

Supplementary Table 2. Prediction of functional relevance of the SNPs found associated with the disorder and those in LD with them, using the FuncPred software*.

SNP	r ²	Chr	Position*	Allele	Nearby Gene	TFBS	Splicing (site)	Splicing (ESE or ESS)	Splicing (abolish domain)	miRNA (miRanda)	miRNA (Sanger)	nsSNP	Stop Codon	Polyphen	SNPs3D (svm profile)	SNPs3D (svm structure)	Regulation Potential Score	Conservation Score
rs222741	assoc	17	3455629	G/A	TRPV1	--	--	--	--	--	--	--	--	--	--	--	0	0.004
rs460716	1	17	3458557	A/G	TRPV1/SHPK	--	--	--	--	--	--	--	--	--	--	--	0	0
rs465563	0.883	17	3460468	A/G	SHPK	--	--	--	--	--	--	--	--	--	--	--	0.052963	0.001
rs7217270	assoc	17	3368225	A/G	TRPV3	--	--	--	--	--	--	--	--	--	--	--	0.07156	0
rs7216486	1	17	3368782	A/G	TRPV3	--	--	--	--	--	--	--	--	--	--	--	0.431906	1
rs7207628	1	17	3369289	G/T	TRPV3	--	--	--	--	--	--	--	--	--	--	--	0.411614	0
rs8079054	1	17	3369103	A/G	TRPV3	--	--	--	--	--	--	--	--	--	--	--	0.288679	0
rs11656938	0.966	17	3367787	C/G	TRPV3	--	--	--	--	--	--	--	--	--	--	--	0	0
rs925102	0.966	17	3369116	A/C	TRPV3	--	--	--	--	--	--	--	--	--	--	--	0.288264	0.015
rs17175319	0.933	17	3370282	A/G	TRPV3	--	--	--	--	--	--	--	--	--	--	--	0	0
rs17763099	0.933	17	3370189	C/T	TRPV3	--	--	--	--	--	--	--	--	--	--	--	0	0
rs925101	0.932	17	3371257	C/T	TRPV3	--	--	--	--	--	--	--	--	--	--	--	0.305059	0

SNP: single nucleotide polymorphism. Chr: Chromosome. TFBS: transcription factor binding site. ESE: exonic splicing enhancer. ESS: exonic splicing silencer. miRNA: microRNA. nsSNP: non-synonymous SNP. Assoc: associated.

* Position from the first nucleotide of 17p according to UCSC Genome Browser (genome.ucsc.edu), build NCBI36/hg18).