Supplementary Table 2. Genetic variants of candidate genes identified by WES and Sanger sequencing

Gene (transcript)	Nucleotide change	AA change	Zygosity	Clinsig† Pharmvar*	Method
CYP3A4	99365943C>A (26)	-	Hom	-	WES
CYP3A5 (NM_0000777.5)	c.219-237A>G (CYP3A5*3)	-	Hom	*Splice defect	Sanger
ABCB1 (NM_001348945)	87168749C>T (78)	-	Hom	-	WES
	c.210A>G (35)	p.70G=	Hom	-	WES
DRD2 (NM016574)	c.852T>C (51)	p.284H=	Het	-	WES
ANKK1 (NM_178510)	c.2137G>A (116)	p.E713K	Het	†Reduce dopamine receptor D2 density in striatum Drug response	WES
	c.1683C>T (126)	p.Y561Y	Hom	-	
	c.1324G>C (194)	p.G442R	Het	-	
	c.453A>C (35)	p.I151I	Het	-	
	c.T255C (96)	p.S85S	Het	-	

The mean coverage of each variant was shown in the parentheses.
AA, amino acid; Het, heterozygous; Hom, homozygous; Clinsig, Clinical significance (ncbi.nlm.nih.gov/clinvar); Pharmvar, Pharmacogene Variation Consortium (pharmvar.org).