

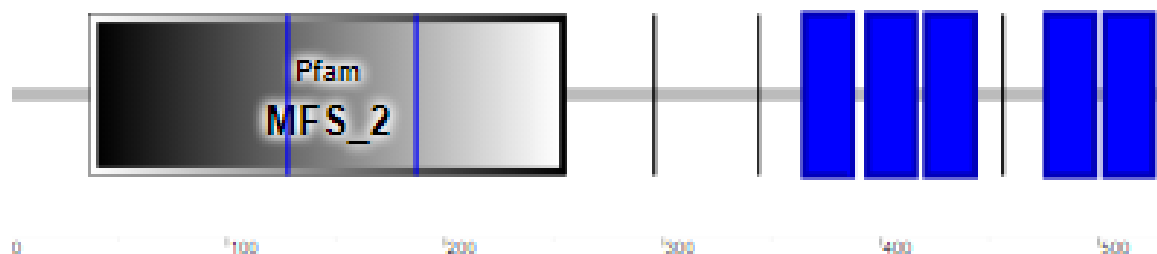
Appendix 1. Genetic models analysis for rs26722 and rs16891982 variants in SCL45A2 gene in case and control groups

SCL45A2_ rs26722 p.E272K association with response group (n=250, adjusted by sex+family)					
Model	Genotype	group=Ca	group=Co	OR (95% CI)	P-value
Codominant	C/C	49 (57.6%)	109 (66.1%)	1.00	0.018
	C/T	0 (0%)	6 (3.6%)	NA (0.00-NA)	
	T/T	36 (42.4%)	50 (30.3%)	0.64 (0.34-1.21)	
Dominant	C/C	49 (57.6%)	109 (66.1%)	1.00	0.36
	C/T-T/T	36 (42.4%)	56 (33.9%)	0.75 (0.40-1.40)	
Recessive	C/C-C/T	49 (57.6%)	115 (69.7%)	1.00	0.12
	T/T	36 (42.4%)	50 (30.3%)	0.61 (0.32-1.14)	
Overdominant	C/C-T/T	85 (100%)	159 (96.4%)	1.00	0.013
	C/T	0 (0%)	6 (3.6%)	NA (0.00-NA)	
Log-additive	---	---	---	0.82 (0.59-1.12)	0.22
SCL45A2_ rs16891982 p.L374F association with response group (n=250, adjusted by sex+family)					
Model	Genotype	group=Ca	group=Co	OR (95% CI)	P-value
Codominant	C/C	47 (55.3%)	84 (50.9%)	1.00	0.78
	C/G	37 (43.5%)	79 (47.9%)	1.24 (0.67-2.30)	
	G/G	1 (1.2%)	2 (1.2%)	1.36 (0.08-23.59)	
Dominant	C/C	47 (55.3%)	84 (50.9%)	1.00	0.48
	C/G-G/G	38 (44.7%)	81 (49.1%)	1.24 (0.67-2.29)	
Recessive	C/C-C/G	84 (98.8%)	163 (98.8%)	1.00	0.88
	G/G	1 (1.2%)	2 (1.2%)	1.25 (0.07-21.51)	
Overdominant	C/C-G/G	48 (56.5%)	86 (52.1%)	1.00	0.5
	C/G	37 (43.5%)	79 (47.9%)	1.23 (0.67-2.28)	
Log-additive	---	---	---	1.23 (0.69-2.20)	0.48

Appendix 2. Association between clinical and genetic factors.

rs26722 p.Glu272Lys

Clinical factor	OR	CI 95%	p-Value
Phototype I-II vs. III-IV	0,508	0,24-1,35	0,059
Eyes color light vs. Black	1,006	0,58-1,73	0,980
Hair color red-blond-brown vs. dark brown-black	0,671	0,35-1,25	0,210
Nevus count <50 vs >50	0,591	0,20-1,69	0,324
rs16891982 p.Phe374Leu			
Phototype I-II vs. III-IV	0,380	0,19-0,75	0,004*
Eyes color light vs. Black	0,75	0,44-1,27	0,285
Hair color red-blond-brown vs. dark brown-black	0,459	0,25-0,84	0,011*
Nevus count <50 vs >50	0,366	0,12-1,05	0,053



Appendix 3. Transmembrane and cytoplasmic of the protein sequence using SMART. In gray box, MFS_2 domain, (Major Facilitator Superfamily type 2) associated with sugar transport proteins. Blue lines within gray box and black lines, representation of introns. Blue boxes, representation of transmembrane regions.

Appendix 4. Prediction of the probably effect of the p.Glu272Lys and p.Phe374Lue variants in the function of the MATP protein using Provean, Polyphen and Pmut. .

Variant	Score PROVEAN	Prediction (cutoff= -2.5)	Score Polyphen	Prediction	Score Pmut	Prediction
p.L374F	-2.675	Deleterious	0,991	Probably damaging	0,42	Neutral
p.E272K	-1.095	Neutral	0,003	Benign	0,19	Neutral