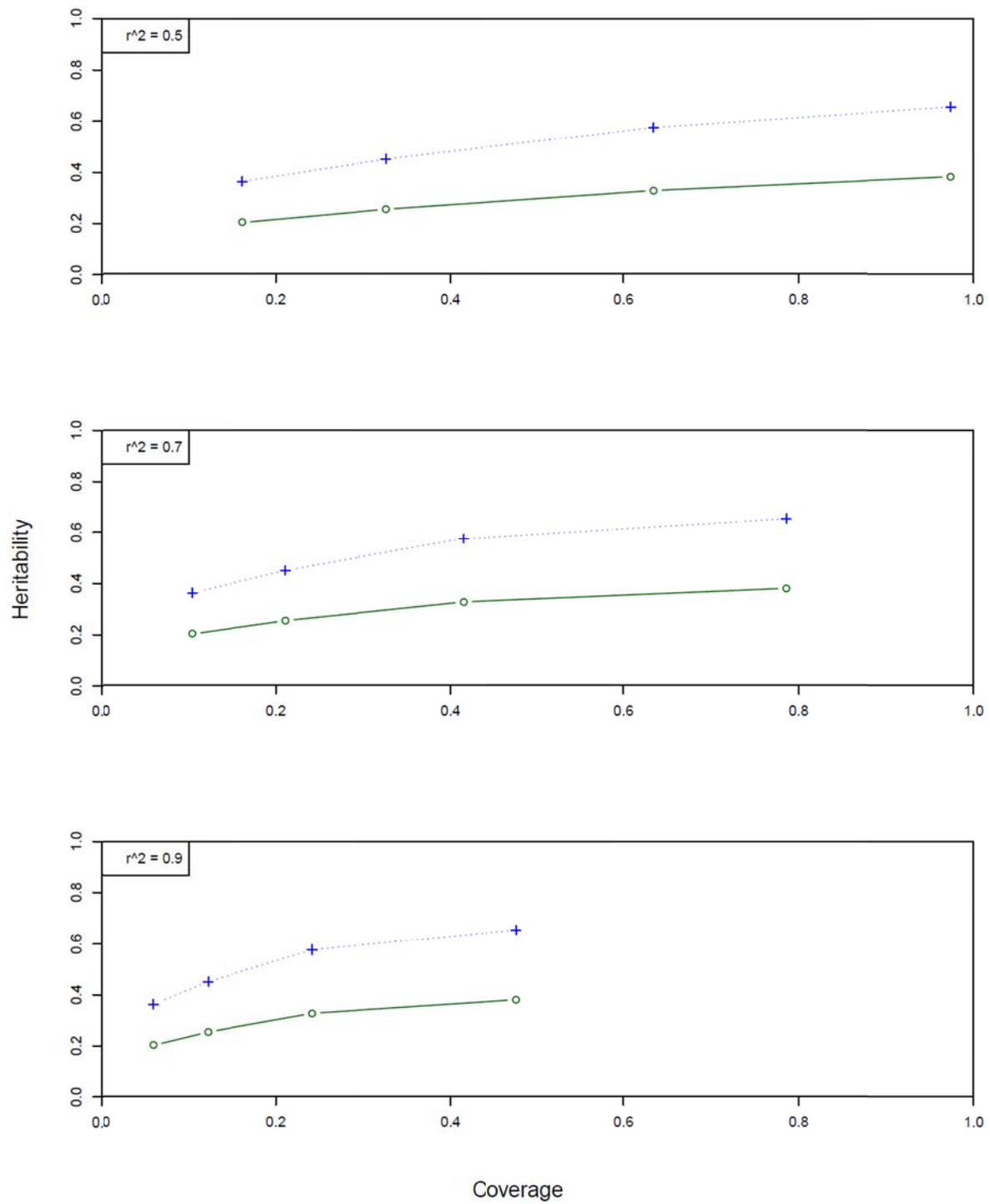




Supplementary Figure 2. Heritability for ASD probands as a function of estimated “genomic coverage” for varying levels of r^2 . Coverage is estimated as the fraction of all known SNPs identified by 1000 Genomes with minor allele frequency > 0.1 tagged by the set of SNPs used to estimate heritability for probands; see Online Methods for more details. From the left points map onto 12.5%, 25%, 50%, and 100% of the SNPs used to estimate heritability. Top line is for probands from multiplex families, bottom for probands from simplex families.