

Table S1: Polymorphisms chosen after applying the criteria of selection

Gene	SNP	Allele	Function	Amino acid substitution	Chromosome	Location
<i>ABCC1</i>	rs28364006	A>G	Missense	Thr1337Ala	16	16134392
<i>ABCC2</i>	rs717620	C>T	5' UTR	-	10	99782821
<i>ABCC3</i>	rs9895420	T>A	5' Flanking	-	17	50634677
<i>AMPD1</i>	rs17602729	G>A	Stop Codon	Gln45Ter	1	114693436
<i>ARID5B</i>	rs10821936	C>T	Intronic	-	10	61963818
<i>ATIC</i>	rs2372536	C>G	Missense	Thr116Ser	2	215325297
<i>ATIC</i>	rs4673993	T>C	Splicing region	-	2	215347616
<i>CCND1</i>	rs9344	G>A	Synonym	Pro241Pro	11	69648142
<i>CDKN2A</i>	rs3731217	A>C	Intra-genic	-	9	21984662
<i>CEBPE</i>	rs2239633	G>A	5' UTR	-	14	23119848
<i>GGH</i>	rs11545078	G>A	Missense	Thr151Ile	8	63026205
<i>GGH</i>	rs1800909	A>G	Missense	Cys6Arg	8	63038753
<i>GGH</i>	rs3758149	G>A	5' Flanking	-	8	63039169
<i>IKZF1</i>	rs4132601	T>G	UTR '3	-	7	50402906
<i>ITPA</i>	rs1127354	C>A	Missense	Pro15Thr	20	3213196
<i>MTHFD1</i>	rs2236225	G>A	Missense	Arg653Gln	14	64442127
<i>MTHFR</i>	rs1801133	G>A	Missense	Ala222Val	1	11796321
<i>MTRR</i>	rs1801394	A>G	Missense	Ile22Met	5	7870860
<i>NALCN</i>	rs7992226	A>G	Intronic	-	13	101145489
<i>NOS3</i>	rs1799983	T>G	Missense	Asp298Glu	7	150999023

<i>PIP4K2A</i>	rs7088318	C>A	Intra-genic	-	10	22564019
<i>SHMT1</i>	rs1979277	G>A	Missense	Leu435Phe	17	18328782
<i>SLCO1B1</i>	rs2306283	A>G	Missense	Asn130Asp	12	21176804
<i>SLCO1B1</i>	rs4149015	G>A	5' Flanking	-	12	21130388
<i>SLCO1B1</i>	rs4149056	T>C	Missense	Val174Ala	12	21178615
<i>TLR4</i>	rs4986790	A>G	Missense	Asp99Gly	9	117713024
<i>TNFAIP3</i>	rs6920220	G>A	Intra-genic	-	6	137685367
<i>TPMT</i>	rs1800460	C>T	Missense	Ala154Thr	6	18138997
<i>TPMT</i>	rs1800462	C>G	Missense	Ala80Pro	6	18143724
<i>TPMT</i>	rs1142345	T>C	Missense	Tyr240Cys	6	18130687
<i>TPMT</i>	rs12201199	A>T	Intrônico	-	6	18139571
<i>TPMT</i>	rs56161402	C>T	Missense	Arg215His	6	18130762

3UTR: 3'UTR regulation; 5UTR: 5'UTR regulation

Table S2: Allelic and genotypic distribution and quality control of the polymorphisms.

Gene/rs	Most Frequent Allele	Nucleotide change	Missings ⁵	AA ¹	Aa ²	aa ³	Missings (%) ⁴	MAF ⁵
<i>TPMT</i> rs1142345	T	T>C	42	90	30	6	25.0	16.7
<i>TPMT</i> rs12201199	A	T>C / T>G	35	95	35	3	20.8	15.4
<i>SLCO1B1</i> rs4149056	T	T>C	31	94	38	5	18.5	17.5
<i>ABCC2</i> rs717620	C	C>T	29	112	25	2	17.3	10.4
<i>ABCC3</i> rs9895420	T	T>A	27	111	29	1	16.1	11.0
<i>GGH</i> rs11545078	G	G>A	21	114	30	3	12.5	12.2
<i>GGH</i> rs3758149	G	G>A	35	66	58	9	20.8	28.6
<i>ATIC</i> rs2372536	C	C>G	25	81	51	11	14.9	25.5
<i>ATIC</i> rs4673993	T	T>C	25	75	55	13	14.9	28.3
<i>AMPD1</i> rs17602729	G	G>A	35	114	17	2	20.8	7.9
<i>CCND1</i> rs9344	G	G>A	18	55	73	22	10.7	39.0
<i>IKZF1</i> rs4132601	T	T>G	26	90	46	6	15.5	20.4
<i>ITPA</i> rs1127354	C	C>A	44	114	10	-	26.2	4.0
<i>MTRR</i> rs1801394	G	A>G	41	47	61	19	24.4	39.0
<i>MTHFD1</i> rs2236225	G	G>A	31	32	74	31	18.5	49.6
<i>NOS3</i> rs1799983	G	T>G	44	121	3	-	26.2	1.2
<i>MTHFR</i> rs1801133	G	G>A	18	69	66	15	10.7	32.0
<i>TLR4</i> rs4986790	A	A>G	31	129	8	-	18.5	2.9
<i>TPMT</i> rs1800460	C	C>T	24/48	127	13	4	14.3	7.3
<i>SLCO1B1</i> rs4149015	G	G>A	82	73	9	4	48.8	9.9
<i>GGH</i> rs1800909	A	A>G	27	132	5	4	16.1	4.6
<i>ARID5B</i> rs10821936	T	C>T	26	42	59	41	15.5	49.6
<i>NALCN</i> rs7992226	A	A>G	46	50	47	25	27.4	39.8
<i>SHMT1</i> rs1979277	A	G>A	67	63	27	11	39.9	24.3
<i>SLCO1B1</i> rs2306283	G	A>G	52	35	59	22	31.0	44.4
<i>CEBPE</i> rs2239633	G	G>A	53	50	53	12	31.5	33.5
<i>PIP4K2A</i> rs7088318	A	C>A	53	31	67	17	31.5	43.9
<i>TNFAIP3</i> rs6920220	G	G>A	58	79	30	1	34.5	14.5
<i>TPMT</i> rs1800462	C	C>G	28	140	-	-	16.7	0.0
<i>TPMT</i> rs56161402	C	C>T	33	270	-	-	19.6	0.0
<i>ABCC1</i> rs28364006	A	A>G	15	153	-	-	8.9	0.0
<i>CDKN2A</i> rs3731217	A	A>C	47	121	-	-	28.0	0.0

¹AA: Most frequent homozygote; ²Aa: Heterozygote; ³aa: Less frequent homozygote; ⁴Genotyping data not obtained; ⁵MAF: minor frequency allele

Table S3. Odds ratio and genotype distributions of the polymorphisms not statistically significant between the patients with response and without response.

Genotype	Responders (%)	No responders (%)	OR (95% CI)	Lower	Upper	p-value
TPMT rs1142345						
TT	57 (71.2)	32 (71.1)	1.00			0.25
CT	21 (26.2)	9 (20.0)	0.76	0.31	1.86	
CC	2 (2.5)	4 (8.9)	3.56	0.62	20.54	
TPMT rs12201199						
AA	54 (67.5)	40 (78.4)	1.00			0.15
AT	25 (31.2)	9 (17.6)	0.49	0.2	1.15	
TT	1 (1.2)	2 (3.9)	2.7	0.24	30.82	
SLC01B1 rs414956						
TT	61 (74.4)	33 (62.3)	1.00			0.30
CT	18 (22.0)	18 (34.0)	1.85	0.85	4.03	
CC	3 (3.7)	2 (3.8)	1.23	0.2	7.75	
ABCC2 rs717620						
CC	66 (80.5)	44 (81.5)	1.00			0.93
CT	15 (18.3)	9 (16.7)	0.9	0.36	2.24	
TT	1 (1.2)	1 (1.9)	1.5	0.09	24.62	
ABCC3 rs9895420						
TT	68 (81.0)	41 (75.9)	1.00			0.63
AT	15 (17.9)	13 (24.1)	1.44	0.62	3.32	
AA	1 (1.2)	0 (0.0)	0.00	0.00		
GGH rs11545078						
GG	68 (78.2)	43 (75.4)	1.00			0.88
AG	17 (19.5)	13 (22.8)	1.21	0.53	2.74	
AA	2 (2.3)	1 (1.8)	0.79	0.07	8.99	
GGH rs3758149						
GG	40 (50.6)	24 (47.1)	1.00			0.59
AG	35 (44.3)	22 (43.1)	1.05	0.5	2.19	
AA	4 (5.1)	5 (2.08)	2.08	0.51	8.52	
ATIC rs2372536						
CC	51 (60.0)	29 (52.7)	1.00			0.22
CG	30 (35.3)	19 (34.5)	1.11	0.53	2.32	
GG	4 (4.7)	7 (12.7)	3.08	0.83	11.41	
ATIC rs4673993						
TT	49 (57.0)	25 (46.3)	1.00			0.33
CT	31 (36.0)	22 (40.7)	1.39	0.67	2.88	
CC	6 (7.0)	7 (13.0)	2.29	0.69	7.53	
AMPD1 rs17602729						
GG	71 (87.7)	41 (82.0)	1.00			0.38
AG	8 (9.9)	9 (18.0)	1.95	0.70	5.44	

AA	2 (2.5)	0 (0.0)	0.00	0.00		
<i>CCND</i> rs9344						
GG	35 (38.5)	20 (35.7)	1.00			0.93
AG	43 (47.3)	27 (48.2)	1.10	0.53	2.28	
AA	13 (14.3)	9 (16.1)	1.21	0.44	3.33	
<i>IKZF1</i> rs4132601						
TT	57 (66.3)	32 (60.4)	1.00			0.43
GT	25 (29.1)	20 (37.7)	1.42	0.69	2.96	
GG	4 (4.7)	1 (1.9)	0.45	0.05	4.16	
<i>ITPA</i> rs1127354						
CC	71 (93.4)	41 (89.1)	1.00			0.40
AC	5 (6.6)	5 (10.9)	1.73	0.47	6.34	
<i>MTRR</i> rs1801394						
AA	26 (32.9)	20 (42.6)	1.00			0.52
AG	41 (51.9)	20 (42.6)	0.63	0.29	1.4	
GG	12 (15.2)	7 (14.9)	0.76	0.25	2.28	
<i>MTHFD1</i> rs2236225						
GG	19 (22.6)	13 (25.5)	1.00			0.79
AG	48 (57.1)	26 (51.0)	0.79	0.34	1.86	
AA	17 (20.2)	12 (23.5)	1.03	0.37	2.87	
<i>NOS3</i> rs1799983						
GG	76 (98.7)	43 (95.6)	1.00			0.29
GT	1 (1.3)	2 (4.4)	3.53	0.31	40.13	
<i>MTHFR</i> rs1801133						
GG	44 (48.9)	25 (43.9)	1.00			0.50
GA	40 (44.4)	25 (43.9)	1.10	0.55	2.22	
AA	6 (6.7)	7 (12.3)	2.05	0.62	6.79	
<i>TLR4</i> rs4986790						
AA	77 (92.8)	50 (96.2)	1.00			0.40
AG	6 (7.2)	2 (3.8)	0.51	0.1	2.64	
<i>TPMT</i> rs1800460						
CC	77 (89.5)	47(85.5)	1.00			0.05
CT	9 (10.5)	4 (7.3)	0.73	0.21	2.50	
TT	0 (0)	4 (7.3)		0.00		
<i>GGH</i> rs1800909						
AA	79 (95.2)	50 (90.9)	1.00			0.35
AG	3 (3.6)	2 (3.6)	1.05	0.17	6.53	
GG	1 (1.2)	3 (5.5)	4.74	0.48	46.84	
<i>ARID5B</i> rs10821936						
TT	22 (25.9)	20(37.0)	1.00			0.30
CT	36 (42.4)	22 (40.7)	0.67	0.30	1.50	
CC	27 (31.8)	12 (22.2)	0.49	0.20	1.22	
<i>NALCN</i> rs7992226						
AA	27 (37.5)	21 (43.8)	1.00			0.38

AG	27 (37.5)	20 (41.7)	0.95	0.42	2.15
GG	18 (25.0)	7 (14.6)	0.50	0.18	1.42
