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SUPPLEMENTAL MATERIAL

Rare genome-wide copy number variation and expression of schizophrenia in 22q11.2 deletion syndrome

Anne S. Bassett, M.D., Chelsea Lowther, B.Sc., Daniele Merico, Ph.D., Gregory Costain, M.D., Ph.D., Eva W. C. Chow, M.D., Therese van Amelsvoort, M.D., Ph.D., Donna McDonald-McGinn, M.Sc., Raquel E. Gur, M.D., Ph.D., Ann Swillen, Ph.D., Marianne Van den Bree, Ph.D., Kieran Murphy, M.D., Ph.D., Doron Gothelf, M.D., Carrie E. Bearden, Ph.D., Stephan Eliez, M.D., Wendy Kates, Ph.D., Nicole Philip, M.D., Vandana Sashi, M.D., Linda Campbell, Ph.D., Jacob Vorstman, M.D., Ph.D., Joseph Cubells, M.D., Ph.D., Gabriela M. Repetto, M.D., Tony Simon, Ph.D., Erik Boot, M.D., Ph.D., Tracy Heung, M.A., Rens Evers M.D., Ph.D., Claudia Vingerhoets, M.Sc., Esther van Duin, M.Sc., Elaine Zakai, M.D., Elfi Vergaelen, M.Sc., Koen Devriendt, M.D., Joris R. Vermeesch, Ph.D., Michael Owen, M.D., Ph.D., Clodagh Murphy, Ph.D., Elena Michaelovosky, Leila Kushan, M.Sc., Maude Schneider, M.Sc., Wanda Fremont, M.D., Tiffany Busa, M.D., Stephen Hooper, Ph.D., Kathryn McCabe, Ph.D., Sasja Duijff, Ph.D., Karin Isaev, B.Sc., Giovanna Pellecchia, Ph.D., John Wei, Ph.D., Matthew J. Gazzellone, M.Sc., Stephen W. Scherer, Ph.D., Beverly S. Emanuel, Ph.D., Tingwei Guo, Ph.D., Bernice E. Morrow, Ph.D., Christian R. Marshall, Ph.D., International 22q11.2DS Consortium on Brain and Behavior.

Supplemental Methods

In order to obtain an unrelated sample of individuals with a typical 22q11.2 deletion of consistent (European) ancestry, we used standard methods to estimate relatedness and ancestry. Genotypes from 272,834 unlinked single nucleotide polymorphisms (SNPs) from the 22q11.2DS subjects, together with genotype data from 778 HapMap subjects used as a reference for known ancestry, were clustered using the PLINK toolset.(1) The majority (n=692; 93.4%) of the 22q11.2DS samples were of European ancestry. Pair-wise identity by descent (IBD) was calculated for every pair of 22q11.2DS subjects. Pairs with a PI_HAT value [defined as P(IBD = 2) + 0.5 x P(IBD = 1)] >0.3 were classified as related. For the n=17 related pairs identified, we chose one sample per family, based on the best quality CNV and phenotypic data.

We generated a heatmap for the 22q11.2 deletion region based on the array intensity files using the Affymetrix Genotyping Console Software. We used these intensity data to select subjects with a "typical" 22q11.2 deletion, which comprise the most common deletion extents. Specifically, typical deletions were defined as low copy repeat (LCR) LCR-A-D deletions, or proximal nested LCR-A-B and LCR-A-C deletions, that would be detected using standard probes (e.g., TUPLE1 or N25) on a fluorescence *in situ* hybridization (FISH) analysis. We also ensured that key genes hypothesized to play a role in the phenotypic expression of 22q11.2DS were overlapped, including *DGCR8* (MIM: 609030), *COMT* (MIM:116760) and *TBX1* (MIM:602054).(2) In further data cleaning, we compared the heatmap results with available multiplex ligation-dependent probe amplification (MLPA) data, and also examined demographic and phenotypic data. We identified two samples with unresolved discrepancies in 22q11.2

deletion length, one with no 22q11.2 deletion, and six with discrepancies between phenotypic sex and observed genotype; these nine samples were excluded. Figure S1 shows the 22q11.2 deletion extent of subjects used in the current study.

Table S1: List of international sites participating in the International Brain and Behavior Consortium on 22q11.2DS

	Current study[1]	
Site	**Number of originating DNA samples (n=866)**	**Number of DNA samples in final cohort (n=329)**
Toronto, ON, Canada	118	97
Maastricht, Netherlands	65	59
Philadelphia, PA, USA	289	41
Leuven, Belgium	51	34
Cardiff, UK/ London, UK/ Dublin, Ireland	25	20
Tel Aviv, Israel	72	19
Los Angeles, CA, USA	38	17
Geneva, Switzerland	61	16
Syracuse, NY, USA	79	6
Marseilles, France	13	6
Durham, NC, USA	7	6
Newcastle, Australia	8	3
Dublin, Ireland	8	3
Utrecht, Netherlands	25	1
Atlanta, GA, USA	1	1
Sacramento, CA, USA	4	-
Santiago, Chile	2	-
Rome, Italy	-	-
Madrid, Spain	-	-
Mallorca, Spain	-	-
Total	**866**	**329**

[1]The current study required as a starting point the availability of Affymetrix 6.0 array data for potential copy number variation analysis, and subsequently DNA samples that passed all QC measures and met strict inclusion criteria. Thus, there are participating sites in the IBBC that have no data that could be included in the current study. The numbers also do not reflect the few subjects that were recruited at more than one site.

Table S2: List of 9,611 population-based controls used to adjudicate CNV rarity in the 22q11.2DS subjects

Control dataset	Number of individuals	Array platform	Description of dataset
ONC (Ontario Familial Colorectal Cancer Registry)	433	Illumina 1M	Cotterchio et al. 2005(3)
SAGE consortium controls	1,769	Illumina 1M	Bierut et al. 2010(4)
Health, Aging, and Body Composition (Health ABC) study controls	2,566	Illumina 1M Duo	Coviello et al. 2012(5)
POPGEN	1,123	Affymetrix 6.0	Krawczak et al. 2006(6)
Ottawa Heart Institute controls	732	Affymetrix 6,0	Stewart et al. 2009(7)
Collaborative Genetic Study of Nicotine Dependence (COGEND) controls	1,213	Illumina OMNI 2.5M Quad	Bierut et al. 2007(8)
KORA controls	1,775	Illumina OMNI 2.5M Quad	Verhoeven et al. 2013(9)
TOTAL	**9,611**		

For our main analyses we used CNVs in the 22q11.2DS subjects that were found in <0.1% of the population controls described above (designated "rare"). All genomic coordinates are provided based on NCBI GRCh37, human genome build 19. Only "high-quality" CNVs were included in the study, defined as (i) identified by at least two of three CNV calling algorithms (iPattern, Birdsuite or Affymetrix Genotyping Console), (ii) spanning 10 consecutive array probes for either deletions or duplications, (iii) were ≥10 kb in size, and (iv) had <75% overlap with segmental duplications. We excluded CNVs likely to represent locus-specific batch effects (e.g., those with identical breakpoints that appeared in >1% of the sample). Larger CNVs that appeared to be fragmented were merged together and retained. We excluded all CNVs in the 22q11.2 deletion region and surrounding structurally complex region (2, 10), i.e., between genomic coordinates chr22:1-24,000,000 (NCBI Build 37/hg19). We also excluded all CNVs located on the sex chromosomes (11, 12).

Table S3: List of 19 gene-sets included in rare CNV gene-set enrichment analysis

Gene-set Name	Number of genes	Source
Human neuro-sets (n=7)		
Neuronal Function Union Inclusive	3,431	Gene Ontology[a]
Blue Module	2,484	Uddin M et al. 2016(13)
Neuronal Function Union Stringent	1,937	Gene Ontology[a]
Brain Specific Illumina Body Map 2.0	1,821	Description below[b]
Neuron Projection	1,720	Gene Ontology[a]
Targets of *FMR1*	927	Ascano M et al. 2012(14)[a]
Synaptic	860	Gene Ontology[a]
Mouse neuro-sets (n=3)		
Neuro Union	3,764	Mouse Genome Informatics[c,a]
Nervous System Phenotype	2,609	Mouse Genome Informatics[c,a]
Neurobehavioral Phenotype	2,602	Mouse Genome Informatics[c,a]
Mouse, other body systems / lethality (n=8)		
Hematological/Immune	2,962	Mouse Genome Informatics[c,a]
Cardiovascular/Muscle	2,327	Mouse Genome Informatics[c,a]
Endocrine/Exocrine/Reproduction	2,298	Mouse Genome Informatics[c,a]
Skeletal/Craniofacial/Limbs	2,057	Mouse Genome Informatics[c,a]
Integumentary/Adipose/Pigment	1,950	Mouse Genome Informatics[c,a]
Digestive/Hepatic	1,645	Mouse Genome Informatics[c,a]
Sensory	1,601	Mouse Genome Informatics[c,a]
Complete Lethality	1,145	Mouse Genome Informatics[c,a]
Mouse, *DGCR8*-related (n=1)		
DGCR8-related gene expression change	3,558	Stark KL et al. 2008(15)

[a]Gene-sets used in Marshall CR, Howrigan DP, Merico D, et al. Nature Genetics(15), updated to November 2016 were retrieved from gene functional databases (e.g., Gene Ontology (GO), Mouse Genome Informatics (MGI).
[b]Illumina Body Map 2.0 RNA-seq data were transformed into Rlog (x+1) scale. The log2 fold change was calculated by having the value of brain as the numerator and the average of other cell types as the denominator; genes having log2 fold change ≥ 1 were selected as brain-specific.
[c]Retrieved from http://www.informatics.jax.org/

Table S4: Additional genome-wide rare (<0.1%) CNV burden analyses in 22q11.2DS (n=329)

		Schizophrenia (n=158)		Non-Psychotic (n=171)		Analysis[b]
		n	%	n	%	p
All Rare (0.1%) CNVs	Loss or Gain	142	89.9	149	87.1	0.4921
	Exonic (loss or gain)[d]	92	58.2	90	52.6	0.3198
	Exonic Loss[d]	38	24.1	47	27.5	0.5291
	Exonic Gain[d]	68	43.0	59	34.5	0.1146
Large (>500 kb) rare (0.1%) CNVs	Loss or Gain	22	13.9	18	10.5	0.3999
	Exonic (loss or gain)[d]	16	10.1	15	8.8	0.7089
	Exonic Loss[d]	4	2.5	6	3.5	0.7521
	Exonic Gain[d]	12	7.6	9	5.3	0.4994
Rare CNV (0.1%) overlapping miRNA	Loss or Gain	16	10.1	8	4.7	0.0878
	Loss	6	3.8	3	1.8	0.3210
	Gain	10	6.3	6	3.5	0.3068
Very rare[c] CNVs	Loss or Gain	108	68.4	125	73.1	0.3957
	Exonic (loss or gain)[d]	67	42.4	65	38.0	0.4325
	Exonic Loss[d]	26	16.5	32	18.7	0.6646
	Exonic Gain[d]	47	29.7	39	22.8	0.1682

[a]Rare autosomal CNVs >10 kb and <6.5 Mb, genome-wide, outside of the 22q11.2 deletion region; see text for details
[b]Fisher's Exact Test, two-sided
[c]Very rare CNVs are defined as those that did not overlap any of the CNVs found in 9,611 population-based controls
[d]Exonic CNVs are defined as those that overlapped at least one bp of coding sequence.

Table S6: Gene overlap between significant gene-sets for rare duplication CNVs in subjects with 22q11.2DS and schizophrenia

Mouse Nervous System	Count	Mouse Neurobehavioral	Count	Mouse Neural Union	Count	Mouse Muscle/Cardio	Count	Mouse Endocrine	Count	GO Synaptic	Count
ABCA4	1			ABCA4	1						
HSD11B1	1	HSD11B1	1	HSD11B1	1			HSD11B1	1		
RYR2	1	RYR2	1	RYR2	1	RYR2	1	RYR2	1		
XRCC5	1	XRCC5	1	XRCC5	1			XRCC5	1		
GRM7	1	GRM7	1	GRM7	1					GRM7	1
SCN11A,SCN5A, SCN10A	3	SCN11A,SCN5A, SCN10A	3	SCN11A,SCN5A, SCN10A	3	SCN5A,SCN10A	2				
APOD	1	APOD	1	APOD	1	APOD	1				
DOK7	1	DOK7	1	DOK7	1	DOK7	1			DOK7	1
CCKAR	1	CCKAR	1	CCKAR	1			CCKAR	1	CCKAR	1
TLR3	1	TLR3	1	TLR3	1	TLR3	1	TLR3	1		
KHDRBS2	1			KHDRBS2	1						
PARK2	1	PARK2	1	PARK2	1	PARK2	1			PARK2	1
MLLT4	1			MLLT4	1	MLLT4	1				
ETV1	1	ETV1	1	ETV1	1	ETV1	1				
CACNA2D1	1	CACNA2D1	1	CACNA2D1	1	CACNA2D1	1				
TDRP	1			TDRP	1			TDRP	1		
DLC1	1			DLC1	1	DLC1	1				
UNC5D	1			UNC5D	1						
LYN	1			LYN	1					LYN	1
SYK	1			SYK	1	SYK	1	SYK	1		
PTEN	1	PTEN	1	PTEN	1	PTEN	1	PTEN	1	PTEN	1
PI4K2A	1	PI4K2A	1	PI4K2A	1			PI4K2A	1	PI4K2A	1
MYO7A,OMP	1	MYO7A, CAPN5	2	MYO7A,OMP,CAPN5	3	B3GNT6	1	MYO7A,B3GNT6	2	MYO7A	1
CADM1	1			CADM1	1			CADM1	1	CADM1	1
FBXW8	1	FBXW8	1	FBXW8	1	FBXW8	1				
C1QTNF9B, TNFRSF19	2	C1QTNF9B,SGCG	2	C1QTNF9B,TNFRSF19, SGCG	3	C1QTNF9B,TNFRSF19, SGCG	3	C1QTNF9B	1		
RPS6KA5	1	RPS6KA5	1	RPS6KA5	1						
CHRNA7,TRPM1	2	CHRNA7,TRPM1	2	CHRNA7,TRPM1	2			CHRNA7,KLF13	2	CHRNA7	1
CHRNA7,TRPM1	-	CHRNA7,TRPM1	-	CHRNA7,TRPM1	-			CHRNA7,KLF13	-	CHRNA7	-
CIB2	1	CIB2	1	CIB2	1	CIB2	1			CIB2	1
SPG7	1	SPG7	1	SPG7	1						
LHX1	1	GGNBP2	1	LHX1,GGNBP2	2	LHX1	1	LHX1	1		
MBP	1	MBP	1	MBP	1						
SLC23A2	1			SLC23A2	1	SLC23A2	1	SLC23A2	1		
VSX1	1			VSX1	1						

Mouse Nervous System	Count	Mouse Neurobehavioral	Count	Mouse Neural Union	Count	Mouse Muscle/Cardio	Count	Mouse Endocrine	Count	GO Synaptic	Count
DSCAM	1	DSCAM	1	DSCAM	1	DSCAM	1	DSCAM	1	DSCAM	1
ADORA2A,MIF, SMARCB1	3	ADORA2A,GGT1	2	ADORA2A,MIF, SMARCB1,GGT1	4	ADORA2A,MMP11	2	SMARCB1,GGT1	2		
		ASL	1	ASL	1	ASL	1	ASL	1		
		ROCK1	1	ROCK1	1	ROCK1	1				
		VWA8	1	VWA8	1	VWA8	1				
		ELMO1	1	ELMO1	1			ELMO1	1		
		NAT2	1	NAT2	1			NAT2	1		
		SYT10	1	SYT10	1					SYT10	1
		AHRR	1	AHRR	1						
		DNAJC15	1	DNAJC15	1						
		CRBN	1	CRBN	1						
		DGAT2	1	DGAT2	1						
		PDE4DIP	1	PDE4DIP	1						
						SLC9A3	1	SLC9A3	1		
						ARL4D	1	RANBP9	1	SLIT1	1
						ARHGAP42	1	BTRC	1		
						UVRAG	1	WDR48	1		
								BLK	1		
								IMMP2L	1		
								AGR2	1		
								THRSP	1		
								ALPPL2	1		
								ALPPL2	-		
Total unique genes	**42**		**42**		**58**		**31**		**32**		**14**

Red font indicates genes included in the Mouse Nervous System Phenotype gene-set, ordered as in Table 3 then by the number of gene-sets in which the gene appears; Count = unique genes within the gene-set, with "-" indicating a CNV overlapping the same gene(s) in another subject, thus repeated genes within a gene-set.

Table S7. Table S7. Connectivity analysis results for comparing 22q11.2 deletion region genes and schizophrenia-related duplication genes

gene_symbol	Entrez_Id	avScoresCS	empPvalueScoreCS	FDRScoreCS
P2RX6	9127	0.008496535	**0.003286148**	0.151162791
SEPT5	5413	0.003328688	**0.014282103**	0.19622093
RTN4R	65078	0.003106461	**0.015925177**	0.19622093
CLTCL1	8218	0.002875936	**0.01706269**	0.19622093
CRKL	1399	0.001201171	**0.033872599**	0.276162791
PI4KA	5297	0.001101492	**0.036021234**	0.276162791
SLC25A1	6576	0.000364188	0.06028817	0.396179402
GP1BB	2812	1.88E-05	0.154764914	0.889898256
CDC45	8318	1.37E-05	0.188195147	0.961886305
CLDN5	7122	1.07E-05	0.216822548	0.997383721
DGCR8	54487	8.04E-06	0.252022245	1
UFD1L	7353	6.31E-06	0.281850354	1
COMT	1312	5.07E-06	0.307381193	1
TRMT2A	27037	4.42E-06	0.324317492	1
TBX1	6899	3.66E-06	0.346309403	1
KLHL22	84861	2.94E-06	0.367542973	1
ZNF74	7625	1.82E-06	0.409567745	1
MRPL40	64976	1.17E-06	0.463978766	1
SCARF2	91179	1.02E-06	0.475606673	1
TSSK2	23617	7.67E-07	0.496524267	1
GNB1L	54584	7.40E-07	0.499368049	1
ZDHHC8	29801	6.13E-07	0.516936299	1
DGCR6L	85359	3.51E-07	0.565596562	1
DGCR6	8214	2.82E-07	0.584934277	1
AIFM3	150209	2.82E-07	0.586830131	1
TANGO2	128989	1.97E-07	0.596498989	1
GSC2	2928	3.13E-08	0.632520222	1
USP41	373856	9.57E-09	0.644021739	1
PRODH	5625	0	1	1
DGCR2	9993	0	1	1
DGCR14	8220	0	1	1
HIRA	7290	0	1	1
C22orf39	128977	0	1	1
TXNRD2	10587	0	1	1
ARVCF	421	0	1	1
RANBP1	5902	0	1	1
MED15	51586	0	1	1
SERPIND1	3053	0	1	1
SNAP29	9342	0	1	1
LZTR1	8216	0	1	1
THAP7	80764	0	1	1
SLC7A4	6545	0	1	1

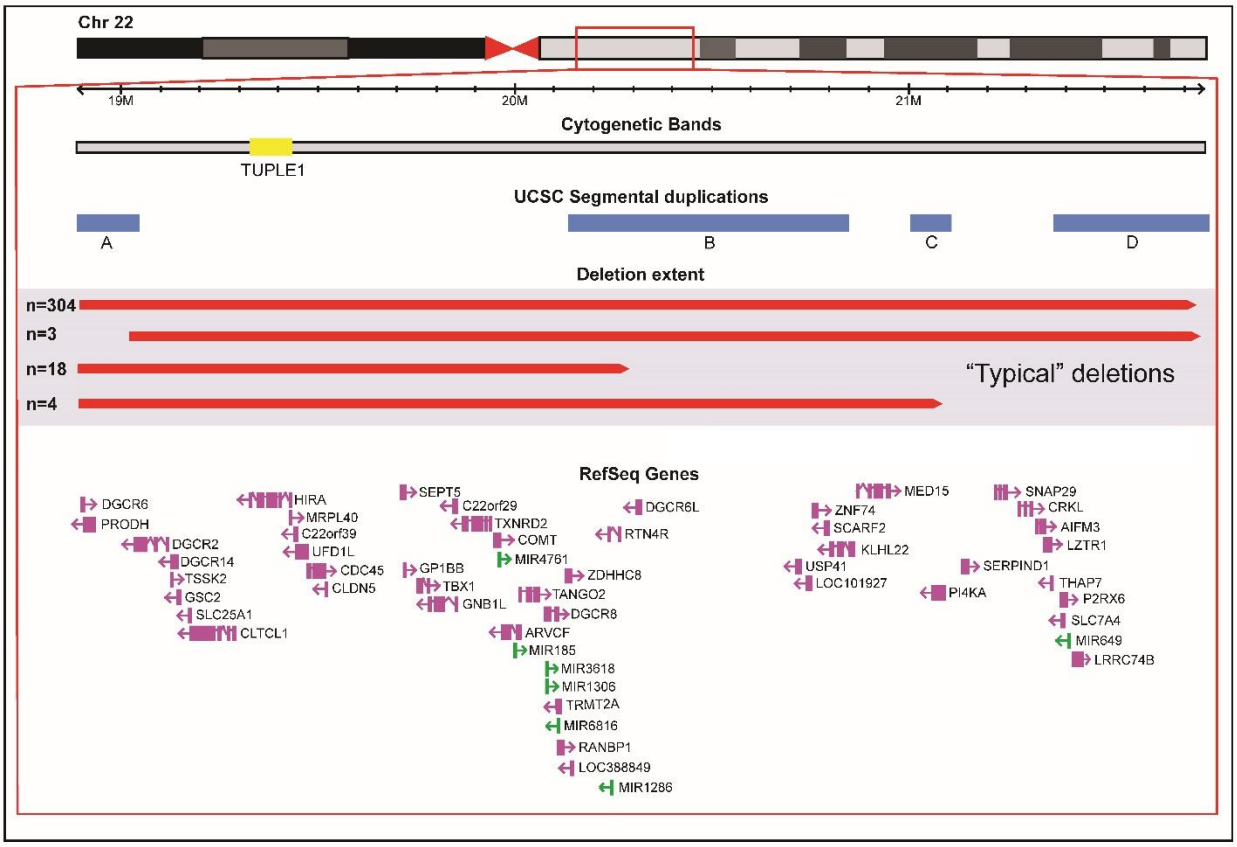

Figure S1. Rare deletions overlapping the 22q11.2 deletion region in 329 cases
The four segmental duplications (A-D) across the 22q11.2 deletion region are shown in blue. The 22q11.2 deletion coordinates estimated from heatmap data for the n=329 22q11.2DS cases included in the study are represented by red bars for 22q11.2 deletions considered "typical", see manuscript for details. All 46 protein-coding genes (pink) and seven microRNAs (green) located within the 22q11.2 deletion syndrome region are shown; 37 other non-coding genes and splice variants of the 46 protein-coding genes are not shown. The approximate position of the 22q11.2 deletion syndrome fluorescence *in situ* hybridization probe, TUPLE1, is shown in yellow along the cytogenetic band. The image was modified from the Database of Genomic variants (http://dgv.tcag.ca), NCBI Build 37 (hg 19).

REFERENCES

1. Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MA, Bender D, Maller J, Sklar P, de Bakker PI, Daly MJ, Sham PC. PLINK: a tool set for whole-genome association and population-based linkage analyses. Am J Hum Genet. 2007;81:559-575.
2. McDonald-McGinn DM, Sullivan KE, Marino B, Philip N, Swillen A, Vorstman JAS, Zackai EH, Emanuel BS, Vermeesch JR, Morrow BE, Scambler PJ, Bassett AS. 22q11.2 deletion syndrome. Nat Rev Dis Prim. 2015:15071.
3. Cotterchio M, Manno M, Klar N, McLaughlin J, Gallinger S. Colorectal screening is associated with reduced colorectal cancer risk: a case-control study within the population-based Ontario Familial Colorectal Cancer Registry. Cancer Causes Control. 2005;16:865-875.
4. Bierut LJ, Agrawal A, Bucholz KK, Doheny KF, Laurie C, Pugh E, Fisher S, Fox L, Howells W, Bertelsen S, Hinrichs AL, Almasy L, Breslau N, Culverhouse RC, Dick DM, Edenberg HJ, Foroud T, Grucza RA, Hatsukami D, Hesselbrock V, Johnson EO, Kramer J, Krueger RF, Kuperman S, Lynskey M, Mann K, Neuman RJ, Nothen MM, Nurnberger JI, Jr., Porjesz B, Ridinger M, Saccone NL, Saccone SF, Schuckit MA, Tischfield JA, Wang JC, Rietschel M, Goate AM, Rice JP, Gene EASC. A genome-wide association study of alcohol dependence. Proc Natl Acad Sci U S A. 2010;107:5082-5087.
5. Coviello AD, Haring R, Wellons M, Vaidya D, Lehtimaki T, Keildson S, Lunetta KL, He C, Fornage M, Lagou V, Mangino M, Onland-Moret NC, Chen B, Eriksson J, Garcia M, Liu YM, Koster A, Lohman K, Lyytikainen LP, Petersen AK, Prescott J, Stolk L, Vandenput L, Wood AR, Zhuang WV, Ruokonen A, Hartikainen AL, Pouta A, Bandinelli S, Biffar R, Brabant G, Cox DG, Chen Y, Cummings S, Ferrucci L, Gunter MJ, Hankinson SE, Martikainen H, Hofman A, Homuth G, Illig T, Jansson JO, Johnson AD, Karasik D, Karlsson M, Kettunen J, Kiel DP, Kraft P, Liu J, Ljunggren O, Lorentzon M, Maggio M, Markus MR, Mellstrom D, Miljkovic I, Mirel D, Nelson S, Morin Papunen L, Peeters PH, Prokopenko I, Raffel L, Reincke M, Reiner AP, Rexrode K, Rivadeneira F, Schwartz SM, Siscovick D, Soranzo N, Stockl D, Tworoger S, Uitterlinden AG, van Gils CH, Vasan RS, Wichmann HE, Zhai G, Bhasin S, Bidlingmaier M, Chanock SJ, De Vivo I, Harris TB, Hunter DJ, Kahonen M, Liu S, Ouyang P, Spector TD, van der Schouw YT, Viikari J, Wallaschofski H, McCarthy MI, Frayling TM, Murray A, Franks S, Jarvelin MR, de Jong FH, Raitakari O, Teumer A, Ohlsson C, Murabito JM, Perry JR. A genome-wide association meta-analysis of circulating sex hormone-binding globulin reveals multiple Loci implicated in sex steroid hormone regulation. PLoS Genet. 2012;8:e1002805.
6. Krawczak M, Nikolaus S, von Eberstein H, Croucher PJ, El Mokhtari NE, Schreiber S. PopGen: population-based recruitment of patients and controls for the analysis of complex genotype-phenotype relationships. Community genetics. 2006;9:55-61.
7. Stewart AF, Dandona S, Chen L, Assogba O, Belanger M, Ewart G, LaRose R, Doelle H, Williams K, Wells GA, McPherson R, Roberts R. Kinesin family member 6 variant Trp719Arg does not associate with angiographically defined coronary artery disease in the Ottawa Heart Genomics Study. J Am Coll Cardiol. 2009;53:1471-1472.
8. Bierut LJ, Madden PA, Breslau N, Johnson EO, Hatsukami D, Pomerleau OF, Swan GE, Rutter J, Bertelsen S, Fox L, Fugman D, Goate AM, Hinrichs AL, Konvicka K, Martin NG, Montgomery GW, Saccone NL, Saccone SF, Wang JC, Chase GA, Rice JP, Ballinger DG. Novel genes identified in a high-density genome wide association study for nicotine dependence. Hum Mol Genet. 2007;16:24-35.

9. Verhoeven VJ, Hysi PG, Wojciechowski R, Fan Q, Guggenheim JA, Hohn R, MacGregor S, Hewitt AW, Nag A, Cheng CY, Yonova-Doing E, Zhou X, Ikram MK, Buitendijk GH, McMahon G, Kemp JP, Pourcain BS, Simpson CL, Makela KM, Lehtimaki T, Kahonen M, Paterson AD, Hosseini SM, Wong HS, Xu L, Jonas JB, Parssinen O, Wedenoja J, Yip SP, Ho DW, Pang CP, Chen LJ, Burdon KP, Craig JE, Klein BE, Klein R, Haller T, Metspalu A, Khor CC, Tai ES, Aung T, Vithana E, Tay WT, Barathi VA, Consortium for Refractive E, Myopia, Chen P, Li R, Liao J, Zheng Y, Ong RT, Doring A, Diabetes C, Complications Trial/Epidemiology of Diabetes I, Complications Research G, Evans DM, Timpson NJ, Verkerk AJ, Meitinger T, Raitakari O, Hawthorne F, Spector TD, Karssen LC, Pirastu M, Murgia F, Ang W, Wellcome Trust Case Control C, Mishra A, Montgomery GW, Pennell CE, Cumberland PM, Cotlarciuc I, Mitchell P, Wang JJ, Schache M, Janmahasatian S, Igo RP, Jr., Lass JH, Chew E, Iyengar SK, Fuchs' Genetics Multi-Center Study G, Gorgels TG, Rudan I, Hayward C, Wright AF, Polasek O, Vatavuk Z, Wilson JF, Fleck B, Zeller T, Mirshahi A, Muller C, Uitterlinden AG, Rivadeneira F, Vingerling JR, Hofman A, Oostra BA, Amin N, Bergen AA, Teo YY, Rahi JS, Vitart V, Williams C, Baird PN, Wong TY, Oexle K, Pfeiffer N, Mackey DA, Young TL, van Duijn CM, Saw SM, Bailey-Wilson JE, Stambolian D, Klaver CC, Hammond CJ. Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. Nat Genet. 2013;45:314-318.
10. Bassett AS, Marshall CR, Lionel AC, Chow EW, Scherer SW. Copy number variations and risk for schizophrenia in 22q11.2 deletion syndrome. Hum Mol Genet. 2008;17:4045-4053.
11. Costain G, Lionel A, Merico D, Forsythe P, Russell K, Lowther C, Yuen T, Husted J, Stavropoulos D, Speevak M, Chow EW, Marshall CR, Scherer SW, Bassett AS. Pathogenic rare copy number variants in community-based schizophrenia suggest a potential role for clinical microarrays. Hum Mol Genet. 2013;22:4485-4501.
12. Silversides CK, Lionel AC, Costain G, Merico D, Migita O, Liu B, Yuen T, Rickaby J, Thiruvahindrapuram B, Marshall CR, Scherer SW, Bassett AS. Rare copy number variations in adults with tetralogy of Fallot implicate novel risk gene pathways. PLoS Genetics. 2012;8:e1002843.
13. Uddin M, Pellecchia G, Thiruvahindrapuram B, D'Abate L, Merico D, Chan A, Zarrei M, Tammimies K, Walker S, Gazzellone MJ, Nalpathamkalam T, Yuen RK, Devriendt K, Mathonnet G, Lemyre E, Nizard S, Shago M, Joseph-George AM, Noor A, Carter MT, Yoon G, Kannu P, Tihy F, Thorland EC, Marshall CR, Buchanan JA, Speevak M, Stavropoulos DJ, Scherer SW. Indexing Effects of Copy Number Variation on Genes Involved in Developmental Delay. Sci Rep. 2016;6:28663.
14. Ascano M, Jr., Mukherjee N, Bandaru P, Miller JB, Nusbaum JD, Corcoran DL, Langlois C, Munschauer M, Dewell S, Hafner M, Williams Z, Ohler U, Tuschl T. FMRP targets distinct mRNA sequence elements to regulate protein expression. Nature. 2012;492:382-386.
15. Stark KL, Xu B, Bagchi A, Lai WS, Liu H, Hsu R, Wan X, Pavlidis P, Mills AA, Karayiorgou M, Gogos JA. Altered brain microRNA biogenesis contributes to phenotypic deficits in a 22q11-deletion mouse model. Nat Genet. 2008;40:751-760.