Background
Common SNPs explain a substantial part of the liability to ADHD. Recently we also found that polygenic scores based on a meta-analysis of ADHD clinical diagnosis predict continuous measures of ADHD symptoms in the general population. Next, we performed a genome-wide association (GWA) meta-analysis in population-based cohorts of ADHD symptoms.

Subjects & Methods
Nine population-based cohorts including 17,560 children with genome-wide genotype data had maternal or teacher rated ADHD symptom data at preschool and school age. Each cohort performed a linear regression of the symptom score on genotype dosages (imputed against the 1000 Genomes reference panel), sex, age and principal components. A p-value based meta-analysis was performed as well as gene-based tests and pathways analyses. In addition, two cohorts assessed SNP-based heritability (total n=2,000). GCTA was ran in two cohorts (NTR and GenR) to estimate SNP-based heritability.

Results
SNP-based heritability was 34% (p < .05) for teacher and 9% (non-significant) for maternal ratings of Attention Problems. In the GWA meta-analysis, no SNPs reached genome-wide significance, and no genes or pathways were associated with ADHD symptoms at a false discovery rate of 5%. In both the individual variant and gene-based association tests the top results included the genes PBX4 and WASL. As both genes are expressed in the brain, these seem promising results. A previous study that analyzed all published GWA studies on ADHD found enrichment of genes involved in directed neurite outgrowth; this finding seems to overlap with our result for WASL.

Conclusion
Our results overlap with previous studies that suggest that genes involved in neurite outgrowth play a role in ADHD etiology. GWA studies of larger samples are needed to detect genetic variants for ADHD; the inclusion of population-based cohorts in GWA studies of ADHD can help to increase sample size and hence improve statistical power for gene finding.

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