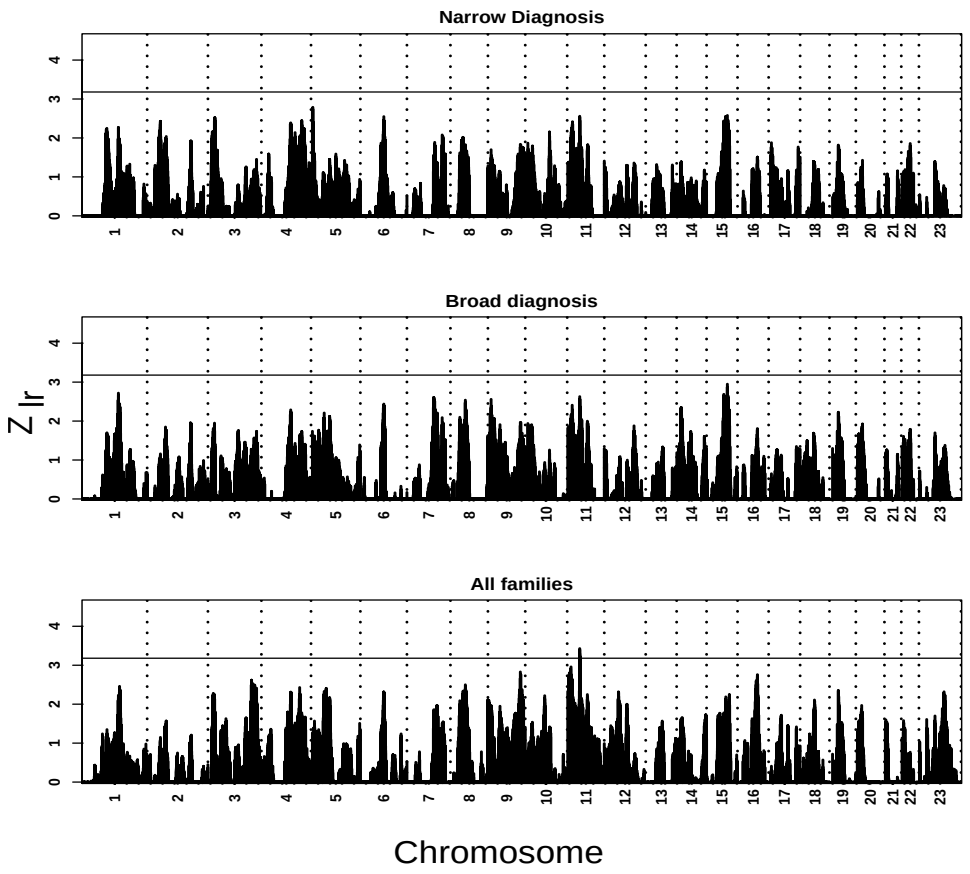
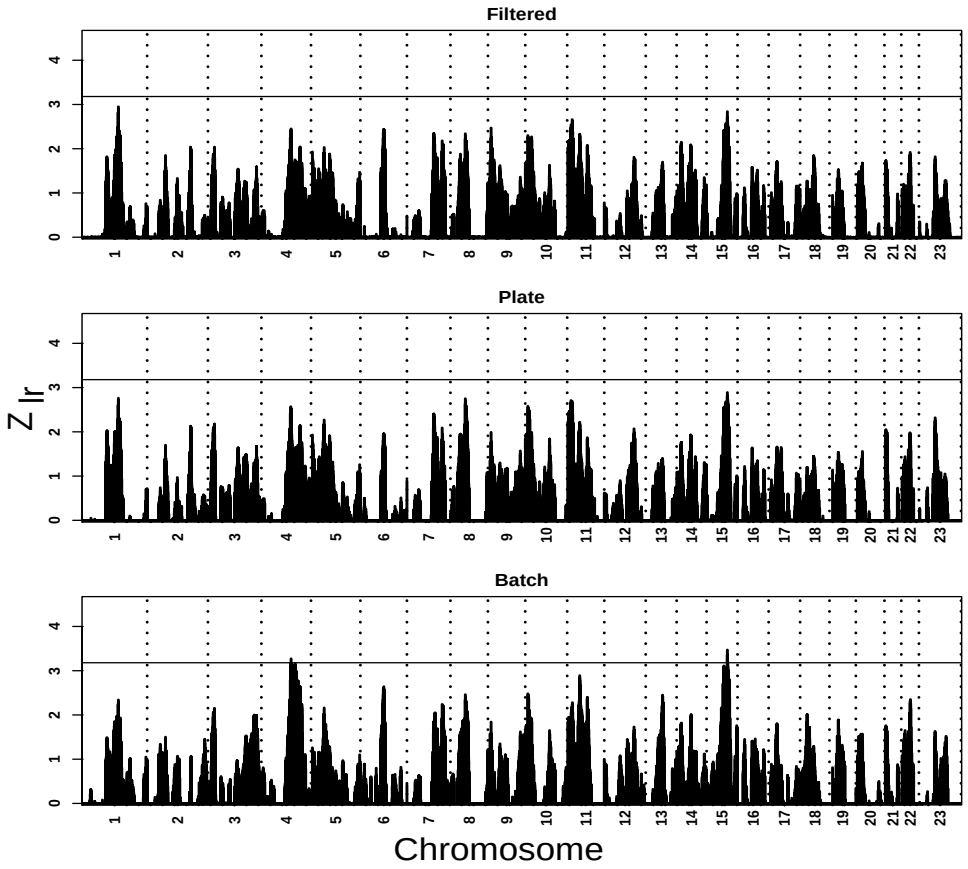
Mapping autism risk loci using genetic linkage and chromosomal rearrangements (The Autism Genome Project (AGP) Consortium)

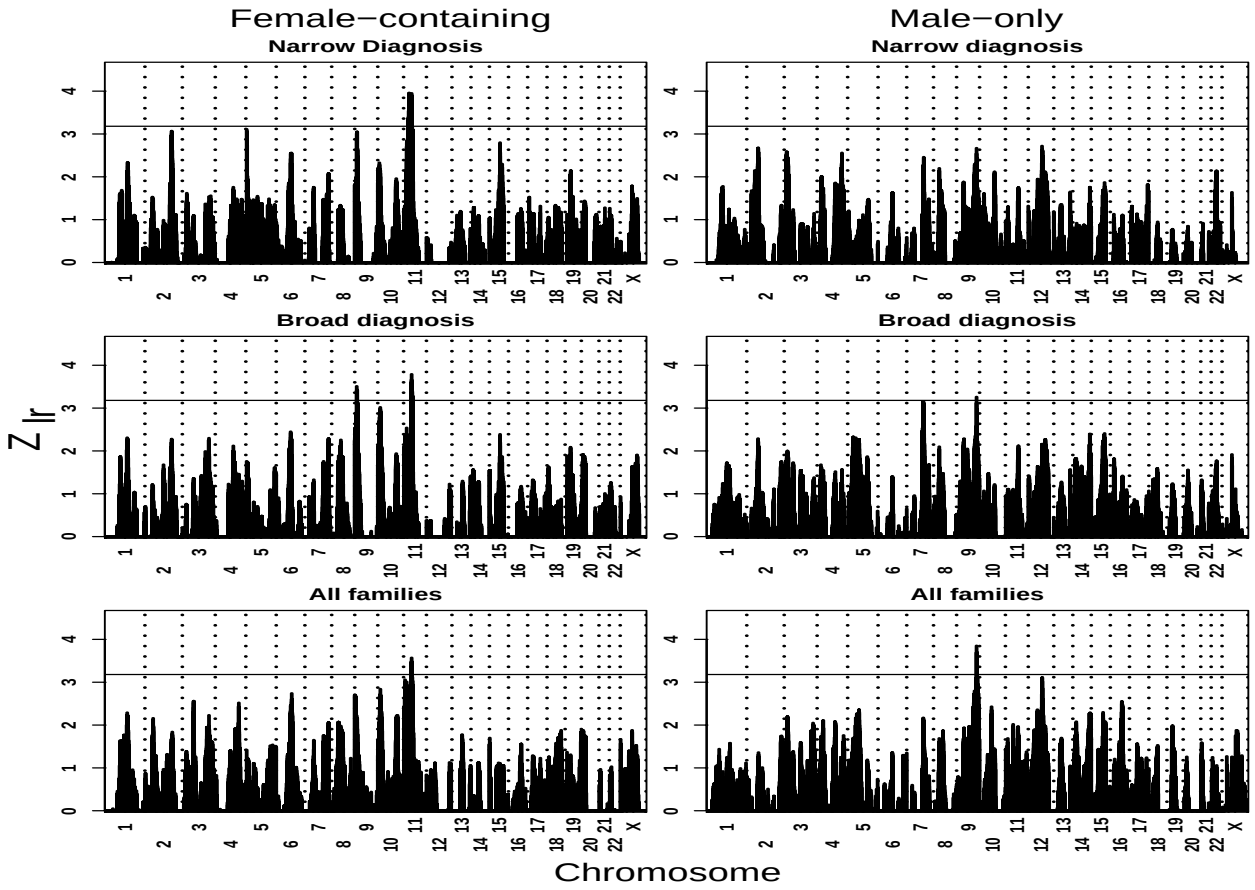
Supplementary Figure 4. Linkage results obtained by analyzing families inferred to be of homogeneous European ancestry (see Supplementary Figure 3 for methods.)



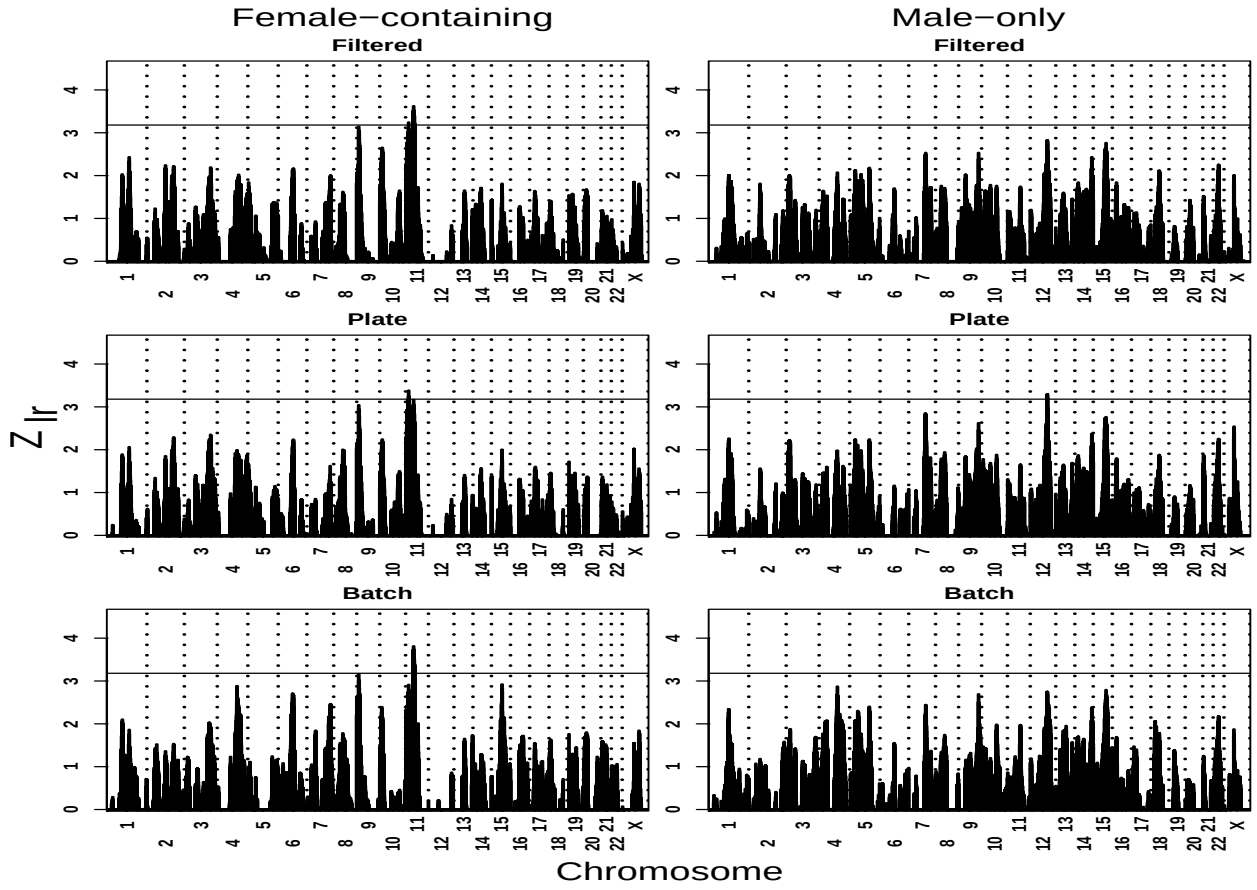
Supplementary Figure 4A. Linkage across the genome for all families of inferred European ancestry, based on levels of diagnostic certainty. Vertical reference lines separate chromosomes, which are ordered. The horizontal reference bar is given at a Zlr of 3.18, the threshold for suggestive linkage according to the Lander/Kruglyak criterion. The suggestive threshold is expected to be crossed, by chance, once per genome scan. It is crossed once, within 11p12 (Zlr = 3.43 at rs2421826).



Supplementary Figure 4B. For families inferred European ancestry, the effect on linkage of removing families in which affected individuals putatively carry CNV. For the batch method of calling CNVs, the suggestive linkage threshold is crossed twice, within 4q31.22 (Zlr = 3.19 at rs720484; m-p = 0.00006) and within 15q25.3 (Zlr = 3.47 at rs1433452; m-p = 0.002).



Supplementary Figure 4C. Linkage peaks by MO/FC for all families of inferred European ancestry, based on levels of diagnostic certainty. Linkage peaks by MO/FC for all families of inferred European ancestry, based on levels of diagnostic certainty. For FC families and narrow diagnosis, the linkage trace in 11p is complex, crossing the suggestive threshold twice. The first maximum is in 11p14.3 (Zlr = 3.96 at rs726859; m-p = 0.002) and the other is in 11p12 (Zlr=3.95 at rs1039205; m-p = 0.005). For FC/Broad, the peak falls within 9p24.1 (Zlr = 3.51 at rs1575284; m-p = 0.015) and 11p12 (Zlr = 3.79 at rs1039205; m-p = 0.009); and for FC/All, to 11p12 (Zlr = 3.57 at rs1039205; m-p = 0.046). For all MO families, peak falls within 9q33.3 (Zlr = 3.26, Broad [m-p = 0.002], and Zlr = 3.85 for All [m-p = 0.0005], both at rs536861).



Supplementary Figure 4D. The effect on linkage of splitting families of inferred European ancestry into FC and MO families while also removing families in which affected individuals putatively carry CNV. For FC families and filtered subset, two peaks cross the suggestive threshold and maximize in two regions on chromosome 11, within 11p15.3 (Zlr=3.24 at rs871704; m-p = 0.335) and 11p12 (Zlr = 3.62 at rs1039205; m-p = 0.291); for FC/Plate, to 11p15.3 (Zlr=3.38 at rs871704; m-p = 0.214); and for FC/Batch, to 11p12 (Zlr = 3.81 at rs1039205; m-p = 0.017). For MO families and plate subset, a single peak crosses the suggestive threshold and maximizes within 12q23.1 (Zlr = 3.29 at rs1560020; m-p = 0.027).