The *cis-*eQTL data was formatted as a “.txt\_besd-dense”, which is a binary file format similar to “.bed”. To transform it to a “.txt” file, we used SMR 1.3.1’s “query” command with the “betql-summary” parameter. We interacted with SMR using bash 3.2. The command we used is the following:

./smr --query 1 --beqtl-summary cis-eQTLs-full\_eQTLGen\_AF\_incl\_nr\_formatted\_20191212.new.txt\_besd-dense --chr 1 --out ./Final\_eQTLs\_per\_chrom/chr1\_whole\_blood\_eQTLs

We used this command for every chromosome just changing the “--chr” flag. The “--query” flag asks for the *p*-value threshold of the variants you want to extract. Since we wanted to extract every variant, we always kept the value for this flag at 1.

Download the full *cis*-eQTL dataset from <https://www.eqtlgen.org/cis-eqtls.html>

Download SMR 1.3.1. from <https://yanglab.westlake.edu.cn/software/smr/#Download>