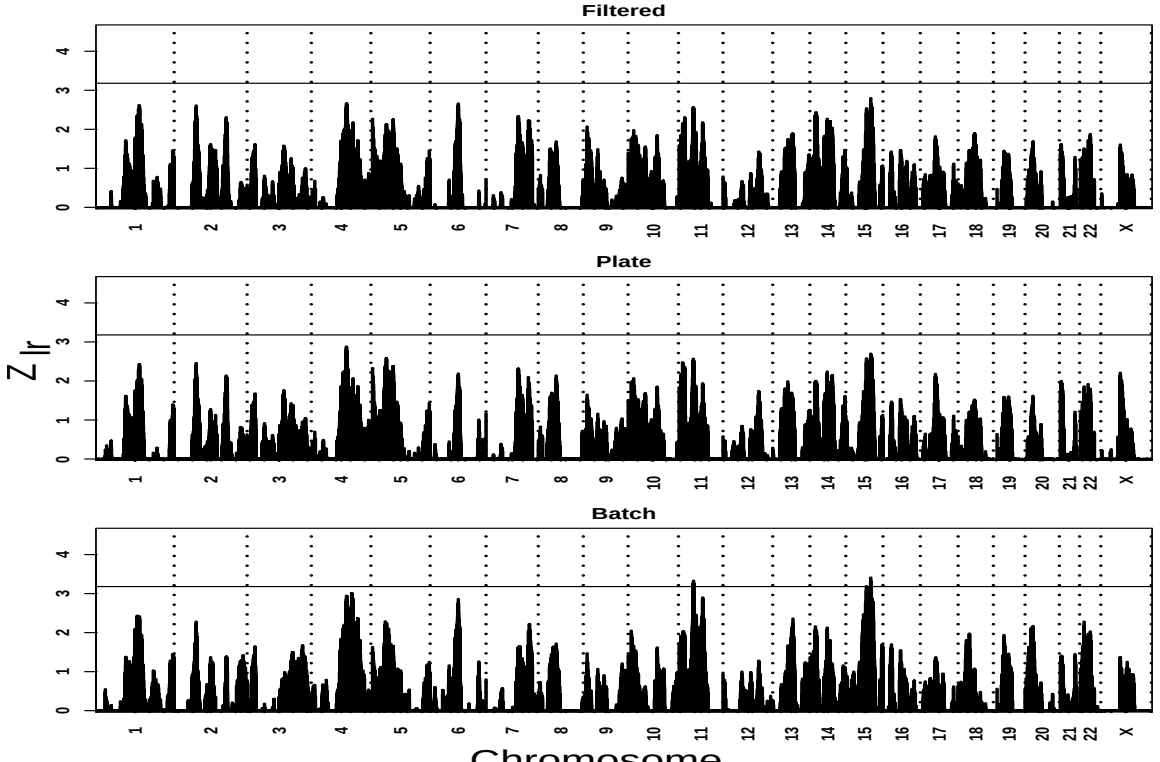
Mapping autism risk loci using genetic linkage and chromosomal rearrangements (The Autism Genome Project (AGP) Consortium)

Supplementary Figure 2. Linkage results due to removing families in which affected individuals putatively carry CNV.



Supplementary Figure 2. Linkage results due to removing families in which affected individuals putatively carry CNV. Families all fall in the broad diagnostic category. For 11p, the maximum occurs in 11p13 (Zlr = 3.33 at rs2421826). For chromosome 15, there are two up-crossings: the smaller peak occurs at in 15q23 (Zlr = 3.19 at rs1372828) and the larger peak in 15q25.3 (Zlr = 3.41 near rs1433452).