

Supplemental information section

Table S1. Call rates for the SNPs in Stage I and Stage II:

SNP	Gene	Call rate Stage I (%)	Call rate Stage II (%)
rs4680	<i>COMT</i>	100	100
rs1611115	<i>DBH</i>	98.6	100
rs1800497	<i>DRD2/ANKK1</i>	100	100
rs6323	<i>MAOA</i>	100	
rs 6295	<i>HTR1A</i>	99.3	
rs 6311	<i>HTR2A</i>	99.3	
rs1799913	<i>TPH1</i>	99	
rs1800532	<i>TPH1</i>	99.7	
rs3785143	<i>NET1</i>	100	

Table S2. Stage I: Genotype distributions of aggression-related SNPs, modulating DA signaling

Abbreviations: *SNP*, single-nucleotide polymorphism; *N*, number of subjects; *HWE*, Hardy-Weinberg equilibrium

SNP	Gene	N	HWE <i>p</i> -value
rs4680	<i>COMT</i>	A/A 91 A/G 127 G/G 72	0.048
rs1611115	<i>DBH</i>	C/C 176 C/T 106 T/T 4	0.017
rs1800497	<i>DRD2/ANKK1</i>	C/C 203 T/C 78 T/T 9	0.670

Table S3. Stage I: Genotype distributions of aggression-related SNPs, modulating NE and 5-HT signaling

Abbreviations: *SNP*, single-nucleotide polymorphism; *N*, number of subjects; *HWE*, Hardy-Weinberg equilibrium

SNP	Gene	N	HWE <i>p</i> -value
rs6295	<i>HTR1A</i>	G/G 73 C/G 143 C/C 72	0.910
rs6311	<i>HTR2A</i>	C/C 99 C/T 144 T/T 45	0.720
rs1799913	<i>TPH1</i>	G/G 119 G/T 127 T/T 41	0.530
rs1800532	<i>TPH1</i>	C/C 120 A/C 127 A/A 42	0.460
rs3785143	<i>NET1</i>	C/C 235 C/T 52 T/T 3	> 0.999

Table S4. Stage I: Associations between genetic modulators of DA signaling, and the side effects of LEV treatment

Abbreviations: **SNP**, single-nucleotide polymorphisms; **N**, number of subjects; **S.E.M.**, standard error of mean; **95% CI**, 95% confidence interval for the mean difference; **AIC**, Akaike Information Criterion

SNP (Gene)	Model	Genotype	N	Response mean (S.E.M.)	Difference (95% CI)	p-value	AIC
rs4680; men (COMT)	Codominant	A/A	46	-0.17 (0.14)	0	0.016	430.5
		A/G	60	-0.08 (0.13)	-0.09 (-0.31 – 0.49)		
		G/G	41	-0.66 (0.18)	-0.48 (-0.92 – -0.05)		
	Dominant	A/A	46	-0.17 (0.14)	0	0.440	436.1
		A/G-G/G	101	-0.32 (0.11)	-0.14 (-0.51 – 0.22)		
	Recessive	A/A-A/G	106	-0.12 (0.1)	0	0.0045	428.7
		G/G	41	-0.66 (0.18)	-0.54 (-0.91 – -0.17)		
rs6323 (MAOA)	Codominant	A/A	181	-0.24 (0.08)	0	0.74	862.4
		A/C	56	-0.12 (0.13)	0.11 (-0.21 – 0.43)		
		C/C	53	-0.26 (0.15)	-0.03 (-0.35 – 0.30)		
Dominant	A/A	181	-0.24 (0.08)	0	0.730	860.9	
	A/C-C/C	109	-0.19 (0.1)	0.04 (-0.21 – 0.30)			
Recessive	A/A-A/C	237	-0.21 (0.07)	0	0.740	860.9	
		C/C	53	-0.26 (0.15)	-0.05 (-0.37 – 0.26)		
rs1611115 (DBH)	Codominant	C/C	176	-0.36 (0.08)	0	0.018	840.3
		C/T	106	0 (0.1)	0.36 (0.11 – 0.61)		
		T/T	4	-0.5 (0.87)	-0.14 (-1.18 – 0.89)		
Dominant	C/C	176	-0.36 (0.08)	0	0.007	839.2	
	C/T-T/T	110	-0.02 (0.1)	0.34 (0.09 – 0.59)			
Recessive	C/C-C/T	282	-0.22 (0.06)	0	0.600	846.1	
		T/T	4	-0.5 (0.87)	-0.28 (-1.32 – 0.76)		
rs1800497 (DRD2/ANKK1)	Codominant	C/C	203	-0.14 (0.08)	0	0.12	858.8
		T/C	78	-0.42 (0.1)	-0.29 (-0.56 – -0.01)		
		T/T	9	-0.33 (0.24)	-0.20 (-0.90 – 0.51)		
Dominant	C/C	203	-0.14 (0.08)	0	0.041	856.8	
	T/C-T/T	87	-0.41 (0.09)	-0.28 (-0.54 – -0.01)			
Recessive	C/C-T/C	281	-0.22 (0.06)	0	0.750	860.9	
		T/T	9	-0.33 (0.24)	-0.12 (-0.82 – 0.59)		

Table S5: Stage I: Rates of LEV side effects for the top-ranked polymorphisms

Abbreviations: **SNP**, single-nucleotide polymorphisms; **Side effects (%)**, rate of LEV treatment-induced adverse side effects, in percent

SNP	Gene	Genotype	Side effects (%)
rs4680	COMT	A/A-A/G	36.8
		G/G	56.1 (19.3% increase)
rs1611115	DBH	C/T-T/T	26.3
		C/C	42.6 (16.3% increase)
rs1800497	DRD2/ANKK1	C/C	35.5
		C/T-T/T	43.7 (8.2% increase)

Table S6. Stage I: Associations between genetic modulators of NE and 5-HT signaling, and the side effects of LEV treatment

Abbreviations: **SNP**, single-nucleotide polymorphisms; **N**, number of subjects; **S.E.M.**, standard error of mean; **95% CI**, 95% confidence interval for the mean difference; **AIC**, Akaike Information Criterion

SNP (Gene)	Model	Genotype	N	Response mean (S.E.M.)	Difference (95% CI)	Difference p-value	AIC
rs6295 (HTR1A)	Codominant	G/G	73	-0.1 (0.12)	0	0.41	848.4
		C/G	143	-0.28 (0.09)	-0.18 (-0.48 – 0.11)		
		C/C	72	-0.29 (0.13)	-0.20 (-0.54 – 0.14)		
rs6295 (HTR1A)	Dominant	G/G	73	-0.1 (0.12)	0	0.180	846.4
		C/G-C/C	215	-0.28 (0.07)	-0.19 (-0.47 – 0.09)		
		C/C	72	-0.29 (0.13)	-0.07 (-0.35 – 0.21)		
rs6295 (HTR1A)	Recessive	G/G-C/G	216	-0.22 (0.07)	0	0.600	847.9
		C/C	72	-0.29 (0.13)	-0.07 (-0.35 – 0.21)		
		C/C	72	-0.29 (0.13)	-0.07 (-0.35 – 0.21)		
rs6311 (HTR2A)	Codominant	C/C	99	-0.1 (0.12)	0	0.32	855.4
		C/T	144	-0.27 (0.08)	-0.17 (-0.44 – 0.10)		
		T/T	45	-0.36 (0.17)	-0.25 (-0.63 – 0.12)		
rs6311 (HTR2A)	Dominant	C/C	99	-0.1 (0.12)	0	0.150	853.6
		C/T-T/T	189	-0.29 (0.07)	-0.19 (-0.45 – 0.07)		
		C/C	99	-0.1 (0.12)	-0.19 (-0.45 – 0.07)		
rs6311 (HTR2A)	Recessive	C/C-C/T	243	-0.2 (0.07)	0	0.370	854.9
		T/T	45	-0.36 (0.17)	-0.15 (-0.49 – 0.18)		
		T/T	45	-0.36 (0.17)	-0.15 (-0.49 – 0.18)		
rs1799913 (TPH1)	Codominant	G/G	119	-0.21 (0.1)	0	0.8	855.3
		G/T	127	-0.27 (0.09)	-0.06 (-0.32 – 0.21)		
		T/T	41	-0.15 (0.17)	0.06 (-0.31 – 0.44)		
rs1799913 (TPH1)	Dominant	G/G	119	-0.21 (0.1)	0	0.830	853.7
		G/T-T/T	168	-0.24 (0.08)	-0.03 (-0.28 – 0.22)		
		G/G	119	-0.21 (0.1)	-0.03 (-0.28 – 0.22)		
rs1799913 (TPH1)	Recessive	G/G-G/T	246	-0.24 (0.07)	0	0.600	853.5
		T/T	41	-0.15 (0.17)	0.09 (-0.26 – 0.44)		
		T/T	41	-0.15 (0.17)	0.09 (-0.26 – 0.44)		
rs1800532 (TPH1)	Codominant	C/C	120	-0.18 (0.1)	0	0.73	857.6
		A/C	127	-0.27 (0.09)	-0.08 (-0.35 – 0.18)		
		A/A	42	-0.14 (0.16)	0.04 (-0.33 – 0.41)		
rs1800532 (TPH1)	Dominant	C/C	120	-0.18 (0.1)	0	0.670	856
		A/C-A/A	169	-0.24 (0.08)	-0.05 (-0.3 – 0.19)		
		C/C	120	-0.18 (0.1)	-0.05 (-0.3 – 0.19)		
rs1800532 (TPH1)	Recessive	C/C-A/C	247	-0.23 (0.07)	0	0.630	856
		A/A	42	-0.14 (0.16)	0.08 (-0.26 – 0.43)		
		A/A	42	-0.14 (0.16)	0.08 (-0.26 – 0.43)		
rs3785143 (NET1)	Codominant	C/C	235	-0.23 (0.07)	0	0.66	862.2
		C/T	52	-0.23 (0.13)	-0.01 (-0.32 – 0.31)		
		T/T	3	0.33 (0.88)	0.56 (-0.65 – 1.77)		
rs3785143 (NET1)	Dominant	C/C	235	-0.23 (0.07)	0	0.870	861
		C/T-T/T	55	-0.2 (0.13)	0.03 (-0.29 – 0.34)		
		C/C	235	-0.23 (0.07)	0.03 (-0.29 – 0.34)		
rs3785143 (NET1)	Recessive	C/C-C/T	287	-0.23 (0.06)	0	0.360	860.2
		T/T	3	0.33 (0.88)	0.56 (-0.64 – 1.76)		
		T/T	3	0.33 (0.88)	0.56 (-0.64 – 1.76)		

Table S7. Stage II: Genotype distributions of SNPsAbbreviations: *SNP*, single-nucleotide polymorphisms; *N*, number of subjects

SNP	Gene	N	HWE <i>p</i> -value
rs4680	<i>COMT</i>	A/A 19 A/G 52 G/G 29	0.69
rs1611115	<i>DBH</i>	C/C 59 C/T 36 T/T 5	> .999
rs1800497	<i>DRD2/ANKK1</i>	C/C 60 T/C 33 T/T 7	0.41

Table S8: Stage II: Rates of LEV side effects for the tested polymorphismsAbbreviations: *SNP*, single-nucleotide polymorphisms; *Side effects (%)*, rate of LEV treatment-induced adverse side effects, in percent

SNP	Gene	Genotype	Side effects (%)
rs4680	<i>COMT</i>	A/A-A/G G/G	22 23.5 (1.5% increase)
rs1611115	<i>DBH</i>	C/T-T/T C/C	22 23.7 (1.7% increase)
rs1800497	<i>DRD2/ANKK1</i>	C/C C/T-T/T	18.3 30.0 (11.8% increase)