Supplementary Text

1 Poisson Mixed Model

To detect differentially expressed genes, we examine one gene at a time with the following Poisson mixed model (PMM):

$$y_i \sim \text{Poi}(r_i \lambda_i), \tag{1}$$

where r_i is the read depth of ith individual; y_i is the read count of the particular gene; λ_i is an unknown rate parameter. We use a log link to model λ_i as a linear function of parameters:

$$\log(\lambda_i) = \mathbf{w}_i^T \boldsymbol{\alpha} + x_i \beta + g_i + e_i, \tag{2}$$

$$\mathbf{g} = c(g_1, \cdots, g_n)^T \sim \text{MVN}(0, \sigma^2 h^2 \mathbf{K}), \tag{3}$$

$$\mathbf{e} = c(e_1, \cdots, e_n)^T \sim \text{MVN}(0, \sigma^2 (1 - h^2) \mathbf{I}_{n \times n}), \tag{4}$$

where $\mathbf{w}_i$ is a c-vector of covariates including an intercept and $\boldsymbol{\alpha}$ is a c-vector of corresponding coefficients; x_i is the predictor of interest and β is its coefficient; $\mathbf{g}$ is an n-vector of genetic random effects that model correlation due to population structure or individual relatedness; $\mathbf{e}$ is an n-vector of environmental residual errors that model independent variation; $\mathbf{K}$ is a known n by n relatedness matrix that can be calculated based on a pedigree or genotype data and that has been standardized to ensure $tr(\mathbf{K})/n = 1$ (this ensures that h^2 lies between 0 and 1, and can be interpreted as heritability, see [1]); $\mathbf{I}$ is an n by n identity matrix; $\sigma^2 h^2$ is the genetic variance component; $\sigma^2(1 - h^2)$ is the environmental variance component; h^2 represents the heritability of the log transformed rate (i.e. $\log(\lambda)$); and MVN denotes the multivariate normal distribution.

The Poisson mixed model proposed here belongs to the generalized linear mixed model family [2]. Both $\mathbf{g}$ and $\mathbf{e}$ model over-dispersion, the increased variance in the data that is not explained by the Poisson model. However, they model different aspects of over-dispersion: $\mathbf{e}$ models the variation that is due to independent environmental noise (a known problem in data sets based on sequencing reads), while $\mathbf{g}$ models the variation that is explained by kinship or population structure. Effectively, our model improves and generalizes the previous negative binomial model by introducing this extra $\mathbf{g}$ term to model individual relatedness due to kinship, population structure, or stratification.

2 Inference Method Overview

We are interested in testing the null hypothesis $H_0 : \beta = 0$. This requires obtaining the maximum likelihood estimate $\hat{\beta}$ from the model. Unlike its linear counter-part, obtaining the estimate of β from the Poisson mixed model is not a trivial task, as the joint likelihood consists of an n-dimensional integral that cannot be solved analytically [2]. Previous frequentist approaches to address this problem include direct numerical integration using Gauss-Hermite quadrature [3], or Laplace approximation that is applied to the likelihood function [4] or the quasi-likelihood function [5–8]. However, both numerical integration and analytic approximation do not scale well with the increasing dimension of the integral, which unfortunately equals the sample size in our model. Even a second order Laplace approximation yields a biased estimate and overly narrow confidence interval, especially when the uncertainty in the variance component estimate is large [9–13]. Therefore, frequentist approaches for estimation and inference in the Poisson mixed model remain notoriously difficult and is still an active area of research [14].

In contrast to the frequentist methods, Markov chain Monte Carlo (MCMC)-based Bayesian approaches provide an appearing alternative [11]. Bayesian methods naturally account for the uncertainty in the variance component estimates and can achieve arbitrary inference accuracy if the chain is allowed to

run long enough. Despite these attractive theoretical features, however, constructing an efficient MCMC algorithm for practical problems is not easy. Previous MCMC approaches for generalized linear mixed models either require a normal approximation to the likelihood function that diminishes its gains over the frequentist methods [15,16], or use n-steps of Metropolis–Hastings algorithm to sample the n-dimensional latent rate variables where efficient proposal distributions for all of them can be hard to construct [17,18]. To improve upon these previous approaches, a new MCMC algorithm [19–21] has been recently developed based on auxiliary variable representation of the Poisson distribution [22]. By introducing latent variables to replace the observed count data, the algorithm makes sampling and computation relatively straightforward.

Therefore, we rely on this particular form of MCMC in the present study. Our main contribution is to further develop an accurate approximation to the distribution of these latent variables, where the approximation form is specifically designed to allow us to adapt recent mixed model innovations [23–26] that substantially reduce the computational burden. By using a mean-normal mixture approximation to the negative log gamma distribution, our approach reduces the per-MCMC iteration computational complexity from $O(n^3)$ to $O(n^2)$, where n is the sample size. This modification allows the Poisson mixed model to be efficiently applied to hundreds of individuals and millions of genes.

Although we use MCMC for posterior sampling, our primary goal is not to perform a Bayesian analysis by producing Bayes factors for model comparison (although this is an interesting area to explore in the future). Rather, our goal is to use MCMC as a convenient and accurate tool to obtain the marginal likelihood of β that is otherwise infeasible or inaccurate to obtain under various frequentist approaches. Under asymptotics, both the likelihood function and the marginal posterior distribution for β will be approximately normal [27]. Since the likelihood function is simply the difference between the posterior and the prior, once we have obtained the posterior mean and standard deviation of β and paired these values to their prior counter-parts, we can easily obtain the approximate likelihood function and compute the approximate maximum likelihood estimate $\hat{\beta}$ and its standard error $se(\hat{\beta})$ using the method of moments. We can then construct approximate Wald test statistics and p values for hypothesis testing.

In the present study, we use flat priors for all nuisance parameters $(\boldsymbol{\alpha}, \sigma^2, h^2)$, or $p(\boldsymbol{\alpha}) \propto 1$, $p(\sigma^2) \propto 1$ and $p(h^2) \propto 1$. (Notice that a uniform distribution for σ^2 on the log scale, or $p(\log(\sigma^2)) \propto 1$, would make the posterior distribution different from the likelihood.) For the parameter of interest, β, we could also use a flat prior, in which case the posterior would be the likelihood. For computational stability reasons, however, we use a relatively informative prior, $\beta \sim N(0, \sigma_b^2)$ instead. A relatively informative prior restricts the sampling space when the likelihood is not informative, allowing efficient posterior sampling. Since we rely on the difference between the posterior and the prior for approximate inference, the choice of prior for β does not influence the eventual results. In the present study, we set $\sigma_b^2 = 1$.

Applications to real data confirm that this procedure produces well-calibrated p-values (Figure 1), suggesting that a few dozen samples are large enough to ensure asymptotic behavior. Moreover, although our approach is inherently stochastic – because the posterior mean and standard deviation of β may be slightly different for different chains – we show that a thousand MCMC iterations per gene is large enough to produce stable estimates of the test statistics and p values (Figure S2).

Finally, it is important to point out that MACAU is not the first PMM applied to RNAseq studies, but only represents the first PMM designed for differential expression analysis in RNAseq studies. Indeed, an early study has presented a special form of PMM, POME method, for quantifying transcript abundance in RNAseq studies [28]. However, POME differs from MACAU in four key areas: (1) Application: POME is designed to quantify gene expression levels, while MACAU is designed for differential expression analysis; (2) Model: POME uses ICAR (intrinsic conditional autoregressive model) to quantify the spatial correlation among reads that are mapped to different base positions on the same transcript, while MACAU uses a general covariance matrix to quantify sample relatedness; (3) Statistics: POME is focused on parameter inference (i.e. obtaining theta estimates), while MACAU is focused on hypothesis testing (i.e. computing p-values); (4) Algorithm: POME uses a standard MCMC algorithm, while one of the

key contributions of MACAU is its use of an alternative sampling algorithm that is n times faster than the standard one.

3 The MACAU Algorithm

Below, we describe the MACAU algorithm, for Mixed model Association for Count data via data AUgmentation, in detail.

3.1 Data Augmentation

To bypass the difficult likelihood function that results from the count nature of the RNAseq data, we introduce two continuous auxiliary variables to replace y_i. This makes our algorithm distinct from, and more complicated than, our early approach of introducing one latent variable for the simpler binomial model [29].

Specifically, for ith individual, observing y_i read counts from a Poisson distribution with rate parameter λ_i is equivalent to observing y_i points within a unit time interval from a Poisson point process with the same rate parameter λ_i. Moreover, observing y_i points in this Poisson process is also equivalent to observing the two arrival times that flank the y_i'th point: the arrival time τ_{i2} of the last point y_i has to occur before unit time, while the arrival time $\tau_{i1} + \tau_{i2}$ of the next point $y_i + 1$ has to occur after the unit time. Therefore, observing y_i read counts is equivalent to observing the two continuous random variables τ_{i1} and τ_{i2}.

The attractive feature of introducing the two continuous random variables τ_{i1} and τ_{i2} is that, conditional on them, the posterior of $(\boldsymbol{\alpha}, \beta, \sigma^2, h^2)$ no longer depends on the observed read counts y_i, hence removing the non-linearity constraint that comes with the Poisson aspect of our model. Specifically, based on the standard properties of the Poisson process, the inter-arrival time τ_{i1} follows an exponential distribution with the same rate parameter λ_i, or $\tau_{i1} \sim Exp(1)$. Similarly, the arrival time of y_i's jump, τ_{i2}, is the summation of y_i independent inter-arrival times and thus follows a Gamma distribution, or $\tau_{i2} \sim Gamma(y_i, 1)$. We can introduce two latent variables z_{i1}, z_{i2} as the negative log of τ_{i1}, τ_{i2}, respectively [19, 20], and we have

$$z_{i1} := -\log(\tau_{i1}) = \log(\lambda_i) + \epsilon_{i1}, \quad \epsilon_{i1} \sim -\log(Exp(1)) \tag{5}$$

$$z_{i2} := -\log(\tau_{i2}) = \log(\lambda_i) + \epsilon_{i2}, \quad \epsilon_{i2} \sim -\log(Gamma(y_i, 1)) \tag{6}$$

where $-\log(Exp(1))$ denotes the negative log exponential distribution; $-\log(Gamma(y_i, 1))$ denotes the negative log gamma distribution. Therefore, using z_{i1} and z_{i2} allows us to bypass y_i, and thus the count feature of the observed data in the algorithm.

3.2 Normal Mixture Approximation

To further circumvent the difficulty introduced by the non-normality of ϵ_i, we follow previous ideas [20, 21] to approximate the non-normal distribution by using a mixture of normals. Importantly, we take advantage of recent innovations in efficient mixed model algorithms [23–26] by using a mean mixture of normals where each normal distribution has a different mean but share the same variance.

Specifically, for every possible integer value of r, we identify a normal approximation in the form of $\sum_{k=1}^{k_r} w_{rk} \mathrm{N}(m_{rk}, s_r^2)$, to the negative log gamma distribution $-\log(\mathrm{Ga}(r, 1))$. Because the mean ($-\Psi(r)$, where Ψ denotes a digamma function) and the variance ($\Psi'(r)$, where Ψ' denotes a trigamma function) of the negative log gamma distribution is a function of r, to ensure approximation stability we work on the standardized version of the negative log gamma distribution, by centering with the mean and standardizing with the standard deviation. Then, we estimate the number of components k_r, the weights

w_{rk}, the means m_{rk} and the variance s_r^2 via the Nelder-Mead algorithm by minimizing the Kullback–Leibler (KL) divergence between the two distributions. These parameter estimates ensure that the KL divergence is smaller than 0.0005, so that the difference between the approximate and the exact distributions are ignorable in practice. Because the negative log gamma distribution asymptotically approximates a normal distribution, the approximation becomes easier for larger r. Therefore, we can use increasingly smaller number of normal components for accurate approximation.

For small values of r ($r \in [1, 5]$), we provide detailed parameter values, directly. For median values of r ($r \in [6, 169]$), we no longer need to store parameters for every r. Instead, we can interpolate the weight, mean and variance estimates across the range of r using rational functions without loss of accuracy. For large values of r ($r \in [170, \infty)$), we use a single normal distribution $\mathrm{N}(0, \Psi'(r))$ for approximation. The mean normal mixture approximations are accurate. Even in the most difficult case where $r = 1$, we only observe small difference between the approximate and the exact distributions. The inferred parameters and functions are available from [29].

3.3 Detailed Sampling Steps and Efficient Computation

Now we are ready to describe the detailed MCMC algorithm. Here, with the normal mixture approximation, we have $2n$ latent observations instead of n observations of the original data

$$z_{ij} = \log(\lambda_i) + \epsilon_{ij} = \mathbf{w}_i^T \boldsymbol{\alpha} + x_i \beta_i + g_i + e_i + \epsilon_{ij}, \quad \epsilon_{ij} \sim \sum_{k=1}^{k_{r_{ij}}} w_{r_{ij},k} \mathrm{N}(m_{r_{ij},k}, s_{r_{ij}}^2), \quad j = 1, 2, \tag{7}$$

where $r_{i1} = 1$ and $r_{i2} = y_i$.

We introduce an $2n$-vector of latent indicators $\boldsymbol{\gamma} = (\gamma_{11}, \gamma_{12}, \gamma_{21}, \gamma_{22}, \cdots, \gamma_{n1}, \gamma_{n2})$, where each $\gamma_{ij} \in (1, \cdots, k_{r_{ij}})$ indicates which normal component the corresponding ϵ_{ij} is from. Conditional on z_{ij} and $(\boldsymbol{\alpha}, \beta, g_i, e_i)$, we have

$$P(\gamma_{ij} = k | z_{ij}, \boldsymbol{\alpha}, \beta, g_i, e_i) \propto w_{r_{ij}k} \Phi(z_{ij} - \log(\lambda_i) - m_{r_{ij}k}, \sigma_{r_{ij}}^2), \tag{8}$$

where $k \in (1, \cdots, k_{r_{ij}})$ and Φ denotes the normal density function.

We denote $\mathbf{z}_1 = (z_{11} - m_{1,\gamma_{11}}, \cdots, z_{n1} - m_{1,\gamma_{n1}})^T$ and $\mathbf{z}_2 = (z_{12} - m_{y_1,\gamma_{12}}, \cdots, z_{n2} - m_{y_n,\gamma_{n2}})^T$ as the current latent variables minus the current sampled mean from the normal mixture distribution. Conditional on $\boldsymbol{\gamma}$, we can integrate out $\boldsymbol{\alpha}$, β, $\mathbf{g}$, $\mathbf{e}$ and $\boldsymbol{\epsilon}$ analytically to obtain the marginal distribution of σ^2 and h^2,

$$\begin{aligned} P(\sigma^2, h^2 | \mathbf{z}, \boldsymbol{\gamma}) \propto & |\mathbf{H}|^{-\frac{1}{2}} |\mathbf{W}^T \mathbf{H}^{-1} \mathbf{W}|^{-\frac{1}{2}} |\sigma_b^2 \mathbf{x}^T \mathbf{P}_w \mathbf{x} + 1|^{-\frac{1}{2}} \\ & e^{-\frac{1}{2}(\mathbf{z}_1^T \mathbf{P}_{x,11} \mathbf{z}_1 + \mathbf{z}_2^T \mathbf{P}_{x,21} \mathbf{z}_1 + \mathbf{z}_1^T \mathbf{P}_{x,12} \mathbf{z}_2 + \mathbf{z}_2^T \mathbf{P}_{x,22} \mathbf{z}_2)}, \end{aligned} \tag{9}$$

where $\mathbf{D}_1 = s_1^2 \mathbf{I}$ is an n by n scaled identity matrix, $\mathbf{D}_2$ is an n by n diagonal matrix with iith element $\sigma_{r_{i2}}^2$, $\mathbf{D} = (\mathbf{D}_1^{-1} + \mathbf{D}_2^{-1})^{-1}$, $\mathbf{V} = h^2 \mathbf{K} + (1 - h^2)\mathbf{I}$, $\mathbf{H} = \sigma^2 \mathbf{V} + (\mathbf{D}_1^{-1} + \mathbf{D}_2^{-1})^{-1}$, $\mathbf{P}_w = \mathbf{H}^{-1} - \mathbf{H}^{-1} \mathbf{W}^T (\mathbf{W}^T \mathbf{H}^{-1} \mathbf{W})^{-1} \mathbf{W} \mathbf{H}^{-1}$ and

$$\mathbf{H}_{11}^{-1} = \mathbf{D}_1^{-1} - \mathbf{D}_1^{-1} (\mathbf{D}^{-1} + \sigma^{-2} \mathbf{V}^{-1})^{-1} \mathbf{D}_1^{-1} \tag{10}$$

$$\mathbf{H}_{22}^{-1} = \mathbf{D}_2^{-1} - \mathbf{D}_2^{-1} (\mathbf{D}^{-1} + \sigma^{-2} \mathbf{V}^{-1})^{-1} \mathbf{D}_2^{-1} \tag{11}$$

$$\mathbf{H}_{12}^{-1} = -\mathbf{D}_1^{-1} (\mathbf{D}^{-1} + \sigma^{-2} \mathbf{V}^{-1})^{-1} \mathbf{D}_2^{-1} \tag{12}$$

$$\mathbf{H}_{21}^{-1} = -\mathbf{D}_2^{-1} (\mathbf{D}^{-1} + \sigma^{-2} \mathbf{V}^{-1})^{-1} \mathbf{D}_1^{-1} \tag{13}$$

$$\mathbf{P}_{w,ab} = \mathbf{H}_{ab}^{-1} - (\mathbf{H}_{a1}^{-1} + \mathbf{H}_{a2}^{-1}) \mathbf{W} (\mathbf{W}^T \mathbf{H}^{-1} \mathbf{W})^{-1} \mathbf{W}^T (\mathbf{H}_{1b}^{-1} + \mathbf{H}_{2b}^{-1}) \tag{14}$$

$$\mathbf{P}_{x,ab} = \mathbf{P}_{w,ab} - (\mathbf{P}_{w,a1} + \mathbf{P}_{w,a2}) \mathbf{x} (\mathbf{x}^T \mathbf{P}_{w,ab} \mathbf{x} + \sigma_b^{-2})^{-1} \mathbf{x}^T (\mathbf{P}_{w,1b} + \mathbf{P}_{w,2b}) \tag{15}$$

for $a, b \in 1, 2$.

We can use the Metropolis–Hastings (MH) algorithm to obtain posterior samples for σ^2 and h^2 jointly. Afterwards, we can obtain posterior samples for $\boldsymbol{\alpha}$, β and $\mathbf{g}+\mathbf{e}$ in turn,

$$P(\beta|\mathbf{z}, \boldsymbol{\gamma}, \sigma_g^2, \sigma_e^2) \sim \mathrm{N}((\mathbf{x}^T\mathbf{P}_w\mathbf{x} + \sigma_b^{-2})^{-1}\mathbf{x}^T((\mathbf{P}_{w,11} + \mathbf{P}_{w,21})\mathbf{z}_1 + (\mathbf{P}_{w,12} + \mathbf{P}_{w,22})\mathbf{z}_2), (\mathbf{x}^T\mathbf{P}_w\mathbf{x} + \sigma_b^{-2})^{-1}), \tag{16}$$

$$P(\boldsymbol{\alpha}|\mathbf{z}, \boldsymbol{\gamma}, \beta, \sigma_g^2, \sigma_e^2) \sim \mathrm{MVN}((\mathbf{W}^T\mathbf{H}^{-1}\mathbf{W})^{-1}\mathbf{W}^T((\mathbf{H}_{11}^{-1} + \mathbf{H}_{21}^{-1})(\mathbf{z}_1 - \mathbf{x}\beta) + (\mathbf{H}_{12}^{-1} + \mathbf{H}_{22}^{-1})(\mathbf{z}_2 - \mathbf{x}\beta)), (\mathbf{W}^T\mathbf{H}^{-1}\mathbf{W})^{-1}), \tag{17}$$

$$P(\mathbf{g}+\mathbf{e}|\mathbf{z}, \boldsymbol{\gamma}, \boldsymbol{\alpha}, \beta, \sigma^2, h^2) \sim \mathrm{MVN}(\sigma^2\mathbf{V}\mathbf{H}^{-1}\mathbf{D}(\mathbf{D}_1^{-1}(\mathbf{z}_1 - \mathbf{m}_{\boldsymbol{\gamma}} - \mathbf{W}\boldsymbol{\alpha} - \mathbf{x}\beta) + \mathbf{D}_2^{-1}(\mathbf{z}_2 - \mathbf{m}_{\boldsymbol{\gamma}} - \mathbf{W}\boldsymbol{\alpha} - \mathbf{x}\beta)), \sigma^2\mathbf{V}\mathbf{H}^{-1}\mathbf{D}). \tag{18}$$

Finally, conditional on y_i and λ_i, the posterior of z_{ij} is easy to sample. In particular, we sample τ_{ij} based on standard properties of Poisson process

$$\tau_{i2}|y_i \sim Beta(y_i, 1), \tag{19}$$

$$\tau_{i1}|y_i \sim 1 - \tau_{i2} + Exp(\lambda_i), \tag{20}$$

and obtain $z_{ij} = -log(\tau_{ij})$. This way, we can perform MCMC based on the two latent variables z_{i1} and z_{i2}, bypass the count likelihood.

The most computationally expensive part of the algorithm is the MH step: a naive approach to evaluate $P(\sigma^2, h^2|z_i, \gamma_i)$ would involve cubic operations. Our mean normal mixture approximation allows us to evaluate this marginal likelihood efficiently as we can apply here the mixed model innovations developed recently [23–26]. This is because given the observed data, $\mathbf{D}$ is a fixed diagonal matrix where the elements do not depend on a $\boldsymbol{\gamma}$ that changes in every MCMC iteration. Therefore, for a given matrix $\mathbf{V}$, we can perform an eigen-decomposition on $\mathbf{D}^{-\frac{1}{2}}\mathbf{V}\mathbf{D}^{-\frac{1}{2}} = \mathbf{U}\mathbf{D}_h\mathbf{U}^T$. This allows us to decompose $\mathbf{H} = \sigma^2\mathbf{V} + \mathbf{D} = \mathbf{D}^{\frac{1}{2}}\mathbf{U}(\sigma^2\mathbf{D}_h + \mathbf{I})\mathbf{U}^T\mathbf{D}^{\frac{1}{2}}$. Afterwards, we can transform the latent variables and other covariates to obtain $\mathbf{D}^{\frac{1}{2}}\mathbf{U}\mathbf{z}_1$, $\mathbf{D}^{\frac{1}{2}}\mathbf{U}\mathbf{z}_2$, $\mathbf{D}^{\frac{1}{2}}\mathbf{U}\mathbf{W}$ and $\mathbf{D}^{\frac{1}{2}}\mathbf{U}\mathbf{x}$. This procedure avoids any cubic operations later on in the MCMC steps. Therefore, with the mean normal mixture approximation, we only need to perform eigen-decompositions at the beginning of the MCMC. Afterwards, each Gibbs step only requires quadratic operations (transformation of $\mathbf{z}_1, \mathbf{z}_2$). In practice, because $\mathbf{V}$ is a function of h^2, we assign a discrete uniform prior for h^2 and evaluate the eigen-decompositions on every discrete values of h^2. In the present study, we found that using either 10 or 100 discrete values of h^2 yields almost identical results (and we present the analyses results for the former in the main text), suggesting that a fine grid for h^2 is not necessary because of our small sample size. Finally, for all analyses in the present study, we ran 1100 Gibbs sampling iterations with the first 100 as burn-in. In each Gibbs iteration, after sampling the latent variables $\mathbf{z}_1, \mathbf{z}_2$ and the latent indicators $\boldsymbol{\gamma}$, we further ran 10 MH steps before continuing the Gibbs iterations.

4 Parameter Estimation and p Value Computation

Denote $\bar{\beta}$ as the posterior mean and σ_β^2 as the posterior variance. Since both the likelihood and the posterior follow normal distributions asymptotically, and because we also use a normal distribution as the prior distribution, we can easily obtain the approximate maximum likelihood estimate and its standard error by the method of moments, or

$$\hat{\beta} = \sigma_b^2\bar{\beta}/(\sigma_b^2 - \sigma_\beta^2), \tag{21}$$

$$se(\hat{\beta}) = \sigma_b\sigma_\beta/\sqrt{\sigma_b^2 - \sigma_\beta^2}. \tag{22}$$

The condition $\sigma_b^2 > \sigma_\beta^2$ is guaranteed by asymptotics. In rare cases, however, this condition may not be satisfied because of the limited MCMC sampling iterations in practice. This may be particularly concerning for genes where the likelihood function is not informative. Arguably, these non-informative genes are the ones that we do not want to perform analysis on in the first place. Therefore, this condition gives us a natural way to perform post-filtering. In the software implementation, we do not analyze genes where $\sigma_\beta^2 \geq c\sigma_b^2$ for a user defined threshold c ($c \leq 1$). We use $c = 0.95$ throughout the present study. This post-filtering step, however, has minimal influence on the results, as only a few dozen genes, out of half a million, are filtered out in each analysis.

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