

Publication

Novel genetic loci underlying human intracranial volume identified through genome-wide association

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Intracranial volume reflects the maximally attained brain size during development, and remains stable with loss of tissue in late life. It is highly heritable, but the underlying genes remain largely undetermined. In a genome-wide association study of 32,438 adults, we discovered five previously unknown loci for intracranial volume and confirmed two known signals. Four of the loci were also associated with adult human stature, but these remained associated with intracranial volume after adjusting for height. We found a high genetic correlation with child head circumference ($r_{\text{hogenetic}} = 0.748$), which indicates a similar genetic background and allowed us to identify four additional loci through meta-analysis ($N_{\text{combined}} = 37,345$). Variants for intracranial volume were also related to childhood and adult cognitive function, and Parkinson's disease, and were enriched near genes involved in growth pathways, including PI3K-AKT signaling. These findings identify the biological underpinnings of intracranial volume and their link to physiological and pathological traits.

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