Supplementary Table 4. Findings from *in silico* Analysis of Risk-associated and Strongly Correlated SNPs

Gene (locus)	Genotyped SNP	# SNPs Tagged*	Tagged SNP(s)	Nucleotide Position (build 36)	Location	Possible function and/or conservation**	r^2 between significant genotyped SNPs
AGO2 (8q24.3)	**rs11996715**	27	-	141716473	flanking 5'UTR	TFBS	
			rs10088475	141739448	intron (PTK2)	intronic enhancer	
			rs10089107	141767633	intron (PTK2)	intronic enhancer	
			rs10104479	141763253	intron (PTK2)	intronic enhancer	
			rs10107434	141741747	intron (PTK2)	intronic enhancer	
			rs10108814	141787496	intron (PTK2)	no known function	
			rs10282830	141740716	intron (PTK2)	no known function	
			rs10283164	141740811	intron (PTK2)	no known function	
			rs10283368	141748999	intron (PTK2)	no known function	
			rs10875457	141772777	intron (PTK2)	no known function	r^2 =0.30 between rs11996715 and rs2176397
			rs11166986	141725337	intron (PTK2)	no known function	
			rs11166990	141733154	intron (PTK2)	no known function	
			rs11166991	141735595	intron (PTK2)	no known function	
			rs11166992	141746652	intron (PTK2)	no known function	r^2 =0.13 between rs11996715 and rs3864659
			rs11776239	141787883	intron (PTK2)	intronic enhancer	
			rs11784281	141735192	intron (PTK2)	no known function	
			rs11995049	141762271	intron (PTK2)	no known function	
			rs11995103	141762443	intron (PTK2)	no known function	
			rs13264524	141723840	intron (PTK2)	no known function	
			rs13268978	141748567	intron (PTK2)	no known function	
			rs13273096	141745113	intron (PTK2)	no known function	
			rs13274713	141734379	intron (PTK2)	no known function	
			rs13275969	141742598	intron (PTK2)	no known function	
			rs4413752	141758154	intron (PTK2)	no known function	
			rs7460	141738042	3'UTR (PTK2)	MBS (miR-137,-335,-539); Conserved	
			rs7820179	141770658	intron (PTK2)	no known function	
			rs9324533	141761186	intron (PTK2)	intronic enhancer	
			rs9644447	141761976	intron (PTK2)	no known function	
	rs2176397	2	-	141691719	intron	no known function	r^2 =0.03 between rs2176397 and rs3864659
			rs4961277	141693901	intron	intronic enhancer	
			rs6995141	141701149	intron	intronic enhancer	
	rs3864659	4	-	141625044	intron	no known function	
			rs2944758	141638360	intron	intronic enhancer	
			rs2944762	141637401	intron	intronic enhancer	

Gene (locus)	SNP	Count	Proxy SNP	Position	Region	Function	LD
			rs2944767	141627062	intron	intronic enhancer	
			rs2977485	141635739	intron	intronic enhancer	
DCP1 **(12p13.33)**	**rs10505725**	0	-	94623895	intron	no known function	r^2 =0.09 between rs10505725 and rs2240610; r^2 =0.11 between rs10505725 and rs6489338; r^2 =0.20 between rs10505725and rs725779
	rs2240610	8	-	1927853	intron	intronic enhancer	r^2 =0.93 between rs2240610 and rs6489338
			rs1860048	1928956	intron	no known function	
			rs2240611	1927962	intron	no known function	
			rs2240612	1928506	intron	splice site	
			rs2470425	1948158	intron	intronic enhancer	
			rs2470427	1946245	intron	no known function	
			rs2470448	1937696	intron	no known function	
			rs4765874	1993943	intron	intronic enhancer	
			rs7966355	1945913	intron	no known function	
			rs7222	1925527	3'UTR	MBS (miR-32, -1279)	
	rs6489338	5	-	1930841	intron	intronic enhancer	
			rs2470425	1948158	intron	intronic enhancer	
			rs2470427	1946245	intron	no known function	
			rs2470448	1937696	intron	no known function	
			rs4765874	1993943	intron	intronic enhancer	
			rs7966355	1945913	intron	no known function	
DICER **(14q32.13)**	**rs1057035**	0	-	94623895	3'UTR	MBS (miR 574-3p); ESE	
	rs1110386	0	-	94623895	flanking 3'UTR	no known function	r^2 =0.10 between rs1110386 and rs11621737; r^2 =0.16 between rs1110386 and rs2353726

	rs11621737	1	- rs11625422	94592587 94595367	flanking 3'UTR flanking 3'UTR	no known function no known function; conserved	r^2=0.38 between rs11621737 and rs2353726
	rs2353726	4	- rs11622458 rs11622522 rs7160684 rs8022945	94604622 94605251 94605456 94607134 94606883	flanking 3'UTR	no known function no known function no known function no known function no known function	
DROSHA **(5p13.3)**	**rs10067066**	0	-	31482473	intron	intronic enhancer	r^2=0.006 between rs10067066 and rs13186629, rs17404622, and rs2161006 r^2=0.002 between rs10067066 and rs6450839
	rs13186629	2	- rs17404622 rs2161006	31411810 31417087 31417271	flanking 3'UTR flanking 3'UTR flanking 3'UTR	no known function no known function no known function	r^2=0.93 between rs13186629, rs17404622, and rs2161006 r^2=0.244 between rs13186629 and rs6450839
	rs6450839	0	-	31419659	flanking 3'UTR	no known function	
FMR1 **(Xq27.3)**	**rs25704**	0	-	146839230	3'UTR	MBS (miR 548b-5p, miR-382)	

Gene (locus)	SNP	tagSNP count	tagSNP	Position	Location	Function	r²
LIN28 (1p36.11)	**rs11247946**	0	-	26591702	flanking 5'UTR	no known function	r²=0.17 between rs11247946 and rs12728900 r²=0.12 between rs11247946 and rs11581746 r²=0.61 between rs11247946 and rs6598964
	rs11581746	0	-	26616674	Intron	no known function	r²=0.60 between rs111581746 and rs12728900
	rs12728900	0	-	26619394	intron	intronic enhancer	r²=0.28 between rs12728900 and rs6598964
	rs6598964	0	-	26618914	intron	no known function	
LIN28B (6q16.3-q21)	**rs12194974**	1	- rs12212292	105510891 105533637	flanking 5'UTR intron	TFBS; Conserved intronic enhancer	r²=0.02 between rs12194974 and rs17065417
	rs17065417	1	- rs1149280	105512967 105561492	intron intron	TFBS no known function	r²=0.07 between rs17065417 and rs314263
PACT (2q31.2)	**rs2059691**	0	-	179010130	intron	no known function	-
SMAD4 (18q21.1)	**rs948588**	1	- rs17663887	46840342 46843716	intron	no known function	-

Abbreviations: TFBS=transcription factor binding site; UTR=untranslated region; MBS=microRNA binding site; miR= miRNA; EXE=exon splicing enhancer

Note: SNPinfo http://snpinfo.niehs.nih.gov/ and FastSNP http://fastsnp.ibms.sinica.edu.tw/pages/input_SNPListAnalysis.jsp/ were used for *in silico* predictions of risk-associated SNPs (Table 2) and their tagSNPs.

[*] TagSNPs defined as r² > 0.80 and within 250kb of genotyped SNP using HapMap2 data (http://hapmap.ncbi.nlm.nih.gov/).

[**] Based on Vertebrate Multi-Alignment and Conservation Score (17 species) downloaded from the UCSC genome bioinformatics web site (http://genome.ucsc.edu/) and obtained through SNPInfo (http://snpinfo.niehs.nih.gov).