CNV_1_67452217_67453437

Insertion Location 95% Confidence Region:
16:77705878-78321065

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
2:102781911-103257560

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
1:146534681-151499635

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
1:121330376-145383170

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
1:121351198-145383170

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
1:121225332-145383170

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
1:121330376-145383170

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
1:121330376-145383170

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
1:121262781-145383170

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
1:16691022-17337391

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
CNV_2_91759300_91821900

Insertion Location 95% Confidence Region:
1:145402354-145626119

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
2:98023626-98307823

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
CNV_2_112177604_112185178

Insertion Location 95% Confidence Region:
2:87061188-88295232

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
2:8588667-88295232

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
2:86183095-86897501

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
6:32350107-32675032

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
15:93718354-93845684

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
3:195652899-195857758

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
3:195652899-195857758

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
CNV_4_4015000_4021500

Insertion Location 95% Confidence Region:
4:8587465-11156745

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
14:19264866-20475208

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
14:19264866-20475208

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
5:34060053-34490529

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
CNV_5_175437826_175440125

Insertion Location 95% Confidence Region:
5:176919656-177408337

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
 insertion location 95% confidence region:
5:176940274-177786775

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
CNV_5_177217820_177221664

Insertion Location 95% Confidence Region:
5:175329033-176045010

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
16:34202307-46534652

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
7:6377836-7143781

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
7:5576680-6416615

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
15:40637622-40988418

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
7:57433043-62504090

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
7:62668534-63313180

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
7:56516052-57350723

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
7:56115321-57353425

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
7:55615076-56513828

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
7:55617815-56704005

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
7:141851540-150205086

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
7:149162885-150004244

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
1:18763894-193484533

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
GS_SD_M2_8_7200001_7436083_8_7600001_7825413

Insertion Location 95% Confidence Region:
8:11860259-12578645

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
8:12584092-12585436

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
8:11714941-11828200

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
8:12583654-12586093

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
CNV_8_8077800_8087700

Insertion Location 95% Confidence Region:
8:11859851-12580568

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
8:12588849-12593045

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
22:32334686-32664241

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
**Figure 1:** Copy number genotypes in the ASD, ID, and SCZ cohorts.

**Figure 2:** LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

**Figure 3:** P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
CNV_10_26913676_26915975

Insertion Location 95% Confidence Region:
10:27210569-27865573

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
10:50862335-52119297

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
10:47703870-48303900

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
**Figure 1:** Copy number genotypes in the ASD, ID, and SCZ cohorts.

**Figure 2:** LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

**Figure 3:** P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
CNV_12_31266000_31407500

Insertion Location 95% Confidence Region:
12:8970652-11630778

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
6:27518819-30365740

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
11:108745546-109045098

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
13:23314312-23545996

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
CNV_13_61461095_61462117

Insertion Location 95% Confidence Region:
5:19609838-23155734

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
15:20173314-23682893

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
CNV_15_28934858_28936946

Insertion Location 95% Confidence Region:
15:20173314-23874362

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
CNV_15_28937648_28943000

Insertion Location 95% Confidence Region:
15:20173314-23619572

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
13:43848721-44191220

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
16:18126929-18821191

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
16:18166840-18969357

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
16:18244090-19090721

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
16:18158085-19181300

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
CNV_16_18615000_18635104

Insertion Location 95% Confidence Region:
16:16291971-17208426

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
16:74171216-74761843

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
1:145514053-150506263

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
17:17496869-18578832

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
17:17325046-17340512

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
17:17322196-18177661

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
17:15402638-16866164

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
17:17848286-18753870

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
17:44076063-44819519

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
CNV_17_62915465_62918489

Insertion Location 95% Confidence Region:
17:44128876-44855683

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
CNV_19_50583100_50594147

Insertion Location 95% Confidence Region:
19:50948550-51244631

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
16:34280305-47986157

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
22:19000061-19091977

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Insertion Location 95% Confidence Region:
22:19000061-19091977

Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.
Figure 1: Copy number genotypes in the ASD, ID, and SCZ cohorts.

Figure 2: LOD scores of insertion locations across the genome (left) and around the 95% confidence interval (highlighted in gray, right).

Figure 3: P-values of association between SNP genotypes and duplication copy number across the genome (left), and around the 95% confidence interval (highlighted in gray, right).

All coordinates refer to GRCh37.