M67. THE UNIQUE EVOLUTIONARY SIGNATURE OF AUTISM GENES.
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**Background** Autism is a prevalent heritable neurodevelopmental disorder characterized by social and communication disabilities, which greatly reduce reproductive fitness. The maintenance of such a heritable and low-reproductive trait in the human population is an evolutionary enigma that has likely left traces in autism genes. High-throughput genomic data from large human samples are an excellent resource to explore such hypotheses.

**Methods** we studied the genomic characteristics of 651 autism genes and of 14,934 non-autism genes in a large whole-exome sequencing dataset, which included data on 503,481 single-nucleotide variants (SNVs) in 2,439 individuals of diverse ethnic backgrounds. We used population genetics methodologies to inquire regarding the types and extent of evolutionary constraints that act on autism genes.

**Results** We show that autism genes are approximately 65% longer and 20% less variable than non-autism genes. The mutational dearth in autism genes was particularly eminent among SNVs with potential damaging effects, which is a hallmark of negative selection. These differences were more prominent when considering only well-established autism genes. We further show that these genomic characteristics could efficiently differentiate between autism genes and other brain-expressed genes, or genes of other closely related diseases.

**Conclusions** Our findings suggest that autism genes have a unique genomic signature, which could be used to identify new candidate genes for the disorder.