Supplementary Table 1

rs	position	Distance (bp)	Hap allele	Saccone *et al*	Bierut *et al*	Zeiger *et al* CADD	Zeiger *et al* Add Health	Greenbaum *et al*	Current study
rs10958726	42655066	12330	T	**T**					
rs1530847	42667396	1408			**T**				
rs1955185	42668804	335			**T**				
rs13277254	42669139	35	G		**A**				
rs13280301	42669174	40			**G**				
rs13277524	42669214	441			**T**				
rs6474412	42669655	566			**T**				
rs6474413	42670221	97		**T**					
rs7004381	42670318	1472	G						G
rs4950	42671790	6953				**G**	**G**		**A**
rs13280604	42678743	750	A			**G**	**A**		**A**
rs6474414	42679493	26729						NS	
rs4952	42706222	594	G	C					
rs4953	42706816	18332	C	G		C			G
rs9298628	42725148	195	C	C					
rs9298629	42725343	1611	G		G			0.035	
rs16891576	42726954	402							
rs2304297	42727356	1652	G	**G**		G	G	NS	**G**
rs35389610	42729008	1151				NS			NS
rs16891583*	42730159	3376		NA					
rs892413	42733535	2490	C		C	NS	NS		NS
rs10087172*	42736025	1578	T		T				
rs2217732	42737603	1555	A					NS	
rs1072003	42739158	9313	C		C	NS		0.053	NS
rs7828365	42748471				C				

SNPs highlighted in bold are those genotyped in this study. Individual risk alleles are shown in bold based on two different significance level cut-offs. For the large genomewide and candidate gene studies (Saccone et al, Bierut et al), SNP achieving $p<0.01$ are in bold, others are $0.01>p>0.10$ and presented only in the context of illustrating putative "risk" allele. For the other studies, SNPs with $p<0.05$ are shown in bold, while others are $0.05<p<0.01$. From the Greenbaum et al paper, we were unable to determine the risk allele, so p-values are presented.
*SNPS indicated with an asterisk are monomorphic in the samples studied.
NS – not significant
NA – not applicable