Abstract: Estimation of heritability is fundamental in genetic studies. Recently, heritability estimation using linear mixed models has gained popularity because these estimates can be obtained from unrelated individuals collected in genome-wide association studies. When evaluating the heritability of a phenotype, it is important to accurately measure the statistical significance of obtaining an estimated heritability value under the null hypothesis of a zero true heritability value. One major problem with the parametric approach detailed above is that it strongly relies on the parametric model at hand. In contrast, permutation testing is a popular nonparametric alternative, whose advantages are that it does not require the assumption of a parametric form of the distribution of the statistic, and that it does not rely on asymptotic assumptions. Indeed, we show that permutation p-values for the heritability of methylation profiles of CpG sites from a cohort of 1799 samples are significantly larger than those calculated by GCTA. In particular, sites which are significantly heritable according to the model, are often deemed to be non-significant, resulting in false positives and demonstrating the need for feasible permutation testing for heritability. Permutation testing, however, is often computationally prohibitive. Here, we propose an efficient method to perform permutation testing for heritability, achieving a speedup of up to several orders of magnitude, resulting in a method which is both highly efficient and does not suffer from asymptotic assumptions.