Supplementary

Table S1 Primers used in the PCR to amplify the coding region

SNPs	Primer sequences (from 5′ to 3′)		Fragment size
rs17209237	F: CTGCCCGACCTTTCTATTCTATGTG	R: CCTGGTGCCAAAGACCTGAAGA	267
rs9324921	F: CCTCTAACCCTTCATTTACAAACATTGG	R: GCCCAGGTTATCTTCCCCAGAT	219
rs1360780	F: TGAGGACAGCCTGCAAAGTCTC	R: TTAATATCTCTTGTGCCAGCAGTAGCA	283
rs4713904	F: GAGATCACAAGTCCAGAATGGGTCT	R: CAGTATTCCCGGCTGAAGATGG	174
rs9296158	F: TTCTGTTATACTCATTCCATGCCCAATA	R: GCCTGGGCTAGGGGTAATTCAA	224
rs10873531	F: TGCAGATCCTTGTAGAGGTGTTGC	R: CCCAAGTGTTTCTCTGGCATCTG	154
rs2298877	F: GCGTGATGTGTCGTCATCTCCT	R: CCTGCTTGCTGCTTGGAGGTAT	284
rs7160651	F: CTGCCTGGTAGGGGAGCTGATAG	R: GCAGAAGCTGACAGGACCAGGTT	213
rs1045642	F: CAGAGAGGCTGCCACATGCT	R: CAGGAGCCCATCCTGTTTGACT	188
rs1128503	F: GCTCTTCCCACAGCCACTGTTT	R: TGTGTCTGTGAATTGCCTTGAAGTTT	125
rs2032582	F: TGAAGACAATGGCCTGAAAACTGA	R: TGTTGTCTGGACAAGCACTGAAAGA	296
rs2242480	F: CTTCTGCCAGTAGCAACCATTTG	R: ACTGCAGGAGGAAATTGATGCAG	218
rs776746	F: CCAGGAAGCCAGACTTTGATCATT	R: TGCCCTTGCAGCATTTAGTCCT	391

PCR, polymerase chain reaction; SNPs, single nucleotide polymorphisms.

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Table S2 The distribution of SNPs in refractory and non-refractory patients

SNPs	Genotype (total =131)	Non-refractory (n=98), n (%)	Refractory (n=33), n (%)	χ^2	P value[a]	Logistic regression	
						OR (95% CIs)	P value[b]
NR3C1 (rs17209237)	TT	68 (69.4%)	23 (69.7%)	0.249	0.883	Reference	
	TC	26 (26.5%)	8 (24.2%)			0.95 (0.31–2.93)	0.925
	CC	4 (4.1%)	2 (6.1%)			0.04 (0.00–56.95)	0.375
	TC + CC	30 (30.6%)	10 (30.3%)	0.001	0.973	0.82 (0.27–2.48)	0.727
	T-allele	162 (82.7%)	54 (81.8%)	0.024	0.877	Reference	
	C-allele	34 (17.3%)	12 (18.2)			0.74 (0.28–1.94)	0.534
NR3C1 (rs9324921)	GG	50 (51.0%)	21 (63.6%)	1.602	0.449	Reference	
	GT	40 (40.8%)	10 (30.3%)			0.47 (0.17–1.36)	0.165
	TT	8 (8.2%)	2 (6.1%)			0.35 (0.04–3.31)	0.358
	GT + TT	48 (49.0%)	12 (36.4%)	1.583	0.208	0.46 (0.17–1.25)	0.127
	G-allele	140 (71.4%)	52 (78.8%)	1.366	0.243	Reference	
	T-allele	56 (28.6%)	14 (21.2%)			0.56 (0.25–1.24)	0.150
FKBP5 (rs1360780)	AA	8 (8.2%)	2 (6.1%)	0.601	0.740	Reference	
	AG	38 (38.8%)	11 (33.3%)			1.74 (0.14–21.90)	0.670
	GG	52 (53.1%)	20 (60.6%)			1.80 (0.15–21.08)	0.640
	AG + GG	90 (91.8%)	31 (93.9%)	0.000	0.988	1.78 (0.16–20.35)	0.644
	A-allele	54 (27.6%)	15 (22.7%)	0.592	0.442	Reference	
	G-allele	142 (72.4%)	51 (77.3%)			0.87 (0.38–1.98)	0.734
FKBP5 (rs4713904)	GG	8 (8.2%)	1 (3.0%)	1.193	0.551	Reference	
	GA	39 (39.8%)	14 (42.4%)			1.80 (0.15–22.07)	0.644
	AA	51 (52.0%)	18 (54.5%)			1.89 (0.16–22.07)	0.612
	GA + AA	90 (91.8%)	32 (97.0%)	0.373	0.542	1.86 (0.16–23.64)	0.618
	G-allele	55 (28.1%)	16 (24.2%)	0.364	0.546	Reference	
	A-allele	141 (71.9%)	50 (75.8%)			1.16 (0.50–2.65)	0.734
FKBP5 (rs9296158)	TT	8 (8.2%)	2 (6.1%)	0.501	0.778	Reference	
	TC	49 (50.0%)	15 (45.5%)			1.63 (0.13–19.96)	0.702
	CC	41 (41.8%)	16 (48.5%)			1.88 (0.16–21.95)	0.615
	TC + CC	90 (91.8%)	31 (93.9%)	0.000	0.988	1.78 (0.16–20.35)	0.644
	T-allele	65 (33.2%)	19 (28.8%)	0.434	0.510	Reference	
	C-allele	131 (66.8%)	47 (71.2%)			1.19 (0.56–2.51)	0.615
HSP90AA1 (rs10873531)	CC	10 (10.2%)	2 (6.1%)	2.526	0.283	Reference	
	CT	38 (38.8%)	9 (27.3%)			1.19 (0.18–7.80)	0.856
	TT	50 (51.0%)	22 (66.7%)			2.20 (0.36–13.36)	0.394
	CT + TT	88 (89.8%)	31 (93.9%)	0.133	0.715	1.70 (0.30–9.56)	0.546
	C-allele	58 (29.6%)	13 (19.7%)	2.447	0.118	Reference	
	T- allele	138 (70.4%)	53 (80.3%)			1.65 (0.73–3.74)	0.226
HSP90AA1 (rs2298877)	AA	8 (8.2%)	2 (6.1%)	1.946	0.378	Reference	
	AG	35 (35.7%)	8 (24.2%)			0.81 (0.11–5.86)	0.833
	GG	55 (56.1%)	23 (69.7%)			1.44 (0.23–9.21)	0.770
	AG + GG	90 (91.8%)	31 (93.9%)	0.000	0.988	1.18 (0.19–7.24)	0.857
	A-allele	51 (26.0%)	12 (18.2%)	1.661	0.197	Reference	
	G-allele	145 (74.0%)	54 (81.8%)			1.45 (0.62–3.34)	0.390
MDR1 (rs1045642)	TT	14 (14.3%)	3 (9.1%)	1.715	0.424	Reference	
	TC	44 (44.9%)	19 (57.6%)			1.43 (0.30–6.79)	0.656
	CC	40 (40.8%)	11 (33.3%)			0.85 (0.17–4.31)	0.841
	TC + CC	84 (85.7%)	30 (90.9%)	0.220	0.639	1.14 (0.26–5.05)	0.865
	T-allele	72 (36.7%)	25 (37.9%)	0.028	0.868	Reference	
	C-allele	124 (63.3%)	41 (62.1%)			0.83 (0.42–1.66)	0.598
MDR1 (rs1128503)	TT	36 (36.7%)	16 (48.5%)	1.976	0.372	Reference	
	TC	50 (51.0%)	15 (45.5%)			0.64 (0.23–1.78)	0.392
	CC	12 (12.2%)	2 (6.1%)			0.31 (0.05–1.82)	0.196
	TC + CC	62 (63.2%)	17 (51.5%)	1.424	0.233	0.55 (0.21–1.45)	0.229
	T-allele	122 (62.2%)	47 (71.2%)	1.734	0.188	Reference	
	C-allele	74 (37.8%)	19 (28.8%)			0.60 (0.29–1.23)	0.162
MDR1 (rs2032582)	TT	13 (13.3%)	3 (9.1%)	3.856	0.570	Reference	
	TG	37 (37.8%)	14 (42.4%)			1.30 (0.26–6.60)	0.754
	GG	17 (17.3%)	6 (18.2%)			0.55 (0.08–3.91)	0.550
	TA	12 (12.2%)	7 (21.2%)			2.16 (0.33–13.96)	0.421
	AA	1 (1.0%)	0 (0.0%)			–	–
	GA	18 (18.4%)	3 (9.1%)			0.63 (0.09–4.43)	0.641
	TG + GG	54 (55.1%)	20 (66.7%)	0.139	0.710	0.99 (0.21–4.69)	0.994
	TA + AA	13 (13.3%)	7 (23.3%)	0.500	0479	2.85 (0.29–11.65)	0.514
	T-allele	75 (38.3%)	27 (40.9%)	0.155	0.926	Reference	
	G-allele	89 (45.4%)	29 (43.9%)			0.66 (0.31–1.38)	0.265
	A-allele	32 (16.3%)	10 (15.2%)			0.84 (0.31–2.25)	0.728
CYP3A4 (rs2242480)	GG	62 (63.3%)	23 (69.7%)	1.734	0.420	Reference	
	GA	31 (31.6%)	7 (21.2%)			0.90 (0.33–2.50)	0.846
	AA	5 (5.1%%)	3 (9.1%)			2.31 (0.39–13.74)	0.359
	GA + AA	36 (36.7%)	10 (30.3%)	0.448	0.503	1.09 (0.43–2.78)	0.861
	G-allele	155 (79.1%)	53 (80.3%)	0.045	0.832	Reference	
	A-allele	41 (20.9%)	13 (19.7%)			1.08 (0.48–2.42)	0.848

The allele frequency was calculated by dividing the number of alleles by twice the number of cases. [a], P value for genotype frequencies using χ^2 test; [b], P value from multivariable logistic regression analysis after adjusting for age, sex, MGFA classification, QMG scores, medicine treatment, and history of thymectomy. SNPs, single nucleotide polymorphisms; OR, odds ratio; CIs, confidence intervals; MGFA, Myasthenia Gravis Foundation of America; QMG, quantified myasthenia gravis.

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