"Large recurrent microdeletions associated with schizophrenia"

Subjects and ascertainment

Iceland

The Icelandic sample consists of 646 cases with schizophrenia and related psychoses and 32,442 controls. Patients and controls are all Icelandic and were recruited from all over Iceland. Diagnoses were assigned according to Research Diagnostic Criteria (RDC) [1] through the use of the lifetime version of the Schizophrenia and Affective Disorders Schedule (SADS-L)[2]. Of the 646 subjects, 619 were diagnosed with schizophrenia, 22 with schizoaffective disorder and five with unspecified functional psychosis.

The 32,442 Icelandic controls used for this study were recruited as a part of various genetic programs at deCODE and were not screened for psychiatric disorders. The individuals came from genetic programs in the following diseases (approximate number of participants in brackets): Abdominal Aortic Aneurism (400), Addiction (5400), Age-related Macular Degeneration (600), Alzheimer's Disease (700), Anxiety and Panic Disorder (1100), Asthma (1400), Attention Deficit Hyperactivity Disorder (500), Benign Prostatic Hyperplasia (900), Breast Cancer (1600), Chronic Obstructive Pulmonary Disease (900), Colon Cancer (1000), Coronary Artery Disease (4000), Deep Vein Thrombosis (1000), Dyslexia (700), Endometriosis (300), Enuresis (900), Obesity (800), Glaucoma (200), Hypertension (2400), Infectious Diseases (2500), Longevity

(1600), Lung Cancer (300), Melanoma (500), Migraine (1300), Osteoarthritis (2600), Osteoporosis (3000), Polycystic Ovary Syndrome (1400), Peripheral Artery Disease (1500), Preeclampsia (800), Prostate Cancer (1400), Psoriasis (900), Restless Legs Syndrome (500), Rheumatoid Arthritis (700), Stroke (1900), Essential Tremor (400), Type II Diabetes (1500), Autism (299) and a set of population controls (900). Because some of the individuals used as controls were participants in more than one program, the numbers of participants in individual programs sum to more than 32,442.

Finland

The Finnish sample consists of 191 schizophrenics and 200 regionally selected controls that had no medical history of schizophrenia. Approximately half of the sample originated from an internal isolate of Finland having a 3.0 % age corrected lifetime risk for schizophrenia compared to the 1.1% of the general population. Two independent psychiatrists blind to family structures made a consensus diagnosis to give best-estimate lifetime diagnoses according to the criteria of Diagnostic and Statistical Manual of Mental Disorders, 4th edition (DSM-IV)[3].

Scotland

The Scottish sample is comprised of 211 schizophrenia cases and 229 controls used in phase I and a replication cohort of 451 schizophrenia cases and 441 controls. All participants self-identified as born in the British Isles (95% in Scotland). All cases met DSM-IV and an ICD-10 criteria for schizophrenia. Diagnosis was made by OPCRIT. Controls were volunteers recruited through general practices in Scotland. Practice lists were screened for potentially suitable volunteers by age and sex and by exclusion of subjects with major mental illness or use of antipsychotic medication.

UK

Samples from the UK subjects (N=105) were drawn from the Maudsley Family Study of psychosis[4], the psychosis twin study[5], and the genetics and psychosis (GAP) study. All controls were unrelated European Caucasians (N=96). All patients were interviewed with the Schedule for Affective Disorders and Schizophrenia Lifetime Version (SADS-L; Endicott and Spitzer, 1978) which was supplemented with information from case notes and other relatives to assign a lifetime DSM-IV diagnosis of schizophrenia. The GAP cases were diagnosed using the Item Group Checklist (IGC) of the Schedule for Clinical Assessment in Neuropsychiatry (SCAN)[6]. Only patients with an ICD-10 research diagnosis of schizophrenia were finally included as cases. Patients were receiving a variety of antipsychotic medications at the time of assessment. The study received approval from the Ethics Committee of the South London and Maudsley Trust and after complete description of the study to the participants, written informed consent was obtained.

Italy

Diagnosis of the 85 Italian subjects was identical to that for the GAP sample (See UK subjects). Patients with a diagnosis of psychotic disorders (ICD-10, F20-F25) attending the South Verona CMHS were identified from the South Verona Psychiatric Case Register, and cases with ICD-10 research diagnosis of schizophrenia were finally included. The controls (N=91) were unrelated volunteers randomly selected from the general population of South Verona. The study received ethical approval and after complete description of the study to the participants, written informed consent was obtained.

Germany - Munich

The Munich sample consisted of 615 cases and 614 controls, all Caucasian. Cases diagnosed with DSM-IV schizophrenia were ascertained from the Munich area in Germany. Samples from 195 cases and 192 controls were typed for phase I and the remaining samples used in the replication phase. Detailed medical and psychiatric histories were collected, including a clinical interview using the Structured Clinical Interview for Axis I DSM-IV Disorders (SCID)[7]. Exclusion criteria included a history of head injury or neurological diseases. The controls were unrelated volunteers randomly selected from the general population of Munich.

Germany - Bonn

The Bonn sample is comprised of 491 patients and 875 controls. Patients were recruited from consecutive hospital admissions and were all of German descent. In patients, lifetime best estimate diagnoses according to DSM-IV criteria were based on multiple sources of information including structured interview with the SCID[7] or SADS-L (Endicott and Spitzer, 1978), the OPCRIT[8], medical records, and the family history. Best estimate diagnoses were obtained from at least two experienced psychiatrists/psychologists. Controls were derived from two German population-based cohorts, PopGen (N=492) and Heinz Nixdorf Recall (N=383). Ethical approval was obtained from the local Ethics Committees. All participants gave written informed consent.

The Netherlands – Utrecht/ Nijmegen

The Dutch sample consisted of 806 patients and 706 controls from Utrecht and on additional 3,333 control individuals from Nijmegen in the Netherlands. Inpatients and outpatients were recruited from different psychiatric hospitals and institutions

throughout the Netherlands, coordinated via academic hospitals in Amsterdam, Groningen, Maastricht and Utrecht. Detailed medical and psychiatric histories were collected, including the Comprehensive Assessment of Symptoms and History (CASH), an instrument for assessing diagnosis and psychopathology. To exclude related patients and controls, all subjects were fingerprinted (Illumina DNA panel, 400 SNPs). Only patients with a DSM-IV diagnosis of schizophrenia were included as cases. All patients and controls were of Dutch descent, with at least three out of four grandparents of Dutch ancestry. The controls were volunteers and were free of any psychiatric history. Ethical approval was obtained from the local Ethics Committees. All participants gave written informed consent.

The additional controls consisted of 3,333 samples, collected by the Radboud University Nijmegen Medical Centre (RUNMC) for genetic studies (cancer and control samples). All 3,333 participants used in the present study are of self-reported European descent. The study protocol was approved by the Institutional Review Board of Radboud University and all study subjects gave written informed consent.

Denmark

The Danish sample included 442 patients who have been recruited to Danish Psychiatric Biobank from the psychiatric departments at the six hospitals in the Copenhagen region. All patients had been clinically diagnosed with schizophrenia according to ICD-10 (F20 and F25) without ever having received a diagnosis of mania or bipolar illness (F30-31). An experienced research- and consultant psychiatrist verified high reliability of the clinical diagnoses, using OPCRIT. Of the 442 patients 30 were schizoaffective and six were diagnosed with persistent delusional disorder. Nine hundred ninety four healthy control subjects were recruited through the Danish Blood Donor Corps in the Copenhagen area. Apparent behavioral abnormality was an exclusion criterion and all

individuals stated that they felt completely healthy and were able to discuss health related issues with a physician. An additional 445 population control samples from the Copenhagen area were recruited by the Danish Headache Center. The Danish Scientific Committees and the Danish Data Protection Agency approved the study and all the patients had given written informed consent prior to inclusion into the project.

Norway

The Norwegian sample included 237 patients who had been recruited to the TOP study from all the psychiatric hospitals in the Oslo area. The patients were diagnosed according to Structural Clinical Interview for DSM-IV (SCID) as schizophrenia (N=153) schizoaffective (N=34), schizophreniform disorder (N=10), psychosis NOS (N=44) and delusional disorder (N=6). The healthy control subjects (N=272) were randomly selected from statistical records of persons from the same catchment area as the patient groups. Only subjects born in Norway, all of Caucasian origin, were contacted by letter and invited to participate. All subjects have given written informed consent prior to inclusion into the project and the Norwegian Scientific-Ethical Committee and the Norwegian Data Protection Agency approved the study.

China

The Chinese sample was from Sichuan Province, Southwest China. Cases (N=438) were ascertained from West China Hospital, and were interviewed by a psychiatrist using the SCID. Diagnosis of schizophrenia was assigned on the basis of the interview and medical records according to DSM-IV criteria. Patients were excluded if they had a history of neurological disorders or head injury, or reported intellectual disability. The unrelated controls (N=463) were volunteers from the local population and were free of

major mental illness. Ethical approval for the project was granted by West China Hospital and written informed consent was obtained from all participants.

The phase I samples were all typed at deCODE using the HumanHap300 chip. The additional samples (phase II) were typed at Duke University (HumanHap300 or HumanHap550), Bonn University (HumanHap550), UCLA (HumanHap550) and Expression Analysis, Durham (Affymetrix GeneChip(r) GenomeWide SNP 6.0 array) and at deCODE (Dosage analysis, Taqman assays). All subjects identified with a CNV using the Taqman assays were confirmed by typing the respective samples on HumanCNV370 chip. A summary of the samples used in the various stages of the study can be found in Supplementary Table 1.

Supplementary Table 1. Summary of the samples used in the various stages of the study

Site	CNV identification		Phase I		Phase II	
	Aff	Ctrl	Aff	Ctrl	Aff	Ctrl
Iceland	-	17596	646	32442	-	-
Scotland	-	-	211	229	451	441
Germany (Munich)	-	-	195	192	420	422
Germany (Bonn)	-	-	-	-	491	875
UK	-	-	105	96	-	-
The Netherlands	-	-	-	-	806	4039
Italy	-	-	85	91	-	-
Finland	-	-	191	200	-	-
Denmark	-	-	-	-	442	1439
Norway	-	-	-	-	237	272
China	-	-	-	-	438	463

For the CNV identification stage, Icelandic trios and parent-offspring pairs, all unaffected with schizophrenia, were used. Phase I included affected and control samples from six research groups - Iceland, Germany (Munich), UK, Italy and Finland. For phase II, additional samples from two sites of the previous six - Scotland and Germany (Munich) – were included (no overlap) as well as data from five additional groups – Germany (Bonn), The Netherlands, Denmark, Norway and China. The Icelandic trios and parent-offspring pairs used for CNV identification were included in the Icelandic controls used in phase I. There were no duplicate samples in the combined phase I and phase II set.

Fluorescent in situ hybridization (FISH)

FISH was carried out at deCODE genetics. Interphases were harvested according to standard cytogenetic methods from human B-lymphoblastoid cell lines (EBV transformed) from six individuals, based on information from the Taqman dosage analysis done previously. We used two BAC probes, RP11-431G14 (covers PRK gene on chromosome 1q21) labelled with biotin (green) and an anchor BAC, RP11-458I7 labelled with digoxigenin (red). The BAC probes were labelled with either Biotin-16-dUTP or Digoxigenin-11-dUTP utilizing a nick translation kit (Roche Applied Science).

The hybridization procedure followed a standard protocol. In short, the probes were denatured at 72°C for 5 minutes and pre-annealed at 37°C for 15 minutes, before being applied to denatured slides. The slides were denatured in 70% formamide at 70°C for 2 minutes, quenched in 2xSSC at 4°C and then dehydrated in an ethanol series. Following an overnight hybridization the slides were washed in 50% formamide at 42°C for 10 minutes and 2xSSC at 42°C for 5 minutes. The biotinylated probe was detected with avidin/streptavidin FITC (Vector Lab) followed by a layer of biotinylated Anti Avidin (Vector Lab) and again one layer of avidin FITC was added. The digoxigenin probe was detected using Sheep anti Digoxigenin Rhodamine (Roche Applied science) followed by a layer of Donkey anti Sheep Texas red (Jackson Immuno Research). After detection the interphases were counter-stained with $9x10^{-3}$µg 4',6-Diamidino-2-phenylindole Dihydrochloride:Hydrate (DAPI) (Sigma) in AF1 mounting medium (Citifluor). The digital imaging was done using a Zeiss Axioplan 2 microscope with Asiocam MRm Zeiss camera and automatic Scanning System Metafer software from Metasystems.

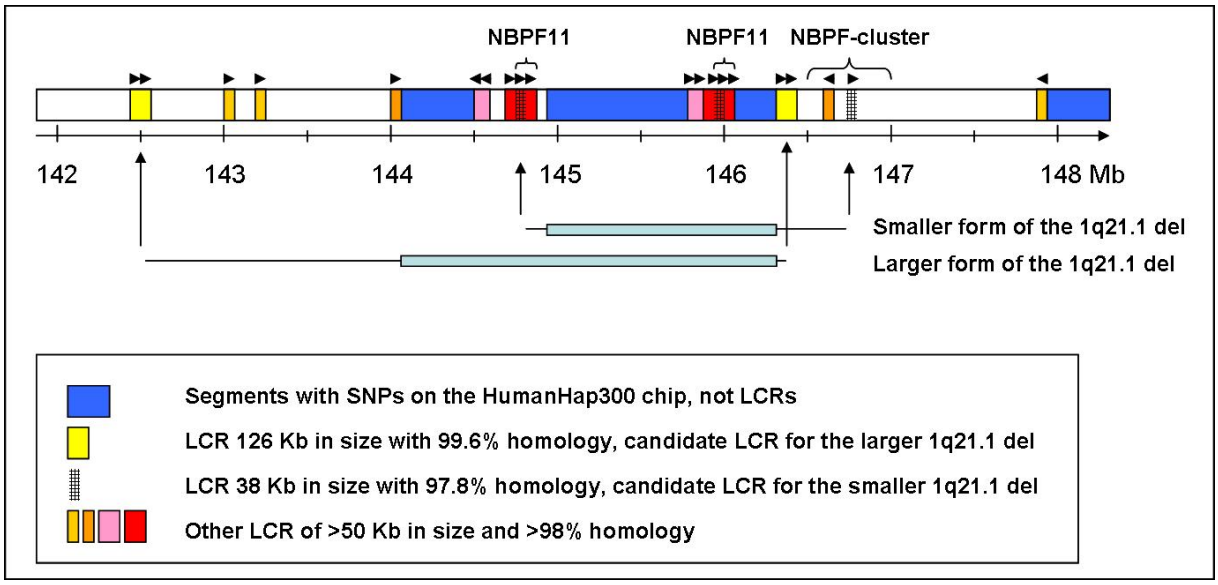
Inheritance of the 1q21.1, 15q11.2 and 15q13.3 deletions in Iceland – evidence for negative selection

Apart from association to schizophrenia, the deletions at 1q21.1, 15q11.2 and 15q13.3 also otherwise exhibited a pattern of negative selection. In the 33,088 Icelanders (646 schizophrenia patients and 32,442 controls) who are CNV typed, nine carry the deletion on 1q21.1, 62 carry the deletion on 15q11.2 and eight carry the deletion on 15q13.3. But not all of these cases resulted from 'first-generation' *de novo* events, i.e. some cases inherited the deletions from their parents. Specifically, by examining the haplotype (sequence of SNPs) background of the deletions and the known familial relationship between the carriers, we deduced that the nine 1q21.1 deletions correspond to six independent mutation/deletion events, the eight 15q13.3 deletions correspond to six independent mutation/deletion events and the 62 15q11.2 deletions correspond to approximately 32 separate events (it is noted that the 15q11.2 deletions in the four Icelandic schizophrenia cases correspond to four separate events, which are shared by a few of the controls). Two conclusions could be drawn from these observations. Firstly, carriers of these deletions are not infertile and, moreover, can pass on the deletion to their children. However, the probability that the carriers pass on the deletion to a child appears to be substantially lower than that under a model of neutrality and fecundity of carriers therefore reduced. All three deletions, particularly the 15q11.2, occurred rather frequently as a *de novo* event. Assuming that the deletions do not repair themselves (or only do so with very low probability) during successive meioses, being neutral, the deletions would be expected to have a much higher frequency in the population than observed. Consider the 15q11.2 deletion. When we study the carriers pair-wise, we find that if two carriers are separated by six meioses (second cousins) or less, their deletions are very likely to result from the same deletion event. For example, if two cousins both carry the deletion, they probably both inherited it from a common grandparent who is also a carrier. However, for two carriers that are separated by more

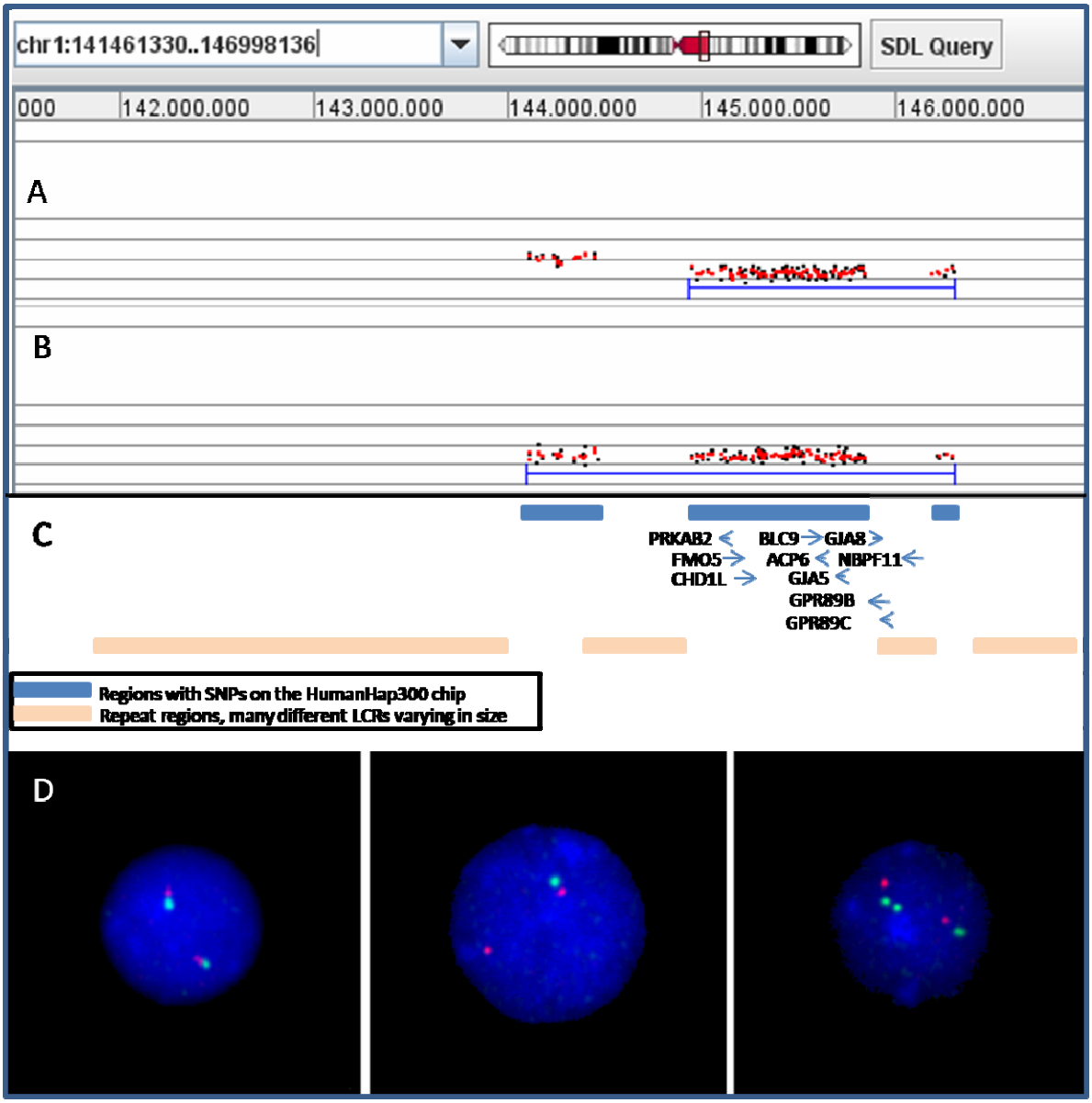
than six meioses, it is nearly always that the deletions they carry are results from two separate deletion events. This implies that the deletions that we observe in carriers, if not first generation *de novo*, would only go back a few generations. If we assume that each deletion carried could be traced back on average five generations, the 62 carriers observed out of 33,088 would correspond to an estimated mutation/deletion rate of 62/(5 x 33088 x 2) (notice that the factor 2 comes in because a person carries two chromosomes), or about 1.9 events in 10,000. This is slightly higher, but not inconsistent, with the 1 in 9878 transmissions that we directly observed. Suppose we assume a mutation rate of 1 in 10,000. Notice that the chromosome a person carried would include all mutations that happened in its history. Even if we consider only the past 30 meioses (or tracing back to about 900 years ago), under a neutral model, the carrier frequency of 15q11.2 in the population would be expected to be around 30 x (1/10,000) x 2 = 0.006, or about 198 carriers in 33088 individuals examined. This is substantially higher than the 62 carriers we actually observed.

We emphasize that the analysis described above is only meant to be descriptive. More rigorous investigation is needed to fully understand the selection pressure on the 1q21.1, 15q11.2 and 15q13.3 deletions. Given that the deletions are associated with schizophrenia patients, who are known to have fewer children than the general population, a pattern of negative selection might be expected. However, further negative selection pressure could result from reduced fecundity of carriers due to other phenotypes, and also transmission disequilibrium from carrier to child, i.e. the normal chromosome has a higher probability to be passed on than the chromosome with the deletion.

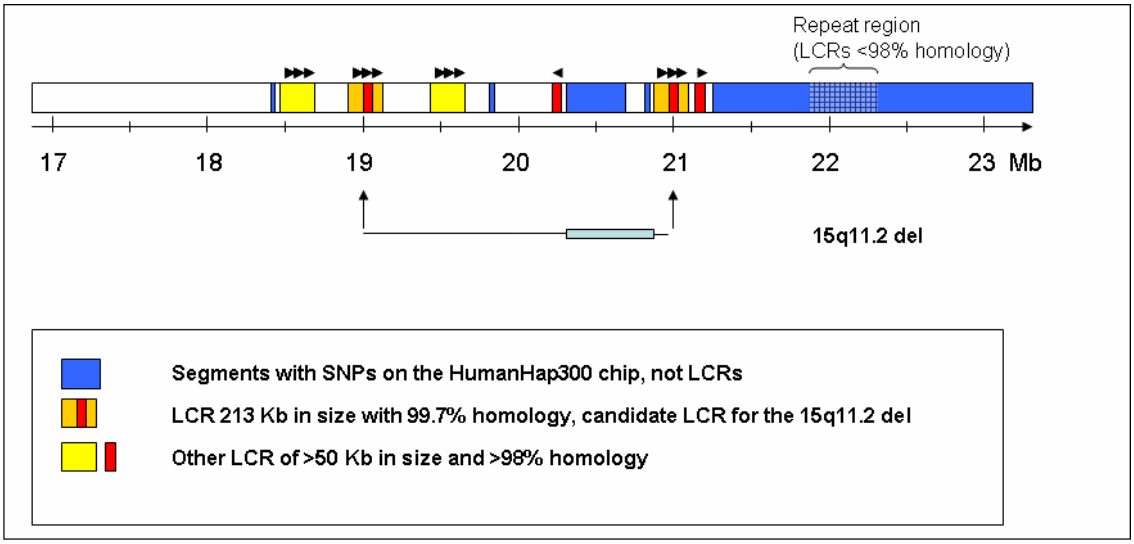
Supplementary Figures



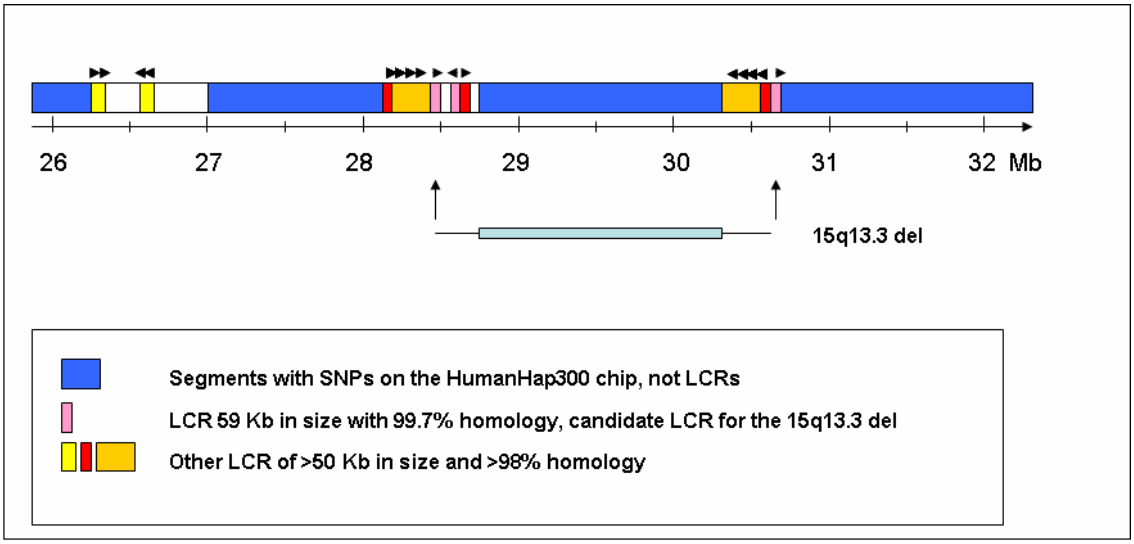
Supplementary Figure 1. Genomic architecture of the 1q21.1 deletions. Many large LCR with high homology are found at the 1q21.1 locus. LCR marked yellow (large arrows) on the picture may mediate NAHR accounting for the larger form of the 1q21.1 deletion. There are also many smaller repeats, 1,000-10,000 bp (not shown on the figure) that potentially could mediate the formation of the deletion. A smaller repeat marked in gray in the figure (smaller arrows) may assist NAHR, accounting for the smaller form of the deletion. Again, for this form of the deletion there are other smaller LCR that potentially could assist with the formation of the deletion (not shown on the figure). The NBPF11 protein (hypothetical protein LOC200030) is duplicated with high sequence homology.Segments marked in blue represent region containing SNPs on the Illumina HumanHap300 chip. Note that there are no SNPs on 1q on the Illumina HumanHap300 chip centromeric to the larger form of the 1q21.1 deletion. Thus, exact size of the larger form of the deletion is not known, the minimum size is 2.19 Mb. Markers on the p-arm are not deleted in the four cases or the control with the larger form of the 1q21.1 deletion.



Supplementary Figure 2. A) DosageMiner output showing the shorter form of the 1q21 deletion (marked in blue). Ninety-nine SNPs on the HumanHap300 chip are affected by the deletion which spans 1.38 Mb. B) DosageMiner output showing the larger form of the 1q21.1 deletion (marked in blue). C) Shows affected genes by both deletions (Coordinates are based on Build 36 of the human genome and positions of genes derived from the UCSC genome browser). LCR flank both deletions (**Supplementary Figure 1**). D) Analysis of the 1q21.1 deletion with fluorescence in situ hybridization (FISH). Two BAC probes, RP11-431G14 (cover the *PRK* gene on chromosome 1q21) labeled with biotin (green) and an anchor BAC, RP11-458I7 labeled with digoxigenin (red) were used as probes for FISH analysis. A cell from a normal control (left) in interphase shows normal FISH signals, one red probe and one green probe per chromosome. A cell from a schizophrenia patient (center) with the 1q21.1 deletion shows aberrant FISH signal, the green signal is missing for one of the chromosomes. A cell from a schizophrenia patient with the 1q21.1 region duplicated (right), two green signals are seen for one of the two chromosomes.



Supplementary Figure 3. A) LCRs flanking the deletion at 15q11.2. Several LCR at this locus can mediate the formation of the deletion. The light blue bar shows the minimum size of the deletion, and vertical arrows point to the regions with longest homologous sequences on both sides of the deletion, harbouring possible breakpoints. Coordinates are in line with Build 36 of the human genome.



Supplementary Figure 4. A) LCRs flanking the deletion at 15q13.3 It is not clear which LCR might mediating the formation of the recurrent deletion. Light blue bar shows the minimum size of the deletion, and vertical arrows point to the only high homology sequence with same orientation on both sides of the deletion in the UCSC human genome reference sequence. Coordinates are in line with Build 36 of the human genome.

Supplementary Table 2. Low copy repeats flanking *de novo* CNVs.

Build 36	CNV	Carriers found in Phase I	Number of flanking LCRs		homology	Reference if present in CNV databases
			Distal	Proximal		
chr1:144943150..146293282	del	8	>5	>5	many	
chr1:144943150..146293282	dup	12	>5	>5	many	
chr1:241675290..241777030	del	1	-	>5	many	
chr1:66487172..66981676	del	2	-	-		
chr2:19443..11594900	dup	1	-	-		
chr2:197605805..204072966	dup	1	-	-		
chr2:198783049..199060613	del	1	-	-		
chr2:239980943..242692820	del	1	-	1	99.30%	
chr2:50947040..51164471	del	1	-	-		
chr2:95514686..97033113	del	1	>5	-	many	
chr3:174806420..176937369	del	1	-	-		
chr3:197326041..197704191	del	1	>5	>5	many	Iafrate/Tuzun:196918333-198862488
chr3:71223511..71819797	dup	1	-	-		
chr3:95019980..99373057	del	1	-	-		
chr3:97879021..101883423	del	1	-	-		
chr4:151856718..151884547	del	4	-	-		
chr5:34603067..34668956	del	1	>5	-	many	
chr5:58116787..72845587	del	1	-	-		
chr6:162767020..162943840	del	35	-	-		Redon: 162760913-163153251
chr6:16699739..16803452	del	1	-	-		
chr7:146077700..147445123	del	1	4	-	98%	
chr7:149081..295765	del	1	-	-		Redon: 106472-298664
chr7:15609872..16251148	dup	1	-	-		
chr7:157553706..158812247	del	1	-	-		
chr7:5050267..5190933	del	1	-	2	99.1%	
chr7:5229720..5653268	dup	1	-	2	99.1%	Iafrate: 5431460-5671684
chr7:57212608..57659300	dup	74	>5	>5	many	
chr7:72388281..73777987	del	1	>5	>5	many	
chr7:83887393..85199723	del	1	-	-		
chr8:3931576..4252805	del	1	2	-	98.7	Iafrate:3586932-5909600 & 3611006-4928252 & 3671288-5942813
chr9:194201..5739305	del	1	>5	-		
chr10:67880428..68013385	del	1	-	-		
chr10:7917790..8021528	del	2	-	-		
chr10:81567594..81962366	del	3	>5	>5	many	
chr11:128201807..134435899	del	1	-	-		
chr11:84603291..85465999	dup	1	-	-		
chr12:115338506..115813464	dup	1	-	-		
chr12:98512325..98707024	del	1	-	-		
chr15:20306549..20777695	del	58	>5	>5	many	Redon/Iafrate: 18263733-21365850 & Iafrate:18403666-21241985
chr15:20306549..20777695	dup	128	>5	>5	many	Redon/Iafrate: 18263733-21365850 & Iafrate:18403666-21241985

chr15:20306549..26208861	dup	6	>5	>5	many	
chr15:28723577..30302218	del	7	>5	>5	many	
chr15:47635303..47679448	del	94	-	-		
chr16:15032942..16197033	del	10	>5	>5	many	
chr16:21515973..21647775	del	31	>5	>5	many	Iafrate:21241957-21833734 & Tuzun:21485317-22595351 & 21500522-22586272 & Redon:21212773-21856623
chr16:21856623..22331199	del	17	>5	>5	many	Tuzun:21485317-22595351 & 21500522-22586272
chr16:29563365..30085308	del	11	>5	>5	many	
chr16:77757915..78273834	del	1	-	-		
chr16:81429793..81491808	del	1	-	-		
chr16:86921984..87097884	del	1	-	-		Redon: 86986674-87137417
chr17:14041754..15390352	del	5	2	>5	many	
chr17:15390352..20231611	del	1	>5	>5	many	
chr17:31889664..33323543	dup	11	>5	>5	many	
chr17:796976..1155912	del	1	2	4	many	
chr17:9071043..9382978	del	1	-	-		
chr18:75020837..75408356	dup	1	-	-		
chr19:20844764..20914290	dup	6	2	1	98%	
chr19:267040..1822341	del	1	-	-		
chr19:54264641..54560863	del	1	>5	>5	many	
chr20:14610721..14884935	del	1	-	-		
chr20:14849776..15034277	del	22	-	-		
chr20:14874333..15174767	del	5	-	-		
chr21:34846103..35391627	dup	1	-	-		
chr22:17257787..17373128	del	56	>5	>5	many	Iafrate: 16931796-17441713 & 17011366-17417535
chr22:19063495..19792353	del	3	>5	>5	many	
chr22:21063401..21394287	del	3	>5	>5	many	McCarroll: 21032391-21564096 & Iafrate: 20487965-21442582 & 20759608-21442582 & 21032391-21564096

Of the 66 identified CNVs tested for association 23 are flanked by large repetitive segments (distal or proximal) likely to harbor LCRs. Those flanked by repetitive segments are in most cases seen in more of the 32,442 controls tested. Reference is given where we have found the CNV in a CNV database. Coordinates are based on Build 36 of the human genome.
Iafrate: BAC microarray analysis of 236 putative CNP regions in 55 individuals[9].
Tuzun: Fosmid mapping paired-end sequences from a human fosmid DNA library (297 ISV sites)[10]. Redon: SNP and BAC microarray analysis of HapMap data phase II (270 Individuals)[11].
Locke: CNP in duplication-rich regions using array CGH in the HapMap populations(269 individuals)[12]. McCarroll: Deletions from analysis of SNP genotypes, using the HapMap Phase I data, release 16a. (269 individuals)[13].

Supplementary Table 3

		Boundaries of CNV		Iceland		Scotland		Germany		UK		Italy		Finland		Combined	
Build36		First SNP	Last SNP	Aff (N=648)	Ctrl (N=32442)	Aff (N=211)	Ctrl (N=229)	Aff (N=195)	Ctrl (N=192)	Aff (N=108)	Ctrl (N=92)	Aff (N=85)	Ctrl (N=91)	Aff (N=191)	Ctrl (N=200)	OR	P-value
chr1:144943150..146293282	del	rs6656361	rs2932454	**1**	**8**	**2**	0	**1**	0	0	0	0	0	0	0	**8.7 (1.0-50)**	**0.02**
chr1:144943150..146293282	dupl	rs6656361	rs2932454	**1**	**12**	0	0	0	0	0	0	0	0	0	**1**	**na.**	**ns.**
chr1:241675290..241777030	del	rs6702982	rs1121276	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr1:66487172..66981676	del	rs6664618	rs604737	0	**2**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr10:67880428..68013385	del	rs1911314	rs2631221	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr10:7917790..8021528	del	rs1244502	rs187821	0	**2**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr10:81567594..81962366	del	rs10885307	rs3000954	0	**3**	0	0	0	0	0	0	0	**1**	0	0	na.	na.
chr11:128201807..134435899	del	rs588407	rs4540845	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr11:84603291..85465999	dupl	rs938727	rs541458	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr12:115338506..115813464	dupl	rs1732325	rs4767470	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr12:98512325..98707024	del	rs3851626	rs11110041	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr15:20306549..20777695	del	rs8040193	rs3883043	**4**	**58**	**2**	0	**3**	0	0	**1**	0	0	0	**1**	**3.2 (1.1-8.0)**	**0.02**
chr15:20306549..20777695	dupl	rs8040193	rs3883043	**2**	**128**	0	0	**1**	**2**	0	0	0	0	**1**	0	**na.**	**ns.**
chr15:20306549..26208861	dupl	rs8040193	rs1635168	0	**6**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr15:28723577..30302218	del	rs2046362	rs4779984	**1**	**7**	**1**	0	**1**	0	0	0	0	0	0	0	**8.9 (0.8-58)**	**0.04**
chr15:47635303..47679448	del	rs1588127	rs7176306	0	**94**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr16:15032942..16197033	del	rs4985124	rs8056397	0	**10**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr16:15032942..16197033	del	rs4985124	rs8056397	0	**10**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr16:21515973..21647775	del	rs194548	rs8050407	**1**	**31**	0	0	0	0	0	0	0	0	0	0	**na.**	**ns.**
chr16:21515973..21647775	del	rs194548	rs8050407	**1**	**31**	0	0	0	0	0	0	0	0	0	0	**na.**	**ns.**
chr16:21856623..22331199	del	rs7498705	rs12446433	0	**17**	0	0	0	0	0	0	0	0	**1**	0	**na.**	**ns.**
chr16:29563365..30085308	del	rs8054172	rs7202714	**1**	**11**	0	0	**1**	0	0	0	0	0	0	0	**na.**	**ns.**
chr16:29563365..30085308	del	rs8054172	rs7202714	**1**	**11**	0	0	**1**	0	0	0	0	0	0	0	**na.**	**ns.**
chr16:77757915..78273834	del	rs11150140	rs7186420	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr16:81429793..81491808	del	rs9934411	rs11150519	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr16:86921984..87097884	del	rs7500421	rs868874	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr17:14041754..15390352	del	rs2856177	rs2938171	0	**5**	0	0	**1**	0	0	0	**1**	0	0	0	**na.**	**ns.**
chr17:15390352..20231611	del	rs2938171	rs9909852	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr17:31889664..33323543	dupl	rs8067765	rs306801	0	**11**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr17:796976..1155912	del	rs4968132	rs12936071	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.

chr17:9071043..9382978	del	rs3785991	rs4239107	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr18:75020837..75408356	dupl	rs9954753	rs383068	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr19:20844764..20914290	dupl	rs1465430	rs10500214	0	**6**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr19:267040..1822341	del	rs7256434	rs4807156	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr19:54264641..54560863	del	rs3810185	rs2303759	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr2:19443..11594900	dupl	rs4637157	rs6758730	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr2:197605805..204072966	dupl	rs13426748	rs2247380	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr2:198783049..199060613	del	rs10170042	rs4413156	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr2:239980943..242692820	del	rs870790	rs12469535	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr2:50947040..51164471	del	rs11884918	rs11896803	0	**1**	0	0	0	0	0	0	0	0	0	**1**	na.	na.
chr2:95514686..97033113	del	rs10201845	rs1256991	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr20:14610721..14884935	del	rs1932954	rs2423873	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr20:14849776..15034277	del	rs2423846	rs431587	0	**22**	0	0	0	0	0	0	0	**1**	0	0	na.	na.
chr20:14849776..15034277	del	rs2423846	rs431587	0	**22**	0	0	0	0	0	0	0	**1**	0	0	na.	na.
chr20:14874333..15174767	del	rs173293	rs6043152	0	**5**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr21:34846103..35391627	dupl	rs2247891	rs1006293	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr22:17257787..17373128	del	rs2543958	rs5993463	**1**	**56**	0	0	0	0	0	0	0	0	0	0	**na.**	**ns.**
chr22:19063495..19792353	del	rs6003971	rs140392	0	**3**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr22:21063401..21394287	del	rs6519260	rs5996362	0	**3**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr3:174806420..176937369	del	rs10513715	rs9858278	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr3:197326041..197704191	del	rs7432894	rs9858020	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr3:71223511..71819797	dupl	rs11128206	rs3796226	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr3:95019980..99373057	del	rs9681884	rs10935259	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr3:97879021..101883423	del	rs1386678	rs1143781	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr4:151856718..151884547	del	rs6535746	rs1451634	0	**4**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr5:34603067..34668956	del	rs7736168	rs408815	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr5:58116787..72845587	del	rs446155	rs2914544	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr6:162767020..162943840	del	rs9456777	rs7756486	0	**35**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr6:16699739..16803452	del	rs236981	rs3812199	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr7:146077700..147445123	del	rs6956550	rs1859539	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr7:149081..295765	del	rs7806592	rs12718123	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr7:15609872..16251148	dupl	rs6946852	rs1295164	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr7:157553706..158812247	del	rs10949695	rs1124425	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr7:5050267..5190933	del	rs7458161	rs6955907	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr7:5229720..5653268	dupl	rs13223581	rs7780518	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.

chr7:57212608..57659300	dupl	rs13240443	rs4870626	0	**74**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr7:72388281..73777987	del	rs1178970	rs810364	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr7:83887393..85199723	del	rs1228960	rs1533029	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr8:3931576..4252805	del	rs10503233	rs10089026	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.
chr9:194201..5739305	del	rs10964134	rs4742122	0	**1**	0	0	0	0	0	0	0	0	0	0	na.	na.

Four deletions, three on 16p and one on 20p, are observed twice *de novo* in our discovery sample, and listed in the table as duplicates. Locations are based on Build 36 of the human genome.

Supplementary Table 4. Diagnosis, family history, age of onset, response to neuroleptics (based on available records) and learning ability in cases carrying the 1q21.1 deletion associating with schizophrenia.

Case ID	Diagnosis	Family history	Age of onset	Gender	Response	Other
Munich 1	DSMIV:295.3	Yes	24	M	Yes	Aggressive, learning disability, not MR
Bonn 1*	DSMIV:295.3	No	33	F	Yes	Not MR
Bonn 2	DSMIV:295.3	No	16	F	Relapse	Not MR, depressive symptoms
Iceland 1	RDC:126.3	No	26	F	Yes	Not MR
Scotland 1	DSMIV:295	No	43	F	Yes	Not MR
Scotland 2*	DSMIV:295	Yes	21	M	Yes	Not MR
Scotland 3*	DSMIV:295	No	32	M	Yes	Not MR, mother with low IQ
Scotland 4*	DSMIV:295	No	33	F	Yes	Not MR, borderline learning disability
Denmark 1	DSMIV: 295	Yes	24	F	Yes	Not MR
Denmark 2	DSMIV: 295	No	23	M	Yes	Borderline mental retardation
Denmark 3	ICD10: Scz (F20)	No	20	M	No	Not MR

* There are two forms of the 1q21.1 deletion, long and short. Those marked with an asterisk in the table above have the larger form. MR=mentally retarded.

Supplementary Table 5. Diagnosis, family history, age of onset, response to neuroleptics based on available records and learning ability in cases carrying the 15q11.2 deletion associating with schizophrenia and related psychoses.

Case ID	Diagnosis	Family history	Age of onset	Gender	Response	Other
Munich 1	DSMIV: 295	Monozygotic twin brother with unknown psychiatric diagnosis	24	M	Yes	Not MR, very aggressive as child
Munich 2	DSMIV: 295	No	25	F	Yes	Not MR
Munich 3	DSMIV: 295	Mother depression	32	M	Yes	Not MR
Munich 4	DSMIV: 295	No	17	M	Yes	Not MR
Munich 5	DSMIV: 295	No	23	F	Yes	Not MR
Bonn 1	.	.	.	M	.	Not MR
Iceland 1	.	No	39	M	Yes	Not MR
Iceland 2	.	No	29	F	Yes	Not MR
Iceland 3	RDC: 126.3	Yes, schizophrenia	33	M	Yes	Not MR
Iceland 4	RDC: 126	Yes, schizophrenia	16	F	Yes	Not MR
Scotland 1	DSMIV: 295	No	37	F	Yes	Not MR, borderline learning difficulties
Scotland 2	DSMIV: 295		23	F	Yes	Not MR
Scotland 3	DSMIV: 295	.	32	F	Yes	Not MR
Scotland 4	DSMIV: 295	No	22	M	Yes	Not MR
Scotland 5	DSMIV: 295	No	31	F	Yes	Not MR, nervous breakdown at 22
Scotland 6	DSMIV: 295	No	15	M	Yes	Not MR, heroin addiction
Scotland 7	.	Yes, schizophrenia	24	F	.	
England 1	.	Yes, schizophrenia (co-twin)	25	M	Yes	Not MR, no drug abuse, primarily negative symptoms
Denmark 1	ICD10: F20	No	26	M	No	Not MR
Denmark 2	ICD10: F20	No	27	M	.	Not MR
Denmark 3	ICD10: F20	No	21	M	.	Not MR , cannabis abuse
Denmark 4	ICD10: F25	Yes	16	M	Yes	Not MR
Holland 1	DSMIV: 295.30	.	19	F	.	Not MR

Holland 2	DSMIV: 295.30	No	20	M	.	Not MR
Holland 3	DSMIV: 295.30	No	20	M	.	Not MR
Holland 4	DSMIV: 295.30	.	22	M	.	Not MR

MR=mentally retarded.

Supplementary Table 6. Diagnosis, family history, age of onset, response to neuroleptics based on available records and learning ability in cases carrying the 15q13.3 deletion associating with schizophrenia.

Case ID	Diagnosis	Family history	Age of onset	Gender	Response	Other
Munich 1	DSMIV: 295	Yes	24	M	Yes	Not MR
Iceland 1	.	Yes	30	M	Yes	Not MR
Scotland 1	DSMIV: 295	.	20	M	Yes	Not MR , IQ 83
Norway 1	DSMIV: 295.4	.	31	F	Yes	Not MR
Holland 1	DSMIV: 295.20	.	23	M	.	Not MR
Holland 2	DSMIV: 295.30	Yes	39	F	.	Not MR
Holland 3	DSMIV: 295.30	.	.	M	.	Not MR

MR=mentally retarded.

Supplementary Table 7. Allelic association results for markers on the Illumina HumanHap300 within the 1q21.1 deletion.

Marker	Allele	OR	P-value	chr	Location (bp)	Gene
rs12406844	C	1.14	0.0010	1	145436035	
rs12141187	C	1.13	0.0023	1	145449387	
rs10465885	C	1.12	0.0033	1	145699364	GJA5
rs6684174	C	1.11	0.0067	1	145683484	
rs2644577	C	0.90	0.0075	1	145409110	
rs4950437	A	0.90	0.0076	1	145394019	OR13Z2P
rs952477	A	1.10	0.0113	1	145716820	GJA5
rs10793705	C	1.10	0.0150	1	145706931	GJA5
rs4132958	C	1.09	0.0258	1	145430649	
rs12755965	C	0.92	0.0300	1	145658465	
rs12022413	A	0.92	0.0328	1	145463869	BCL9
rs613089	C	1.09	0.0356	1	145547811	BCL9
rs4950322	A	1.10	0.0372	1	145321460	
rs10900321	C	0.92	0.0431	1	145096540	PRKAB2|LOC400780
rs1342709	C	1.08	0.0432	1	145744388	
rs3766510	A	0.89	0.0434	1	145596846	ACP6
rs4950361	A	1.09	0.0472	1	145025789	LOC441904
rs2236570	A	0.92	0.0495	1	145560511	BCL9
rs1932977	A	0.92	0.0603	1	145155565	FMO5
rs11240007	C	1.08	0.0662	1	145304073	
rs945742	A	0.93	0.0728	1	145251781	
rs4950402	G	1.08	0.0787	1	145258026	
rs903786	C	1.09	0.0839	1	145830625	LOC391092|GJA8
rs11240147	A	1.13	0.0856	1	145824905	LOC391092|GJA8
rs10494251	A	1.14	0.1012	1	145490518	BCL9
rs903784	A	0.92	0.1020	1	145830723	LOC391092|GJA8
rs999095	A	0.92	0.1048	1	145676851	
rs11811023	C	1.07	0.1075	1	145047742	LOC440678
rs21327	C	1.07	0.1119	1	144995145	LOC440677
rs3820129	A	1.06	0.1145	1	145558596	BCL9
rs11239984	A	0.94	0.1174	1	145258353	
rs1417279	A	1.09	0.1212	1	145574517	BCL9
rs2883318	G	1.06	0.1216	1	145315767	
rs2353974	A	1.06	0.1297	1	145322880	
rs1932978	C	0.95	0.1532	1	145194387	CHD1L
rs12408395	A	1.07	0.1535	1	145372992	
rs11239953	T	1.06	0.1559	1	145184188	CHD1L
rs2275552	C	1.06	0.1566	1	145598569	ACP6
rs647596	G	1.05	0.1593	1	145002018	LOC440677
rs6593752	C	1.06	0.1766	1	145196592	CHD1L
rs2353986	C	0.95	0.1781	1	145288493	
rs2077749	A	1.05	0.1810	1	145119261	PRKAB2|LOC400780 |FMO5
rs11576760	C	1.09	0.1956	1	145806592	LOC391092
rs2353987	G	0.95	0.2020	1	145294180	
rs4950328	C	1.05	0.2235	1	145471435	BCL9
rs2353544	A	0.95	0.2365	1	145515224	BCL9
rs2353983	C	1.04	0.2809	1	145279761	
rs7541090	C	1.04	0.3058	1	145353686	OR13Z1P

rs627219	G	0.92	0.3068	1	145539979	BCL9
rs10900403	G	0.95	0.3305	1	145807358	
rs2999613	A	1.06	0.3586	1	146286966	
rs10494246	A	1.10	0.3592	1	145614928	ACP6
rs2354432	A	1.05	0.3811	1	145159853	FMO5
rs885239	A	0.95	0.3831	1	145594226	ACP6
rs1353431	C	0.94	0.3926	1	145764604	LOC391092
rs1390510	A	1.07	0.3975	1	145497947	BCL9
rs4950392	G	0.96	0.4064	1	145203172	CHD1L
rs10494245	A	1.04	0.4135	1	145637476	
rs1853782	C	1.04	0.4300	1	144975398	LOC440677
rs4504949	A	1.06	0.4304	1	145368301	OR13Z2P
rs584323	C	0.97	0.4348	1	145442845	
rs1541187	A	1.04	0.4534	1	145518117	BCL9
rs1572825	A	0.97	0.4567	1	145473996	BCL9
rs6664767	G	1.03	0.4681	1	145776067	LOC391092
rs1814653	A	0.96	0.4757	1	146209659	LOC440679 |LOC388684
rs894469	A	1.05	0.4853	1	145139530	FMO5
rs1015235	A	0.97	0.5032	1	145510166	BCL9
rs894467	C	0.94	0.5305	1	145128642	PRKAB2|FMO5
rs1908627	C	0.95	0.5319	1	145727389	GJA5
rs4950574	A	1.03	0.5358	1	146216845	LOC440679 |LOC388684
rs6937	A	0.97	0.5686	1	145093546	PRKAB2
rs946904	C	0.98	0.5768	1	145589455	ACP6
rs2992453	A	0.98	0.5966	1	146253348	LOC440680
rs596561	C	0.97	0.6110	1	145447612	
rs1353428	G	0.98	0.6115	1	145792846	
rs7526407	C	1.03	0.6163	1	145537233	BCL9
rs11804045	A	1.03	0.6551	1	145628401	ACP6
rs4950494	A	1.02	0.6672	1	145838200	LOC391092|GJA8
rs10494257	A	0.98	0.6923	1	145721193	GJA5
rs1495956	C	1.02	0.7095	1	145705110	GJA5
rs1344	A	1.01	0.7439	1	145585897	ACP6
rs12141387	A	1.01	0.7529	1	144970465	LOC440677
rs11261254	C	0.98	0.7631	1	146185099	
rs10494243	C	1.03	0.7723	1	145146427	FMO5
rs6593746	A	1.03	0.8049	1	145153273	FMO5
rs2932454	G	1.01	0.8354	1	146293282	FLJ39739|RNU1P10
rs12061877	C	0.99	0.8369	1	145730876	GJA5
rs1763457	C	0.99	0.8455	1	146262302	LOC440680
rs7530962	A	1.01	0.8523	1	145614797	ACP6
rs2452	A	0.99	0.8609	1	145220003	CHD1L
rs6693109	A	1.01	0.8686	1	145287960	
rs11240009	A	0.99	0.8697	1	145308966	
rs9661159	A	0.99	0.8740	1	145224547	CHD1L
rs1001193	C	1.01	0.8784	1	145633001	
rs1857208	A	1.01	0.9070	1	145758611	
rs671205	C	1.00	0.9479	1	144989346	LOC440677
rs2000072	A	1.00	0.9581	1	145437192	

Significant association with SNP alleles was not found with schizophrenia after Bonferroni correction. Data from 2,687 cases and 13,484 controls were used in the association analysis. Locations are based on Build 36 of the human genome.

Supplementary Table 8. Allelic association results for markers on the Illumina HumanHap300 within the 15q11.2 deletion.

Marker	Allele	OR	P-value	chr	Location (bp)	Gene
rs8029320	A	1.17	0.0008	15	20437666	CYFIP1
rs1897786	A	1.15	0.0061	15	20545323	CYFIP1
rs999842	C	0.91	0.0163	15	20551713	CYFIP1|NIPA2
rs4778413	C	1.09	0.0507	15	20560833	NIPA2|CYFIP1
rs6606817	C	1.08	0.0647	15	20567999	NIPA2
rs4778370	C	0.91	0.0764	15	20578289	NIPA2
rs8034210	C	0.93	0.0810	15	20347960	
rs12911925	C	1.10	0.0917	15	20568493	NIPA2
rs4778334	A	0.93	0.1100	15	20592297	
rs7168000	G	1.08	0.1283	15	20564567	CYFIP1|NIPA2
rs7170838	C	0.93	0.1334	15	20572679	NIPA2
rs4778464	A	0.93	0.1518	15	20537129	CYFIP1
rs2289819	C	0.93	0.1522	15	20512379	CYFIP1
rs4778575	T	0.95	0.2031	15	20605280	NIPA2|NIPA1
rs1009153	C	0.95	0.2039	15	20528352	CYFIP1
rs4293342	C	1.05	0.2069	15	20455753	CYFIP1
rs1991922	C	0.92	0.2168	15	20610835	NIPA1
rs12594495	A	1.05	0.2193	15	20499445	CYFIP1
rs7181789	A	0.96	0.2454	15	20595337	NIPA2|NIPA1
rs12441373	A	1.13	0.2619	15	20541359	CYFIP1
rs2289824	C	0.94	0.2680	15	20477670	CYFIP1
rs2028794	A	0.96	0.2818	15	20470856	CYFIP1
rs2278458	A	0.90	0.3075	15	20551298	CYFIP1|NIPA2
rs8031642	C	1.04	0.3118	15	20351272	LOC390544
rs3693	A	1.04	0.3290	15	20556334	CYFIP1|NIPA2
rs2289815	G	0.96	0.3483	15	20421301	TUBGCP5
rs4778470	C	0.96	0.3797	15	20523005	CYFIP1
rs7167658	C	1.04	0.4210	15	20460862	CYFIP1
rs1347314	C	0.94	0.4450	15	20585443	NIPA2|NIPA1
rs7168367	C	1.04	0.4805	15	20618177	NIPA1
rs5006363	A	0.95	0.4848	15	20398953	TUBGCP5
rs722410	A	1.03	0.4896	15	20475538	CYFIP1
rs765763	C	0.97	0.5022	15	20428330	TUBGCP5|CYFIP1
rs6606825	A	1.04	0.5038	15	20614243	NIPA1
rs4932679	C	1.03	0.5296	15	20322108	LOC390544
rs2289823	A	0.97	0.5390	15	20479393	CYFIP1
rs956120	C	1.02	0.5545	15	20489279	CYFIP1
rs4592619	C	0.97	0.5620	15	20585244	NIPA2|NIPA1
rs8040193	C	1.05	0.6146	15	20306549	LOC390544
rs7182576	G	0.98	0.6284	15	20546036	CYFIP1
rs1579821	C	1.02	0.6338	15	20501269	CYFIP1
rs3812924	A	1.02	0.6381	15	20599983	NIPA2|NIPA1
rs3751566	C	0.98	0.6918	15	20492111	CYFIP1
rs2304341	C	0.97	0.7614	15	20542471	CYFIP1
rs722411	A	1.01	0.7741	15	20475585	CYFIP1
rs7174982	C	1.01	0.8269	15	20517099	CYFIP1
rs7168653	C	0.99	0.8308	15	20516088	CYFIP1
rs3883043	A	1.01	0.8321	15	20777695	LOC339005
rs11636068	A	0.99	0.8639	15	20629449	NIPA1|LOC400320

rs8043036	A	1.00	0.9396	15	20434983	CYFIP1
rs1544285	A	1.00	0.9665	15	20405438	TUBGCP5
rs4778298	A	1.00	0.9740	15	20505022	CYFIP1
rs11263687	G	1.00	0.9838	15	20635884	LOC400320|NIPA1
rs2289816	G	1.00	0.9906	15	20506454	CYFIP1

Significant association with SNP alleles was not found with schizophrenia after Bonferroni correction. Data from 2,687 cases and 13,484 controls were used in the association analysis. Locations are based on Build 36 of the human genome.

Supplementary Table 9. Allelic association results for markers on the Illumina HumanHap300 within the 15q13.3 deletion.

Marker	Allele	OR	P-value	chr	Location (bp)	Gene
rs1463408	A	0.88	0.0055	15	29243936	
rs12915265	C	0.89	0.0089	15	30196358	CHRNA7
rs8038654	C	0.83	0.0095	15	30072156	
rs10438342	A	0.91	0.0169	15	30189338	
rs4779824	C	0.91	0.0174	15	29191586	TRPM1
rs1223889	A	0.92	0.0243	15	29258764	
rs2241494	A	0.92	0.0301	15	29155896	TRPM1
rs10152238	A	1.15	0.0377	15	30057610	
rs1647992	A	0.91	0.0459	15	29245430	
rs4779984	A	0.89	0.0520	15	30302218	
rs1863279	A	1.08	0.0530	15	29282405	
rs1477534	A	0.93	0.0539	15	29271979	
rs4779536	A	1.08	0.0598	15	29574400	C15orf16
rs2651418	A	0.93	0.0642	15	30226573	CHRNA7
rs999876	A	0.93	0.0642	15	29272626	
rs7173280	C	0.93	0.0759	15	29128656	TRPM1
rs1035706	A	1.10	0.0795	15	29130377	TRPM1
rs1978801	A	0.94	0.0880	15	29294328	LOC283710
rs919001	A	1.07	0.0893	15	29144430	TRPM1
rs6493543	G	0.94	0.0923	15	29324788	LOC283710
rs8042511	A	1.16	0.0971	15	29222034	
rs803534	C	0.94	0.1062	15	29215548	
rs6493688	A	0.94	0.1139	15	29560167	LOC400347|C15orf16
rs4779937	C	1.06	0.1178	15	29975287	
rs7162289	C	1.08	0.1310	15	29373158	
rs1672407	C	1.06	0.1344	15	29227096	
rs12442141	C	1.16	0.1345	15	29266578	
rs1672409	A	0.95	0.1446	15	29228600	
rs1001555	A	1.12	0.1452	15	30060958	
rs1514254	A	0.94	0.1456	15	29998226	
rs1465778	C	1.06	0.1460	15	29408613	KLF13
rs1580141	A	1.05	0.1981	15	29232062	
rs3784595	A	1.07	0.2043	15	29129507	TRPM1
rs6493540	A	1.05	0.2115	15	29321882	LOC283710
rs1465779	C	1.07	0.2226	15	29397182	KLF13
rs1865873	C	1.05	0.2226	15	29303300	LOC283710
rs2278133	A	1.05	0.2238	15	29140680	TRPM1
rs8034505	A	1.05	0.2270	15	29460239	KLF13|LOC440262
rs2241493	C	1.06	0.2295	15	29149644	TRPM1
rs8035668	A	0.94	0.2296	15	30178638	CHRNA7
rs2879262	C	0.95	0.2459	15	29344873	
rs4417522	C	1.04	0.2735	15	29974412	
rs7179733	C	0.96	0.2814	15	30160985	CHRNA7
rs1459200	A	1.04	0.2991	15	29594877	C15orf16
rs2288242	A	1.05	0.3062	15	29117572	TRPM1
rs2338834	C	1.04	0.3069	15	29125017	TRPM1
rs890158	C	1.04	0.3097	15	29157929	TRPM1
rs12900301	C	0.95	0.3122	15	29619936	C15orf16
rs1503004	A	1.06	0.3286	15	29827425	

rs3964705	C	0.96	0.3343	15	28822861	LOC440261
rs6494039	C	1.07	0.3401	15	29979194	
rs12440180	C	1.04	0.3677	15	30072148	
rs1606659	A	0.96	0.3731	15	30119745	CHRNA7
rs4779939	C	0.95	0.3764	15	29985165	
rs4779814	C	0.97	0.3814	15	29143717	TRPM1
rs7169523	A	0.96	0.3831	15	29250670	
rs2137856	A	0.97	0.3882	15	30016646	
rs7163696	C	0.96	0.3902	15	29313681	LOC283710
rs11630449	C	0.96	0.3953	15	29402033	KLF13
rs7163763	A	0.94	0.3977	15	29609507	C15orf16
rs953326	C	1.03	0.4090	15	30004979	
rs3784601	C	0.96	0.4097	15	29180766	TRPM1
rs3096464	C	1.03	0.4122	15	29256215	
rs898212	G	1.03	0.4134	15	29579128	C15orf16
rs4779862	C	1.03	0.4200	15	29420453	KLF13
rs4779759	A	1.03	0.4212	15	28751864	
rs1456212	A	1.05	0.4215	15	29211346	
rs3743234	A	1.03	0.4329	15	29126965	TRPM1
rs1459198	A	1.03	0.4337	15	29649740	C15orf16
rs12901022	C	0.97	0.4341	15	29100035	TRPM1
rs11638348	A	1.03	0.4352	15	29714219	C15orf16
rs1524878	G	1.03	0.4370	15	28941992	
rs2125615	A	1.03	0.4493	15	29587441	C15orf16
rs2046362	C	0.97	0.4581	15	28723577	
rs8041717	G	1.03	0.4719	15	29063737	FLJ20313
rs4779816	A	0.97	0.4730	15	29156415	TRPM1
rs3865090	C	1.06	0.4734	15	29319602	LOC283710
rs8026705	A	0.97	0.4835	15	29704566	C15orf16
rs16956362	A	1.07	0.4848	15	28986264	KIAA1018
rs12439925	C	1.03	0.4852	15	29386793	KLF13
rs971330	C	1.03	0.4885	15	29538956	LOC400347
rs7174744	A	0.97	0.4961	15	28971039	KIAA1018 |LOC388104
rs12442622	A	1.03	0.4971	15	30045195	
rs11071179	C	0.97	0.4975	15	29635750	C15orf16
rs7175258	A	1.04	0.5180	15	29484934	LOC440262
rs2337980	C	0.98	0.5194	15	30231488	CHRNA7
rs10519712	A	1.03	0.5230	15	29997162	
rs4779889	G	1.03	0.5245	15	29601495	C15orf16
rs7169662	A	0.98	0.5292	15	29438608	KLF13
rs11632955	C	0.98	0.5400	15	29336409	
rs9672615	A	1.03	0.5436	15	30298847	
rs8025698	C	1.02	0.5444	15	29186010	TRPM1
rs7175507	C	1.02	0.5606	15	30007740	
rs6493623	A	1.03	0.5622	15	29444540	KLF13
rs4779809	C	0.98	0.5771	15	29131323	TRPM1
rs12439621	C	1.05	0.5937	15	30096476	CHRNA7
rs12442954	A	0.98	0.5955	15	30029658	
rs1060493	G	1.02	0.6020	15	29303762	LOC283710
rs7402321	C	1.02	0.6061	15	30207700	CHRNA7
rs16956762	A	0.98	0.6140	15	29539275	LOC400347
rs964925	C	1.02	0.6145	15	29093271	TRPM1
rs2337233	C	0.98	0.6206	15	30094507	CHRNA7
rs7182946	G	0.98	0.6232	15	29182160	TRPM1
rs7178760	C	0.97	0.6243	15	29318665	LOC283710
rs17228178	C	0.98	0.6295	15	29257220	
rs6493352	C	1.02	0.6331	15	29021356	FLJ20313|KIAA1018

rs11070871	C	0.97	0.6503	15	29299944	LOC283710
rs11636101	A	0.98	0.6721	15	30061449	
rs1524876	C	0.98	0.6726	15	29050564	FLJ20313
rs4779948	C	0.98	0.6730	15	30046352	
rs8042404	A	0.98	0.6904	15	29467308	KLF13|LOC440262
rs2113945	C	0.98	0.6905	15	29111823	TRPM1
rs7174211	A	0.98	0.6930	15	29425288	KLF13
rs1474380	A	0.98	0.6997	15	29056527	FLJ20313
rs2338679	A	0.99	0.7029	15	29608133	C15orf16
rs13329490	A	1.02	0.7102	15	30195523	CHRNA7
rs4321165	A	0.98	0.7117	15	29863575	LOC440263
rs12323980	C	0.97	0.7147	15	29363969	
rs4238558	A	0.99	0.7193	15	29933027	
rs11636160	C	0.98	0.7239	15	29489142	LOC440262
rs4268714	A	0.99	0.7304	15	29462745	KLF13|LOC440262
rs965435	C	1.02	0.7400	15	30104501	CHRNA7
rs7167632	A	1.01	0.7425	15	29935438	
rs4779520	C	0.99	0.7456	15	29452735	KLF13
rs8028220	A	1.01	0.7461	15	29214684	
rs12441324	A	1.01	0.7535	15	28830254	LOC440261
rs7182547	C	1.01	0.7558	15	29084964	FLJ20313|TRPM1
rs9302175	C	0.99	0.7596	15	29530870	LOC400347
rs2289126	G	0.99	0.7710	15	29308957	LOC283710
rs798081	A	0.98	0.7775	15	28910527	LOC390561
rs2611605	C	0.99	0.7856	15	30228925	CHRNA7
rs11070619	C	1.02	0.7926	15	28896081	LOC390561
rs753636	A	0.98	0.7935	15	29478345	LOC440262
rs1514260	A	1.01	0.7981	15	30086242	
rs1567885	A	1.01	0.8297	15	30088094	
rs2063722	A	0.99	0.8311	15	30083665	
rs10519688	C	0.99	0.8362	15	29921270	
rs10519726	A	0.99	0.8404	15	29109167	TRPM1
rs12594231	C	0.99	0.8540	15	29963596	
rs17816055	C	1.01	0.8543	15	29619386	C15orf16
rs4779527	C	1.01	0.8566	15	29523383	LOC440262 |LOC400347
rs1524877	C	0.99	0.8618	15	29058472	FLJ20313
rs2293314	A	0.99	0.8680	15	28997943	KIAA1018
rs1035707	C	1.01	0.8721	15	29172089	TRPM1
rs2081455	C	0.99	0.8741	15	29210624	
rs6493741	C	1.01	0.8747	15	29609127	C15orf16
rs11638086	A	0.99	0.8765	15	28853522	LOC440261 |LOC390561
rs9672180	C	1.01	0.8818	15	30300468	
rs1088475	C	1.01	0.8880	15	28927992	LOC390561
rs2219507	A	1.01	0.8928	15	29646927	C15orf16
rs2873	A	1.00	0.9116	15	29018547	FLJ20313|KIAA1018
rs2339046	A	1.01	0.9146	15	29059962	FLJ20313
rs798104	C	1.01	0.9313	15	28894118	LOC390561
rs3784589	A	0.99	0.9331	15	29082006	FLJ20313|TRPM1
rs8027035	C	1.01	0.9334	15	30149996	CHRNA7
rs1392808	G	1.00	0.9471	15	30198807	CHRNA7
rs4779556	C	1.00	0.9564	15	29960537	
rs4779910	C	1.00	0.9612	15	29734334	C15orf16
rs1075232	A	1.00	0.9619	15	29528508	LOC400347
rs1378847	C	1.00	0.9674	15	29234640	
rs12898600	A	1.00	0.9694	15	29816985	
rs6494223	C	1.00	0.9697	15	30183749	CHRNA7

rs1983459	A	1.00	0.9703	15	28996041	KIAA1018
rs7178637	C	1.00	0.9774	15	29665644	C15orf16
rs4779794	A	1.00	0.9844	15	28984856	KIAA1018
rs905426	A	1.00	0.9955	15	29870041	

Significant association with SNP alleles was not found with schizophrenia after Bonferroni correction. Data from 2,687 cases and 13,484 controls were used in the association analysis. Locations are based on Build 36 of the human genome.

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