

***Supplementary table 1: Sample breakdown by population and genotyping platform***

<b>Site</b>	<b>Population</b>	<b>Affected</b>	<b>Controls</b>	<b>Genotyping platform</b>
<i>Discovery sample</i>				
Roskilde	Danish	22	0	HumanCNV370
<i>SGENE+ follow-up samples</i>				
Roskilde	Danish	502	477	Human610-Quad
Bonn	German	491	881	Human550v3
Helsinki	Finnish	63	150	HumanHap300
Verona	Italian	86	91	HumanHap300
Kuusamo	Finnish	128	50	HumanHap300
London (Kings college)	British	104	95	HumanHap300
Munich	German	611	612	HumanHap300
Nijmegen	Dutch	0	3,333	HumanCNV370
Oslo	Norwegian	245	272	Affy 6.0
Reykjavik <sup>1</sup>	Icelandic	684	28,730	HumanHap300/ HumanCNV370
Utrecht	Dutch	806	706	Human550v3
<i>ISC follow-up samples</i>				
Aberdeen	Scottish	727	694	Affy 5.0 <sup>2</sup>
Cardiff	Bulgarian	479	646	Affy 6.0
Dublin	Irish	280	914	Affy 6.0
Edinburgh	Scottish	403	290	Affy 6.0
Karolinska Institutet	Swedish	622	437	Affy 5.0/6.0
London (University college)	British	547	0	Affy 5.0
Portuguese Island Collection	Portuguese	333	200	Affy 5.0
<i>Cardiff follow-up samples</i>				
Cardiff	British	471	2,792	Affy 500K
<b>Total (follow-up)</b>		<b>7,582</b>	<b>41,370</b>	

<sup>1</sup>A further 5,773 Icelandic samples were evaluated for 15q11.2-q13.1 duplications, but excluded from analysis of association with schizophrenia owing to a psychiatric or developmental diagnosis other than schizophrenia or schizoaffective disorder, or to a first degree relationship with a schizophrenia affected individual.

<sup>2</sup>A large part (661 affected and 670 controls) of the Aberdeen sample was also typed by the SGENE+ Consortium on HumanHap300 and Human550v3 arrays.