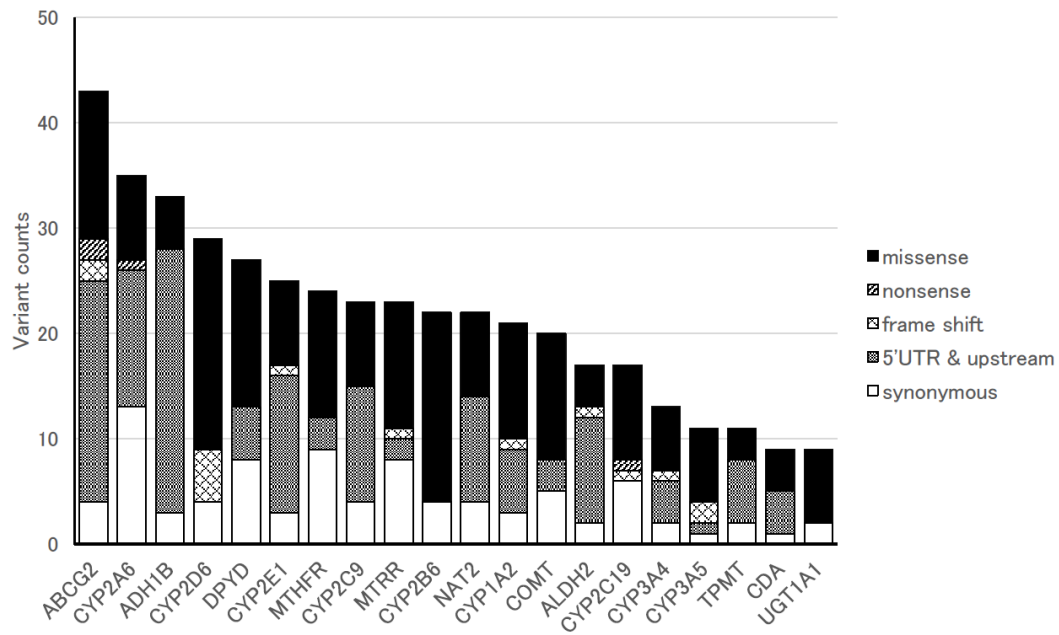


Supplementary Information

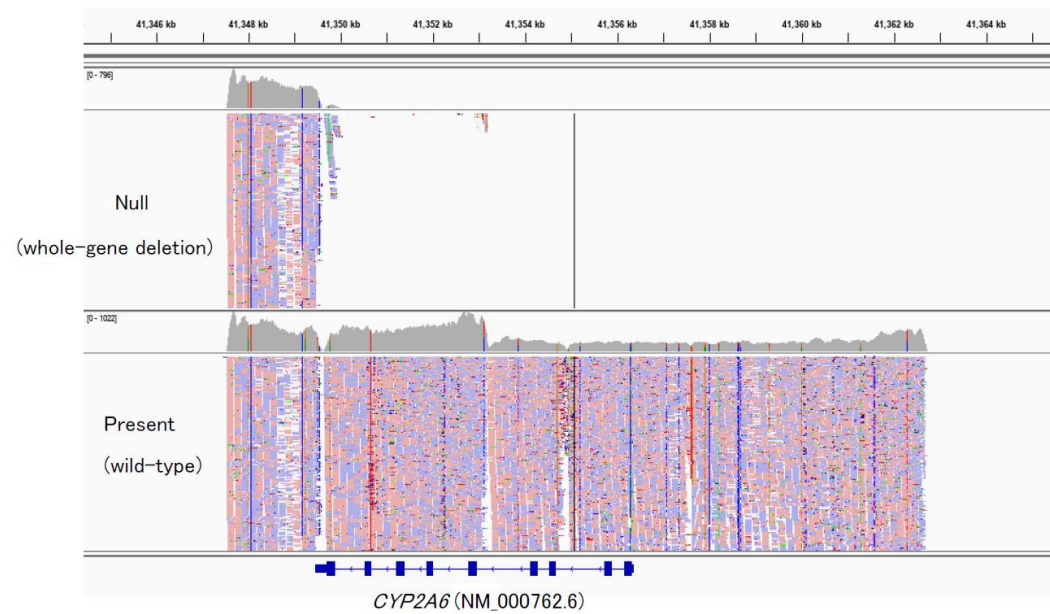
Comparison of genetic susceptibility to lung adenocarcinoma and squamous cell carcinoma in Japanese patients using a novel panel for cancer-related drug-metabolizing enzyme genes

Sumiko Ohnami, Akane Naruoka, Maki Mizuguchi, Sou Nakatani, Fukumi Kamada, Yuji Shimoda, Ai Sakai, Keiichi Ohshima, Keiichi Hatakeyama, Kouji Maruyama, Mitsuhiro Isaka, Yasuhisa Ohde, Hirotsugu Kenmotsu, Toshiaki Takahashi, Yasuto Akiyama, Takeshi Nagashima, Kenichi Urakami, Shumpei Ohnami, Ken Yamaguchi



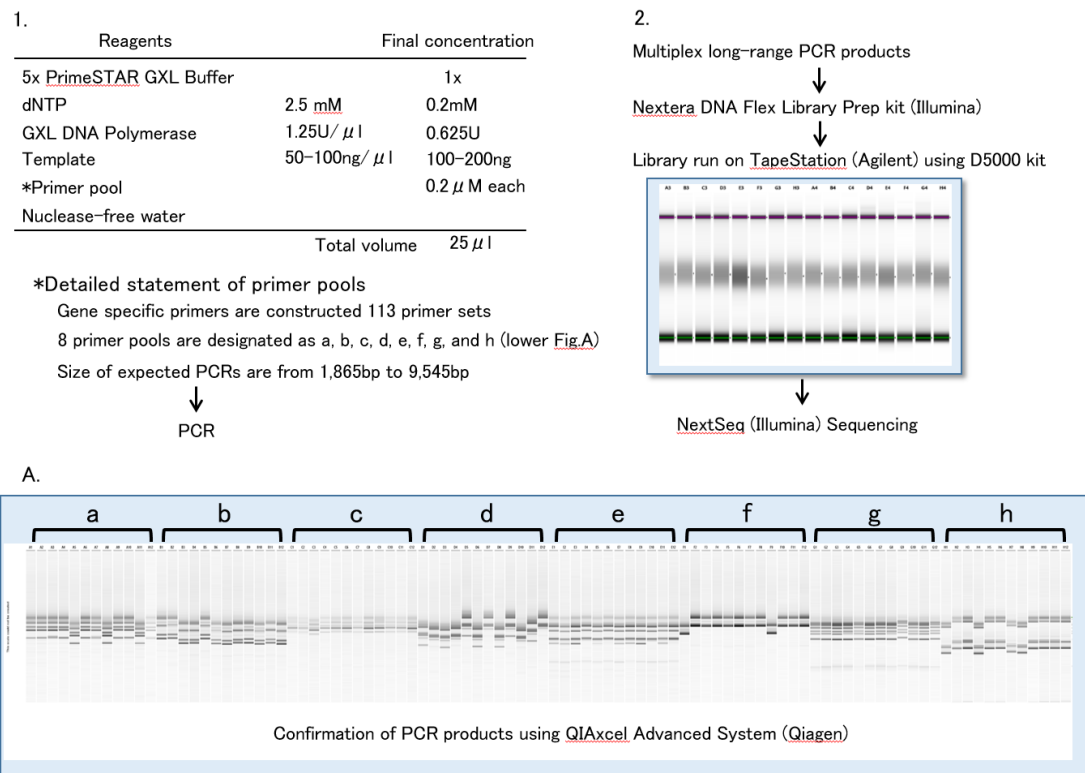
Supplementary Fig. S1

Distribution of genetic variants across the 20 drug-metabolizing enzymes in 710 cases.



Supplementary Fig. S2

Visualization of the *CYP2A6* whole-gene deletion and wild-type calls using Integrative Genomics Viewer (IGV).



Supplementary Fig. S3

Multiplex long-range PCR method (1) and subsequent DNA library preparation and targeted sequencing using an Illumina sequencer (2). An indication of the electrophoresis pattern of long-range PCR.

Supplementary Table S1

Association of variants between adenocarcinoma and squamous cell carcinoma in lungs

Gene symbol	rs No. or chr. position	nucleotide change	Adenocarcinoma (N=559)			Squamous cell carcinoma (N=151)			P value	OR (95%CI)
			AA	Aa	aa	AA	Aa	aa		
1 <i>MTHFR</i>	rs2274976	C>T	476	75	4	133	17	1	0.508	0.82(0.47-1.41)
2 <i>MTHFR</i>	chr1:11852436	C>A	559	0	0	150	1	0	0.213	
3 <i>MTHFR</i>	rs750510348	G>A	550	4	0	148	1	0	1.000	
4 <i>MTHFR</i>	rs1801131	T>G	367	167	20	103	40	6	0.557	0.88(0.59-1.29)
5 <i>MTHFR</i>	chr1:11854881	G>A	554	0	0	148	1	0	0.212	
6 <i>MTHFR</i>	rs2066462	G>A	474	76	4	131	17	1	0.508	
7 <i>MTHFR</i>	rs755483936	C>T	557	1	0	151	0	0	1.000	0.81(0.47-1.40)
8 <i>MTHFR</i>	rs45498098	G>A	558	0	0	150	1	0	0.213	
9 <i>MTHFR</i>	rs781214043	C>T	557	1	0	151	0	0	1.000	
10 <i>MTHFR</i>	rs45459991	T>C	551	1	0	148	0	0	1.000	0.96(0.66-1.40)
11 <i>MTHFR</i>	rs1801133	G>A	200	250	101	55	68	25	0.848	
12 <i>MTHFR</i>	rs1018203291	C>T	549	2	0	148	0	0	1.000	
13 <i>MTHFR</i>	chr1:11861246	G>A	558	1	0	151	0	0	1.000	0.72(0.42-1.23)
14 <i>MTHFR</i>	chr1:11861247	C>A	558	1	0	151	0	0	1.000	
15 <i>MTHFR</i>	rs781158269	C>G	553	1	0	149	0	0	1.000	
16 <i>MTHFR</i>	rs201618781	C>T	553	1	0	149	0	0	1.000	0.72(0.42-1.23)
17 <i>MTHFR</i>	rs749729349	G>A	553	1	0	149	0	0	1.000	
18 <i>MTHFR</i>	rs2066470	G>A	461	90	3	130	18	1	0.258	
19 <i>MTHFR</i>	chr1:11863124	C>T	553	1	0	149	0	0	1.000	0.72(0.42-1.23)
20 <i>MTHFR</i>	rs768905024	G>A	552	2	0	149	0	0	1.000	
21 <i>MTHFR</i>	rs773463208	G>A	553	1	0	148	1	0	0.379	
22 <i>MTHFR</i>	rs764973403	A>G	554	0	0	148	1	0	0.212	0.72(0.42-1.23)
23 <i>MTHFR</i>	chr1:11865961	A>G	558	1	0	150	1	0	0.380	
24 <i>MTHFR</i>	chr1:11866090	G>A	559	0	0	150	1	0	0.213	
25 <i>CDA</i>	rs67820925	G>A	480	68	1	137	10	0	0.057	0.50(0.25-1.01)
26 <i>CDA</i>	rs602950	A>G	349	174	26	92	49	6	0.847	
27 <i>CDA</i>	rs3215400	C>-	178	262	109	47	65	35	1.000	
28 <i>CDA</i>	rs749081273	C>T	548	1	0	147	0	0	1.000	1.02(0.69-1.50)
29 <i>CDA</i>	rs777342792	G>A	548	1	0	147	0	0	1.000	
30 <i>CDA</i>	rs2072671	A>C	351	172	26	95	46	6	0.923	
31 <i>CDA</i>	rs201761717	C>T	557	1	0	150	0	0	1.000	0.97(0.66-1.41)
32 <i>CDA</i>	rs60369023	G>A	514	44	0	145	5	0	0.068	
33 <i>CDA</i>	rs76249360	T>C	551	7	0	148	2	0	1.000	
34 <i>DPYD</i>	rs1462320422	C>A	536	0	0	138	1	0	0.206	2.48(0.96-6.37)
35 <i>DPYD</i>	chr1:97564054	A>G	554	2	0	150	0	0	1.000	
36 <i>DPYD</i>	rs188052243	T>C	554	2	0	149	1	0	0.512	
37 <i>DPYD</i>	chr1:97658771	C>T	551	1	0	149	0	0	1.000	1.70(0.72-4.00)
38 <i>DPYD</i>	rs55725052	A>G	547	1	0	146	0	0	1.000	
39 <i>DPYD</i>	rs56005131	G>T	530	18	0	138	8	0	0.222	
40 <i>DPYD</i>	rs1801160	C>T	531	19	0	145	2	0	0.277	0.38(0.08-1.67)
41 <i>DPYD</i>	chr1:97847963	C>T	556	1	0	151	0	0	1.000	
42 <i>DPYD</i>	rs17376848	A>G	417	124	6	107	36	2	0.586	
43 <i>DPYD</i>	rs1801159	T>C	292	218	42	69	67	11	0.227	1.13(0.74-1.73)
44 <i>DPYD</i>	rs777368221	A>C	551	1	0	147	0	0	1.000	
45 <i>DPYD</i>	rs772264512	G>A	551	1	0	147	0	0	1.000	
46 <i>DPYD</i>	rs752985272	C>G	550	1	0	146	0	0	1.000	1.26(0.88-1.82)
47 <i>DPYD</i>	rs754745863	G>A	556	1	0	150	1	0	0.381	
48 <i>DPYD</i>	rs139863300	C>T	554	1	0	149	1	0	0.381	
49 <i>DPYD</i>	rs190048823	G>A	549	7	0	147	1	0	1.000	0.40(0.09-1.77)
50 <i>DPYD</i>	rs776973423	C>T	556	1	0	149	0	0	1.000	
51 <i>DPYD</i>	rs2297595	T>C	539	18	0	147	2	0	0.276	
52 <i>DPYD</i>	rs190771411	A>G	552	0	0	148	2	0	0.045	0.40(0.09-1.77)
53 <i>DPYD</i>	rs200562975	T>C	554	0	0	148	2	0	0.045	
54 <i>DPYD</i>	rs201841475	C>T	554	1	0	148	0	0	1.000	
55 <i>DPYD</i>	rs1801265	G>A	1	32	523	0	8	140	1.000	0.90(0.40-2.00)
56 <i>DPYD</i>	chr1:98386518	T>C	535	1	0	141	0	0	1.000	
57 <i>DPYD</i>	rs72981743	C>T	531	3	0	141	2	0	0.286	
58 <i>DPYD</i>	rs145248180	G>T	481	52	1	132	11	0	0.520	0.75(0.38-1.48)
59 <i>DPYD</i>	rs61787828	A>C	505	29	0	138	4	0	0.273	
60 <i>DPYD</i>	chr1:98386981	G>T	533	1	0	142	0	0	1.000	
61 <i>CYP2C19</i>	rs17885098	T>C	390	148	18	111	34	4	0.311	0.80(0.53-1.21)
62 <i>CYP2C19</i>	rs145328984	C>T	553	1	0	149	0	0	1.000	
63 <i>CYP2C19</i>	rs368767518	C>T	553	1	0	149	0	0	1.000	
64 <i>CYP2C19</i>	rs181297724	G>C	547	7	0	147	2	0	1.000	0.91(0.58-1.41)
65 <i>CYP2C19</i>	rs765456449	C>A	556	1	0	151	0	0	1.000	
66 <i>CYP2C19</i>	rs4986893	G>A	430	117	10	119	29	3	0.742	
67 <i>CYP2C19</i>	rs4244285	G>A	261	246	49	80	59	12	0.199	0.78(0.54-1.12)
68 <i>CYP2C19</i>	rs778258371	G>A	557	0	0	150	1	0	0.213	
69 <i>CYP2C19</i>	rs559628884	C>A	541	1	0	149	0	0	1.000	
70 <i>CYP2C19</i>	rs745503497	A/G	540	0	0	147	1	0	0.215	0.79(0.55-1.14)
71 <i>CYP2C19</i>	rs3758580	C>T	256	238	47	78	58	11	0.227	

72	CYP2C19	rs3758581	G>A	498	41	4	140	7	0	0.216	0.55(0.24-1.25)
73	CYP2C19	chr10:96602697	C>T	544	2	0	147	0	0	1.000	
74	CYP2C19	rs17886522	A>C	425	111	13	118	29	3	0.825	0.92(0.59-1.44)
75	CYP2C19	rs779501712	C>T	547	1	0	150	0	0	1.000	
76	CYP2C19	rs28399514	G>A	547	0	1	149	1	0	0.384	
77	CYP2C19	chr10:96612671	A>G	547	1	0	150	0	0	1.000	
78	CYP2C9	rs530860659	C>T	553	1	0	150	0	0	1.000	
79	CYP2C9	rs9332098	G>A	531	22	1	146	4	0	0.482	0.63(0.21-1.85)
80	CYP2C9	chr10:96697516	C>G	553	1	0	150	0	0	1.000	
81	CYP2C9	chr10:96697711	G>A	553	1	0	150	0	0	1.000	
82	CYP2C9	chr10:96697799	->T	548	6	0	149	1	0	1.000	
83	CYP2C9	rs397843768	T>-	553	1	0	150	0	0	1.000	
84	CYP2C9	chr10:96698030	T>C	553	1	0	150	0	0	1.000	
85	CYP2C9	rs1184084119	C>A	554	0	0	149	1	0	0.213	
86	CYP2C9	chr10:96698167	C>T	553	1	0	150	0	0	1.000	
87	CYP2C9	rs1309328671	A>G	552	2	0	150	0	0	1.000	
88	CYP2C9	chr10:96698425	AAG>-	553	1	0	150	0	0	1.000	
89	CYP2C9	rs114071557	A>G	553	1	0	150	0	0	1.000	
90	CYP2C9	rs17847036	G>A	544	13	0	150	0	0	0.082	
91	CYP2C9	rs201856860	T>C	555	2	0	149	1	0	0.512	
92	CYP2C9	rs12414460	G>A	555	2	0	150	0	0	1.000	
93	CYP2C9	rs1253395922	G>T	556	1	0	150	0	0	1.000	
94	CYP2C9	rs774550549	C>T	555	1	0	151	0	0	1.000	
95	CYP2C9	chr10:96707668	T>A	555	1	0	151	0	0	1.000	
96	CYP2C9	rs182132442	C>A	552	2	0	149	0	0	1.000	
97	CYP2C9	rs1057910	A>C	523	22	1	145	4	0	0.481	0.62(0.21-1.84)
98	CYP2C9	rs141283168	T>C	537	8	1	142	7	0	0.056	2.94(1.07-8.03)
99	CYP2C9	rs1057911	A>T	528	22	1	147	4	0	0.481	0.62(0.21-1.83)
100	CYP2C9	rs781583846	G>A	549	2	0	151	0	0	1.000	
101	CYP2E1	rs2031921	T>C	362	165	22	97	42	7	1.000	0.97(0.66-1.43)
102	CYP2E1	chr10:135339913	T>C	546	1	0	147	0	0	1.000	
103	CYP2E1	rs3813870	A>G	331	189	31	81	56	10	0.299	1.22(0.84-1.76)
104	CYP2E1	chr10:135340070	A>T	548	1	0	146	0	0	1.000	
105	CYP2E1	rs2031922	T>C	362	165	22	96	43	7	1.000	1.00(0.68-1.48)
106	CYP2E1	rs1219486901	G>A	545	1	0	146	0	0	1.000	
107	CYP2E1	rs2070672	A>G	332	189	31	81	56	9	0.344	1.21(0.83-1.75)
108	CYP2E1	rs2070673	A>T	98	261	193	30	72	44	0.471	
109	CYP2E1	chr10:135340594	A>G	545	2	0	146	0	0	1.000	
110	CYP2E1	chr10:135340995	G>A	546	1	0	145	0	0	1.000	
111	CYP2E1	rs72559710	G>A	555	2	0	151	0	0	1.000	
112	CYP2E1	chr10:135342066	A>G	556	1	0	151	0	0	1.000	
113	CYP2E1	chr10:135345205	C>T	546	1	0	147	0	0	1.000	
114	CYP2E1	rs141280653	C>T	546	1	0	147	0	0	1.000	
115	CYP2E1	rs778316659	G>A	546	1	0	147	0	0	1.000	
116	CYP2E1	rs2070674	C>T	365	158	22	96	40	11	0.695	1.07(0.73-1.58)
117	CYP2E1	rs28371742	C>G	533	12	0	145	2	0	0.745	0.61(0.13-2.76)
118	CYP2E1	rs566294180	A>G	544	2	0	147	0	0	1.000	
119	CYP2E1	rs41299426	A>G	545	1	0	147	0	0	1.000	
120	CYP2E1	rs1390074994	G>C	546	0	0	146	1	0	0.212	
121	CYP2E1	chr10:135347317	G>C	545	1	0	147	0	0	1.000	
122	CYP2E1	rs28371746	C>A	517	27	1	138	9	0	0.679	1.20(0.55-2.61)
123	CYP2E1	rs199856651	A>G	552	4	0	148	2	0	0.613	0.67(0.04-11.29)
124	CYP2E1	rs2515641	T>C	17	144	395	5	43	102	0.481	1.15(0.78-1.70)
125	CYP2E1	chr10:135352305	A>-	555	1	0	150	0	0	1.000	
126	ALDH2	chr12:112203692	T>A	551	0	0	147	1	0	0.212	
127	ALDH2	chr12:112203720	T>C	550	1	0	148	0	0	1.000	
128	ALDH2	rs568781254	A>C	549	1	0	145	3	0	0.032	11.3(1.17-110.0)
129	ALDH2	rs551263044	C>T	549	1	0	148	0	0	1.000	
130	ALDH2	rs1480473723	C>T	549	1	0	148	0	0	1.000	
131	ALDH2	rs1414849157	C>T	548	2	0	148	0	0	1.000	
132	ALDH2	rs886205	A>G	32	166	352	12	49	87	0.251	1.24(0.86-1.80)
133	ALDH2	chr12:112204571	G>A	549	1	0	148	0	0	1.000	
134	ALDH2	rs991114674	G>A	549	1	0	148	0	0	1.000	
135	ALDH2	chr12:112204719	G>A	549	1	0	148	0	0	1.000	
136	ALDH2	rs141574314	A>G	522	1	0	142	0	0	1.000	
137	ALDH2	rs13306164	C>T	509	12	0	139	3	0	1.000	
138	ALDH2	chr12:112229894	CAGGTTGCTGCTGGG>-	557	1	0	151	0	0	1.000	
139	ALDH2	chr12:112230450	G>A	556	0	0	150	1	0	0.214	
140	ALDH2	rs1331843613	G>A	534	1	0	146	0	0	1.000	
141	ALDH2	rs671	G>A	280	228	46	73	65	11	0.782	1.06(0.74-1.52)
142	CYP1A2	chr15:75040196	T>G	548	1	0	0	147	0	1.000	
143	CYP1A2	rs2069523	G>T	548	1	0	147	0	0	1.000	
144	CYP1A2	rs2069524	A>G	512	37	0	141	6	0	0.334	0.58(0.24-1.42)
145	CYP1A2	rs2069525	T>C	496	51	1	138	9	0	0.251	0.62(0.29-1.29)
146	CYP1A2	chr15:75040864	G>C	555	4	0	150	1	0	1.000	
147	CYP1A2	rs143211242	A>C	557	2	0	151	0	0	1.000	
148	CYP1A2	rs941101723	G>A	558	1	0	151	0	0	1.000	
149	CYP1A2	rs3743482	G>A	559	0	0	150	1	0	0.213	
150	CYP1A2	rs752037611	G>A	559	0	0	150	1	0	0.213	

151	CYP1A2	rs138652540	C>T	557	2	0	151	0	0	1.000	
152	CYP1A2	rs773366123	T>A	559	0	0	150	1	0	0.213	
153	CYP1A2	rs56037745	G>A	556	2	0	151	0	0	1.000	
154	CYP1A2	rs35796837	G>A	555	3	0	150	1	0	1.000	
155	CYP1A2	rs55918015	G>A	554	4	0	151	0	0	0.583	
156	CYP1A2	rs56107638	G>A	557	1	0	150	1	0	0.381	
157	CYP1A2	rs45486893	C>T	539	16	0	148	3	0	0.778	
158	CYP1A2	rs72547517	G>A	547	7	0	150	1	0	1.000	
159	CYP1A2	rs199528490	G>C	552	2	0	151	0	0	1.000	
160	CYP1A2	chr15:75047379	C>T	553	1	0	151	0	0	1.000	
161	CYP1A2	rs111900570	C>T	554	1	0	150	1	0	0.382	
162	CYP1A2	rs2470890	C>T	348	180	27	101	44	5	0.339	0.81(0.55-1.19)
163	CYP2A6	CYP2A6(*4/*4)	CYP2A6>deletion	537	0	22	151	0	0	0.007	
164	CYP2A6	rs539466327	G>A	534	1	0	151	0	0	1.000	
165	CYP2A6	rs143731390	T>A	533	2	0	150	1	0	0.526	
166	CYP2A6	rs2002977	G>A	522	11	3	147	2	2	1.000	
167	CYP2A6	rs143336165	G>A	534	2	0	150	1	0	0.526	
168	CYP2A6	rs28399462	G>A	535	0	1	150	0	1	0.392	
169	CYP2A6	rs56314118	A>G	535	1	0	151	0	0	1.000	
170	CYP2A6	rs59389036	G>A	535	1	0	151	0	0	1.000	
171	CYP2A6	rs561177628	G>A	535	1	0	151	0	0	1.000	
172	CYP2A6	rs28399455	G>A	535	1	0	151	0	0	1.000	
173	CYP2A6	rs2644907	G>C	533	3	0	151	0	0	1.000	
174	CYP2A6	rs140471703	C>T	534	2	0	151	0	0	1.000	
175	CYP2A6	rs1809811	G>A	524	11	2	148	2	1	1.000	
176	CYP2A6	rs28399447	A>G	520	15	2	150	1	0	0.144	0.20(0.02-1.54)
177	CYP2A6	rs199916117	T>C	501	4	0	136	1	0	1.000	
178	CYP2A6	rs72549434	T>C	522	4	2	144	2	0	0.686	
179	CYP2A6	rs1355151029	C>T	527	1	0	146	0	0	1.000	
180	CYP2A6	rs199545200	G>A	521	6	1	146	0	0	0.356	
181	CYP2A6	rs747840206	C>T	530	1	0	146	0	0	1.000	
182	CYP2A6	rs8192721	C>T	515	11	2	143	2	1	1.000	
183	CYP2A6	rs1137115	T>C	38	104	385	7	31	108	0.916	0.95(0.62-1.44)
184	CYP2A6	rs8192720	G>A	356	118	53	96	37	13	0.691	1.08(0.73-1.59)
185	CYP2A6	rs28399434	C>T	516	8	2	146	0	0	0.129	
186	CYP2A6	rs28399433	A>C	323	135	70	97	32	17	0.289	0.79(0.54-1.17)
187	CYP2A6	rs535847711	C>T	532	0	0	145	1	0	0.215	
188	CYP2A6	chr19:41356623	T>G	531	1	0	146	0	0	1.000	
189	CYP2A6	chr19:41356790	T>G	527	0	0	145	1	0	0.217	
190	CYP2A6	rs371984288	T>C	525	3	0	146	0	0	1.000	
191	CYP2A6	rs1357380496	C>A	527	0	1	146	0	0	1.000	
192	CYP2A6	chr19:41356848	G>A	532	0	0	145	1	0	0.215	
193	CYP2A6	rs539519931	G>A	526	2	0	146	0	0	1.000	
194	CYP2A6	chr19:41356946	C>T	527	1	0	146	0	0	1.000	
195	CYP2A6	rs61663607	T>C	348	121	58	93	38	15	0.623	1.10(0.75-1.62)
196	CYP2A6	rs1452707033	C>G	524	1	0	146	0	0	1.000	
197	CYP2A6	rs1439083763	G>T	521	2	0	146	0	0	1.000	
198	CYP2A6	rs4803381	T>C	131	166	226	38	43	65	0.830	0.94(0.62-1.44)
199	CYP2B6	rs8192709	C>T	476	76	3	136	12	1	0.099	0.57(0.31-1.06)
200	CYP2B6	rs367708702	G>A	537	0	0	145	1	0	0.214	
201	CYP2B6	chr19:41509928	T>C	535	1	0	146	0	0	1.000	
202	CYP2B6	rs2279341	G>C	457	74	3	133	11	1	0.053	0.53(0.28-1.01)
203	CYP2B6	rs757472041	C>T	536	1	0	146	0	0	1.000	
204	CYP2B6	rs375508968	C>T	536	1	0	146	0	0	1.000	
205	CYP2B6	rs3826711	C>G	530	8	0	142	4	0	0.296	1.86(0.55-6.28)
206	CYP2B6	rs3745274	G>T	378	142	20	90	45	11	0.058	1.45(0.99-2.12)
207	CYP2B6	rs565530668	C>T	558	0	0	150	1	0	0.213	
208	CYP2B6	rs139029625	G>A	557	1	0	151	0	0	1.000	
209	CYP2B6	rs142806708	G>C	555	2	0	151	0	0	1.000	
210	CYP2B6	rs201500445	T>C	557	0	0	150	1	0	0.213	
211	CYP2B6	rs200238771	T>A	556	1	0	151	0	0	1.000	
212	CYP2B6	rs35661880	C>T	554	3	0	148	3	0	0.115	
213	CYP2B6	rs147991149	C>T	557	0	0	150	1	0	0.213	
214	CYP2B6	rs3211369	A>G	552	5	0	151	0	0	0.590	
215	CYP2B6	rs373442191	G>A	556	1	0	151	0	0	1.000	
216	CYP2B6	rs117872433	G>A	557	0	0	150	1	0	0.213	
217	CYP2B6	rs200993638	C>T	552	5	0	151	0	0	0.590	
218	CYP2B6	rs3211370	A>T	552	5	0	151	0	0	0.590	
219	CYP2B6	rs564083989	G>A	556	1	0	151	0	0	1.000	
220	CYP2B6	rs3211371	C>T	544	13	0	146	5	0	0.558	1.43(0.50-4.08)
221	UGT1A1	rs4148323	G>A	343	148	20	92	38	6	1.000	0.97(0.65-1.46)
222	UGT1A1	rs200412341	C>T	518	0	0	134	1	0	0.207	
223	UGT1A1	rs1029804751	G>A	516	1	0	135	0	0	1.000	
224	UGT1A1	rs35350960	C>A	516	2	0	134	1	0	0.501	
225	UGT1A1	rs34946978	C>T	549	4	0	146	1	0	1.000	
226	UGT1A1	rs201427749	C>T	550	1	0	148	0	0	1.000	
227	UGT1A1	rs115944950	G>C	551	0	0	147	1	0	0.212	
228	UGT1A1	rs34993780	T>G	548	3	0	146	2	0	0.287	
229	UGT1A1	rs867885761	G>C	550	1	0	147	1	0	0.379	

230	COMT	chr22:19948728	C>T	554	1	0	149	0	0	1.000	
231	COMT	rs558998170	A>G	552	3	0	148	1	0	1.000	
232	COMT	rs1171801279	G>T	554	1	0	149	0	0	1.000	
233	COMT	rs74745580	C>T	557	2	0	151	0	0	1.000	
234	COMT	rs1261617944	T>C	558	1	0	151	0	0	1.000	
235	COMT	rs4633	C>T	282	224	53	67	73	11	0.200	1.27(0.88-1.83)
236	COMT	rs6267	G>T	463	93	3	131	20	0	0.267	0.73(0.43-1.23)
237	COMT	rs373611092	A>G	557	2	0	151	0	0	1.000	
238	COMT	rs76452330	G>A	532	27	0	146	5	0	0.513	1.48(0.56-3.91)
239	COMT	rs199710929	C>T	558	1	0	151	0	0	1.000	
240	COMT	rs4818	C>G	280	236	43	67	73	11	0.233	1.25(0.87-1.80)
241	COMT	rs201835143	C>T	557	2	0	151	0	0	1.000	
242	COMT	rs4680	G>A	277	225	57	64	72	15	0.120	1.33(0.92-1.91)
243	COMT	rs1460479393	G>A	558	1	0	151	0	0	1.000	
244	COMT	rs769224	G>A	515	43	1	141	9	1	0.730	0.83(0.40-1.69)
245	COMT	rs4646315	G>C	425	120	14	117	31	3	0.747	0.92(0.60-1.41)
246	COMT	rs201656482	A>C	549	10	0	151	0	0	0.131	
247	COMT	chr22:19956087	T>C	558	1	0	151	0	0	1.000	
248	COMT	rs749437638	C>T	559	0	0	150	1	0	0.213	
249	COMT	rs201407028	G>A	558	1	0	151	0	0	1.000	
250	CYP2D6	rs1440526469	C>T	555	1	0	149	0	0	1.000	
251	CYP2D6	rs1135840	G>C	168	253	135	52	62	34	0.273	0.79(0.54-1.17)
252	CYP2D6	rs765776661	-/CAGTGGGCA	554	1	1	149	0	0	1.000	
253	CYP2D6	rs1135835	T>C	553	3	0	149	0	0	1.000	
254	CYP2D6	rs1372322657	G>A	555	1	0	149	0	0	1.000	
255	CYP2D6	rs28371733	C>T	555	1	0	149	0	0	1.000	
256	CYP2D6	rs747089665	G>A	555	1	0	149	0	0	1.000	
257	CYP2D6	rs769157652	C>T	555	0	1	149	0	0	1.000	
258	CYP2D6	rs141739595	G>A	556	0	0	148	1	0	0.211	
259	CYP2D6	rs76088846	C>T	556	0	0	148	1	0	0.211	
260	CYP2D6	chr22:42523850	C>T	555	1	0	149	0	0	1.000	
261	CYP2D6	chr22:42523883	A>G	555	1	0	149	0	0	1.000	
262	CYP2D6	rs16947	A>G	23	141	392	3	35	111	0.360	1.22(0.81-1.84)
263	CYP2D6	rs1135829	T>C	554	2	0	148	1	0	0.510	
264	CYP2D6	rs72549352	->G	545	7	2	147	1	0	0.697	0.41(0.05-3.27)
265	CYP2D6	rs749182114	G>T, G>C	552	2	0	148	0	0	1.000	
266	CYP2D6	rs28371718	G>T	528	0	0	139	1	0	0.210	
267	CYP2D6	chr22:42524247	G>A	554	0	0	148	1	0	0.212	
268	CYP2D6	rs72549353	AGTT>-	553	1	0	149	0	0	1.000	
269	CYP2D6	rs3892097	C>T	554	2	0	149	0	0	1.000	
270	CYP2D6	rs5030865	C>T	551	5	0	148	1	0	1.000	
271	CYP2D6	rs1058164	G>C	164	239	124	49	57	34	0.415	0.83(0.56-1.24)
272	CYP2D6	rs1135822	A>T	519	8	1	139	1	0	0.697	0.41(0.05-3.30)
273	CYP2D6	chr22:42525739	C>T	521	1	0	139	0	0	1.000	
274	CYP2D6	rs1081003	G>A	220	215	86	54	55	30	0.499	1.15(0.78-1.68)
275	CYP2D6	chr22:42525787	G>T	552	0	0	147	1	0	0.211	
276	CYP2D6	rs28371705	G>C	548	4	0	148	0	0	0.584	
277	CYP2D6	rs1065852	G>A	235	222	92	57	58	32	0.398	1.18(0.81-1.71)
278	CYP2D6	rs267608313	G>A	550	1	0	148	0	0	1.000	
279	ABCG2	rs763740151	G>A	557	1	0	150	0	0	1.000	
280	ABCG2	rs748531218	T>C	555	3	0	150	0	0	1.000	
281	ABCG2	rs759701118	G>A	550	1	0	147	0	0	1.000	
282	ABCG2	rs868217328	G>-	550	1	0	147	0	0	1.000	
283	ABCG2	rs192169063	A>G	544	7	0	146	1	0	1.000	
284	ABCG2	rs1354553769	C>T	550	1	0	147	0	0	1.000	
285	ABCG2	rs35622453	C>T	522	12	0	140	4	0	0.757	1.24(0.39-3.91)
286	ABCG2	rs140207606	G>A	512	0	0	137	1	0	0.212	
287	ABCG2	chr4:89042907	T>C	521	1	0	141	0	0	1.000	
288	ABCG2	chr4:89052224	C>T	555	0	1	150	0	0	1.000	
289	ABCG2	chr4:89052257	T>C	555	1	0	150	0	0	1.000	
290	ABCG2	rs769012528	C>T	555	1	0	150	0	0	1.000	
291	ABCG2	rs201006821	C>G	555	1	0	150	0	0	1.000	
292	ABCG2	rs2231142	G>T	268	239	49	61	71	18	0.117	1.35(0.94-1.95)
293	ABCG2	rs149106245	T>A	555	1	0	149	1	0	0.380	
294	ABCG2	rs72552713	G>A	528	26	1	142	8	0	0.832	1.10(0.48-2.47)
295	ABCG2	rs2231139	G>A	552	2	0	150	0	0	1.000	
296	ABCG2	rs199473672	G>A	551	4	0	149	1	0	1.000	
297	ABCG2	rs146682354	T>C	556	1	0	151	0	0	1.000	
298	ABCG2	rs1319203095	G>A	556	1	0	151	0	0	1.000	
299	ABCG2	rs2231137	C>T	356	181	20	90	57	4	0.343	1.20(0.83-1.73)
300	ABCG2	rs4148151	C>A	556	1	0	151	0	0	1.000	
301	ABCG2	chr4:89079596	G>C	544	1	0	149	0	0	1.000	
302	ABCG2	rs2231136	G>A	537	10	0	143	5	0	0.334	0.53(0.17-1.58)
303	ABCG2	chr4:89079887	C>T	545	1	0	148	0	0	1.000	
304	ABCG2	chr4:89079919	G>C	544	2	0	147	1	0	0.514	
305	ABCG2	rs1400423296	C>T	554	3	0	151	0	0	1.000	
306	ABCG2	rs72554040	G>A	274	231	52	68	73	10	0.409	1.18(0.82-1.69)
307	ABCG2	rs182367277		550	7	0	147	4	0	0.260	0.46(0.13-1.61)
308	ABCG2	rs186907101		557	0	0	150	1	0	0.213	

309	ABCG2	rs1334731718	C>T	554	3	0	151	0	0	1.000	
310	ABCG2	rs62309960	G>C	540	15	2	149	2	0	0.393	0.42(0.09-1.86)
311	ABCG2	rs546576886	G>A	544	13	0	149	2	0	0.749	
312	ABCG2	rs766442580	C>T	556	1	0	151	0	0	1.000	
313	ABCG2	rs36111742	A>G	549	8	0	149	2	0	1.000	
314	ABCG2	chr4:89152786	CTGAGGGT>-	556	1	0	151	0	0	1.000	
315	ABCG2	rs542537786	A>-	555	2	0	150	1	0	0.514	
316	ABCG2	rs62309962	A>C	540	15	2	149	2	0	0.393	0.42(0.09-1.86)
317	ABCG2	rs7681726	G>A	0	8	548	0	2	149	1.000	
318	ABCG2	rs562002915	T>C	545	11	1	148	3	0	1.000	
319	ABCG2	chr4:89153301	->A	556	1	0	151	0	0	1.000	
320	ABCG2	chr4:89153381	A>T	556	1	0	151	0	0	1.000	
321	ABCG2	chr4:89153436	T>C	556	1	0	151	0	0	1.000	
322	ADH1B	rs150939574	T>C	553	1	0	151	0	0	1.000	
323	ADH1B	rs74451421	C>T	552	2	0	150	1	0	0.515	
324	ADH1B	rs1789882	A>G	4	68	482	0	11	140	0.063	0.52(0.27-1.01)
325	ADH1B	chr4:100235107	G>C	555	1	0	151	0	0	1.000	
326	ADH1B	rs1181667845	C>A	554	1	0	151	0	0	1.000	
327	ADH1B	rs750389182	A>C	554	1	0	151	0	0	1.000	
328	ADH1B	rs772635726	T>G	556	0	0	149	1	0	0.212	
329	ADH1B	rs1229984	T>C	341	176	39	99	41	10	0.342	0.81(0.55-1.19)
330	ADH1B	chr4:100240130	T>C	556	0	0	149	1	0	0.212	
331	ADH1B	rs1440331692	C>T	555	1	0	150	0	0	1.000	
332	ADH1B	rs28913910	TGG>-	550	5	0	148	2	0	0.645	
333	ADH1B	rs993180442	C>T	553	2	0	150	0	0	1.000	
334	ADH1B	chr4:100240742	G>A	554	1	0	149	1	0	0.381	
335	ADH1B	rs1258284878	G>A	553	3	0	150	0	0	1.000	
336	ADH1B	chr4:100240879	A>G	554	1	0	150	0	0	1.000	
337	ADH1B	chr4:100240976	A>G	555	1	0	150	0	0	1.000	
338	ADH1B	chr4:100241124	G>A	555	1	0	150	0	0	1.000	
339	ADH1B	chr4:100241340	T>C	556	0	0	149	1	0	0.212	
340	ADH1B	rs1353621	T>C	533	23	1	143	7	0	0.824	1.08(0.45-2.57)
341	ADH1B	chr4:100241826	G>A	555	1	0	150	0	0	1.000	
342	ADH1B	chr4:100241832	C>A	555	1	0	150	0	0	1.000	
343	ADH1B	chr4:100242490	T>A	555	1	0	150	0	0	1.000	
344	ADH1B	chr4:100242813	->T	553	2	0	149	1	0	0.513	
345	ADH1B	rs927053190	C>T	554	1	0	150	0	0	1.000	
346	ADH1B	rs1302702778	A>G	553	2	0	149	1	0	0.513	
347	ADH1B	rs1159918	A>C	12	126	416	3	26	121	1.000	0.92(0.25-3.30)
348	ADH1B	chr4:100243086	C>T	554	1	0	150	0	0	1.000	
349	ADH1B	rs573647108	A>T	554	1	0	150	0	0	1.000	
350	ADH1B	rs2070898	G>A	16	144	396	4	31	115	1.000	0.92(0.30-2.80)
351	ADH1B	rs2070897	G>A	12	127	417	3	26	121	1.000	0.92(0.25-3.32)
352	ADH1B	rs6810842	T>G	12	127	418	3	25	122	1.000	0.92(0.25-3.32)
353	ADH1B	rs28913903	G>C	247	247	63	74	61	15	0.310	0.81(0.57-1.17)
354	ADH1B	rs1034245804	G>T	555	1	0	150	0	0	1.000	
355	MTRR	rs1182239347	G>A	552	0	0	147	1	0	0.211	
356	MTRR	rs72716536	T>C	382	157	13	104	39	5	0.841	0.95(0.63-1.41)
357	MTRR	rs778827432	G>A	550	1	0	147	0	0	1.000	
358	MTRR	rs1355632408	T>G	550	1	0	147	0	0	1.000	
359	MTRR	rs148267849	G>T	548	1	0	147	0	0	1.000	
360	MTRR	rs114748706	T>C	535	14	0	143	4	0	1.000	
361	MTRR	rs1801394	A>G	237	254	54	73	58	16	0.192	0.78(0.54-1.12)
362	MTRR	rs149300444	G>A	546	1	0	146	0	0	1.000	
363	MTRR	chr5:7875409	G>A	556	1	0	149	0	0	1.000	
364	MTRR	rs577851734	T>C	556	1	0	148	1	0	0.378	
365	MTRR	rs1532268	C>T	429	119	6	112	34	2	0.660	1.10(0.72-1.68)
366	MTRR	rs161870	T>C	409	140	5	105	40	3	0.531	
367	MTRR	rs752182014	A>G	552	2	0	148	0	0	1.000	
368	MTRR	rs201557658	C>T	552	2	0	148	0	0	1.000	
369	MTRR	rs2303080	T>A	428	121	5	117	29	2	0.739	0.90(0.57-1.40)
370	MTRR	rs162036	A>G	398	136	5	105	39	3	0.599	1.12(0.75-1.69)
371	MTRR	rs2287779	G>A	375	159	9	109	29	6	0.125	0.71(0.46-1.09)
372	MTRR	rs2287780	C>T	372	162	8	109	30	6	0.153	0.72(0.47-1.09)
373	MTRR	rs16879334	C>G	368	156	8	106	30	6	0.216	0.76(0.50-1.16)
374	MTRR	rs139206262	G>A	543	1	0	147	0	0	1.000	
375	MTRR	rs10380	C>T	423	120	2	110	34	3	0.508	1.16(0.76-1.78)
376	MTRR	rs12347	G>A	422	118	2	110	34	3	0.439	1.18(0.77-1.80)
377	MTRR	rs1802059	G>A	417	119	6	109	36	2	0.512	1.16(0.76-1.76)
378	TPMT	rs1142345	T>C	510	12	0	134	4	0	0.755	1.26(0.40-3.99)
379	TPMT	rs2842949	C>A	46	179	284	13	49	71	0.739	1.09(0.57-2.08)
380	TPMT	rs75543815	T>A	516	4	0	138	1	0	1.000	
381	TPMT	rs2842934	G>A	48	193	290	15	48	84	0.633	1.14(0.62-2.10)
382	TPMT	rs750424422	C>T	554	1	0	151	0	0	1.000	
383	TPMT	rs376768623	A>T	555	1	0	151	0	0	1.000	
384	TPMT	rs747281890	C>T	555	1	0	151	0	0	1.000	
385	TPMT	rs141028204	G>T	531	2	0	141	0	0	1.000	
386	TPMT	rs1256925667	G>C	531	1	0	141	1	0	0.377	
387	TPMT	rs1002196683	G>T	527	1	0	141	0	0	1.000	

388	TPMT	rs1279888446	A>G	523	5	0	142	0	0	0.590	
389	CYP3A5	rs749945666	G>T	547	2	0	148	0	0	1.000	
390	CYP3A5	rs28365085	A>G	536	14	0	143	5	0	0.572	1.33(0.47-3.77)
391	CYP3A5	rs776843927	G>A	549	1	0	148	0	0	1.000	
392	CYP3A5	rs756271054	T>C	550	0	0	147	1	0	0.212	
393	CYP3A5	rs761366357	C>T	559	0	0	150	1	0	0.213	
394	CYP3A5	chr7:99261713	A>G	558	1	0	151	0	0	1.000	
395	CYP3A5	rs56411402	T>C	558	1	0	151	0	0	1.000	
396	CYP3A5	rs1445725863	G>T	558	1	0	151	0	0	1.000	
397	CYP3A5	rs55965422	A>G	557	2	0	151	0	0	1.000	
398	CYP3A5	rs759812876	C>A	558	1	0	151	0	0	1.000	
399	CYP3A5	chr7:99277540	T>G	557	1	0	150	0	0	1.000	
400	CYP3A4	rs147125009	G>A	543	0	0	146	1	0	0.213	
401	CYP3A4	rs142425279	T>C	542	1	0	146	0	0	1.000	
402	CYP3A4	rs1309748501	G>A	544	2	0	148	0	0	1.000	
403	CYP3A4	rs28371759	A>G	549	10	0	149	2	0	1.000	
404	CYP3A4	rs34784390	->T	553	1	0	149	0	0	1.000	
405	CYP3A4	rs55901263	G>C	557	1	0	150	1	0	0.381	
406	CYP3A4	rs12721627	G>C	536	22	0	149	2	0	0.134	3.05(0.71-13.1)
407	CYP3A4	rs55951658	T>C	555	2	0	151	0	0	1.000	
408	CYP3A4	chr7:99370267	G>A	557	1	0	151	0	0	1.000	
409	CYP3A4	rs55679469	A>G	553	1	0	150	0	0	1.000	
410	CYP3A4	rs36231115	C>T	551	3	0	149	1	0	1.000	
411	CYP3A4	rs1296063536	G>A	553	1	0	150	0	0	1.000	
412	CYP3A4	rs1298207919	T>C	552	2	0	149	1	0	0.513	
413	NAT2	rs934550523	G>T	525	1	0	140	0	0	1.000	
414	NAT2	rs4646267	A>G	114	262	149	31	78	30	0.908	0.96(0.61-1.51)
415	NAT2	rs55736132	A>G	488	35	1	125	15	0	0.152	1.62(0.86-3.06)
416	NAT2	rs4345600	A>G	332	178	15	91	45	4	0.767	0.92(0.62-1.36)
417	NAT2	rs4345601	A>T	332	178	15	91	45	4	0.767	0.92(0.62-1.36)
418	NAT2	rs35436619	->AATT	304	196	26	83	47	10	0.773	0.94(0.64-1.37)
419	NAT2	rs4271002	G>C	333	177	15	91	46	3	0.767	0.93(0.63-1.37)
420	NAT2	chr8:18248305	A>G	524	1	0	140	0	0	1.000	
421	NAT2	rs1426644302	AGAG>-	526	1	0	140	0	0	1.000	
422	NAT2	rs4646246	A>G	117	279	154	33	80	34	0.736	0.93(0.60-1.44)
423	NAT2	rs1805158	C>T	553	1	0	149	0	0	1.000	
425	NAT2	rs1041983	C>T	278	225	51	73	64	12	0.854	1.04(0.73-1.50)
426	NAT2	rs1801280	T>C	530	24	0	143	6	0	1.000	
427	NAT2	chr8:18257976	G>A	553	1	0	149	0	0	1.000	
428	NAT2	rs770612696	G>A	553	1	0	149	0	0	1.000	
429	NAT2	rs1799929	C>T	529	25	0	142	7	0	1.000	
430	NAT2	rs139512288	T>C	553	1	0	149	0	0	1.000	
431	NAT2	rs1799930	G>A	362	167	25	91	51	7	0.337	1.20(0.82-1.74)
432	NAT2	rs1309998351	G>A	553	1	0	149	0	0	1.000	
433	NAT2	rs1208	G>A	0	41	513	1	13	135	0.212	
434	NAT2	rs1799931	G>A	448	103	3	127	21	1	0.234	0.73(0.44-1.20)

Supplementary Table S2

The sequeces of the primer sets used in this study

Gene	Primer name	Forward: Primer sequence	Primer name	Reverse: Primer sequence	Product size (bp)
MTHFR	MTHFR_1_F	5'-TAAACGCGCTCTTGCCAGGGAA-3'	MTHFR_1_R	5'-CCTGTCAAACCAGTTGCTGC-3'	7784
MTHFR	MTHFR_2_F	5'-CACTTCCCCTCTCCTCCTTG-3'	MTHFR_2_R	5'-AGTTCGCTGAGTTCCTCCCA-3'	4546
MTHFR	MTHFR_3_F	5'-CCTGAGGCTGAGTCTTCCA-3'	MTHFR_3_R	5'-AACTACTGTGCCTGGAGAC-3'	6351
MTHFR	MTHFR_4_F	5'-GTCGAGGTCAAGAGGTGAA-3'	MTHFR_4_R	5'-ATCGTGGGAGTTGGCTTACA-3'	4197
MTHFR	MTHFR_5_F	5'-CAGAACAAAAGCTGCCCAT-3'	MTHFR_5_R	5'-GACCAGGCCACTCACTACTT-3'	3247
CDA	CDA_1_F	5'-CATCTGAAAGCTGCGTACC-3'	CDA_1_R	5'-CACCATGCCCCACTATTGTG-3'	2088
CDA	CDA_2_F	5'-CACGGAACAAAATACTGCATAATCACAATG-3'	CDA_2_R	5'-GTTTGTGCTCACCTTGGTCACACACTGAGG-3'	6260
CDA	CDA_3_F	5'-ACCTGTGTGCAGGCTTGAATTTTCCATC-3'	CDA_3_R	5'-GAAGATGGAAGTGTCTGCATCCCCAGATGC-3'	5076
CDA	CDA_4_F	5'-ATGCAGACACTTCCATCTTCC-3'	CDA_4_R	5'-GTCTAGACAAACCGTGCTTG-3'	2822
DPYD	DPYD_1_F	5'-TTCCTTGCCATCTCTCCACG-3'	DPYD_1_R	5'-TCTCAGAAGACCGGTGCTTT-3'	3014
DPYD	DPYD_2_F	5'-TCATCCTAAGTATTGAGAGAGTAGTAGCTG-3'	DPYD_2_R	5'-CAGAAGACCTGAAATATACAAAAGTGCCAA-3'	5012
DPYD	DPYD_3_F	5'-GTGCTTCTACATATGGTTCCTTGAAGCATAA-3'	DPYD_3_R	5'-AGTGATTTGTAAACTCGGATACCTGACAAGA-3'	5970
DPYD	DPYD_4_F	5'-GCCTAGTGAAAACCTCTAAGTTGTTTTCTTG-3'	DPYD_4_R	5'-GTGTGTGTGTGTAGGGCTTTATTAAGATAT-3'	7131
DPYD	DPYD_5_F	5'-GATCCTCTGGATTTTCTATGAATTTTAGG-3'	DPYD_5_R	5'-GGGAACAGGTGACTTTTTGTACACTGGTA-3'	8013
DPYD	DPYD_6_F	5'-TGGTGATGCCATCCTCTGAG-3'	DPYD_6_R	5'-TGGGCAGGCAGTTTCCTAAA-3'	7211
DPYD	DPYD_7_F	5'-TTTGCTTCAGGAGATGCTGGGAAATGGATT-3'	DPYD_7_R	5'-CTGGGTCTGGATATAATCAGGTTATGTTA-3'	4910
DPYD	DPYD_8_F	5'-CAGAGACTTTTCACTATCTCTCTCAAT-3'	DPYD_8_R	5'-GTGCCTTCTCCACAAATACCCACCTC-3'	5838
DPYD	DPYD_9_F	5'-ATCCGGTCAGCCACATTCTG-3'	DPYD_9_R	5'-CCGGCTCTTGAAAGACAA-3'	7492
DPYD	DPYD_10_F	5'-CATAGGGATGTGGTGATCAGGGAGCAGGTG-3'	DPYD_10_R	5'-GTTGAGGCATTTATCATTTTATGATAGGGA-3'	7271
DPYD	DPYD_11_F	5'-ACATAACAGAAAAATCCCCCGTTTATAA-3'	DPYD_11_R	5'-TAGAGAGTTACACAGCAGGAGGTAAGATTA-3'	8053
DPYD	DPYD_12_F	5'-TGGCTTTTCTCCTTCGATTGA-3'	DPYD_12_R	5'-CAGATATTCATTAGCTCTCTTTGGC-3'	7701
DPYD	DPYD_13_F	5'-GAAATAAAGCCCGTTTTGCTATAAAGACA-3'	DPYD_13_R	5'-CCATTGGTAGGAGTATTTTCCAGGAAAAAT-3'	5125
DPYD	DPYD_14_F	5'-GCACTTGTTTTCCCTTCTTCCC-3'	DPYD_14_R	5'-ACCCCTTGCTCCTAAACCTC-3'	4559
DPYD	DPYD_15_F	5'-TTCTAGCTTCTCTGACTTGATGTTTTCTT-3'	DPYD_15_R	5'-GCTGCCTAGATTCTCATTCATAAAGTAAA-3'	7203
DPYD	DPYD_16_F	5'-TGCCATGCTCTGAGACAACA-3'	DPYD_16_R	5'-GTTGACTGCCTGTCTGTTTT-3'	7226
DPYD	DPYD_17_F	5'-TGCCCATGGTCACATCTGAC-3'	DPYD_17_R	5'-ACCCCATGTAGATGAGGGCT-3'	7026
DPYD	DPYD_18_F	5'-AGGCCAGGTTTTCTGCTGAA-3'	DPYD_18_R	5'-TTTCTAACCATGGGGCTGG-3'	6841
DPYD	DPYD_19_F	5'-CAATGCACAAAGAAAATCCTGTAGGAATCT-3'	DPYD_19_R	5'-AGGCTTATGTAAATGTAAACCAAGGACA-3'	5031
DPYD	DPYD_20_F	5'-ATTCCTTCTCTGCTCGAGGGA-3'	DPYD_20_R	5'-CCCACCTACAAACAGACTGCA-3'	7248
CYP2C19	CYP2C19_1_F	5'-CCCCTCCCTTTTCAGGTACAG-3'	CYP2C19_1_R	5'-TCACCGAATCCCAACAGCA-3'	7529
CYP2C19	CYP2C19_2_F	5'-CAAGTGAAAGGGATCCAGTGGTACTTACTG-3'	CYP2C19_2_R	5'-TGGGGTGTGTTGTAGGAGATCCATCAGAGT-3'	5286
CYP2C19	CYP2C19_3_F	5'-CTGCTCAGGGAATTAAGAGATTACAAAAAC-3'	CYP2C19_3_R	5'-CTCTTTTCCATCACACACCTCTACACCTCC-3'	6275
CYP2C19	CYP2C19_4_F	5'-GCATCCACTACACCATACAGTATTTTCT-3'	CYP2C19_4_R	5'-GCAAAATGTGCAAGTCTGAAAACACACTATT-3'	7547
CYP2C19	CYP2C19_5_F	5'-GGGTATCTGATCTAAAAATACCTAGGTCTA-3'	CYP2C19_5_R	5'-AAATGGCCAGAGTGTCTATTACAGGGCAT-3'	8574
CYP2C19	CYP2C19_6_F	5'-GACACTCTGGCCATTTCCCA-3'	CYP2C19_6_R	5'-TTCCTCCCAATACCTGATCCTCT-3'	6500
CYP2C9	CYP2C9_1_F	5'-TGACCTTGATCAGCAATGGTTTTTAA-3'	CYP2C9_1_R	5'-TCCATGCAGCACCATATGG-3'	7157
CYP2C9	CYP2C9_2_F	5'-CATCTTTTATTGCATCCACAACCTGTGGTTC-3'	CYP2C9_2_R	5'-TTCCCATTTGAATACCCCTTGACTGATTG-3'	7224
CYP2C9	CYP2C9_3_F	5'-CCTGACTTCTGAAACATATAGATGTGAAT-3'	CYP2C9_3_R	5'-CAGGTTACATATGCTGTGAGTCTTTATAT-3'	8143
CYP2C9	CYP2C9_4_F	5'-CAGTATCCTTACTCTCTCTTTATCCCCTG-3'	CYP2C9_4_R	5'-GTACCCCCAAACATATTGATATATACCTAC-3'	5248
CYP2C9	CYP2C9_5_F	5'-CTCTAGATACGTGAACCTGTTTCTGAATTC-3'	CYP2C9_5_R	5'-AGTTGAAAGCCAGTCTTTGGAATCTTGTGC-3'	6243
CYP2C9	CYP2C9_6_F	5'-CAGCACTGTGTGGCCAAATTC-3'	CYP2C9_6_R	5'-TCTCTCTCTCTGTCCAGGTG-3'	7659
CYP2E1	CYP2E1_1_F	5'-TGGAAGCTGCCTTTGTAGGG-3'	CYP2E1_1_R	5'-GGGGCCAGCAGAAGGTTATT-3'	7146
CYP2E1	CYP2E1_2_F	5'-CCGCTACGACTGTTGTGAA-3'	CYP2E1_2_R	5'-TGGTTCCTCTAGTGAGAGT-3'	7636
CYP2E1	CYP2E1_3_F	5'-GTGCCCATCCCTGGCCTTTGCTTTTTCAA-3'	CYP2E1_3_R	5'-GTAGTGAAAGTCTCTAACAAAAAGAGGAAGT-3'	5272
ALDH2	ALDH2_1_F	5'-CCTCATCTCTCTGCCTCTGG-3'	ALDH2_1_R	5'-GGGGCTTACTCTGGAAAGTT-3'	5095
ALDH2	ALDH2_2_F	5'-GGAACAGCTTGCTGGGAGAT-3'	ALDH2_2_R	5'-AGGATTTTCCCATGAGCTGG-3'	6027
ALDH2	ALDH2_3_F	5'-AGCTTTCTTCCAGGGTCACA-3'	ALDH2_3_R	5'-GACACGAAGGTTACAGAGC-3'	4467
ALDH2	ALDH2_4_F	5'-TCCTGTCTTTCTGTCCCCAC-3'	ALDH2_4_R	5'-CGGAGGCTCTTACCACACAGT-3'	8037
ALDH2	ALDH2_5_F	5'-ACCACTCATGCACACACAGT-3'	ALDH2_5_R	5'-CAGCAAAATGACCGCATAGGC-3'	7774
ALDH2	ALDH2_6_F	5'-ATGAGCCTCTGTATCCCCAC-3'	ALDH2_6_R	5'-TTTACCCACAGCAGAGGAGG-3'	3100
CYP1A2	CYP1A2_1_F	5'-GTTTCAAGCAAAGGGATCAGCTTTGGAGAA-3'	CYP1A2_1_R	5'-TGCTCACATGCTCCTCCAGGTAGCAGGAGG-3'	7566
CYP1A2	CYP1A2_2_F	5'-TCATCTAATCTCCAGTCCGTGCTTACATGT-3'	CYP1A2_2_R	5'-AGTTGATTCTGTGCACTAAAGTTTGTGAA-3'	5299
CYP1A2	CYP1A2_3_F	5'-GTTACAGGTGATGGTTCCCC-3'	CYP1A2_3_R	5'-AGGAGAGGAGTGAAGGAGGT-3'	2995
CYP2A6	CYP2A6_1_F	5'-GTGCTCAATCCAGCCTCGTTAAATACCT-3'	CYP2A6_1_R	5'-AATATTGCTTCTTCTAATCTCACTGTGTGC-3'	5682
CYP2A6	CYP2A6_2_F	5'-AAAGTCTAATCTTACCTAAGGAAAGGACC-3'	CYP2A6_2_R	5'-TATCCAGGTTTCAAGTATTTAAACAGAGGCT-3'	9545
CYP2B6	CYP2B6_1_F	5'-AACACCATAGGTACAACCTCAGGGAATG-3'	CYP2B6_1_R	5'-TTACCAGGCCAACTACAAATGAATGTCTCT-3'	8514
CYP2B6	CYP2B6_2_F	5'-GCAGGGGTGGCTACAAGAAT-3'	CYP2B6_2_R	5'-CTTGCCCCGAATTCCTCTCT-3'	7694
CYP2B6	CYP2B6_3_F	5'-GTTTCATTCCAGCTGGGGTGTAGTGTGCC-3'	CYP2B6_3_R	5'-TCTCTTAAAAACAAATTAGCAGGCCAGTCGC-3'	7133
CYP2B6	CYP2B6_4_F	5'-GAAATAAGACAAAGGGCTATGTGGCAGG-3'	CYP2B6_4_R	5'-AAGCTTGTCTGTGGAATCCCAACCCAAAGTA-3'	6178
UGT1A1	UGT1A1_1_F	5'-TTTCTACGCGTCCGACAACA-3'	UGT1A1_1_R	5'-AATAGCAGCAAGACGGGCAT-3'	7894
UGT1A1	UGT1A1_2_F	5'-CCCTGCCAGGGTAAGATAGCAGTGGTTACAC-3'	UGT1A1_2_R	5'-GCTGTGTTACTATTATCACCTGAAAGGTTA-3'	8097
UGT1A1	UGT1A1_3_F	5'-CCTAAGAACAACCTGGTGAAAGTCC-3'	UGT1A1_3_R	5'-GGGATGGTGGGAGCCATGTTTT-3'	5574
COMT	COMT_1_F	5'-CCAACCTCTGCCCATTCACAC-3'	COMT_1_R	5'-CTACACGTCAGCCCTTACCA-3'	3343
COMT	COMT_2_F	5'-AGCCAGTTGTGGTAGCAGAC-3'	COMT_2_R	5'-GCCTACACCTTGGCCTATCAG-3'	6726
COMT	COMT_3_F	5'-AGTCTCTGCTCTCTCTT-3'	COMT_3_R	5'-GCTCGCAGTAGGTGTCAATG-3'	7912
COMT	COMT_4_F	5'-ACACACCTGCTCTGTCTACC-3'	COMT_4_R	5'-GTGTCTTTCTGCCCCAAGTG-3'	3656
COMT	COMT_5_F	5'-CCTTGTCACTCCAGAACCT-3'	COMT_5_R	5'-GCACTGCATCTCACTCATG-3'	5488
COMT	COMT_6_F	5'-GGGCAGAAAGTGGAAACCTG-3'	COMT_6_R	5'-ATCTGGTTGTTGCTCCACCT-3'	2809
CYP2D6	CYP2D6_1_F	5'-TATAGCTCCCTGACGCCATG-3'	CYP2D6_1_R	5'-CATTTCCAGCTGGAATCCG-3'	3425
CYP2D6	CYP2D6_2_F	5'-TGGCCATGAAGGCATTAGCCCCA-3'	CYP2D6_2_R	5'-CGCCATCTCCAAAACAAAAGAAAGGCC-3'	6124
ABCG2	ABCG2_1_F	5'-CTGGGATTCAATGGCTATATTGCTAAATTC-3'	ABCG2_1_R	5'-AGAAACCCCAAAGCACAGAGATAGCCATCA-3'	5619
ABCG2	ABCG2_2_F	5'-GCACCAAGGCATCATTTTCT-3'	ABCG2_2_R	5'-TAACGGCCAGGTCTGAAAC-3'	2105
ABCG2	ABCG2_3_F	5'-AGGAAGCACCATTGTGGACAG-3'	ABCG2_3_R	5'-CAGGTGCTGCTTTATGCGTA-3'	4481
ABCG2	ABCG2_4_F	5'-CAGGGCTAGGATGGGATA-3'	ABCG2_4_R	5'-GGTGCATACAGATCTGGCCA-3'	7417
ABCG2	ABCG2_5_F	5'-TGGATGCTTCCCTAACACCT-3'	ABCG2_5_R	5'-CGGCTCTACCCAGTTTCAAT-3'	8938
ABCG2	ABCG2_6_F	5'-CAATAGACAGGCTATTCTCTGTAGTTTTC-3'	ABCG2_6_R	5'-CTCATCTACCTCAATAAAAGAATGACAT-3'	7178
ABCG2	ABCG2_7_F	5'-CTTCCACATGACTTACATTCTTTGTTCAAC-3'	ABCG2_7_R	5'-GCAATCATAGAAAAGGCACGTGTTACTAAA-3'	8216

ABCG2	ABCG2_8_F	5'-CACTTGAATAAGTTGAGAAAAAAACCCCGT-3'	ABCG2_8_R	5'-GCTGCTCTTCTTGAAGGTAGTTGAAAAAAA-3'	5217
ADH1B	ADH1B_1_F	5'-CACCCAGCAACAGGTAGTGT-3'	ADH1B_1_R	5'-GCAGCCTTGACCTAGGACAG-3'	6519
ADH1B	ADH1B_2_F	5'-TATGCCCAAGGTAGAGGAGC-3'	ADH1B_2_R	5'-CTGTGGCAGGCATTGAAAGA-3'	5317
ADH1B	ADH1B_3_F	5'-AGTCGAGAATCCACAGCCAA-3'	ADH1B_3_R	5'-CCACAAAAGAGAATGGGCC-3'	7201
MTRR	MTRR_1_F	5'-TGAGAGAACACTGGTCCACC-3'	MTRR_1_R	5'-GAGAACACTGCCCTTACCCT-3'	7557
MTRR	MTRR_2_F	5'-AGACTTTACCCAGAGCCAC-3'	MTRR_2_R	5'-GCTGCCATGAACTGATCCTG-3'	5608
MTRR	MTRR_3_F	5'-GTTTCAGTGTGTCATCCCCAGG-3'	MTRR_3_R	5'-TGCAGTCACCTCCATCACTG-3'	6538
MTRR	MTRR_4_F	5'-AGAGCACTGCGTCCTTTTGA-3'	MTRR_4_R	5'-GAAGCAACCAACAAGGCCAG-3'	7045
MTRR	MTRR_5_F	5'-TTCTCCCTGTGGCCTTCATT-3'	MTRR_5_R	5'-CACTGTCCTCGCCAAACAAA-3'	6173
MTRR	MTRR_6_F	5'-ATCGTGCCTAAGTCGGGTAG-3'	MTRR_6_R	5'-AGAAAAGGTCCCTCACTGCT-3'	4703
TPMT	TPMT_1_F	5'-TTTCACACAAACTTGAAGTGC-3'	TPMT_1_R	5'-GAGGTATCCGTCCCTGGG-3'	1865
TPMT	TPMT_2_F	5'-ATCCACTCACATCACCTACATTATAAGCC-3'	TPMT_2_R	5'-GCTTCTTATAGATGAAATCACACACAAGCA-3'	6113
TPMT	TPMT_3_F	5'-CCGGCCACAAGTATGGACTT-3'	TPMT_3_R	5'-ACGAGGAACCAATGTGGCTAA-3'	6093
TPMT	TPMT_4_F	5'-AGGCAGGGCAAGGCATTTAT-3'	TPMT_4_R	5'-ACACAGGCATCCAAGGTCAG-3'	6004
CYP3A5	CYP3A5_1_F	5'-GCCTTTGGGTCCAGTGAAGA-3'	CYP3A5_1_R	5'-CCGAGACGCACCATTACACT-3'	6233
CYP3A5	CYP3A5_2_F	5'-AGACAAGACTGCACGTCTTTTCAAATATAC-3'	CYP3A5_2_R	5'-AAGTGAGTTAAACCTGTGTCTTCAAGTTGA-3'	8247
CYP3A5	CYP3A5_3_F	5'-TATCTTTACTATGTTTCAGCCTTTCATCCCG-3'	CYP3A5_3_R	5'-CAGTTTCTTTCGAATTCTGGGAGTCAATCA-3'	5514
CYP3A5	CYP3A5_4_F	5'-CATGAAGATCACACAACTAATGTGAGAAA-3'	CYP3A5_4_R	5'-GGCCATCTTCTCGCCACACTCCTTTTTTTT-3'	6925
CYP3A5	CYP3A5_5_F	5'-AGCCCTGGCATCAGCTATTT-3'	CYP3A5_5_R	5'-TGTGAGGCAGACACAAAGGG-3'	7066
CYP3A4	CYP3A4_1_F	5'-AACCTGTGGTTTTTGAAGCTCCCATGCA-3'	CYP3A4_1_R	5'-GCAGGATCCCACCAGTGAGAGGATTCATCC-3'	7418
CYP3A4	CYP3A4_2_F	5'-GGATGCAAGGCTGGGTTCAA-3'	CYP3A4_2_R	5'-AACAGGAGGGAATGTGGACA-3'	7270
CYP3A4	CYP3A4_3_F	5'-ACACACGCTACACTTCAGCA-3'	CYP3A4_3_R	5'-ACGCTGACTTGATCCTGGTG-3'	7838
CYP3A4	CYP3A4_4_F	5'-GCAGTAAAAACAGGTGTAATCTGAGTTGT-3'	CYP3A4_4_R	5'-ACACCCAGGGCCAGGCTCCGTCAGACTACA-3'	6070
CYP3A4	CYP3A4_5_F	5'-GATTTGAGGGCTTCACTTAGATTTCTCTTC-3'	CYP3A4_5_R	5'-CAAGTCATTTGGAAATGTCATTGGGAAGTC-3'	8033
NAT2	NAT2_1_F	5'-CACCCGTACCAAGGTTCTCTC-3'	NAT2_1_R	5'-TCTGGCTACAAGTCTGCAAAGT-3'	7073
NAT2	NAT2_2_F	5'-AGCTGTTGTGTTTGAAGTGGT-3'	NAT2_2_R	5'-GGCCAGATCTCCTATCCACC-3'	3173