
				14399419	0.0000118							
Recessive	2	6	rs9403521	9	4	PHACTR2	4	78	67	46	121	126
					0.0000119							
Recessive	3	7	rs4141275	29079870	3	CPVL	52	68	29	47	161	85
Recessive	4	13	rs1782805	40946993	0.0000191	TTL	16	48	85	4	97	192
					0.0000195							
Recessive	5	8	rs2942213	23427919	2	SLC25A37	4	74	71	45	120	128
				14400498	0.0000217							
Recessive	6	6	rs9403523	1	9	PHACTR2	5	80	64	48	121	124
				11961079	0.0000311							
Recessive	7	3	rs6782799	3	8	GSK3B	16	86	47	81	127	85
				11977688	0.0000311							
Recessive	7	3	rs17204878	0	8	GSK3B	16	86	47	81	127	85
					0.0000341							
Recessive	9	4	rs9306994	76576116	5	G3BP2	0	63	86	25	98	169
					0.0000380							
Recessive	10	5	rs4362905	52927597	2	NDUFS4	2	71	76	35	115	143
					0.0000380							
Recessive	10	5	rs11745611	53011223	2		2	73	74	35	116	142
					0.0000454							
Recessive	12	12	rs10437774	20139160	6		12	77	59	69	136	88
				11045157								
Recessive	13	9	rs10816556	9	0.0000477		9	34	106	0	74	219
				11045163								
Recessive	13	9	rs10759254	7	0.0000477		9	34	106	0	74	219

Recessive	15	3	rs7651125	6401420	0.0000482		3	65	81	39	105	148
				11622768	0.0000485							
Recessive	16	11	rs482795	7	5		14	84	51	74	130	89
				11963181	0.0000488							
Recessive	17	3	rs6438552	4	6	<i>GSK3B</i>	16	85	47	80	128	85
					0.0000610							
Recessive	18	21	rs2268284	36220679	1	<i>RUNX1</i>	48	69	32	44	169	79
					0.0000613							
Recessive	19	6	rs403606	40493903	4	<i>LRFN2</i>	15	73	61	76	144	73
				13085344								
Recessive	20	8	rs837065	7	0.0000622	<i>FAM49B</i>	10	86	53	62	139	92

B/B, homozygote for the major allele infor each

SNP

Model, the genetic model in which candidate SNPs were selected by the GWAS; CHR, chromosome number; Position, chromosomal position (bp); Related gene, the nearest gene from the SNP site; A/A, homozygote for the minor allele for each SNP; A/B, heterozygote for each SNP; B/B, homozygote for the major allele for each SNP.

Table S6. Top 20 candidate SNPs selected from the GWAS for PONV in patients who received propofol.

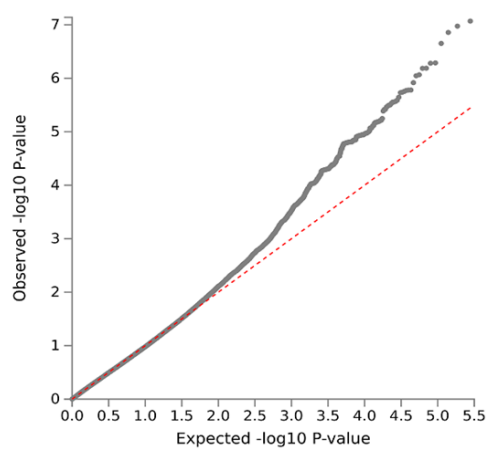
Model	Rank	CHR	SNP	Position	p	Related gene	Genotype (Nausea +)			Genotype (Nausea -)		
							A/A	A/B	B/B	A/A	A/B	B/B
					0.00000242							
Trend	1	13	rs1752136	48726219	5		0	25	135	0	9	273
					0.00000269							
Trend	2	6	rs7356878	40494855	5	<i>LRFN2</i>	55	82	23	53	140	89
					0.00000368							
Trend	3	17	rs11079308	55604585	2	<i>MSI2</i>	9	57	94	1	64	217
					0.00000447							
Trend	4	9	rs4977887	23718520	9	<i>ELAVL2</i>	11	64	85	49	141	92
					0.00000505							
Trend	5	15	rs11072390	73136716	6		44	78	38	37	128	117
Trend	6	2	rs1922717	11024358	0.00000913		4	41	115	0	35	247
					0.00000941							
Trend	7	5	rs7719723	2137758	6		14	75	71	70	130	82
Trend	8	6	rs403606	40493903	0.00001074	<i>LRFN2</i>	17	79	64	74	138	70
Trend	9	6	rs1433742	40503796	0.00001093	<i>LRFN2</i>	28	77	55	21	110	151
			exm-									
Trend	10	3	rs2286720	42448471	0.00001378	<i>LYZL4</i>	3	63	94	27	142	113
Trend	10	3	rs2286720	42448471	0.00001378	<i>LYZL4</i>	3	63	94	27	142	113

Trend	12	7	rs4141275	29079870	0.00001401	CPVL	55	75	30	44	154	84
Trend	13	3	rs1529047	98252027	0.00001439		16	70	74	11	84	187
Trend	14	6	rs382023	40491240	0.00001476	LRFN2	17	83	60	73	144	65
Trend	15	15	rs12439063	73150166	0.00001589		23	86	51	23	107	152
Trend	16	5	rs28558979	68820348	0.00001621	OCLN	3	52	105	25	126	131
Trend	17	17	rs4644888	64745690	0.00002141	PRKCA	22	64	74	65	145	72
Trend	18	17	rs8070561	64747056	0.00002539	PRKCA	22	64	74	64	146	72
Trend	19	3	rs4682737	42484782	0.0000284		3	64	93	27	141	114
Trend	20	2	rs17036833	69851974	0.00002911	AAK1	1	34	125	0	23	259
Domi-					0.00000464							
nant	1	18	rs1942295	66544809	3	CCDC102B	10	43	107	21	137	124
Domi-					0.00000701							
nant	2	13	rs1752136	48726219	1		0	25	135	0	9	273
Domi-					0.00000770							
nant	3	15	rs12439063	73150166	9		23	86	51	23	107	152
Domi-					0.000011							
nant	4	1	rs1571549	86050965			25	68	67	67	154	61
Domi-					0.00001418	PRKCA	22	64	74	65	145	72
nant	5	17	rs4644888	64745690		PRKCA	22	64	74	64	146	72
Domi-					0.00001418	PRKCA	22	64	74	64	146	72
nant	5	17	rs8070561	64747056			22	64	74	64	146	72
Domi-					0.00002622							
nant	7	14	rs4983168	26851322			28	93	39	46	111	125
Domi-				13447063								
nant	8	7	rs1982436	2	0.00002819	CALD1	5	65	90	5	63	214
Domi-					0.00002928							
nant	9	23	rs1318834	39345412			43	83	20	48	104	75
Domi-				24051196								
nant	10	1	rs6658239	5	0.0000307	FMN2	17	86	57	25	98	159
Domi-					0.00003229	ELAVL2	11	64	85	49	141	92
nant	11	9	rs4977887	23718520			11	64	85	49	141	92
Domi-					0.00003232	C4orf19	0	1	159	2	26	254
nant	12	4	rs2380737	37536119			0	1	159	2	26	254
Domi-				16732370								
nant	13	3	rs9837095	9	0.00003708	WDR49	2	27	131	14	89	178
Domi-				16732001								
nant	14	3	exm363153	0	0.0000384	WDR49	2	27	131	14	89	179
Domi-					0.00004003	FLYWCH1	18	89	51	36	97	149
nant	15	16	rs2074365	2964283			18	89	51	36	97	149

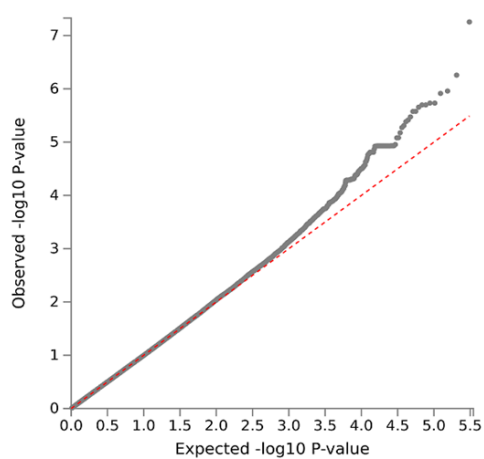
Domi-				18192651								
nant	16	4	rs11946898	8	0.00004213		34	96	30	54	123	105
Domi-												
nant	17	9	rs7869201	5551261	0.00004234	<i>PDCD1LG2</i>	26	84	50	36	101	145
Domi-												
nant	18	8	rs13258851	55330814	0.00004506		12	53	95	29	143	110
Domi-												
nant	19	10	rs10828239	21679527	0.00005148		31	92	37	38	124	118
Domi-												
nant	20	3	rs1529047	98252027	0.00005312		16	70	74	11	84	187
					0.00000517							
Recessive	1	8	rs2942213	23427919	1	<i>SLC25A37</i>	4	81	75	45	113	124
					0.00000925	<i>CPVL,CPV</i>						
Recessive	2	7	rs4141275	29079870	3	<i>L</i>	55	75	30	44	154	84
Recessive	3	5	rs4362905	52927597	0.0000095	<i>NDUFS4</i>	2	78	80	35	108	139
Recessive	3	5	rs11745611	53011223	0.0000095		2	80	78	35	109	138
				15814560								
Recessive	5	7	rs12698219	6	0.00001116	<i>PTPRN2</i>	11	32	117	0	51	231
Recessive	6	3	rs7651125	6401420	0.00001256		3	69	88	39	101	141
Recessive	7	5	rs567	52979097	0.00001627	<i>NDUFS4</i>	2	78	80	34	109	139
Recessive	8	1	rs1195866	81678254	0.00001682		16	47	96	3	98	178
Recessive	9	17	rs7219495	64722145	0.00002003	<i>PRKCA</i>	41	75	44	28	141	113
				11622768								
Recessive	10	11	rs482795	7	0.00002028		15	93	52	73	121	88
Recessive	11	5	rs7719723	2137758	0.00002501		14	75	71	70	130	82
Recessive	12	3	rs6796561	6409144	0.00002696		0	57	103	23	99	160
				12348387								
Recessive	12	10	rs2420953	9	0.00002696		0	65	95	23	102	157
				12348662								
Recessive	12	10	rs2935689	6	0.00002696		0	65	95	23	102	157
						<i>CPVL,CPV</i>						
Recessive	15	7	rs505532	29084392	0.00003413	<i>L</i>	55	73	31	47	149	84
Recessive	16	8	rs2942201	23419176	0.0000366	<i>SLC25A37</i>	3	76	81	36	105	141
Recessive	17	1	rs11165660	96993561	0.00003954		16	90	54	73	127	80
Recessive	18	14	rs10483614	53151428	0.00004454	<i>ERO1L</i>	20	62	78	7	114	161
Recessive	19	7	rs6964887	17728255	0.00004826		50	69	38	42	147	92
Recessive	20	5	rs6886811	53020039	0.00005066		2	75	82	32	106	144

Model, the genetic model in which candidate SNPs were selected by the GWAS; CHR, chromosome number; Position, chromosomal position (bp); Related gene, the nearest gene from the SNP site; A/A, homozygote for the minor allele for each SNP; A/B, heterozygote for each SNP; B/B, homozygote for the major allele for each SNP.

(a) Additive:



(b) Dominant:



(c) Recessive:

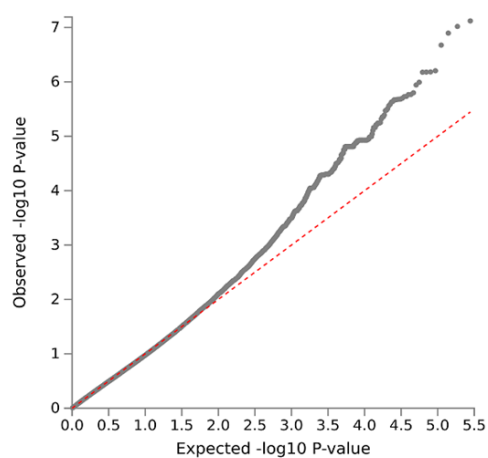


Figure S1. Log quantile-quantile (QQ) p -value plot as a result of the GWAS for the frequency of nausea in all patients. (a) Plot of the results from the additive model. (b) Plot of the results from the dominant model. (c) Plot of the results from the recessive model.

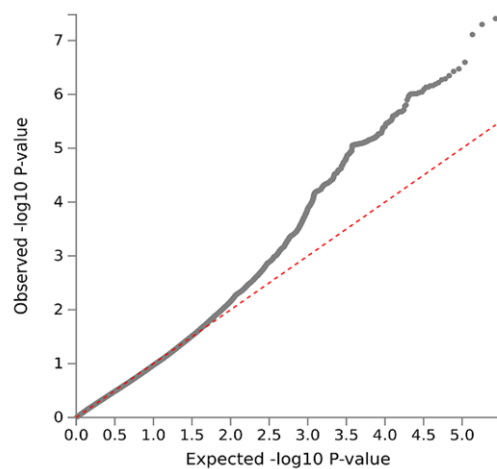
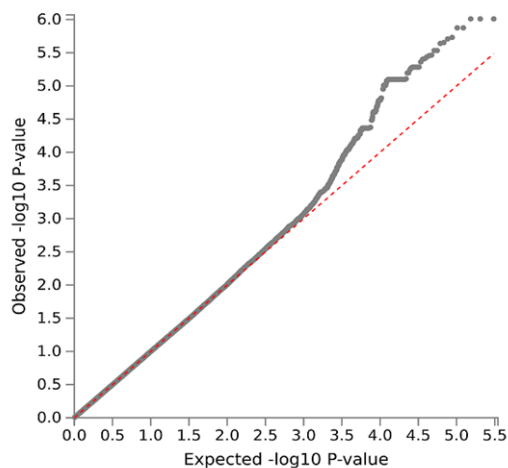
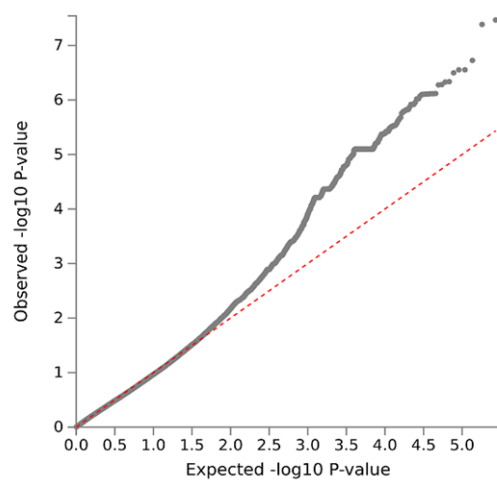
(a) Additive:**(b) Dominant:****(c) Recessive:**

Figure S2. Log quantile-quantile (QQ) p -value plot as a result of the GWAS for the frequency of nausea in patients with propofol. (a) Plot of the results from the additive model. (b) Plot of the results from the dominant model. (c) Plot of the results from the recessive model.

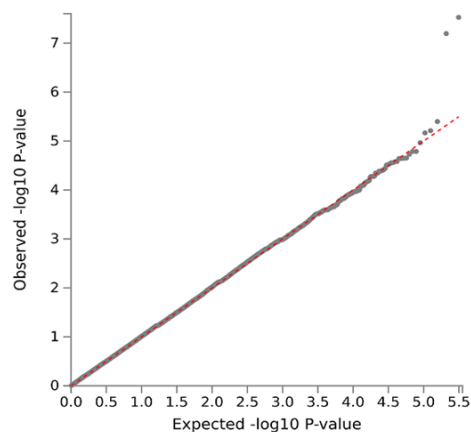
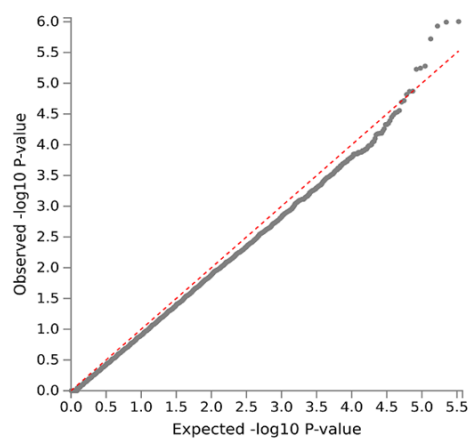
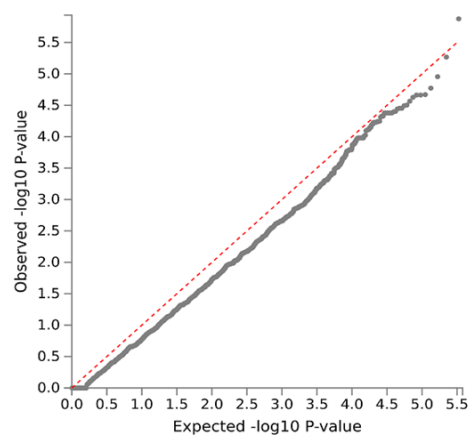
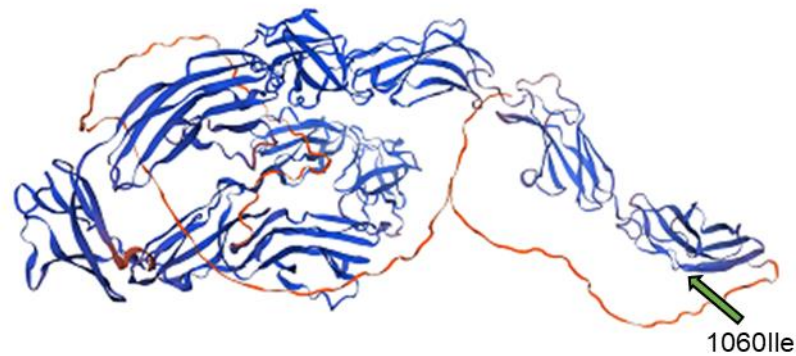
(a) Trend:**(b) Dominant:****(c) Recessive:**

Figure S3. Log quantile-quantile (QQ) p -value plot as a result of the GWAS for vomiting in patients who received propofol. (a) Plot of the results from the trend model. (b) Plot of the results from the dominant model. (c) Plot of the results from the recessive model.

(a) rs140703637-A:



(b) rs140703637-C:

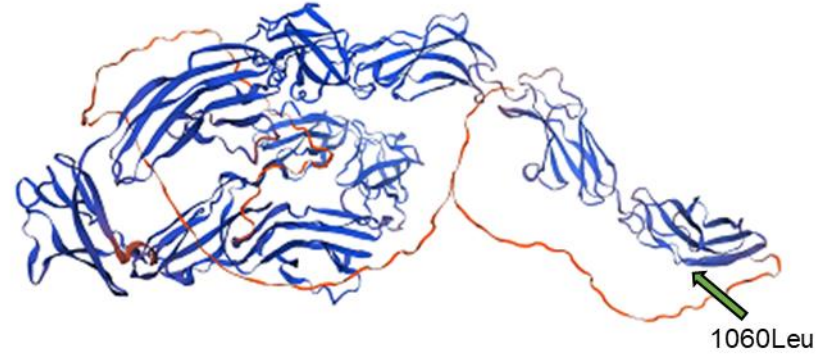
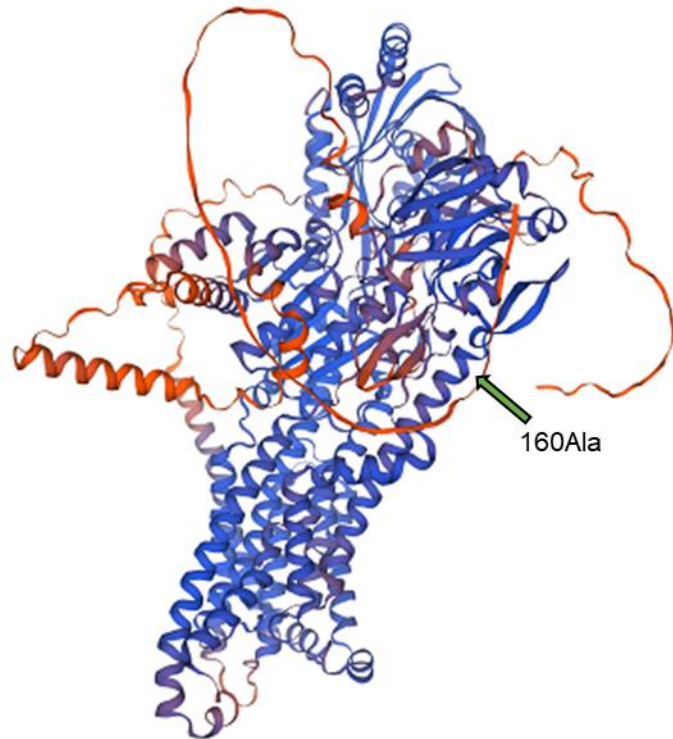


Figure S4. Protein structures of contactin 5 predicted from amino acid sequence (NCBI accession no. NP_001230199.1). (a) Protein structure predicted from amino acid sequence, including isoleucine residue, that corresponds to the A allele of the rs140703637 SNP. (b) Protein structure predicted from amino acid sequence, including leucine residue, that corresponds to the C allele of the rs140703637 SNP. The amino acids that correspond to the position of the rs140703637 SNP are indicated by the arrowheads.

(a) rs45574836-G:



(b) rs45574836-A:

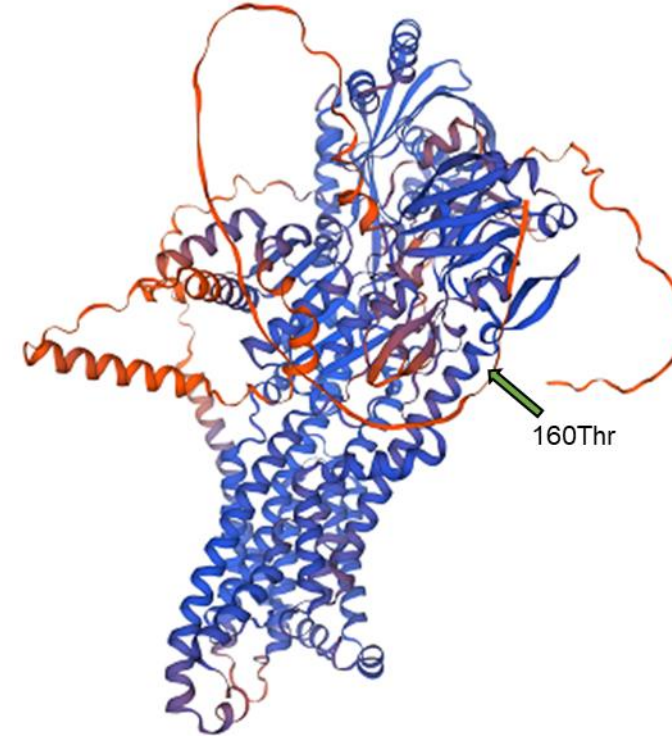


Figure S5. Protein structures of ATPase phospholipid transporting 8B3 predicted from amino acid sequence (NCBI accession no. NP_001171473.1). (a) Protein structure predicted from amino acid sequence, including alanine residue, that corresponds to the G allele of the rs45574836 SNP. (b) Protein structure predicted from amino acid sequence, including threonine residue, that corresponds to the A allele of the rs45574836 SNP. The amino acids that correspond to the position of the rs140703637 SNP are indicated by the arrowheads.