Supplemental Table 1: Number of CNVs Observed in Probands, Parents, and CEU Controls by Standard Criteria. Criteria for inclusion in this analysis are CNVs that encompass ≥ 20 SNP markers, are ≥ 100 kilobases in length, and cannot overlap more than 60% with a previously identified variant (20m100k60o). The frequency of CNVs is much greater in the patients than parents; frequency in parents is greater than controls (Kruskal-Wallis non-parametric test, $p < 0.00005$).

Subjects	Total CNVs	Gains	Losses
Autism Probands, n = 69	**107**	**87**	**20**
Proband Frequency	**1.6**	**1.3**	**0.3**
Parents, n = 35	**33**	**19**	**14**
Parent Frequency	**0.94**	**0.54**	**0.4**
CEU Controls, n = 89[#]	**14**	**9**	**5**
CEU Frequency	**0.16**	**0.1**	**0.05**

of 90 CEU HapMap subject cell lines, one was excluded because it had previously been shown to harbor multiple rearrangements.

Supplemental Table 2: Number of CNVs Observed in Probands, Parents, and CEU Controls by Standard Criteria. Criteria for inclusion in this analysis are CNVs that encompass ≥ 20 SNP markers, are ≥ 10 kilobases in length, but do not overlap with any previously identified variant (20m10k0o). The frequency of CNVs is much greater in the patients than parents; frequency in parents is greater than controls (Kruskal-Wallis non-parametric test, $p < 0.00005$).

Subjects	Total CNVs	Gains	Losses
Autism Probands, n = 69	**621**	**530**	**91**
Proband Frequency	**9**	**7.7**	**1.3**
Parents, n = 35	**89**	**60**	**29**
Parent Frequency	**2.5**	**1.7**	**0.8**
CEU Controls, n = 89[#]	**13**	**6**	**7**
CEU Frequency	**0.14**	**0.06**	**0.08**

of 90 CEU HapMap subject cell lines, one was excluded because it had previously been shown to harbor multiple rearrangements.