

**Table S1. Genotype distribution of the studied *COMT*, and *DRD2* SNPs.**

<i>COMT</i> rs4680	N	%	<i>DRD2</i> rs1076560	n	%	<i>DRD2</i> rs1800497	N	%
<b>Genotype</b>			<b>genotype</b>			<b>genotype</b>		
GG	77	25,41%	CC	206	68,21%	GG	198	65,35%
GA	164	54,13%	CA	86	28,48%	GA	93	30,69%
AA	62	20,46%	AA	10	3,31%	AA	12	3,96%
<b>Allele</b>			<b>allele</b>			<b>allele</b>		
G	318	52,48%	C	498	82,45%	G	489	80,69%
A	288	47,52%	A	106	17,55%	A	117	19,31%

*COMT* rs4680 n=303; HWE p=0,14; MAF 0.4752; *DRD2* rs1076560 n=302; HWE p=0,78; MAF 0.1755;  
*DRD2* rs1800497 n=303; HWE p=0,80; MAF 0.1931

**Table S2. Linkage disequilibria between the studied loci in *DRD2* gene.**

<b>DRD2</b>	<b>rs1076560:C&gt;A</b>	<b>rs1800497:G&gt;A</b>
rs1076560:C>A	$r^2 \downarrow$ $D' \rightarrow$	0.952
rs1800497:G>A	0.590	

distance (kbp) – 12.86

**Table S3. Comparison of estimated haplotype frequencies of *DRD2* gene between FASD and NFC groups.**

<b>haplotype</b>	<b>FASD</b>	<b>NFC</b>	<b>p*</b>
GC	0.784	0.829	0.14
AA	0.183	0.154	0.28
AC	0.028	0.013	0.21

\*Fisher Exact Test