

Figure 1: Comparison of standard deviation σ per gene for data set 1. Left: Raw data versus LEMming. Right: $\Delta\Delta CT$ normalized data (reference gene: *Gapdh*) versus LEMming processed data. Both cases show that σ 's per gene of LEMming processed are smaller.

Error variance of $\Delta\Delta C_t$ method in comparison with LEMming

Here, we want to proof, that LEMming results in a decreased standard deviation compared $\Delta\Delta C_t$ with one reference gene (RG). In the following we use abbreviations for *ref* - *r*, *target* - *t*, *sample* - *s* and *control* - *c*. For sake of simplicity we make three simplifying assumptions: We assume that the PCR efficiency $E_t = E_r$, the $\Delta\Delta C_t$ is

$$\Delta\Delta C_t = (C_t^{r,s} - C_t^{t,s}) - (C_t^{r,c} - C_t^{t,c})$$

We assume that control and sample measurements originate from different animals. According to LEMming the C_t -values can be decomposed (e.g. $C_t^{r,s} = \epsilon_{P:A,r} + \epsilon_{S,s} + \Delta_{T,s} + \Delta_{T:G,r,s} + \epsilon_{r,s}$). Calculating the $\Delta\Delta C_t$ value the probe and sample errors cancel out. The variables $\Delta_{T,-}$ and $\Delta_{T:G,-,-}$ with the according indices are not classified as random variables. Thus, their variance is zero. The random variables $\epsilon_{r,s}$, $\epsilon_{r,c}$, $\epsilon_{t,s}$ and $\epsilon_{t,c}$ are independently distributed.

$$Var(\Delta\Delta C_t) = Var(\epsilon_{r,s} - \epsilon_{t,s} - \epsilon_{r,c} + \epsilon_{t,c})$$

Assuming that all ϵ 's have the same variance σ_ϵ^2 , the variance of $\Delta\Delta C_t$ is given by $4\sigma_\epsilon^2$. The ΔC_t (distance to the mean of the control) of LEMming has the variance

$$Var(\Delta C_t) = Var(\epsilon_{t,s}) + Var(Mean(\epsilon_{t,c}))$$

With all ϵ 's being equal the variance is of the ΔC_t is $\sigma_\epsilon^2 + \frac{\sigma_\epsilon^2}{n}$ where n is the size of the control group. This means that $Var(\Delta C_t) < Var(\Delta\Delta C_t)$, proving that LEMming has lower variance compared to the $\Delta\Delta C_t$ method. If the variances of control group and treated group are different, as we have shown for DS1 in the main manuscript, only $Var(\epsilon_{t,s})$ cancel out and the variances are:

$$Var(Mean(\epsilon_{t,c})) < Var(\epsilon_{r,s}) + Var(\epsilon_{r,c}) + Var(\epsilon_{t,c}).$$

If sample and control are from the same animals, the random variables ϵ are not statistically independent. The covariance of ϵ 's can reduce the variances of the $\Delta\Delta C_t$ method.

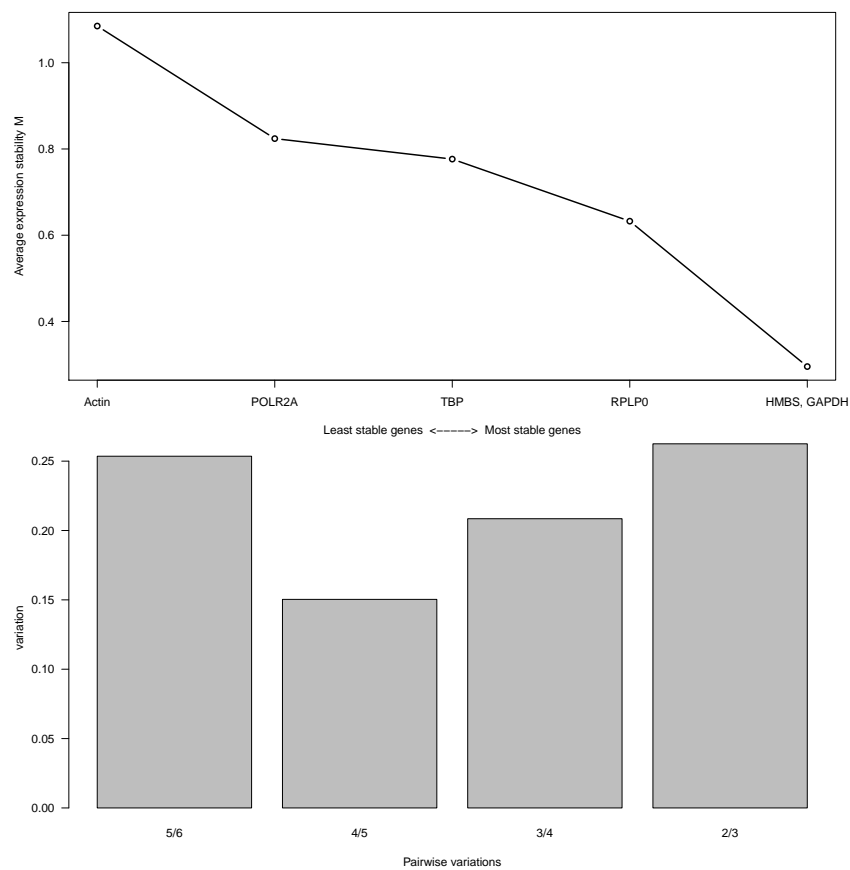
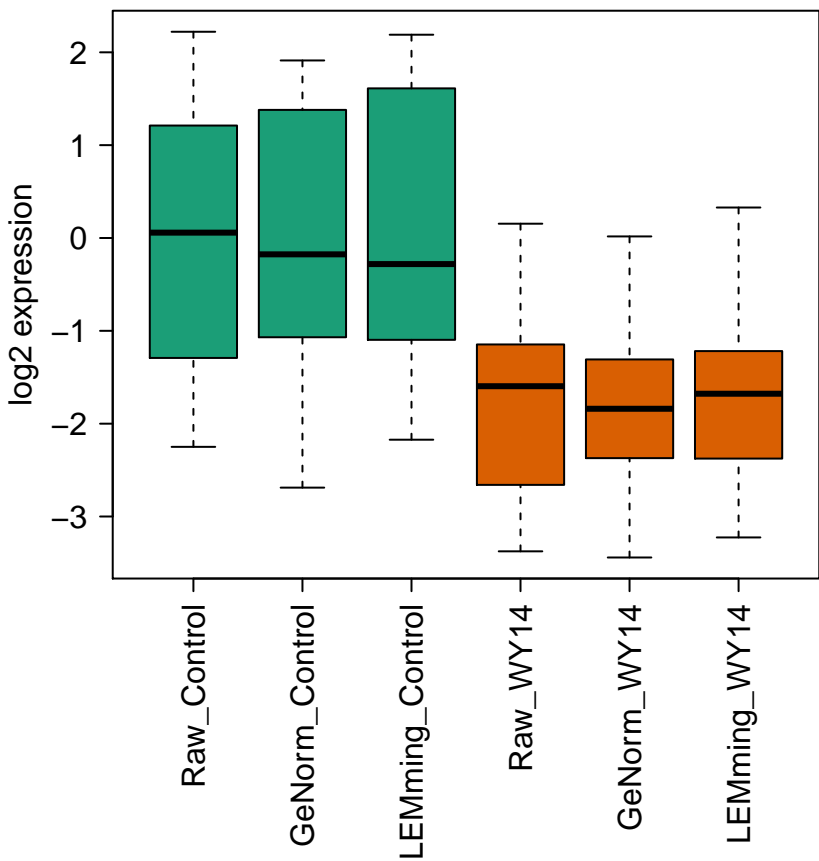
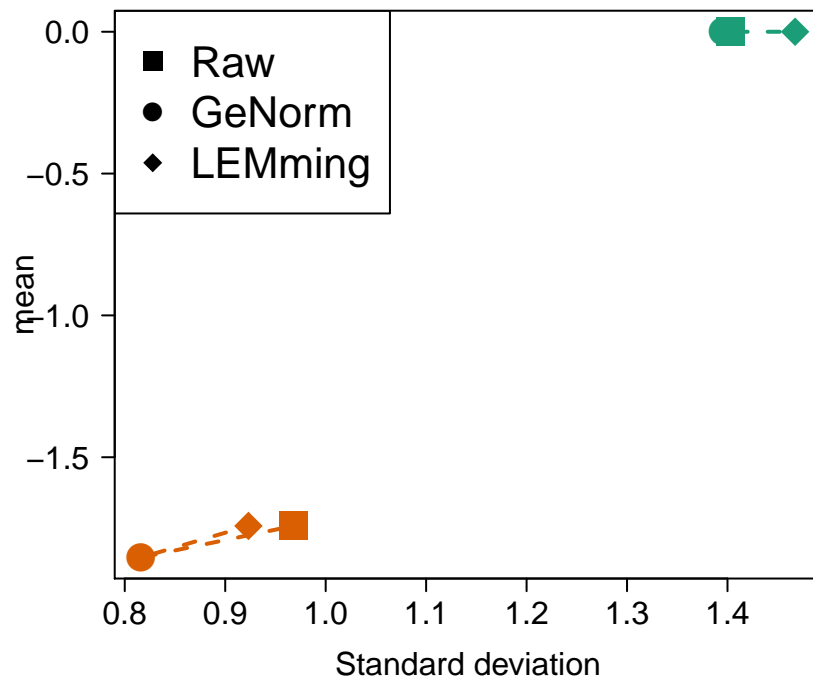
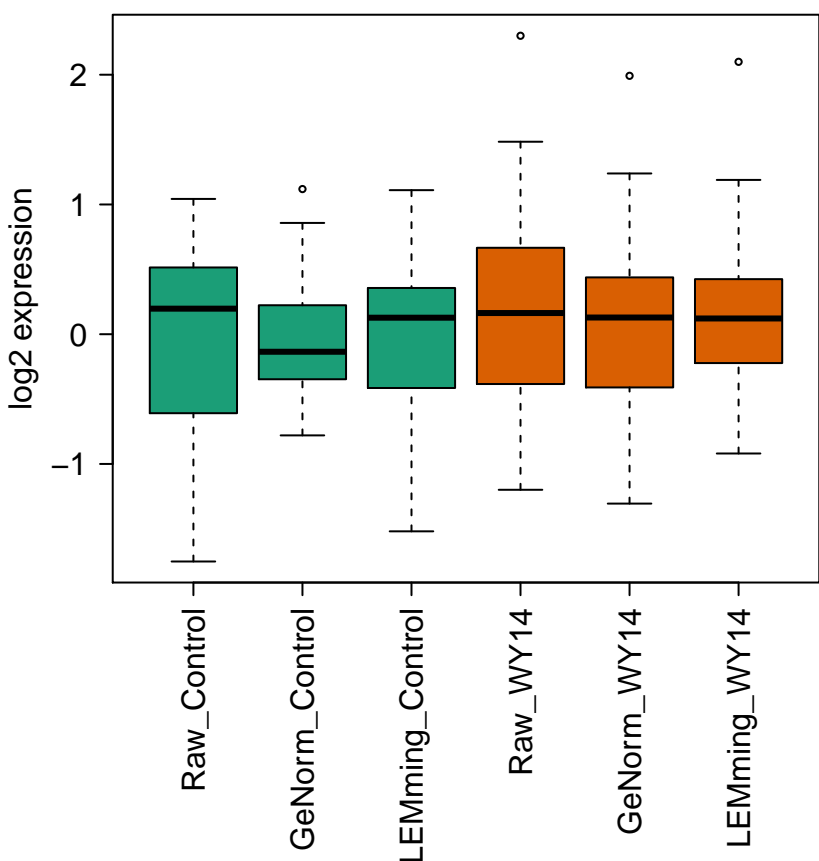
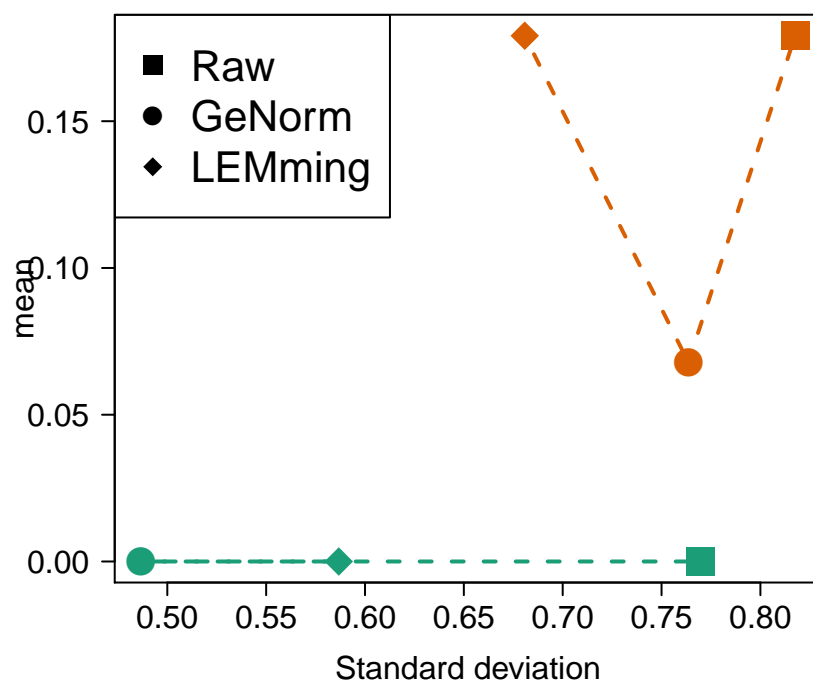
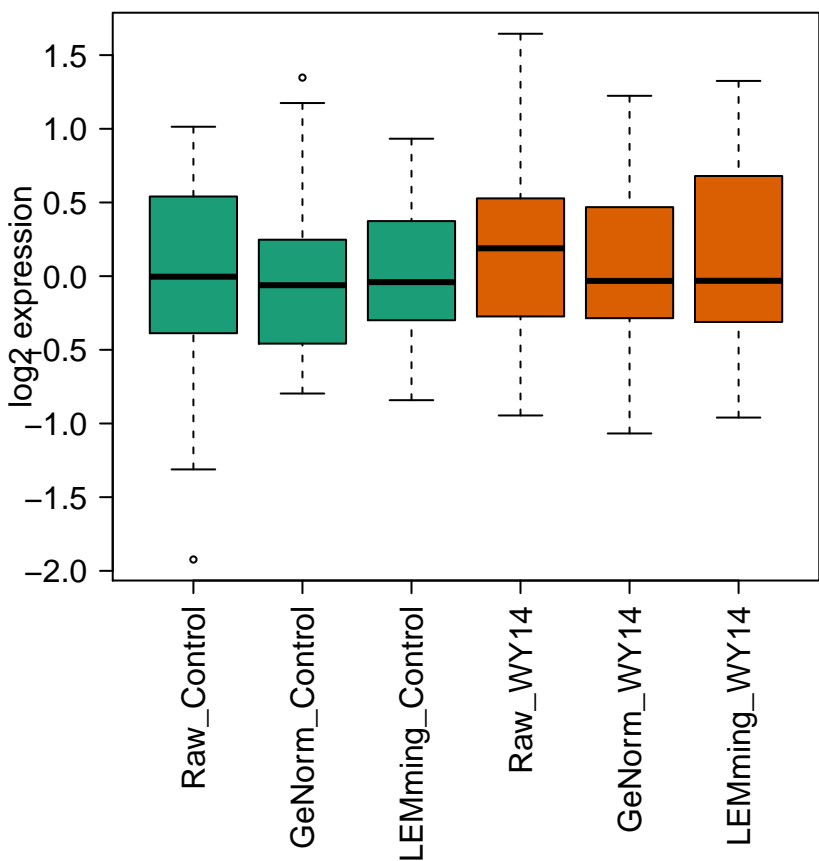
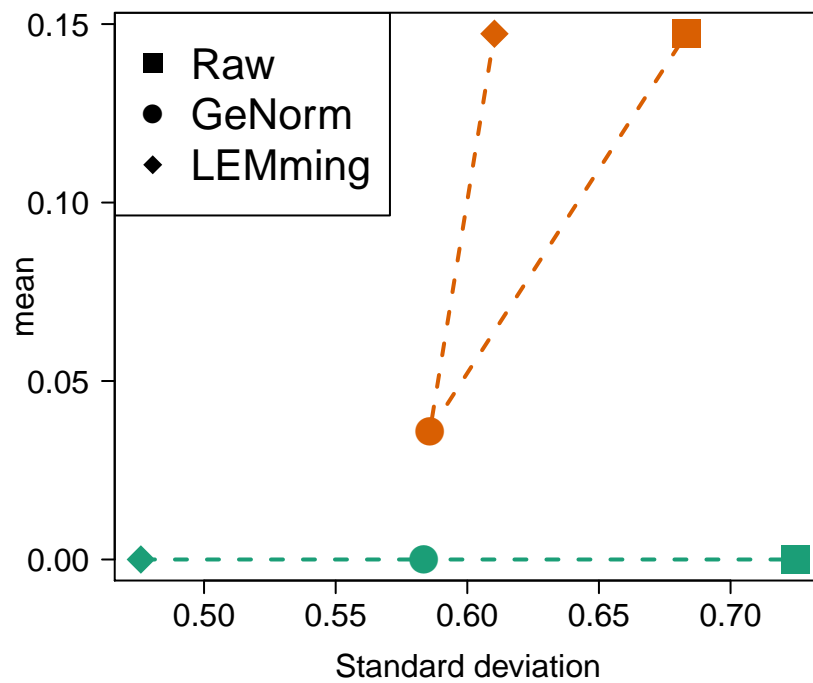
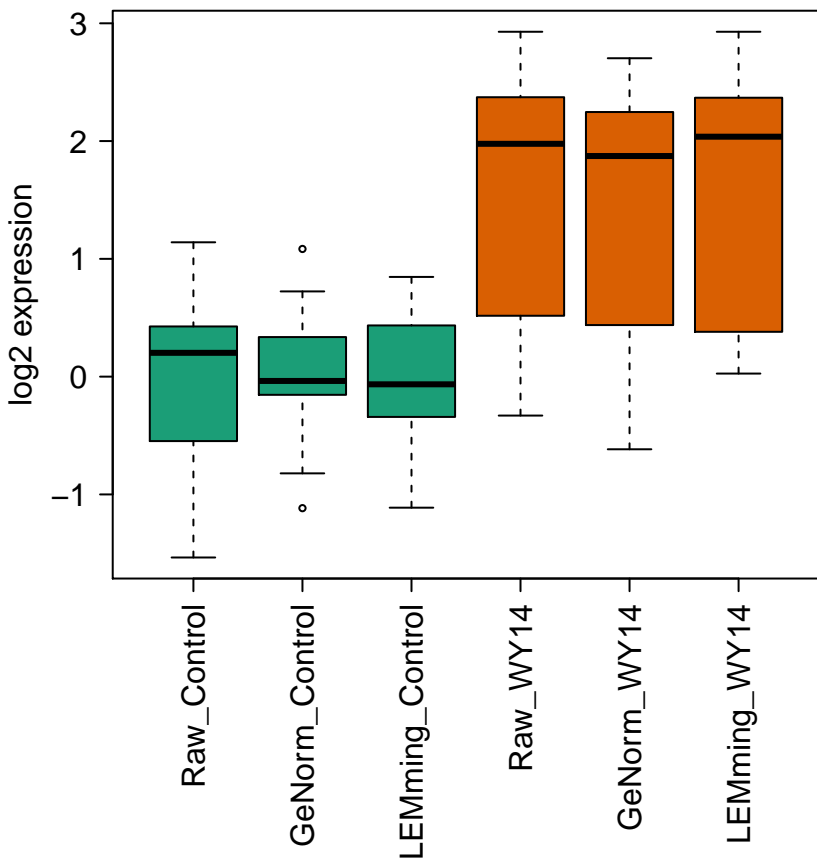
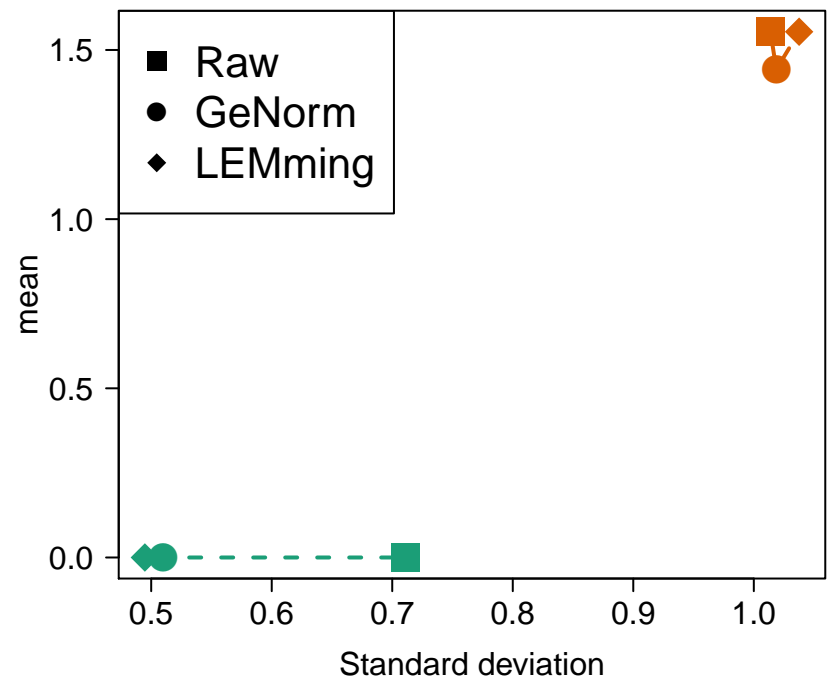
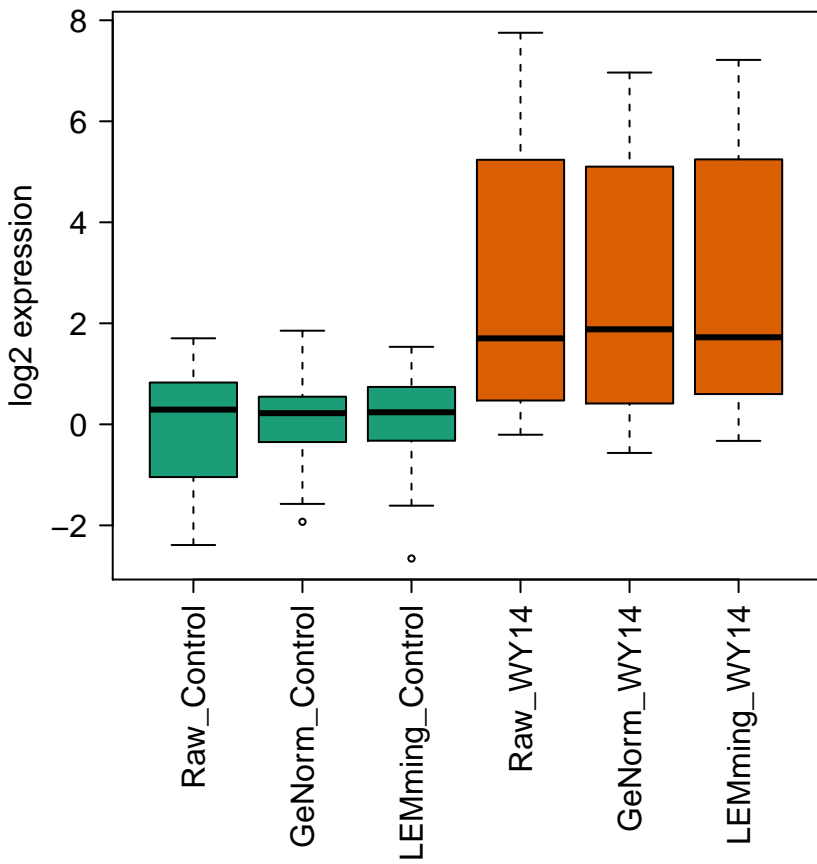
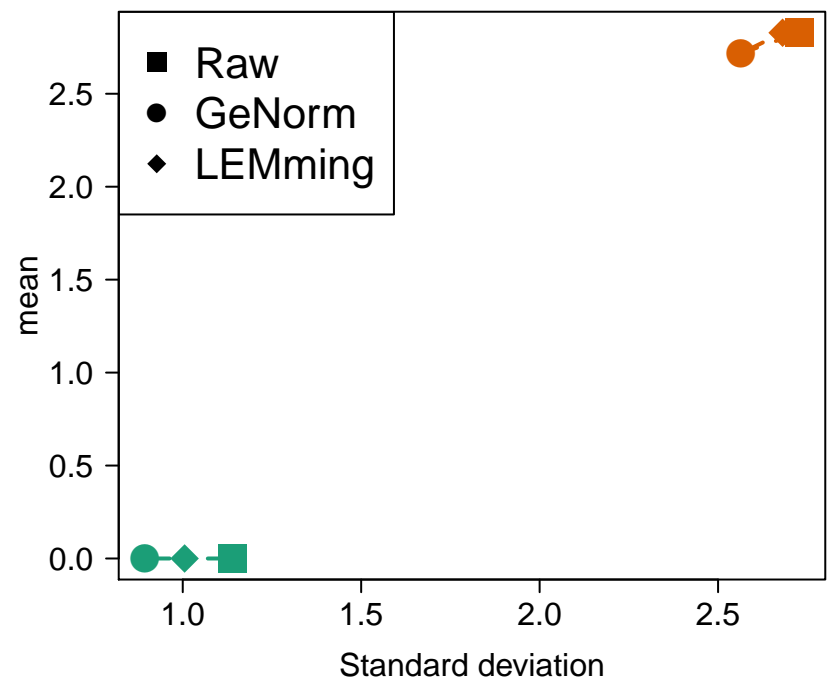
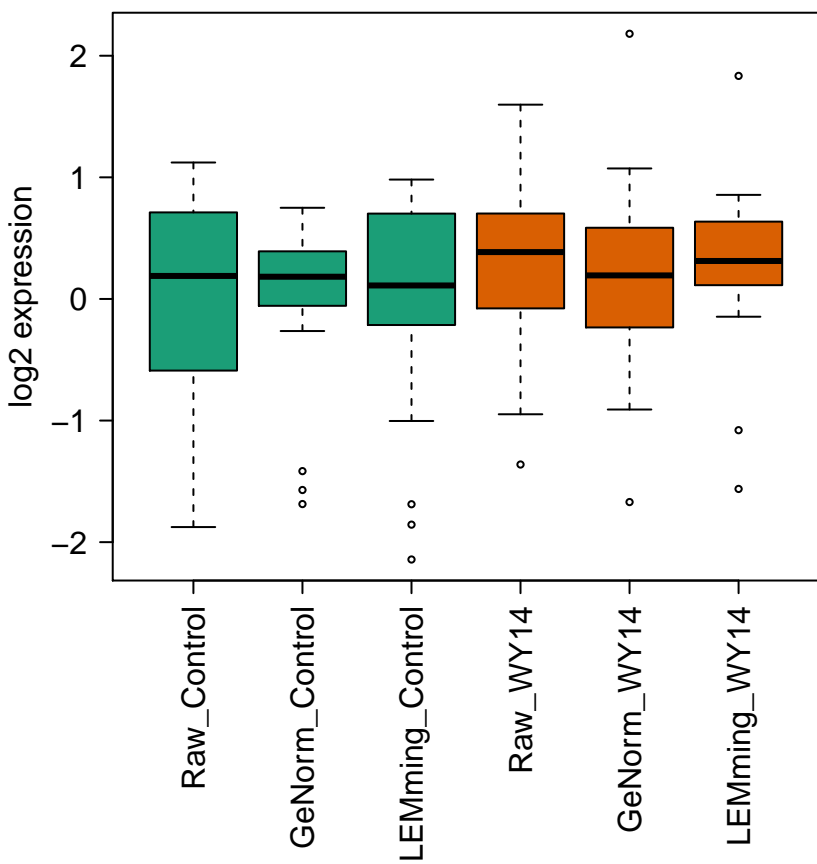
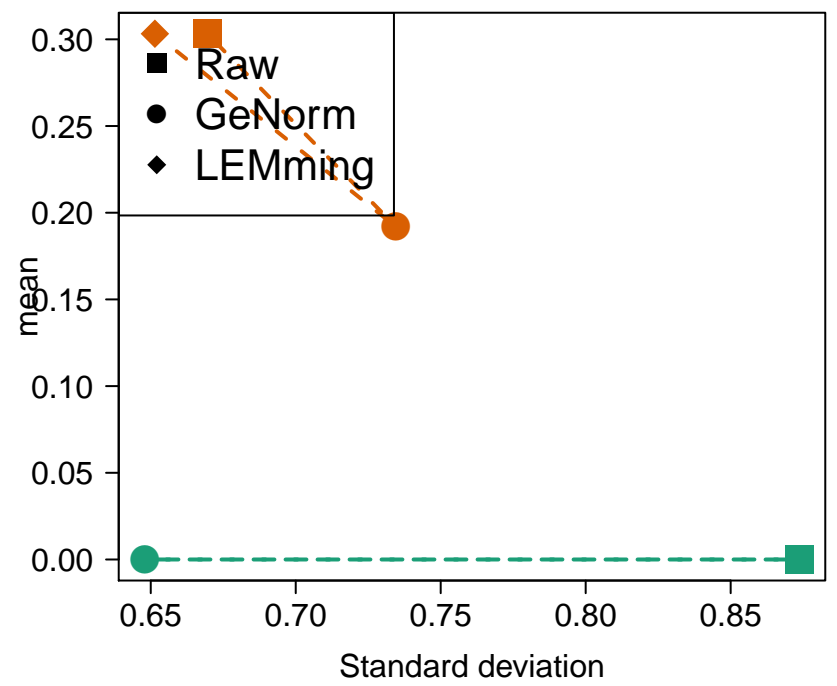
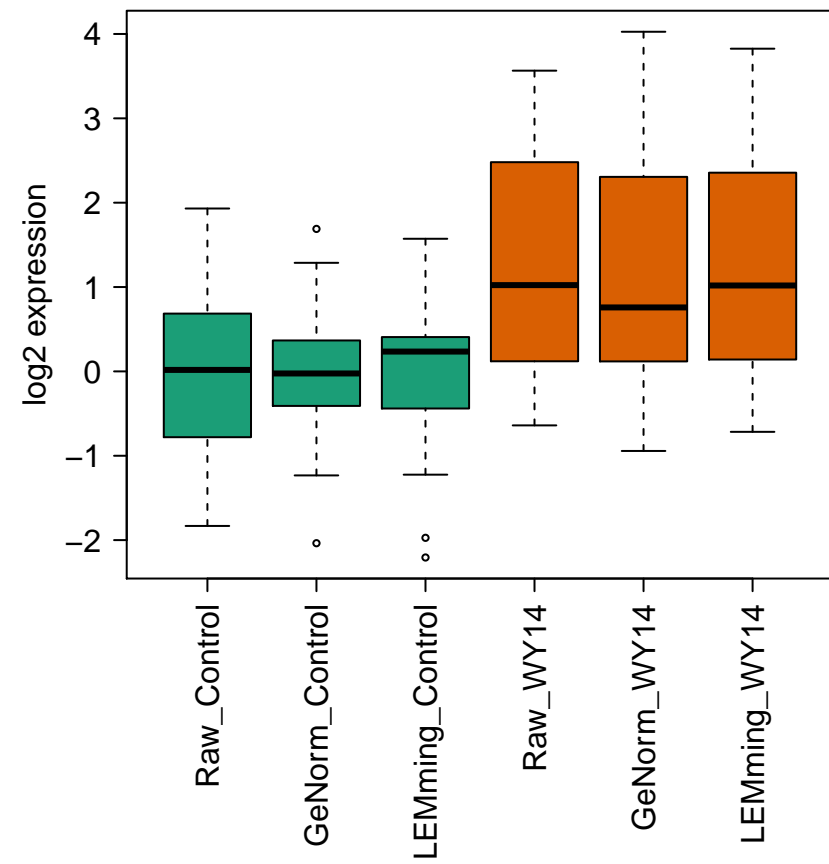
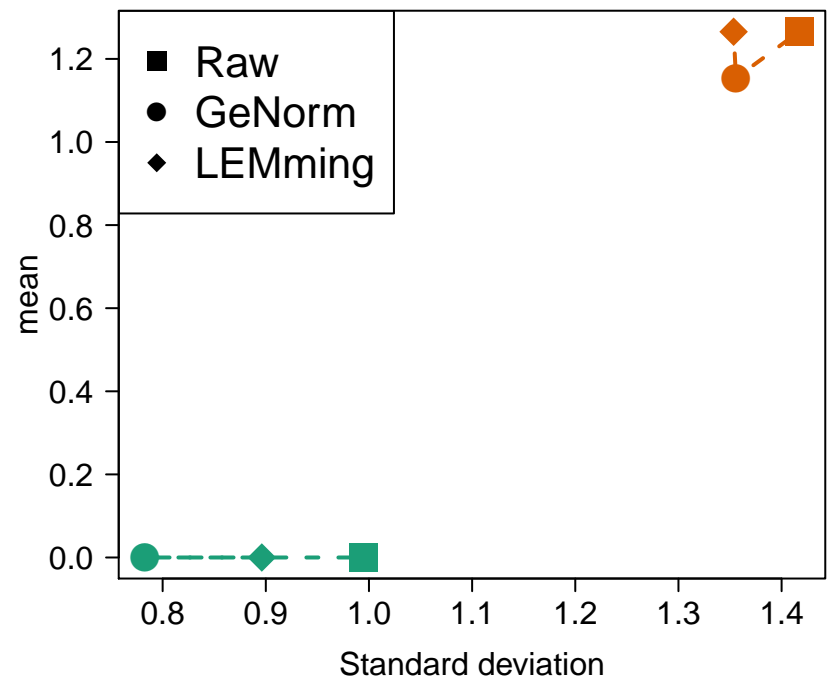
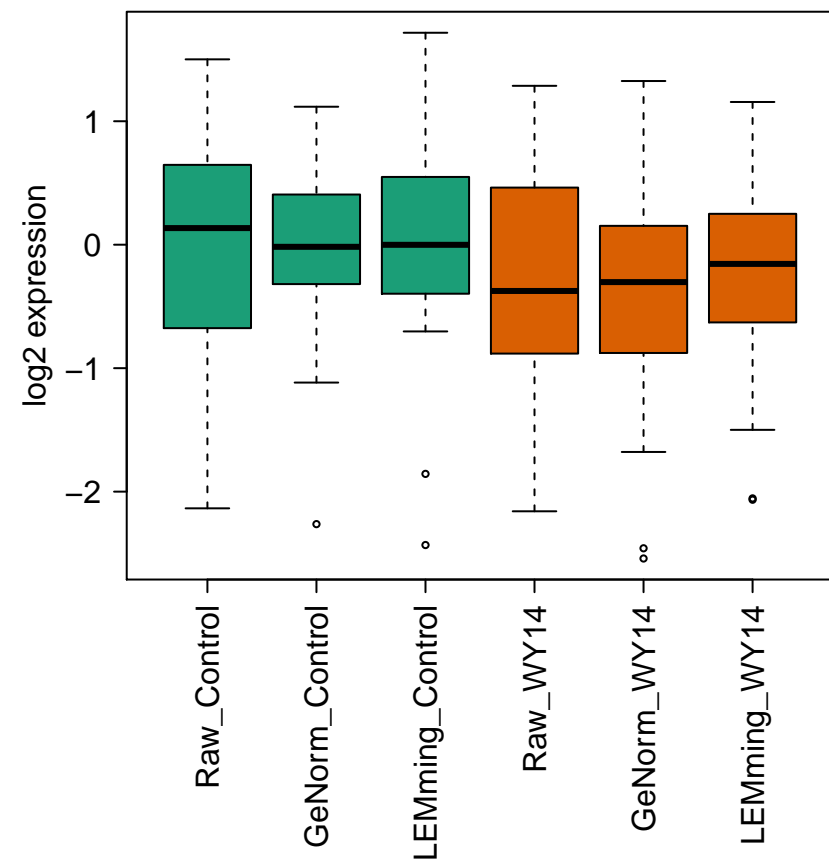
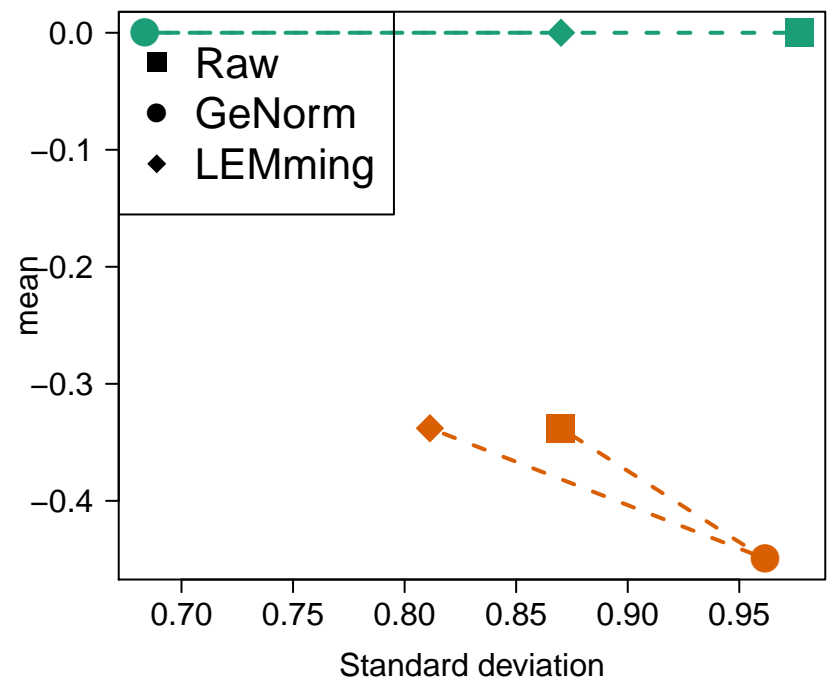
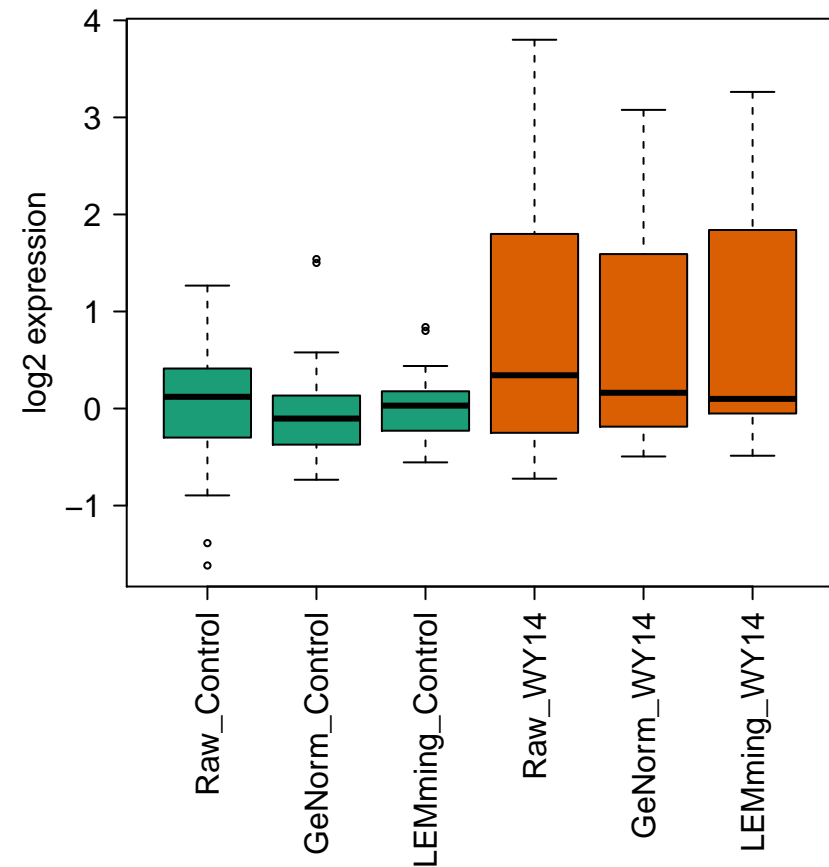
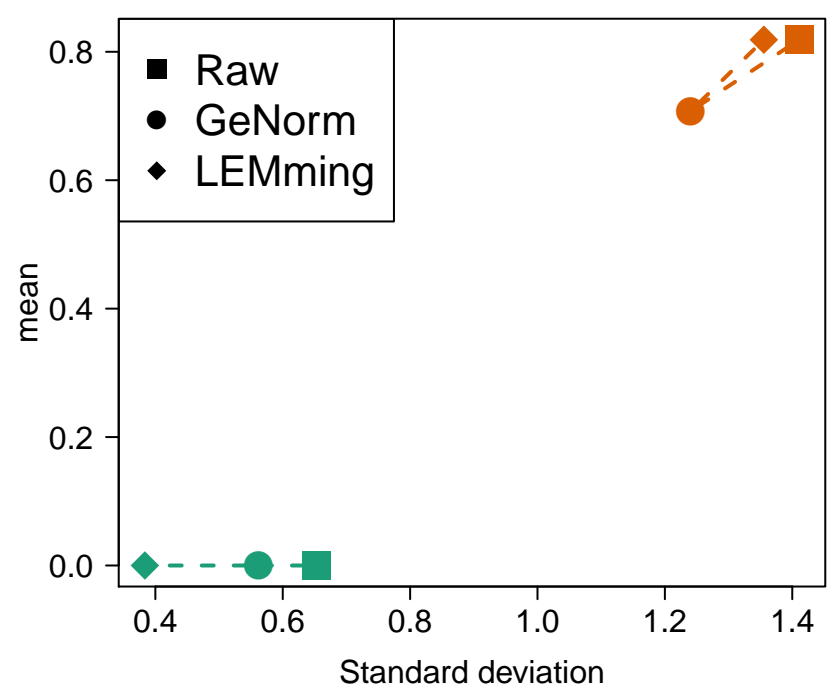
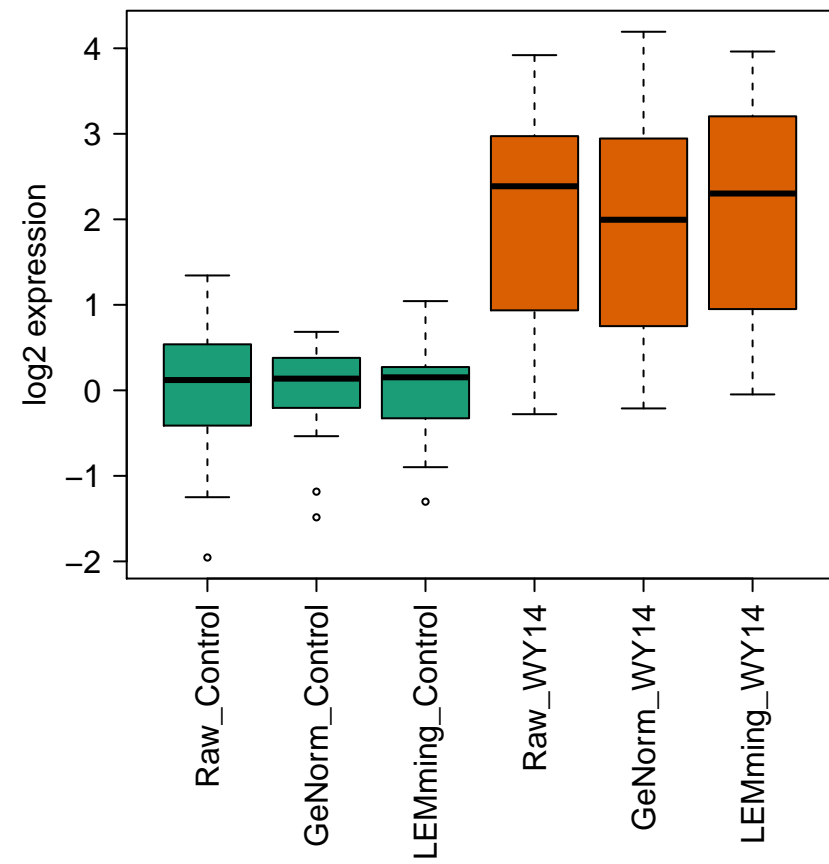
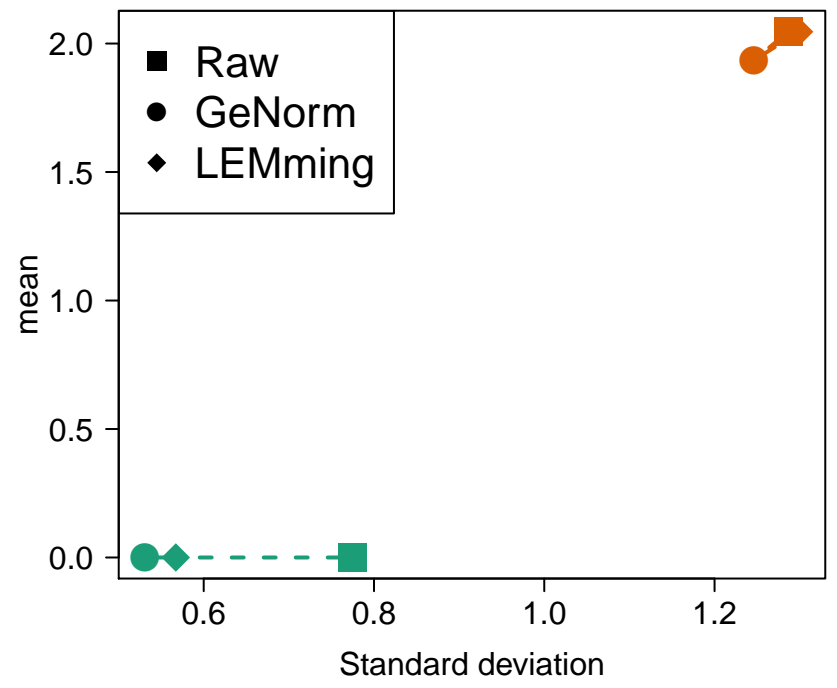
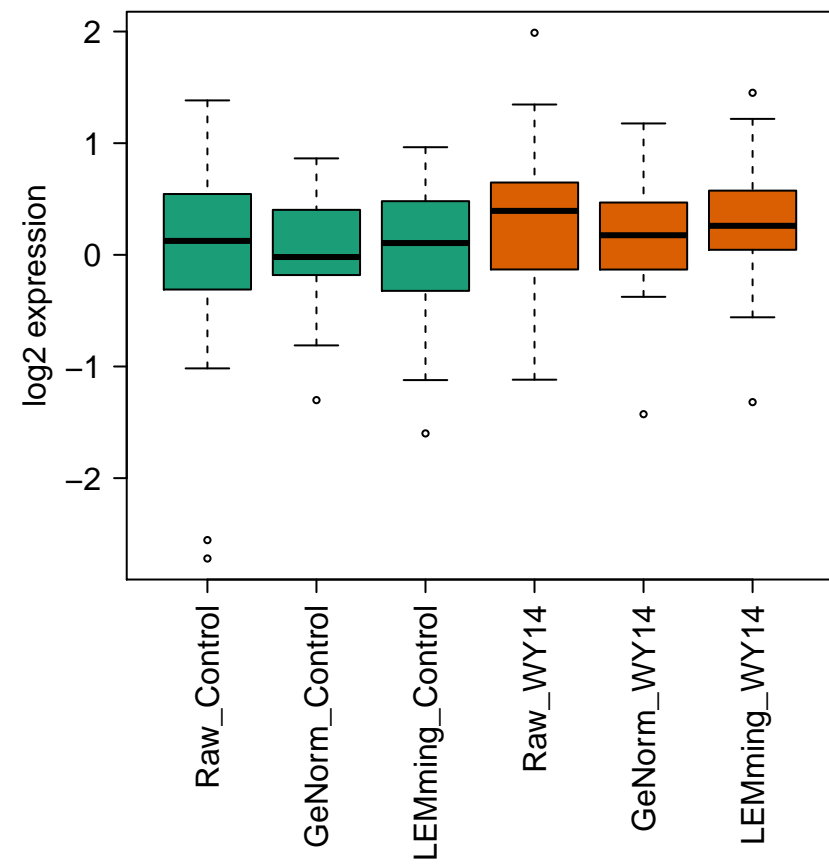
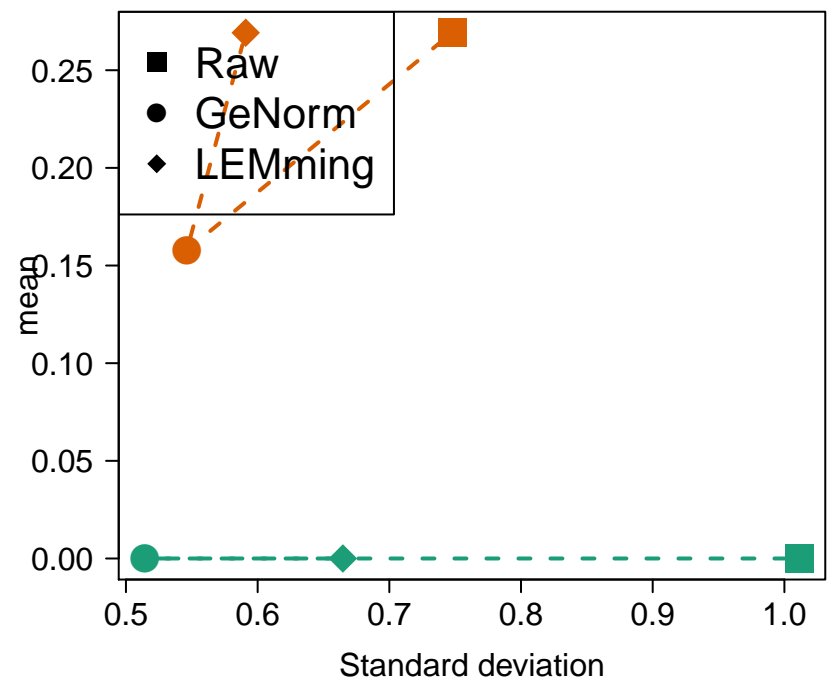
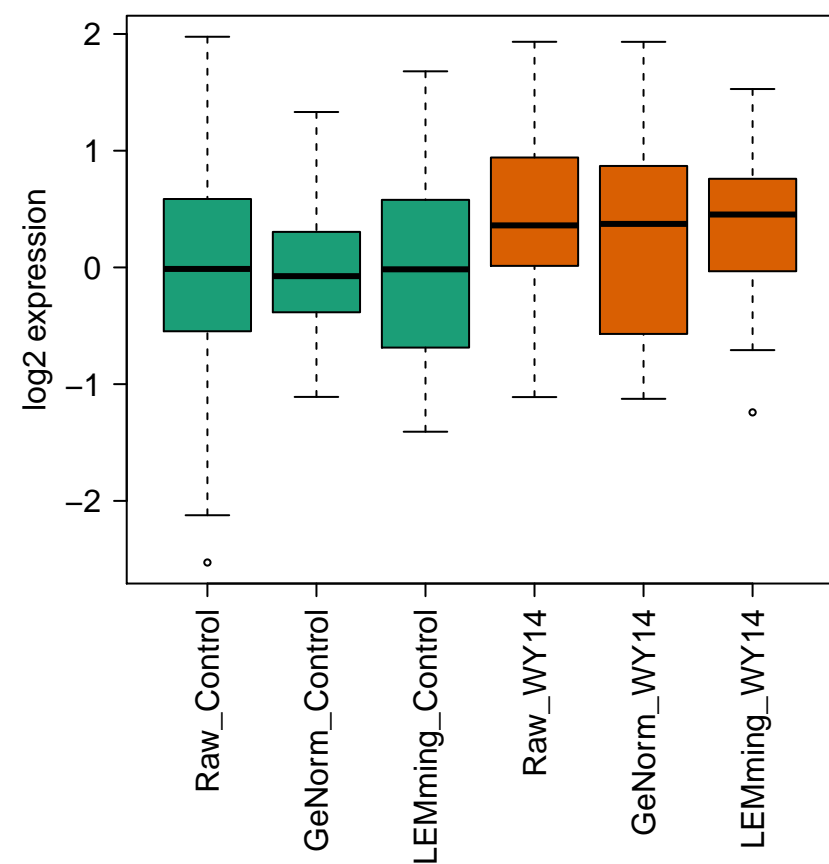
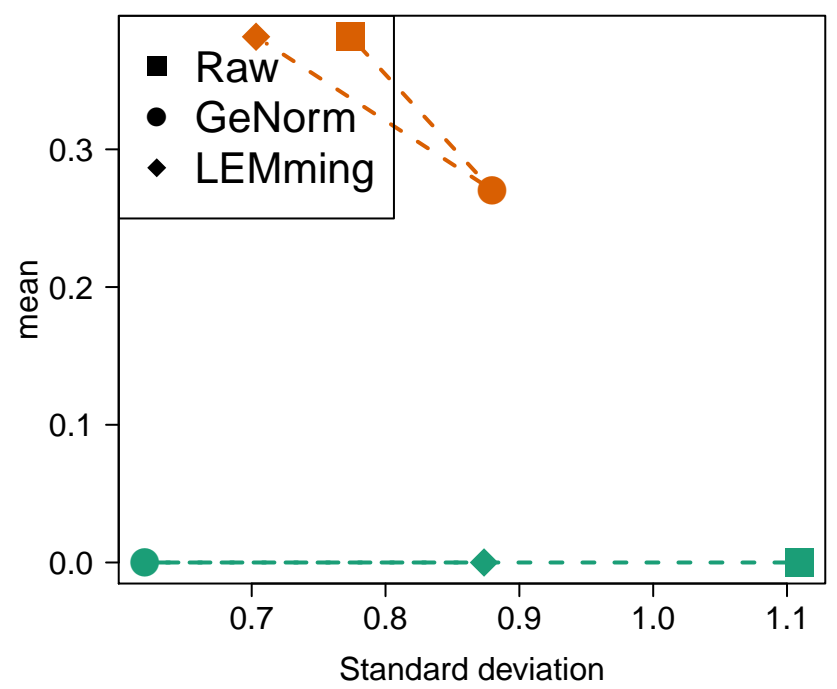


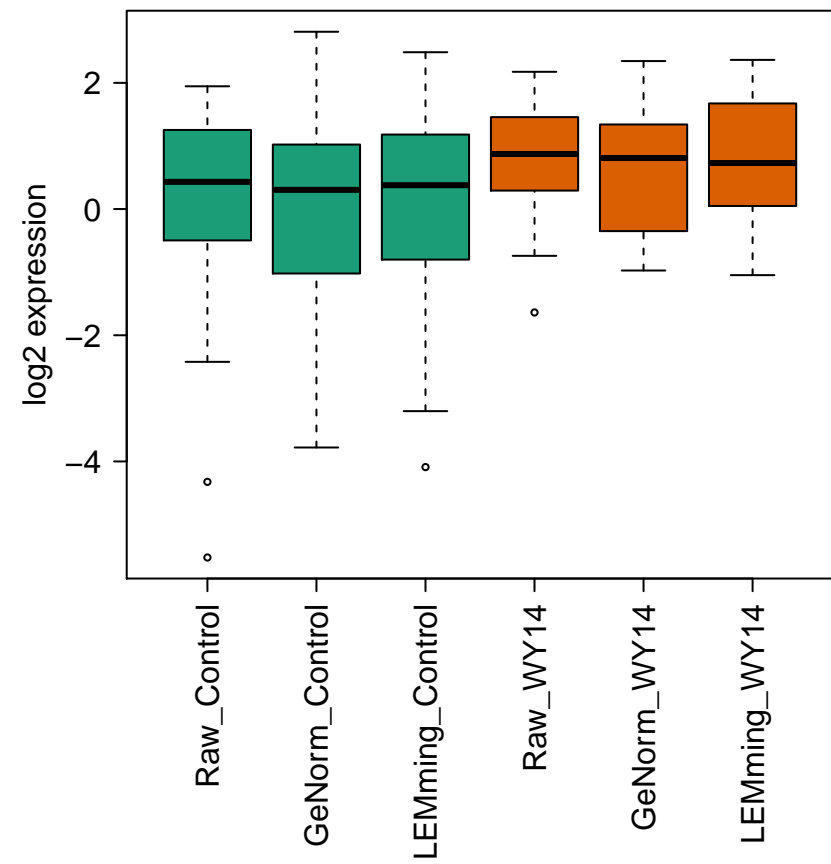
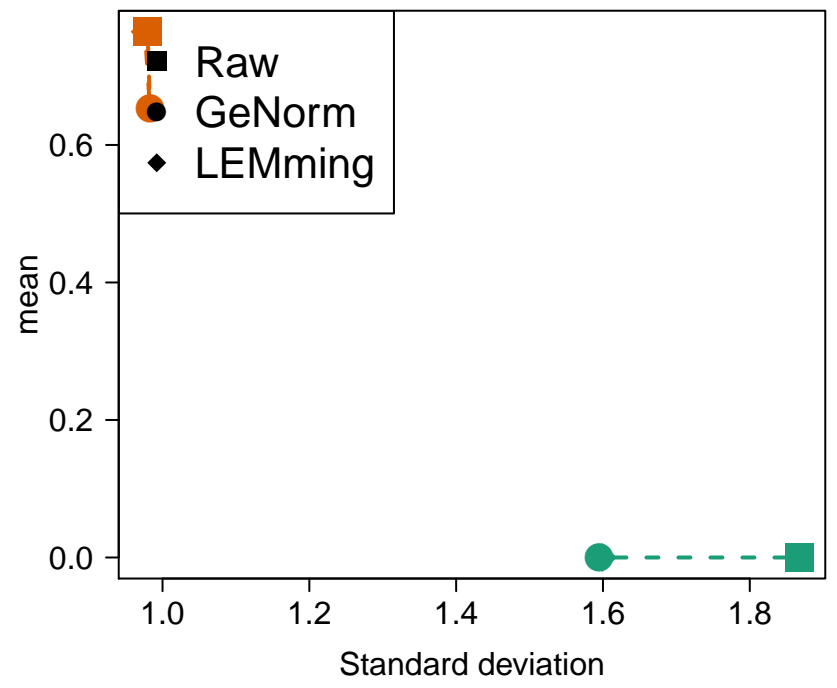
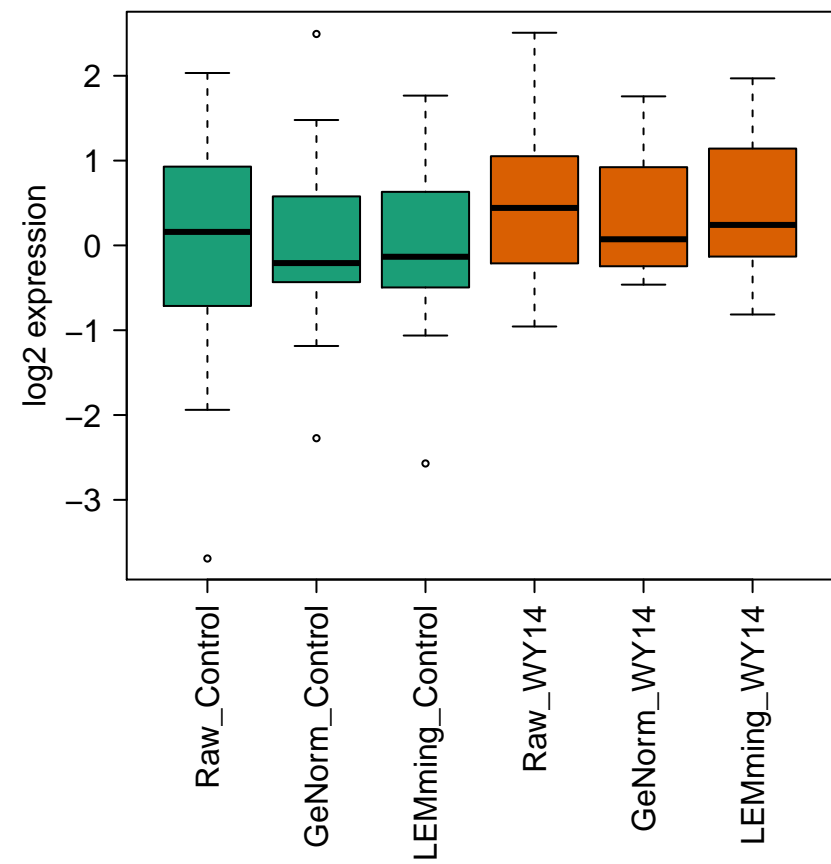
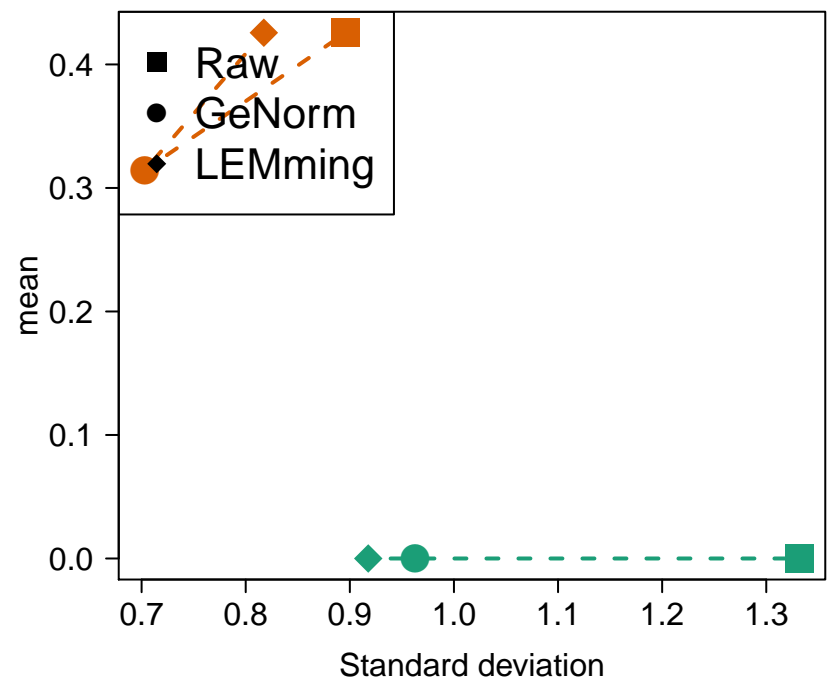
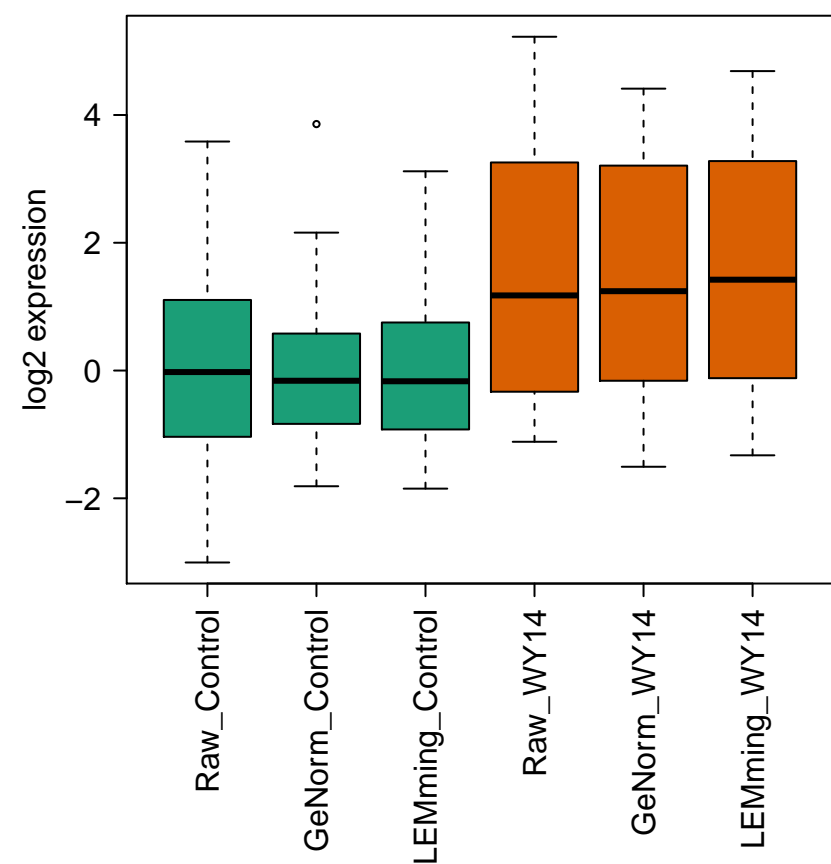
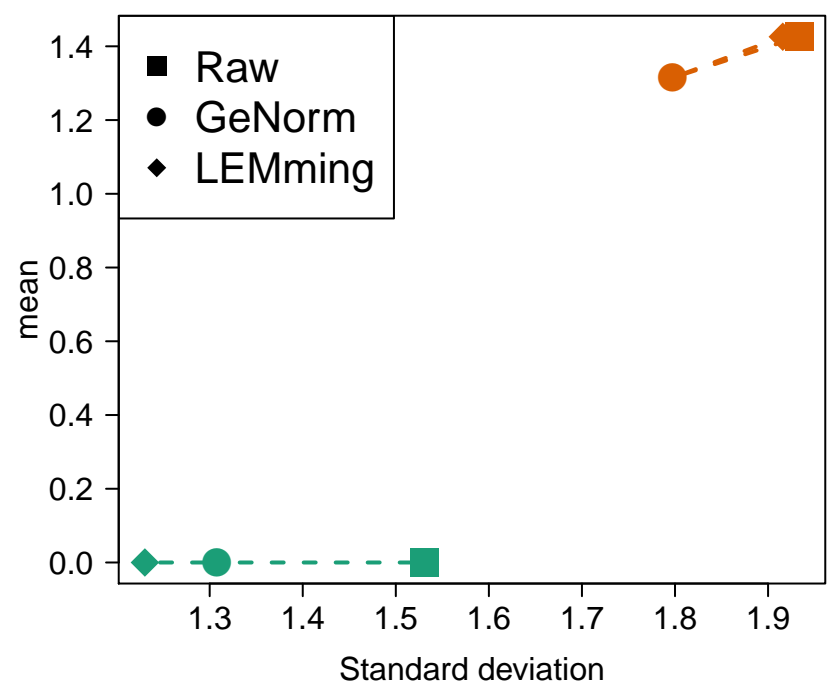
Figure 2: Average expression stability and pairwise variation of data set 1 according to Vandesompele et al. 2002. We selected *GAPDH*, *HMBS*, *RPLP0* and *TBP* with a pairwise variation of 0.15 and M-values below 0.8 as RGs for *geNorm* normalization.

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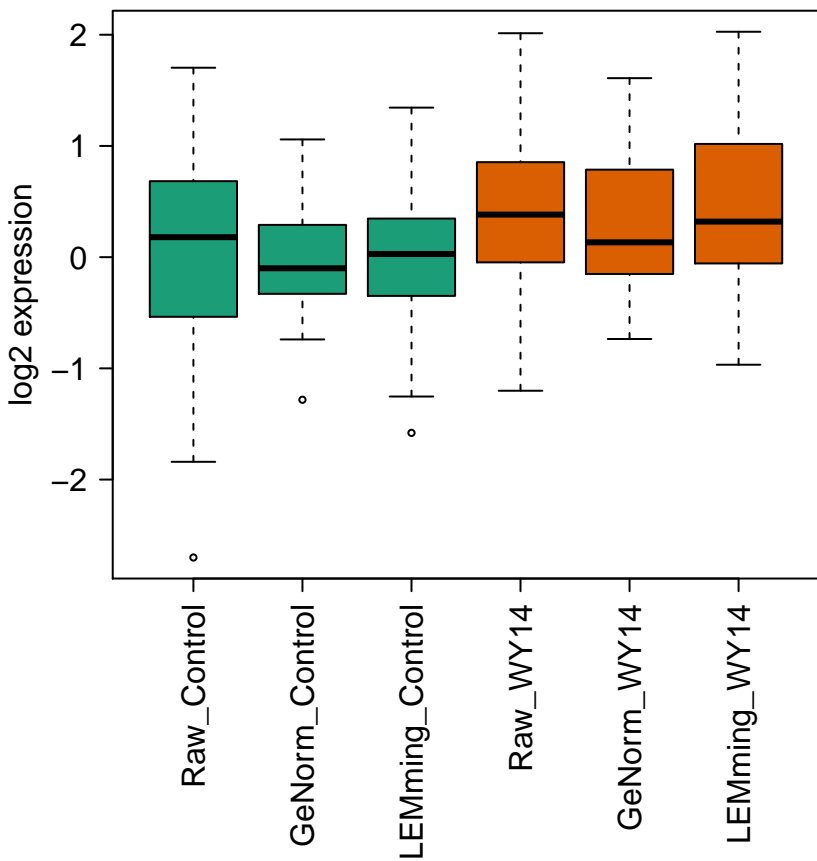
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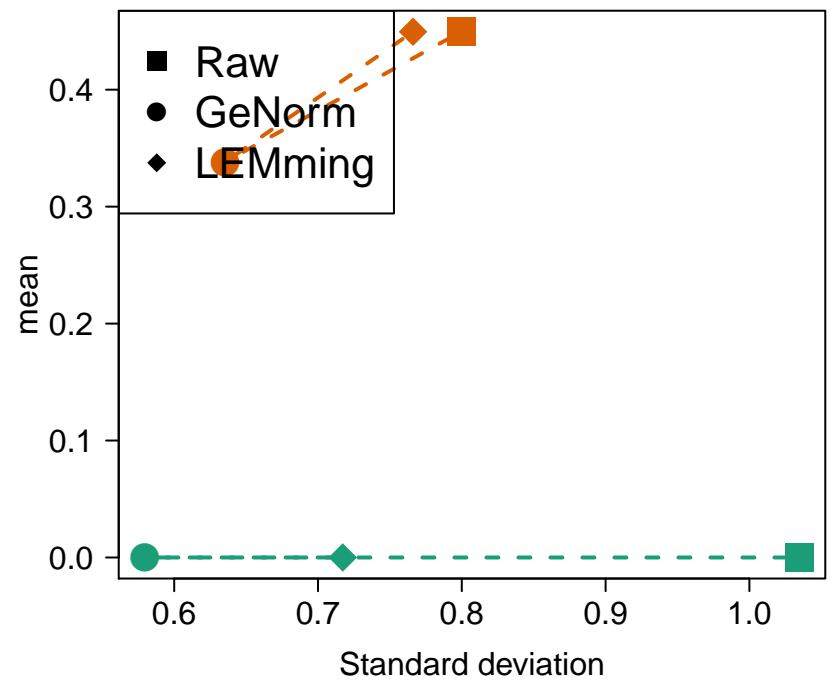
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CYP1A1**Variance–mean plot****SULT1A1****Variance–mean plot****SULT1B1.****Variance–mean plot**

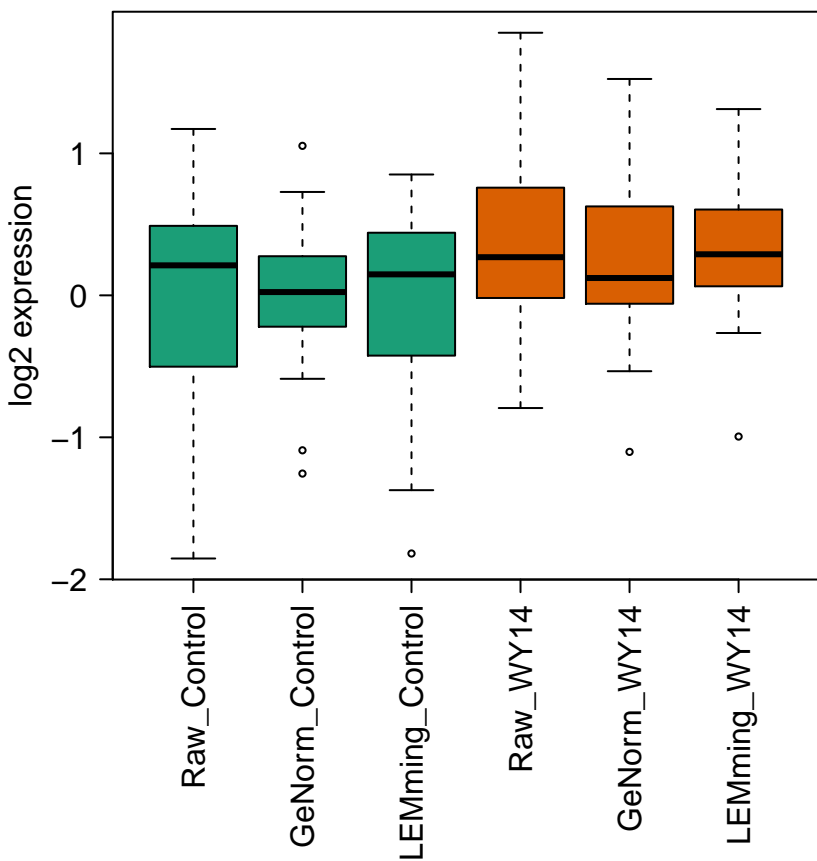
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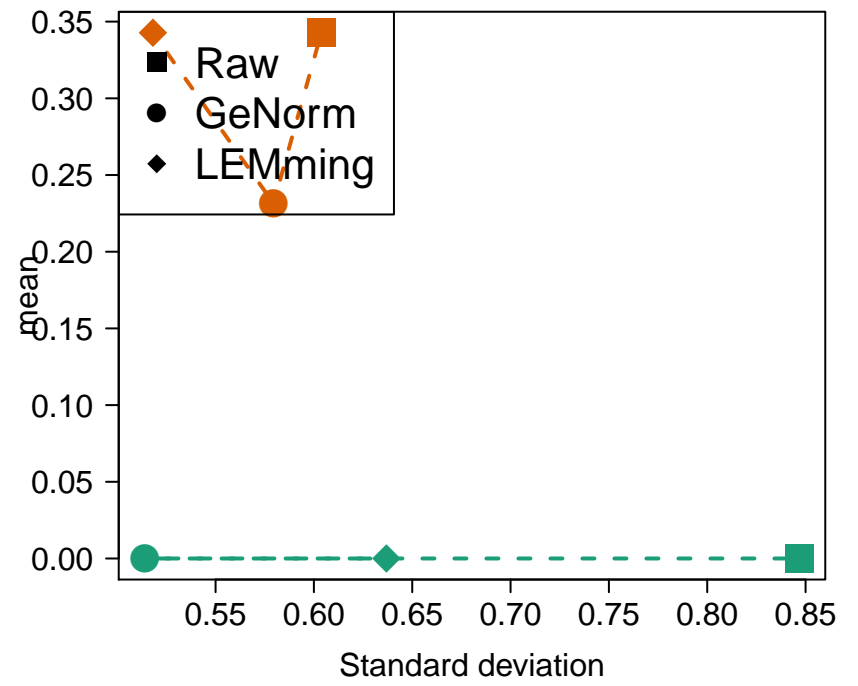
Variance-mean plot



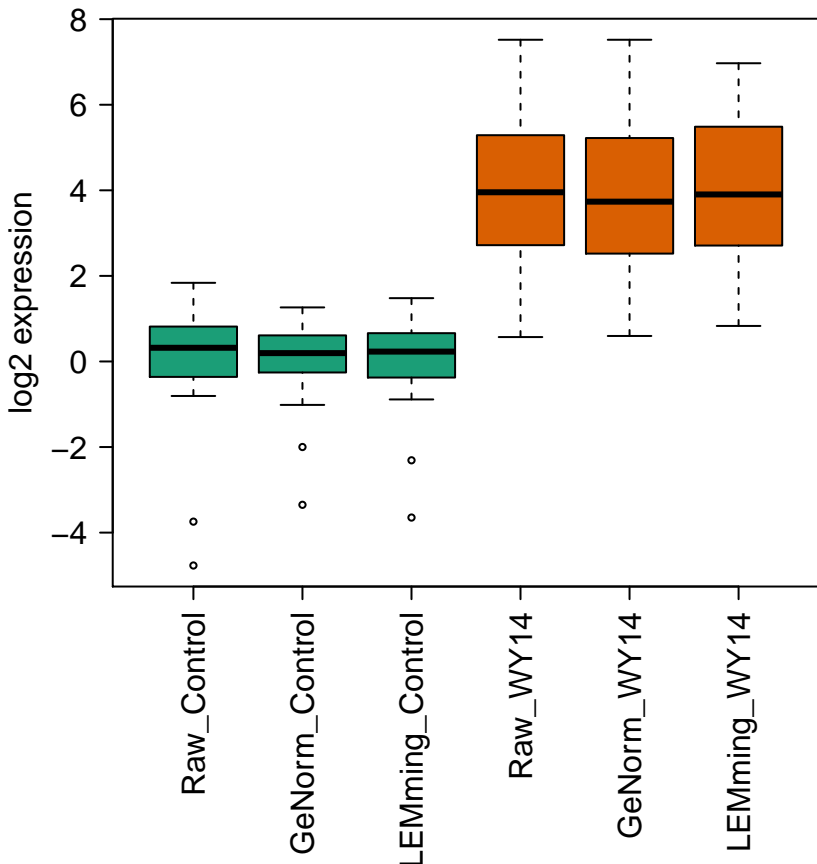
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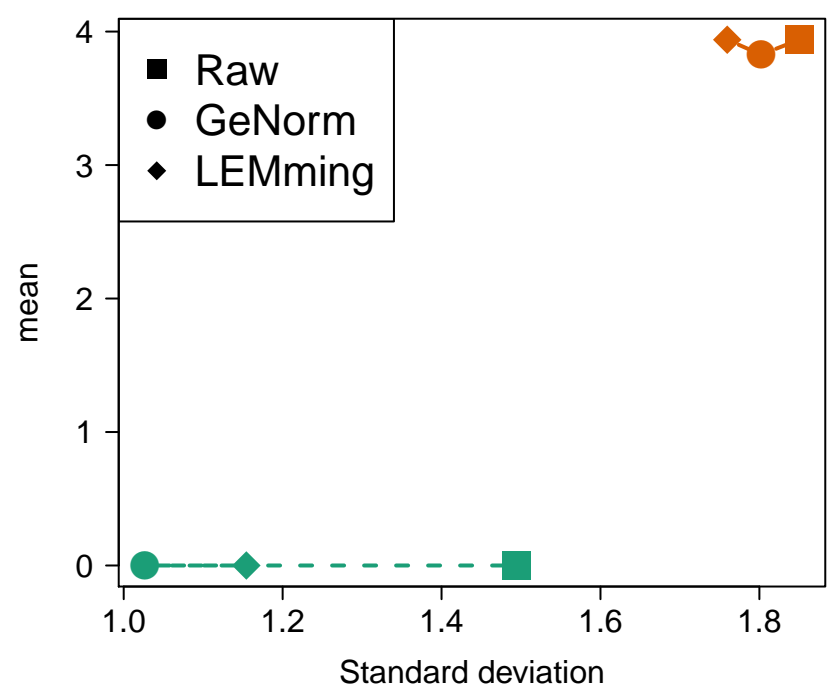
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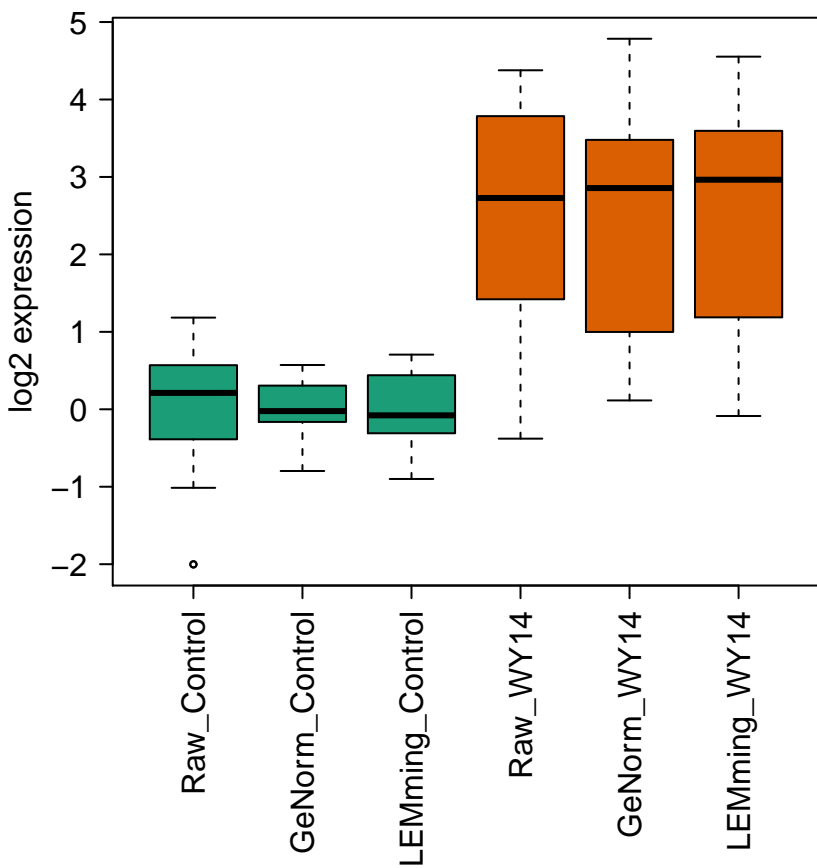
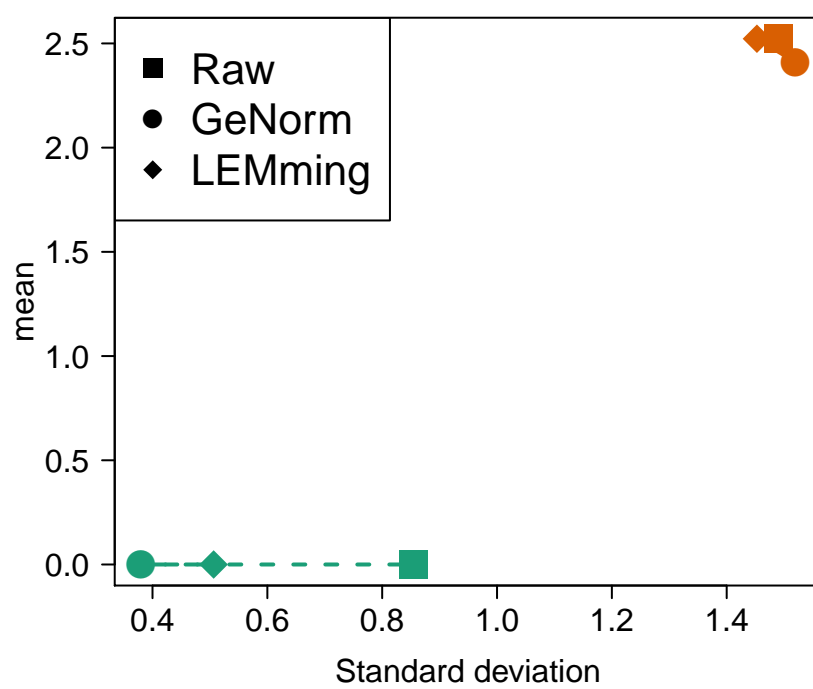
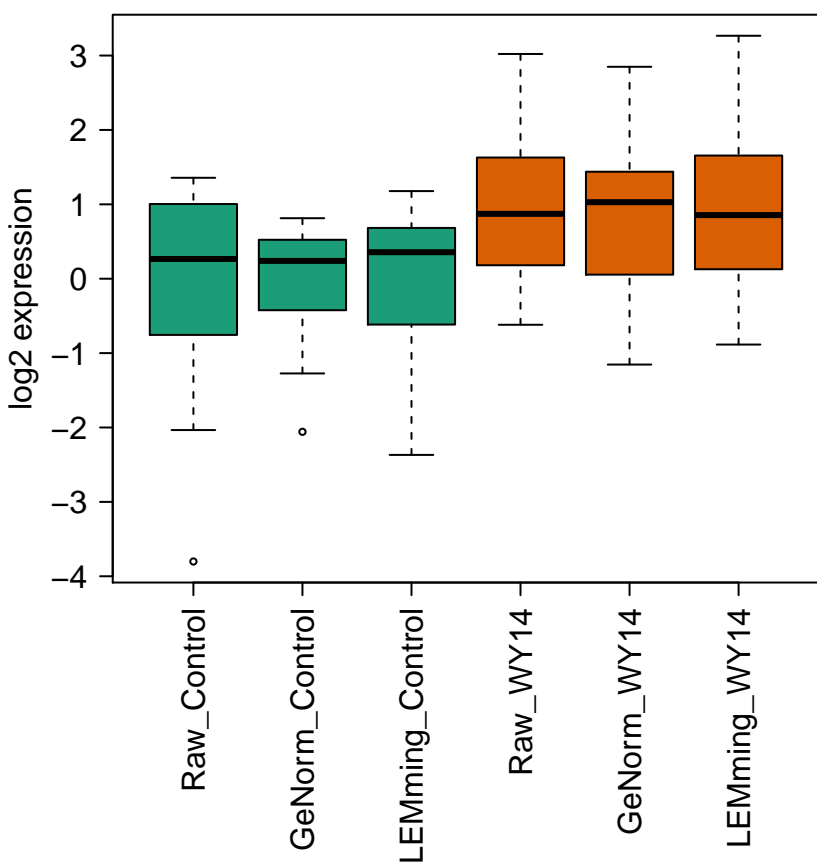
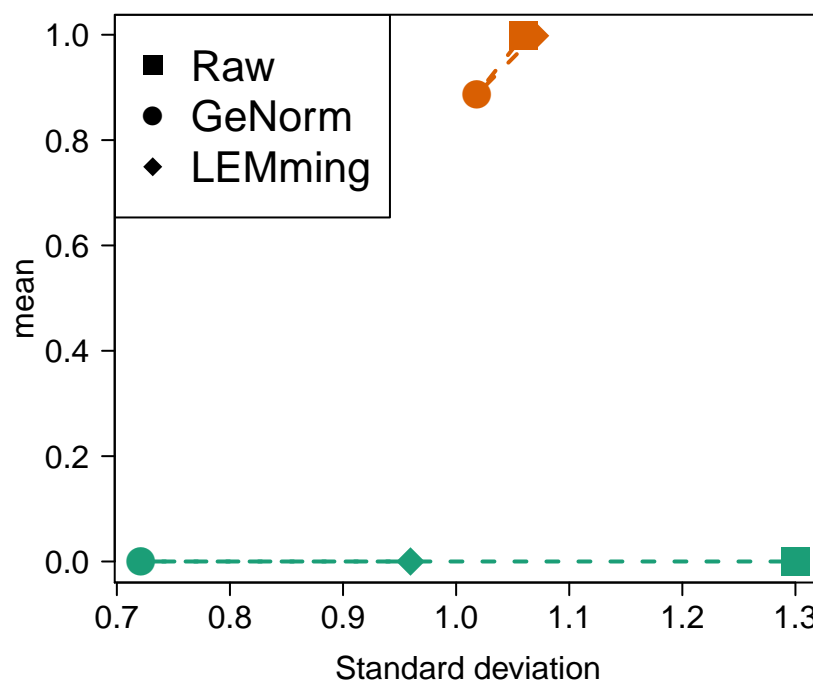
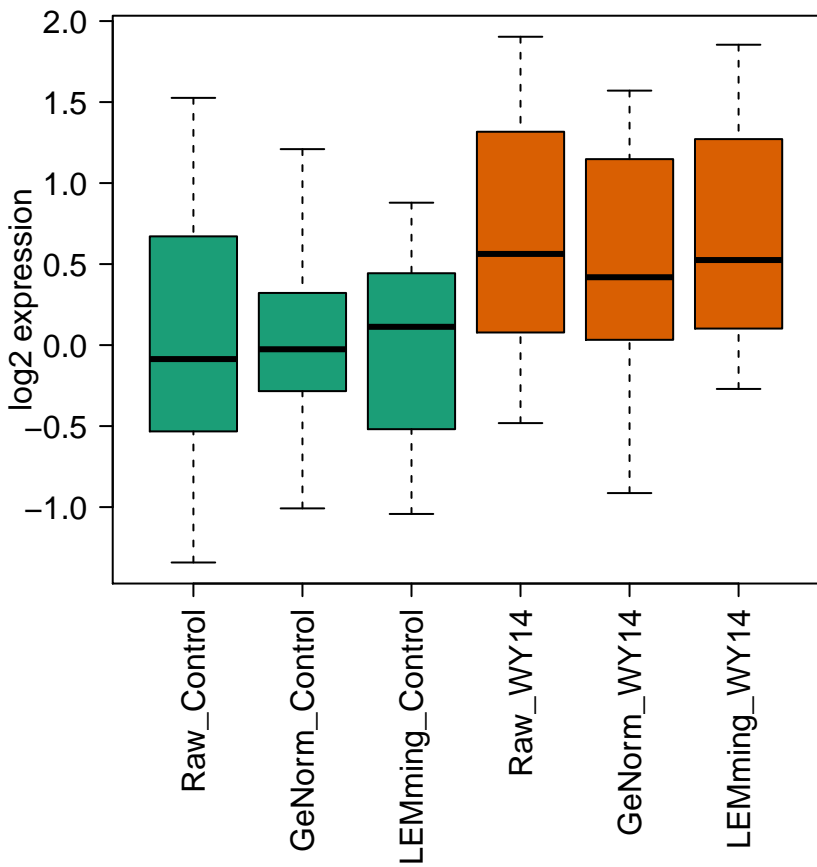
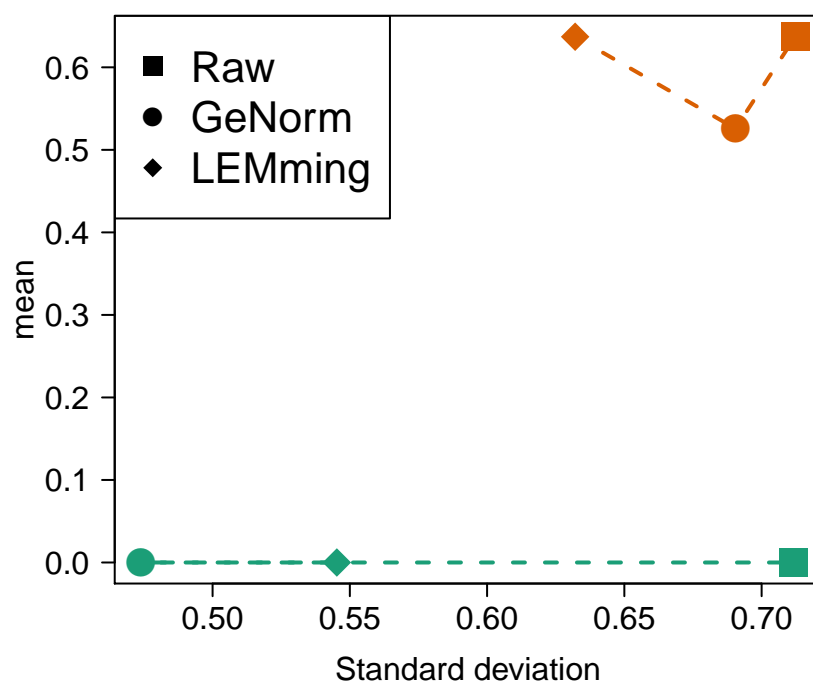


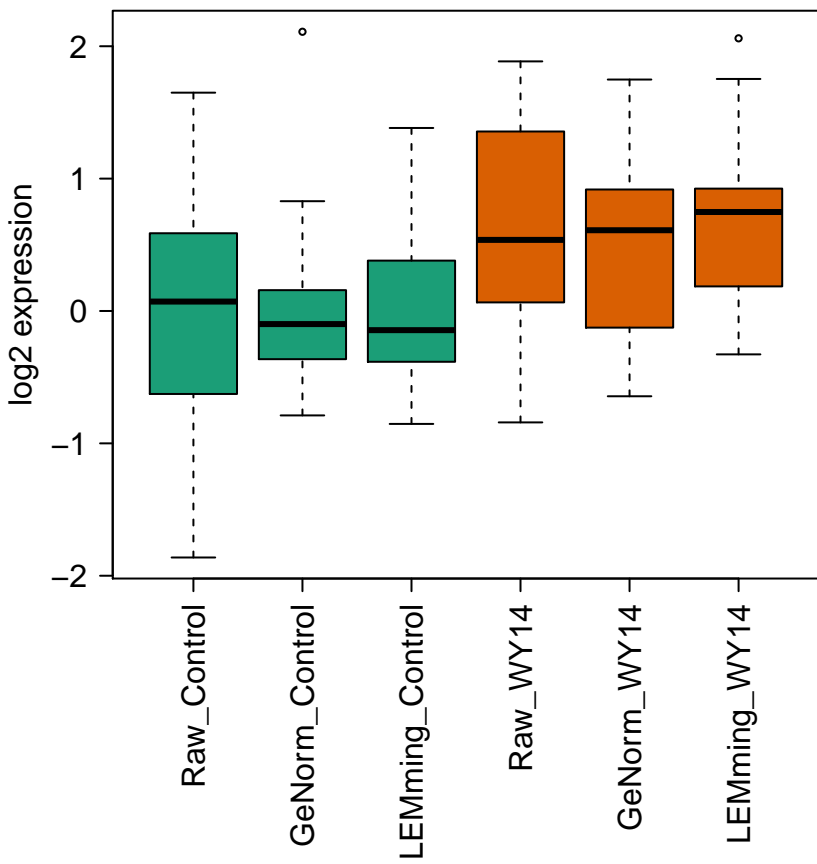
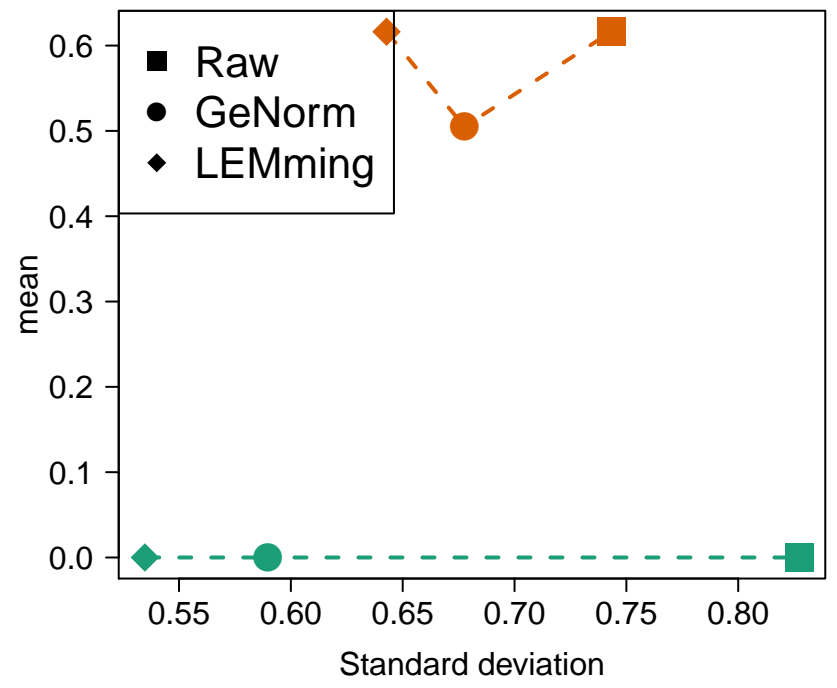
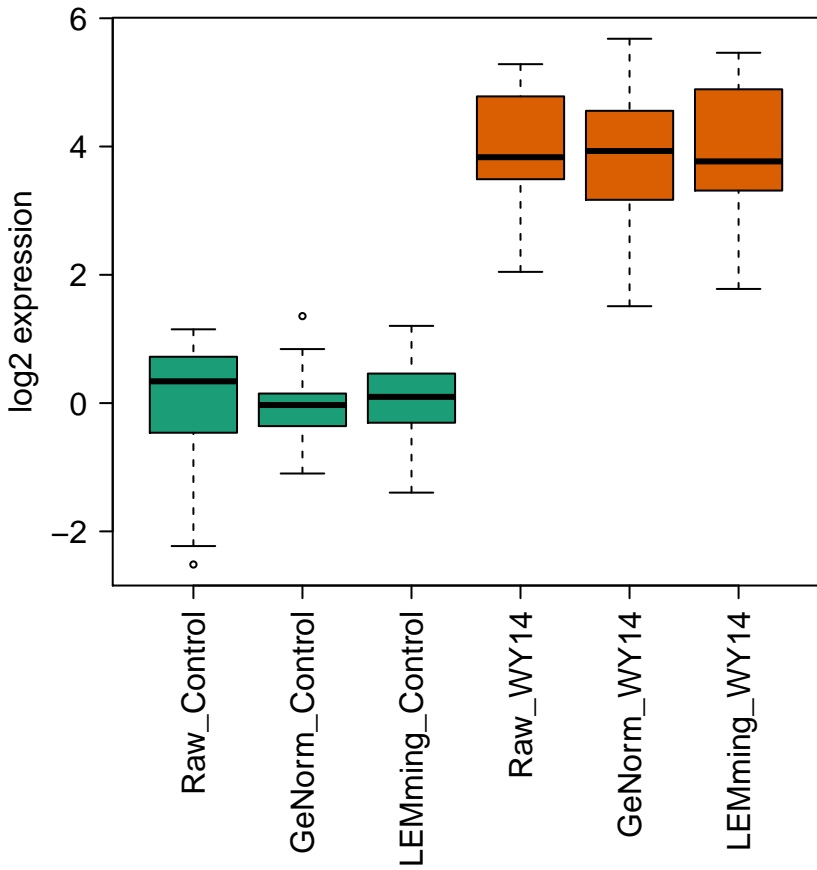
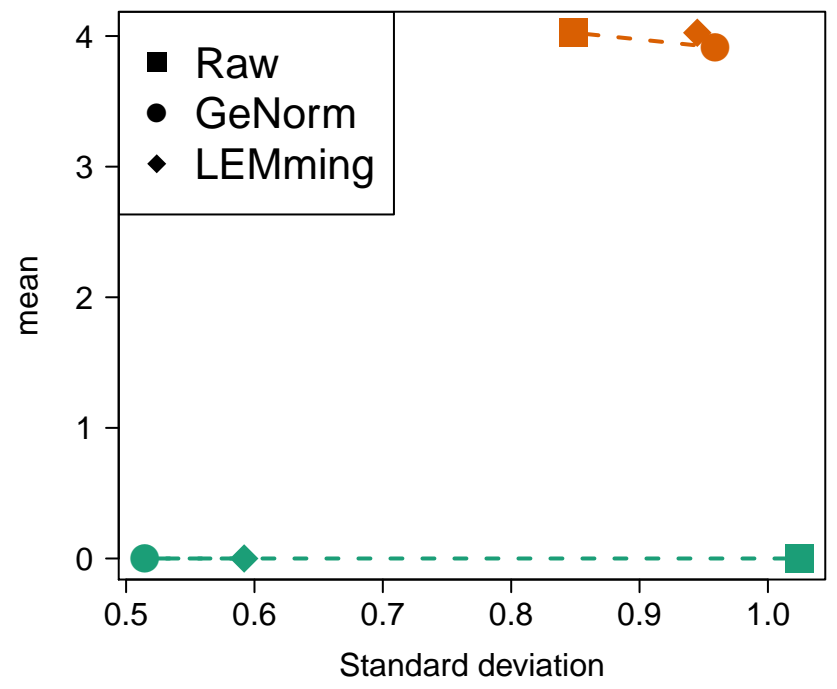
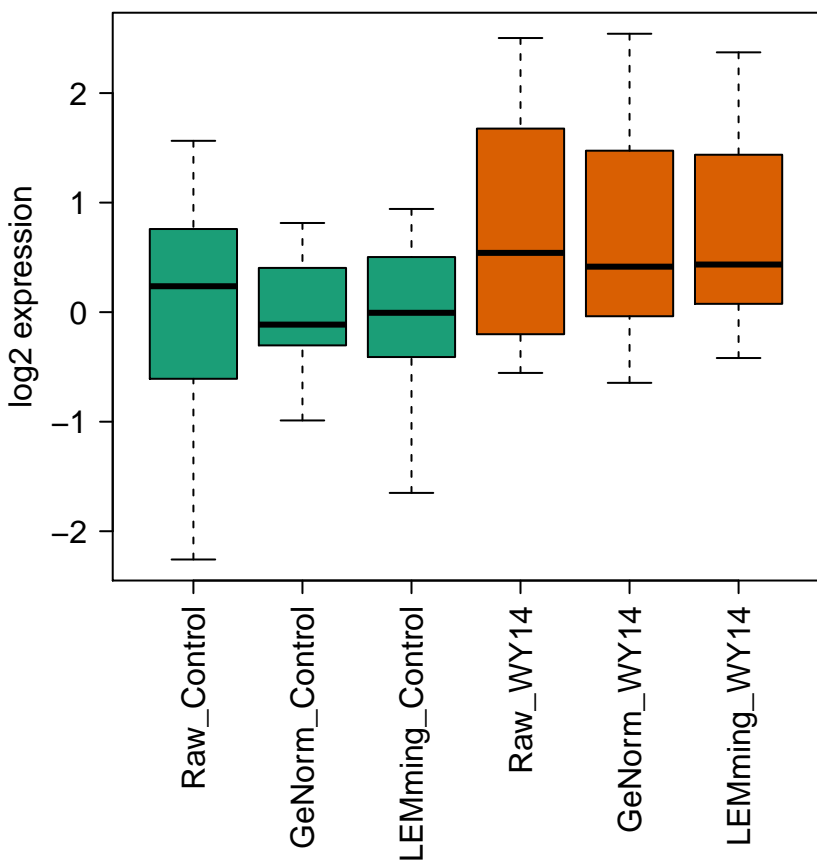
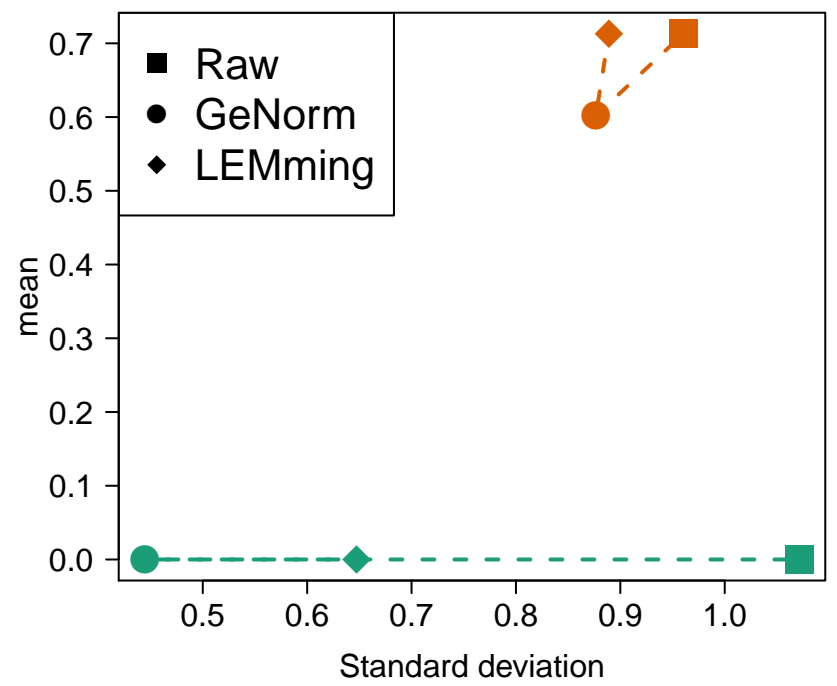
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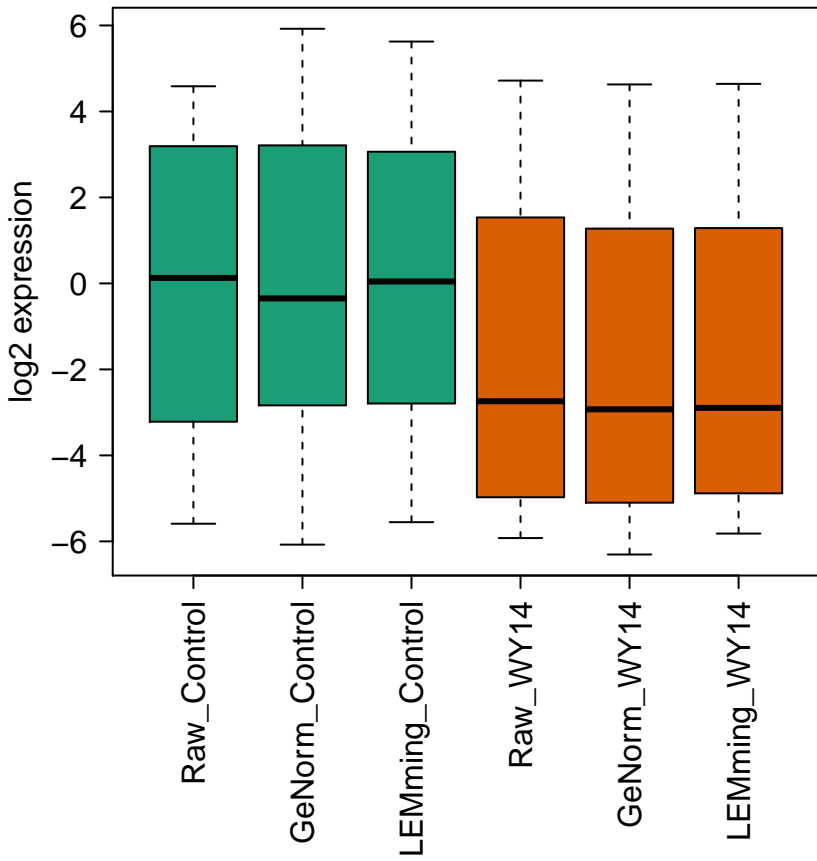
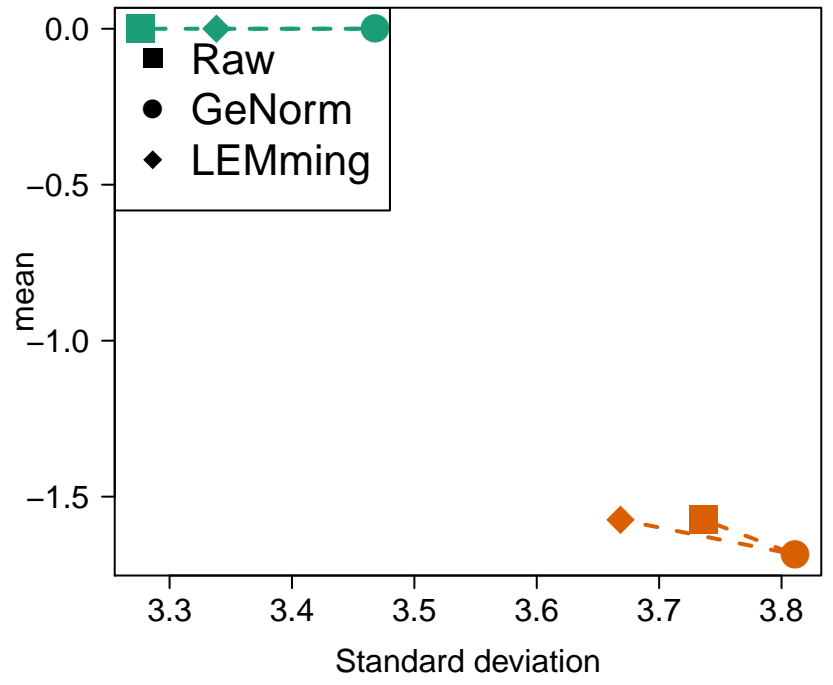
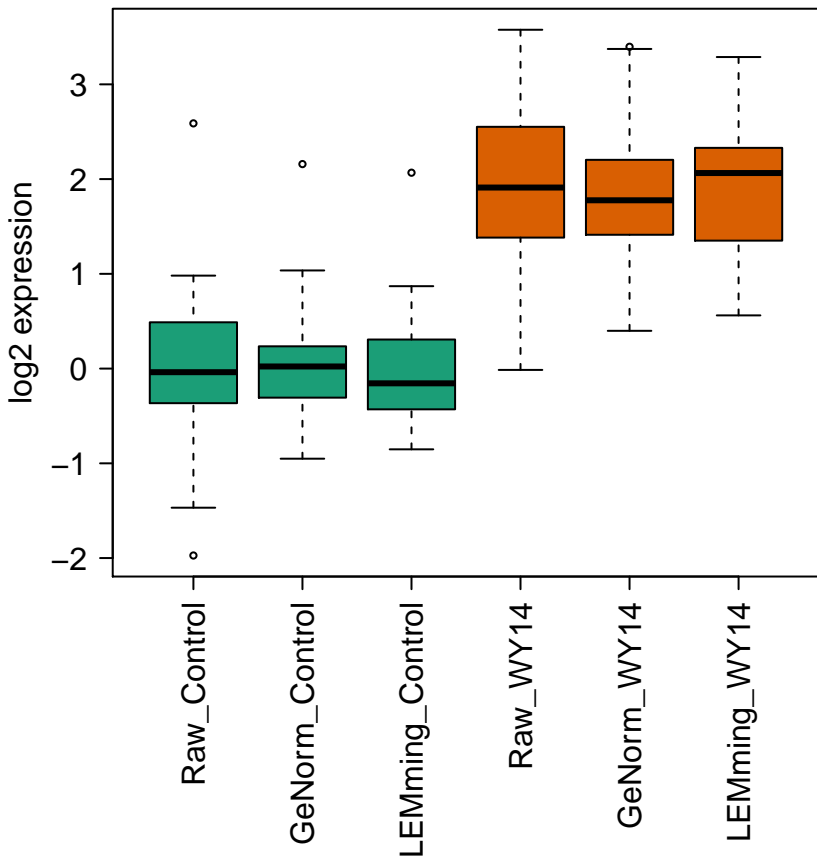
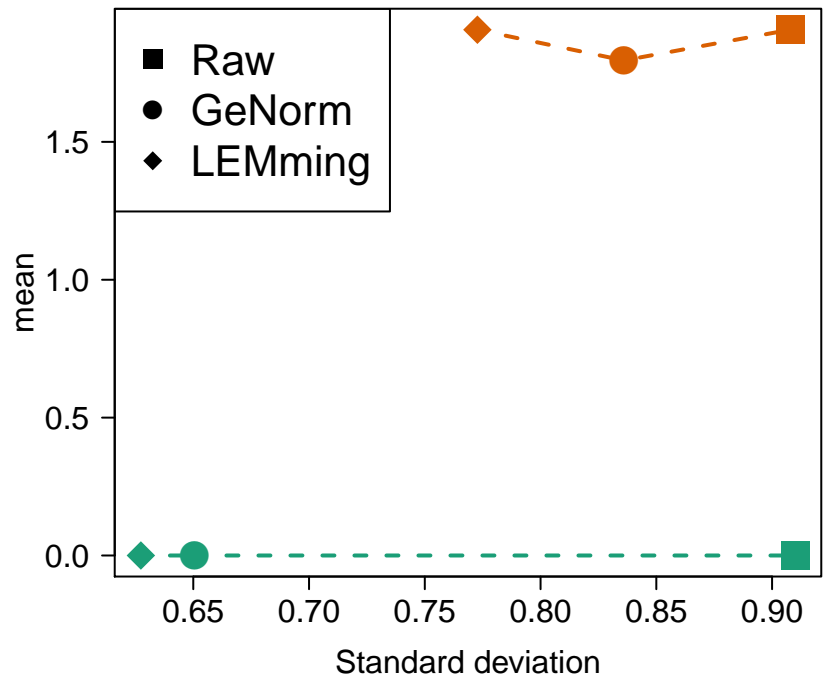
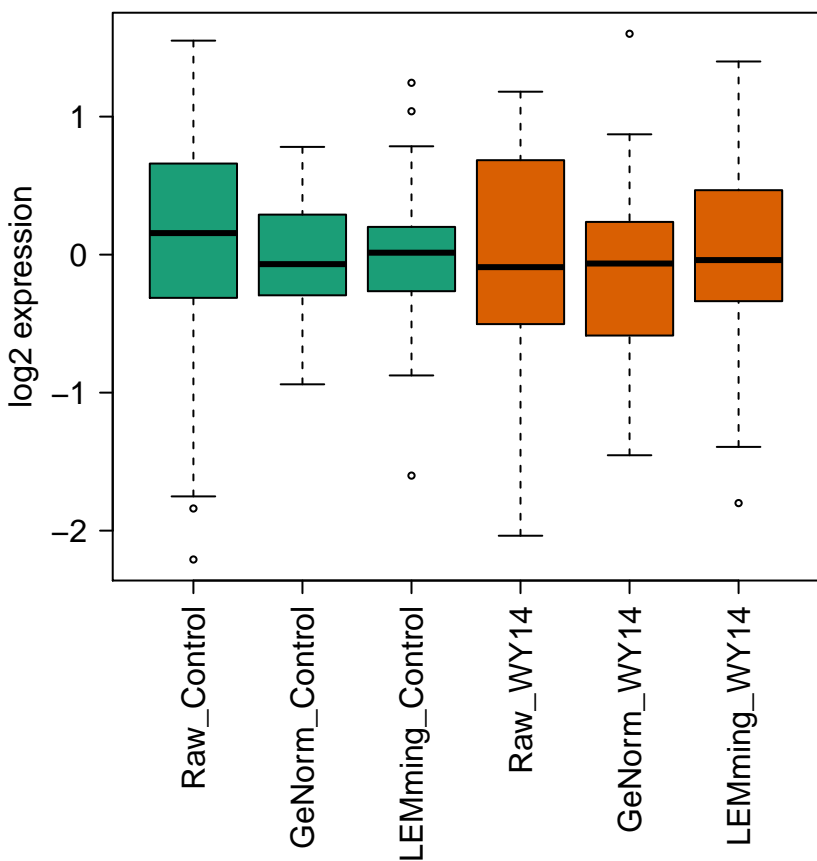
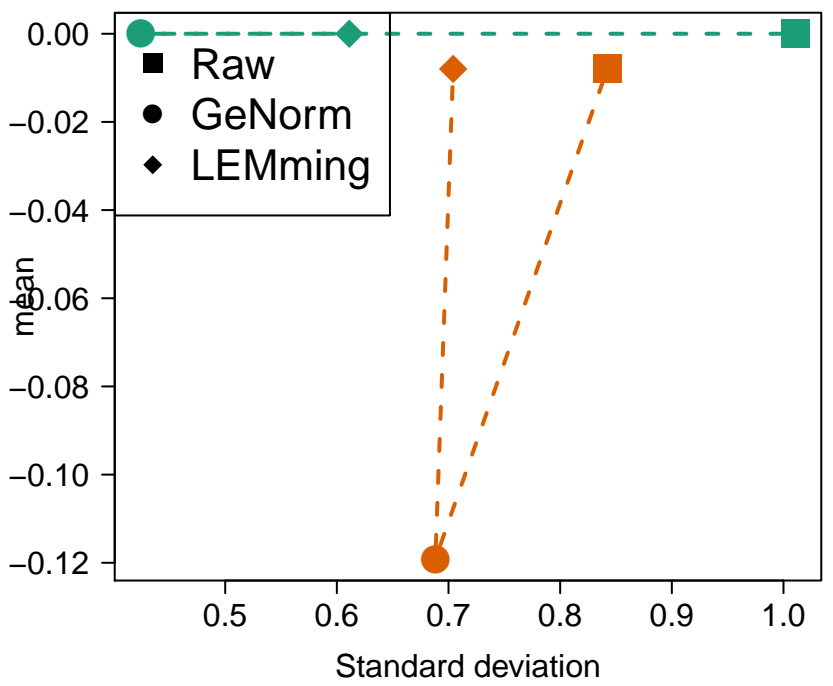


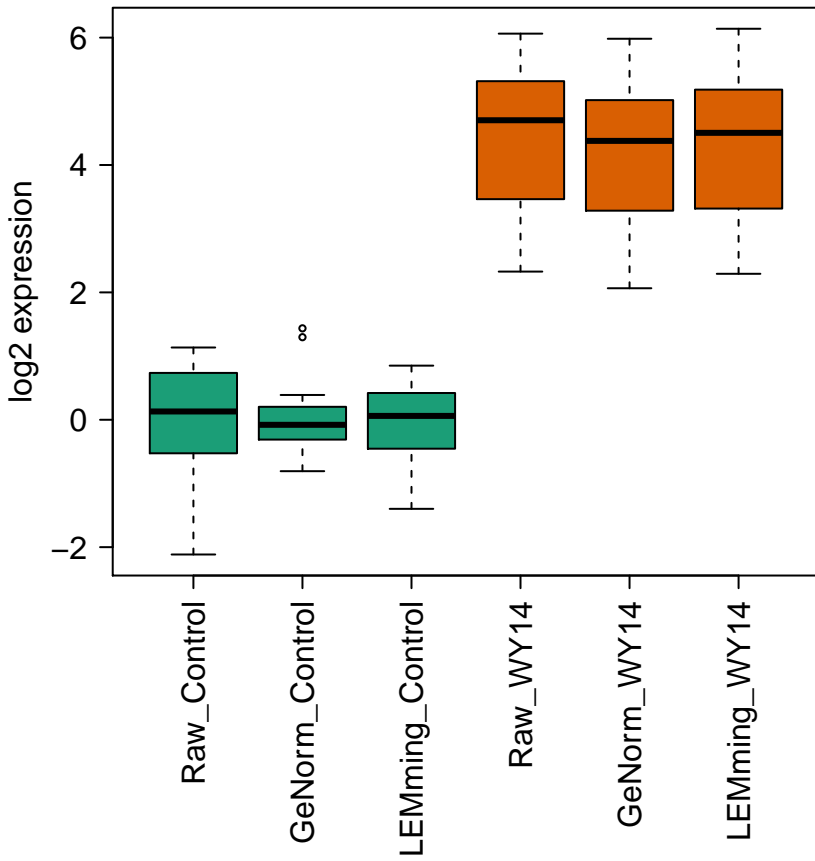
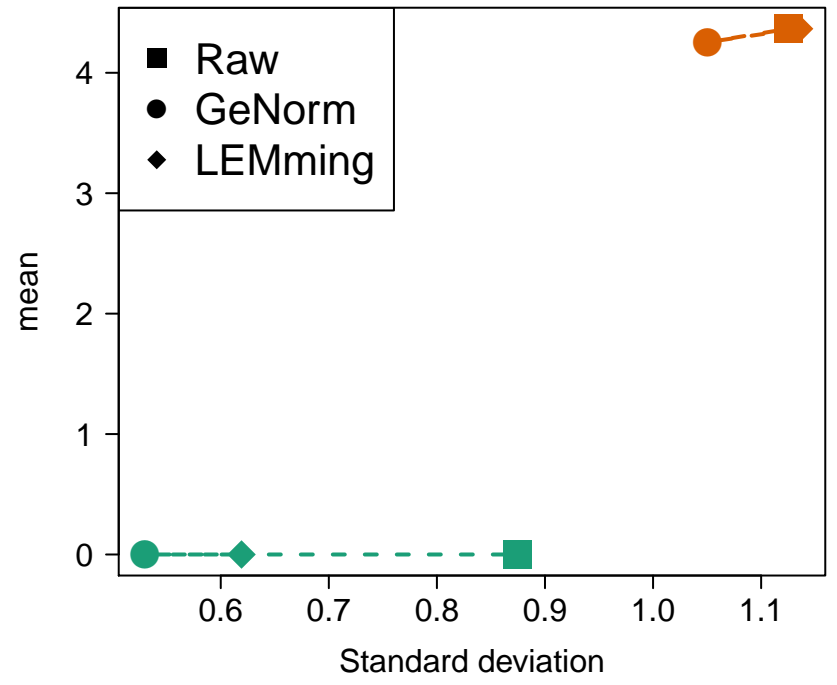
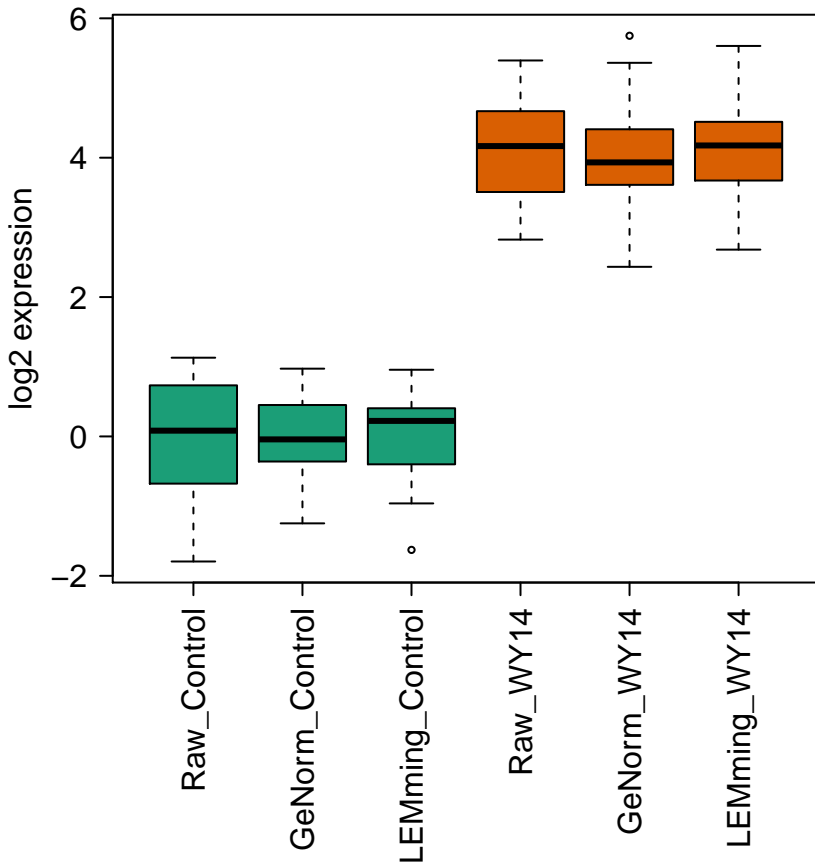
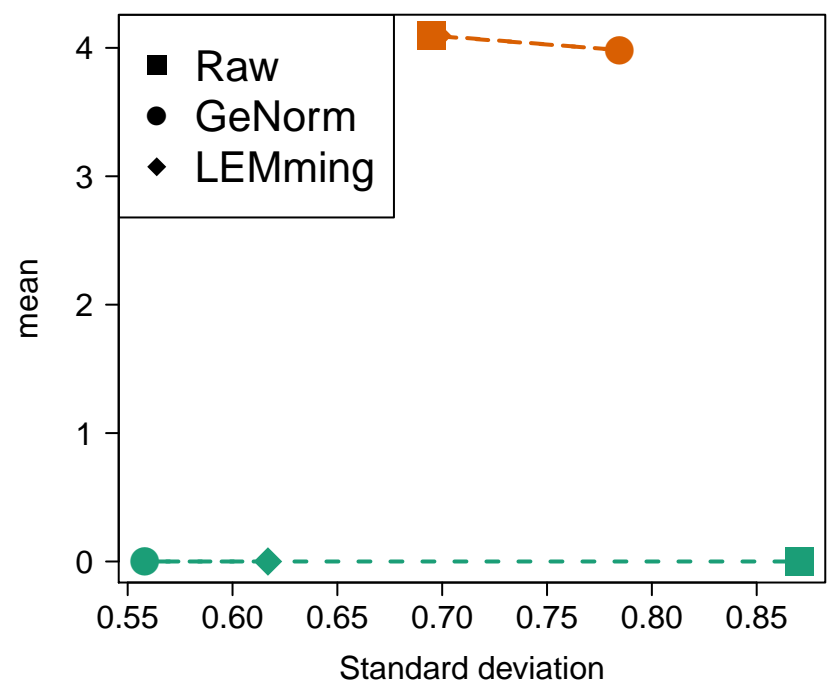
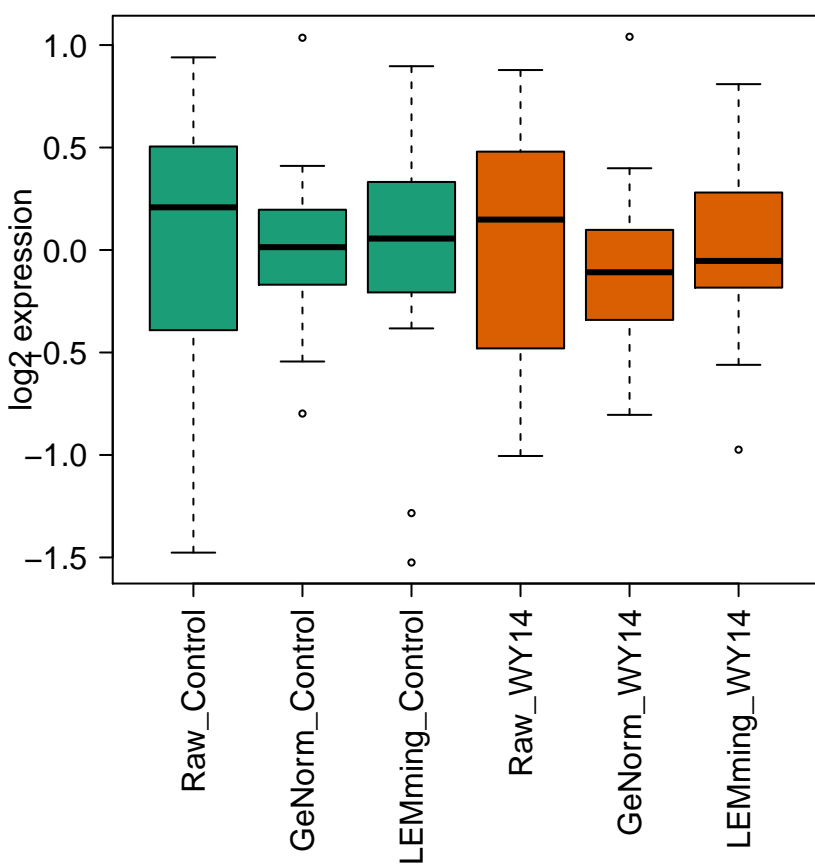
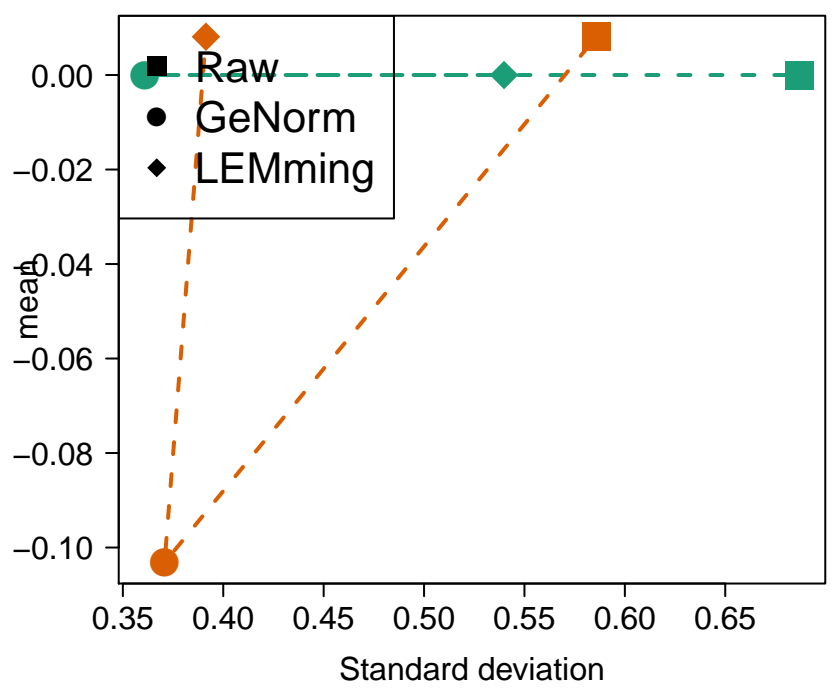
Variance-mean plot

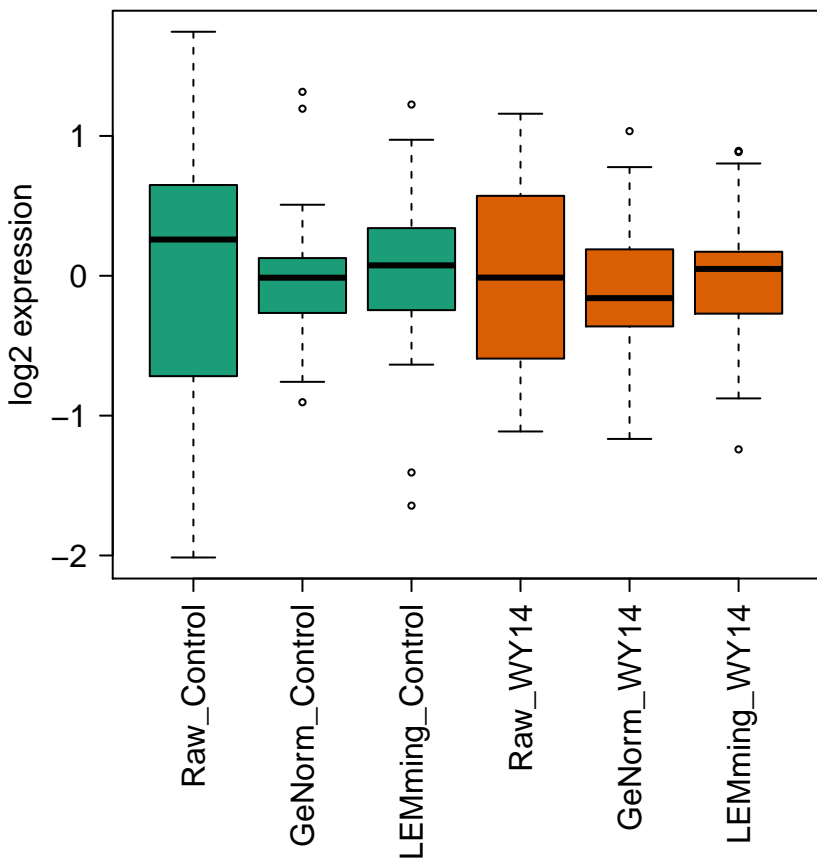
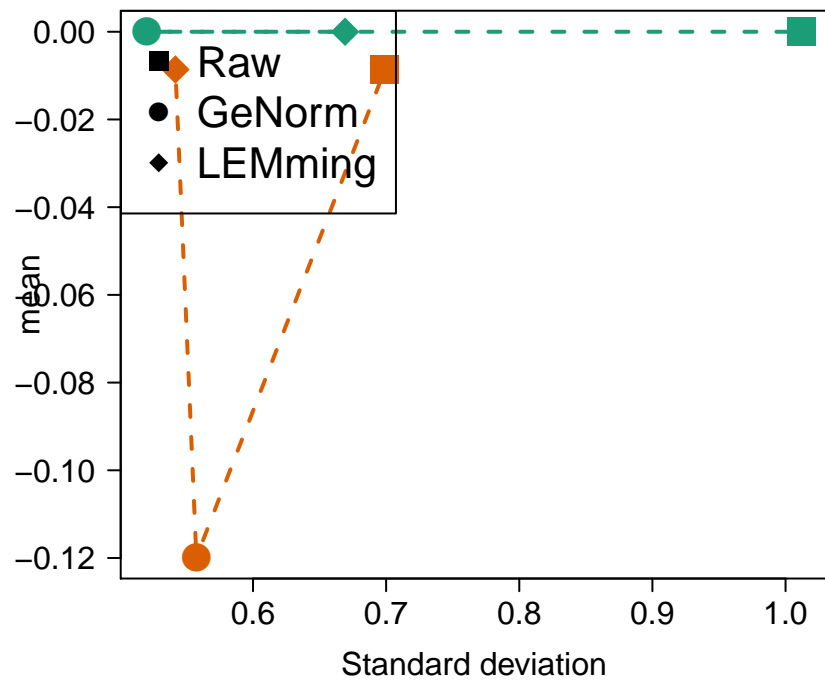
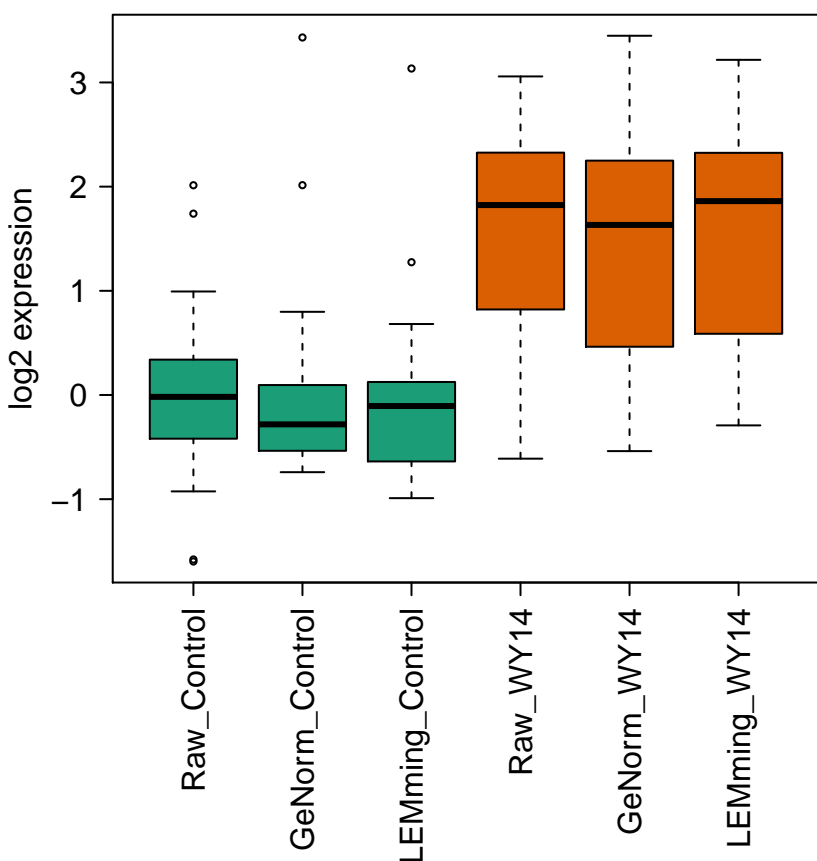
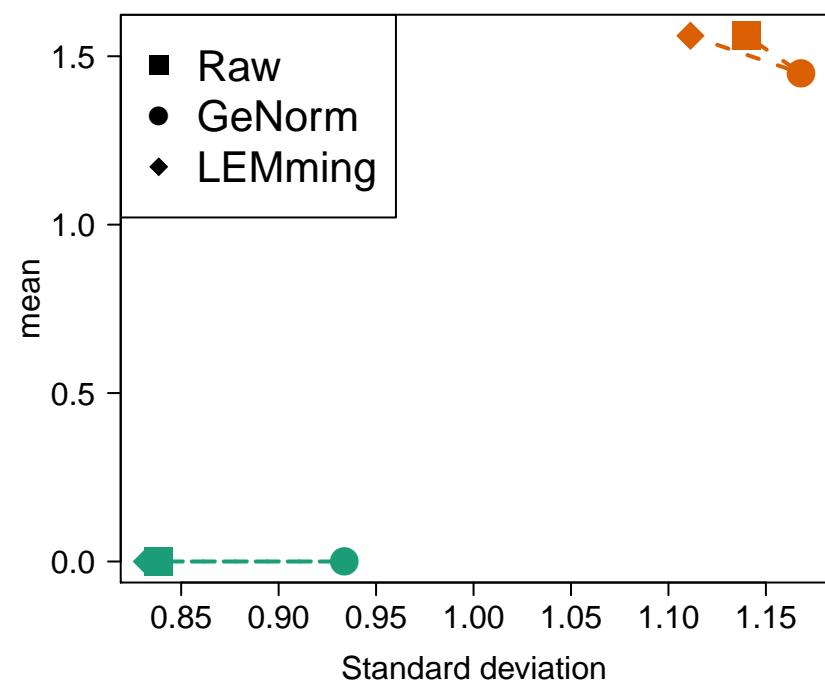
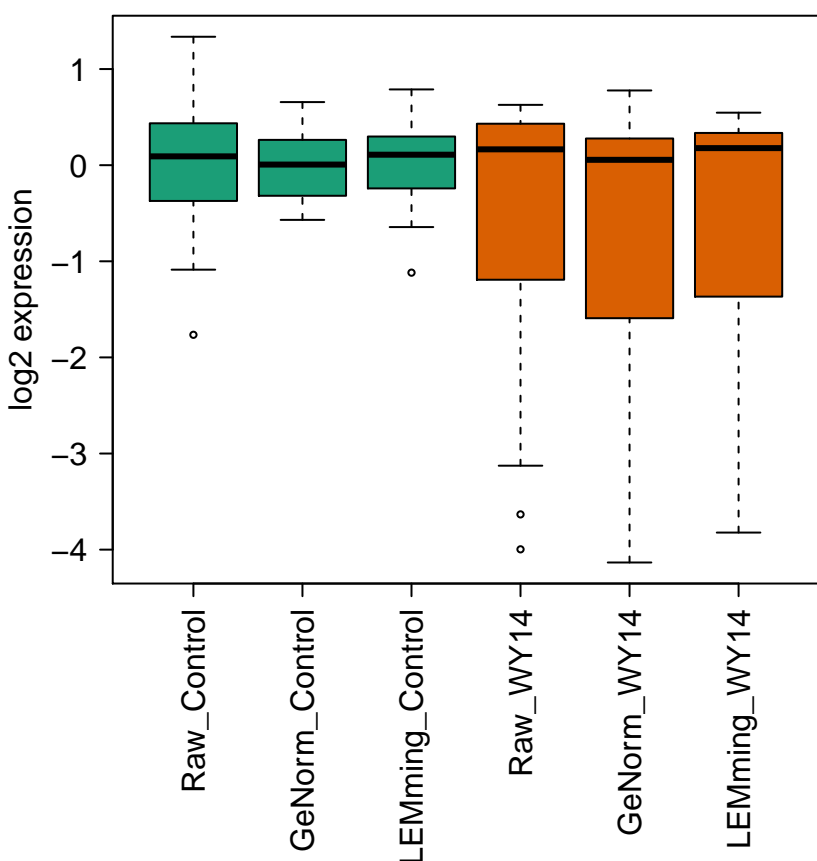
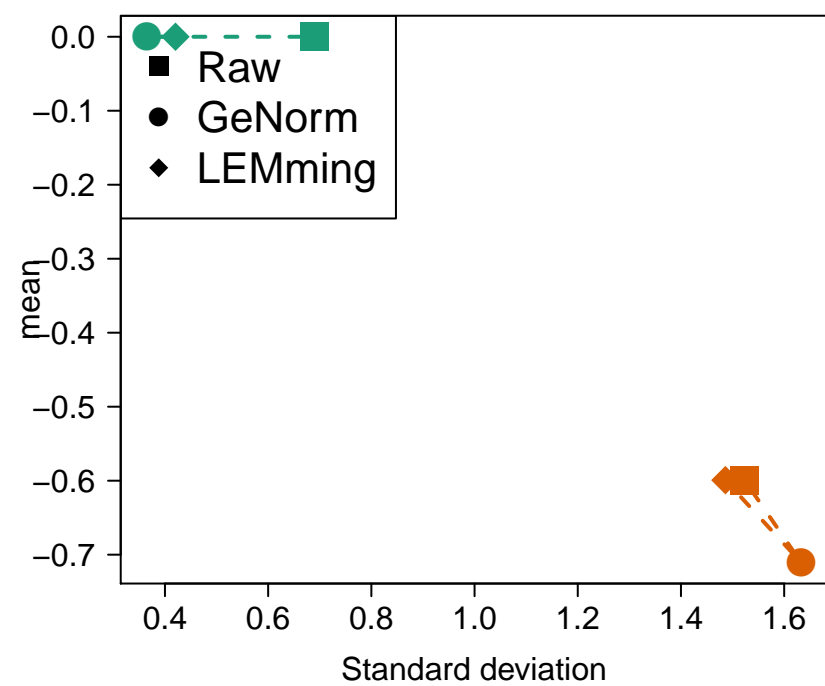


UGT2B7**Variance–mean plot****VDR****Variance–mean plot****VEGFA****Variance–mean plot**

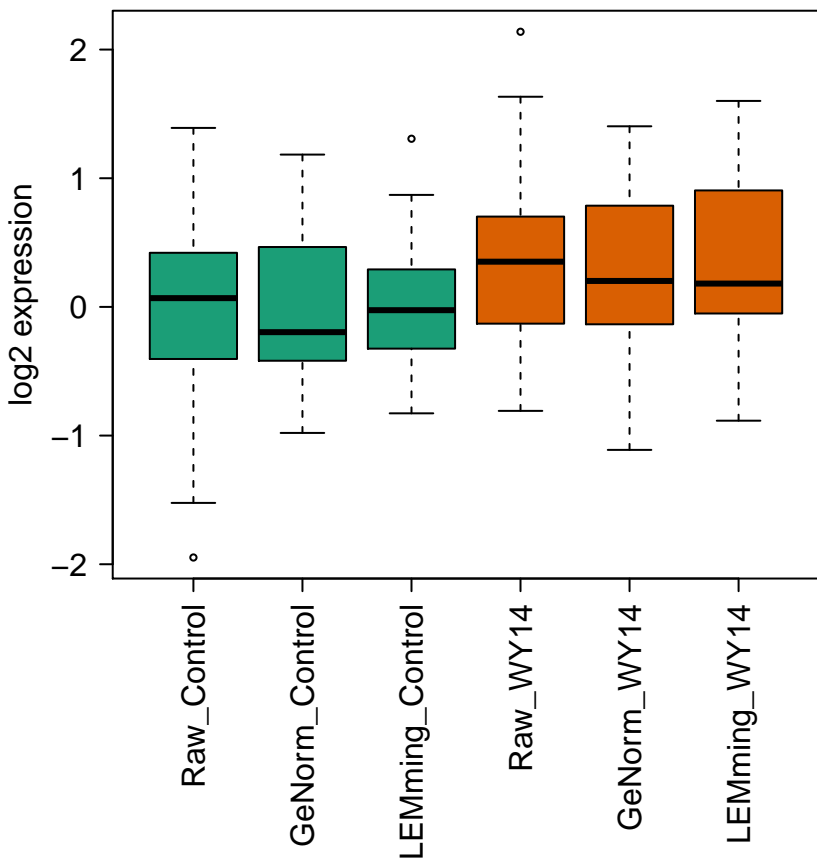
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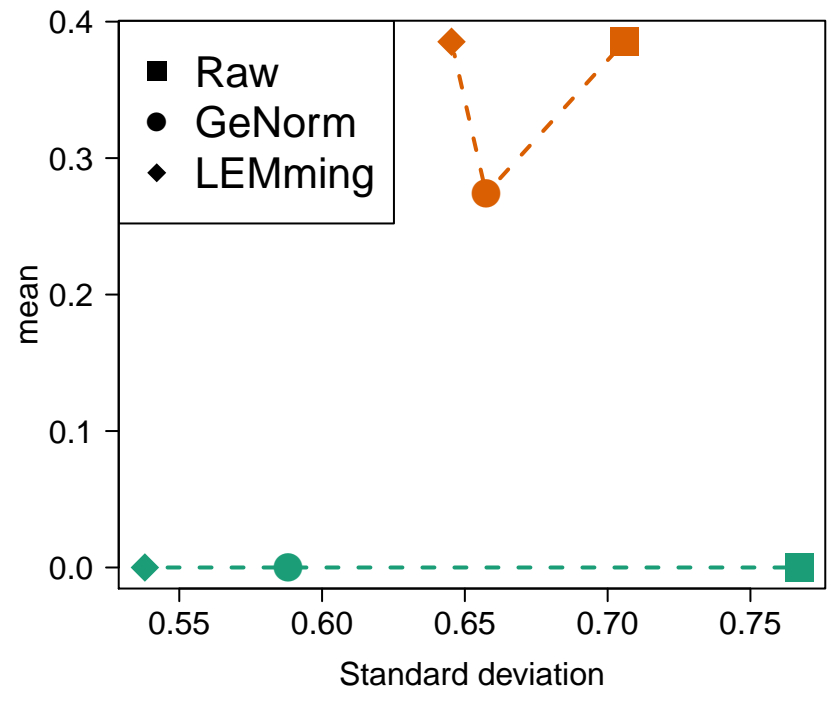
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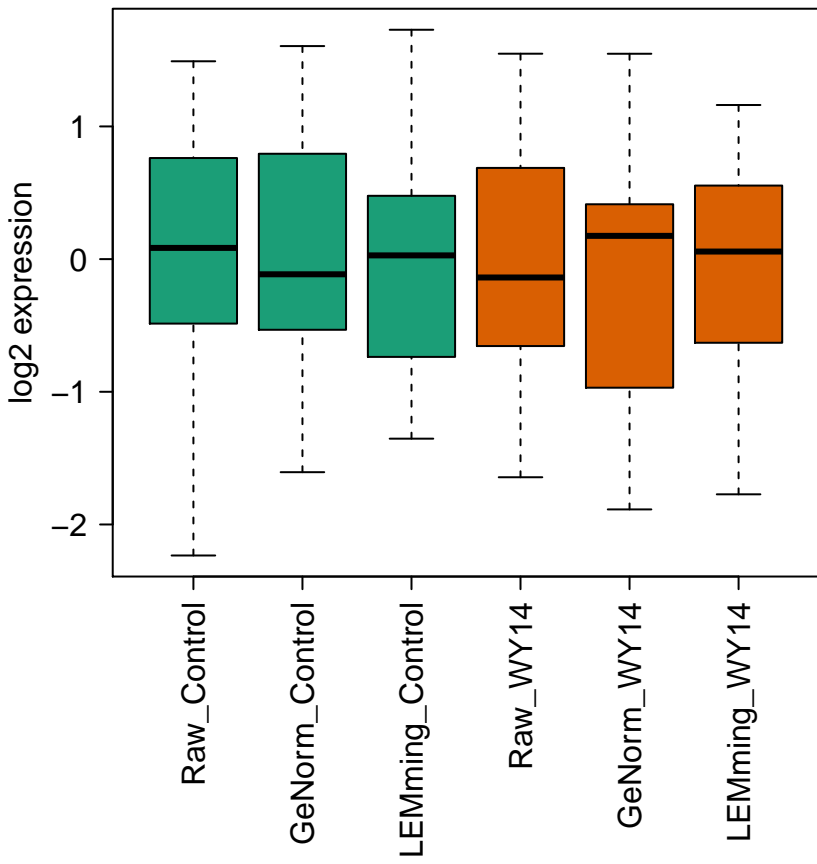
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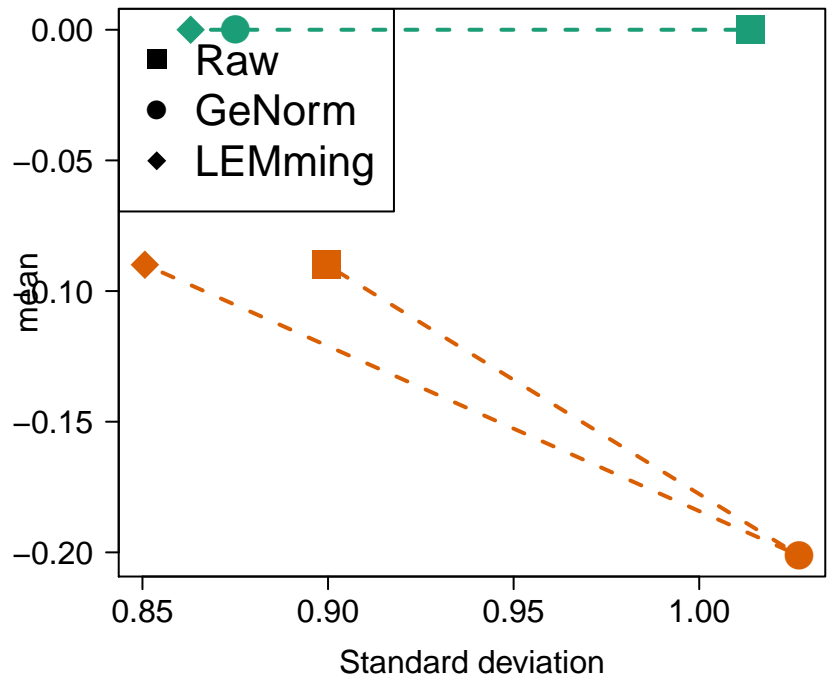
Variance-mean plot



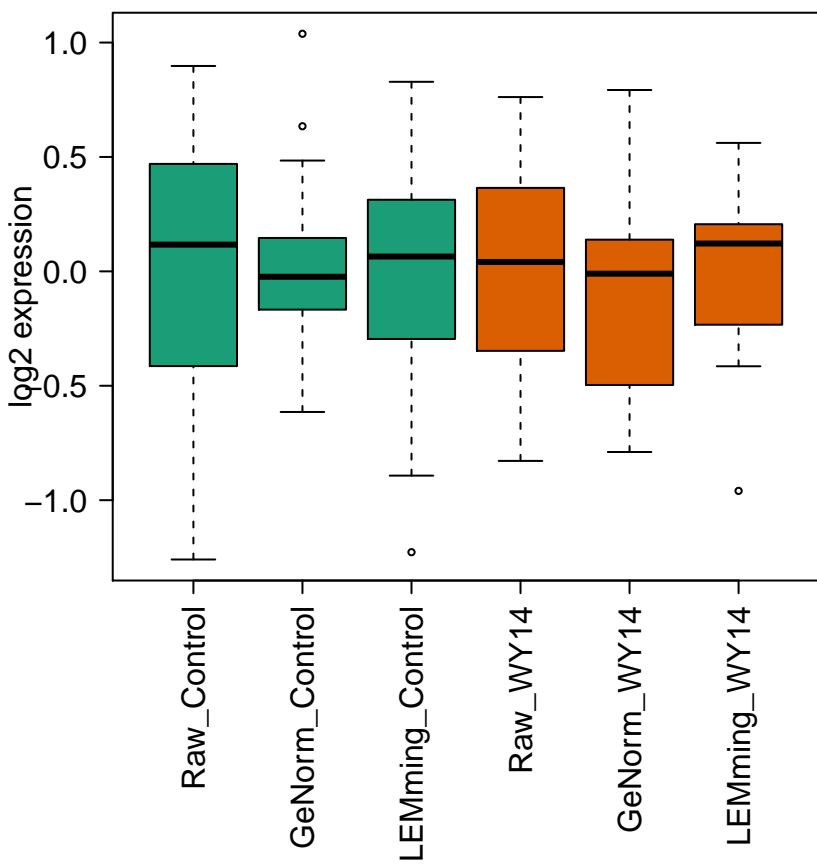
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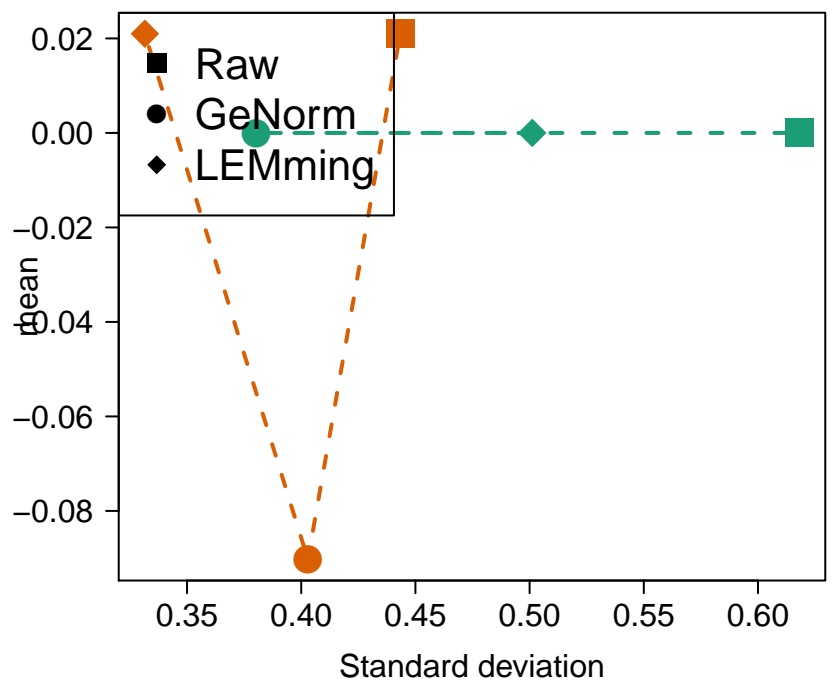
Variance-mean plot

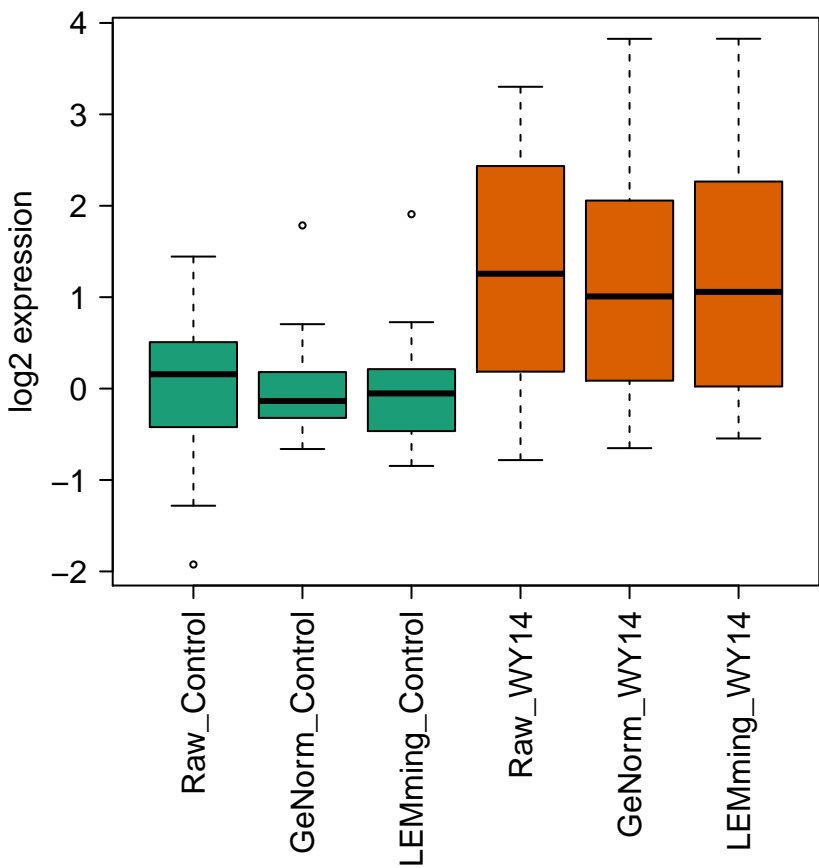
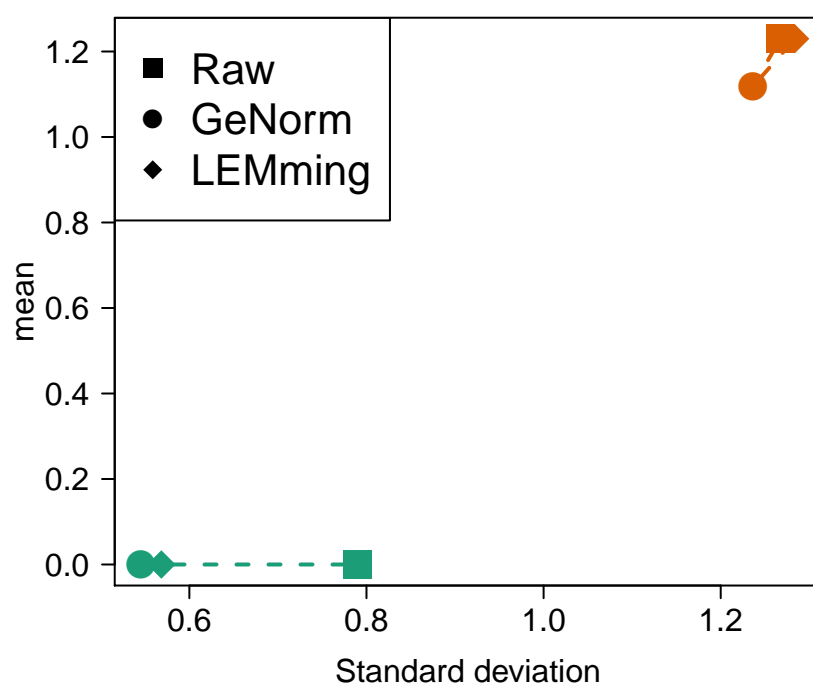
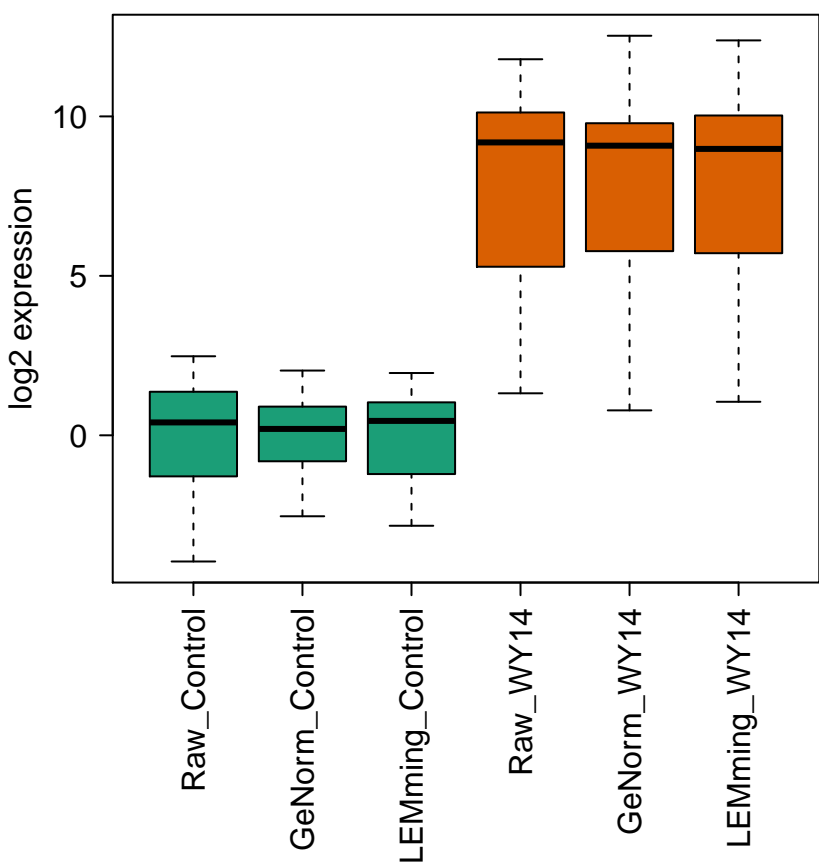
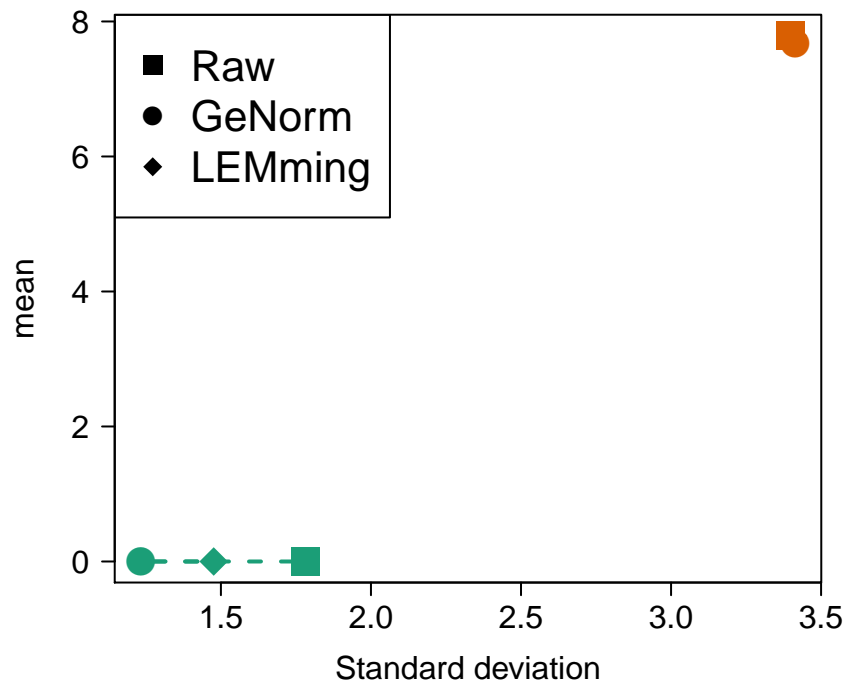
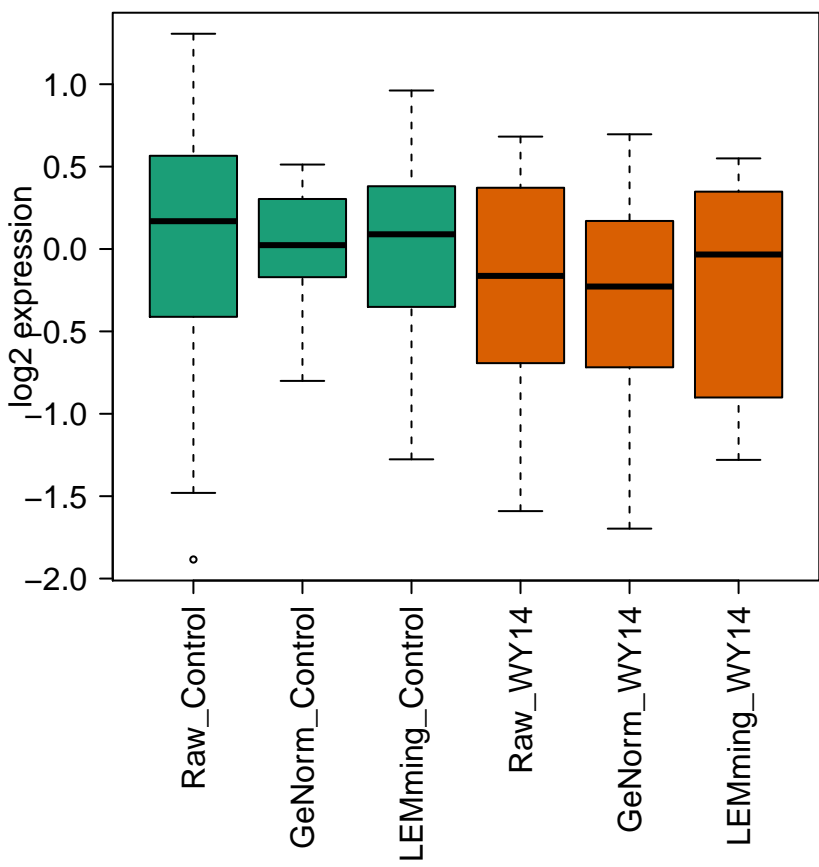
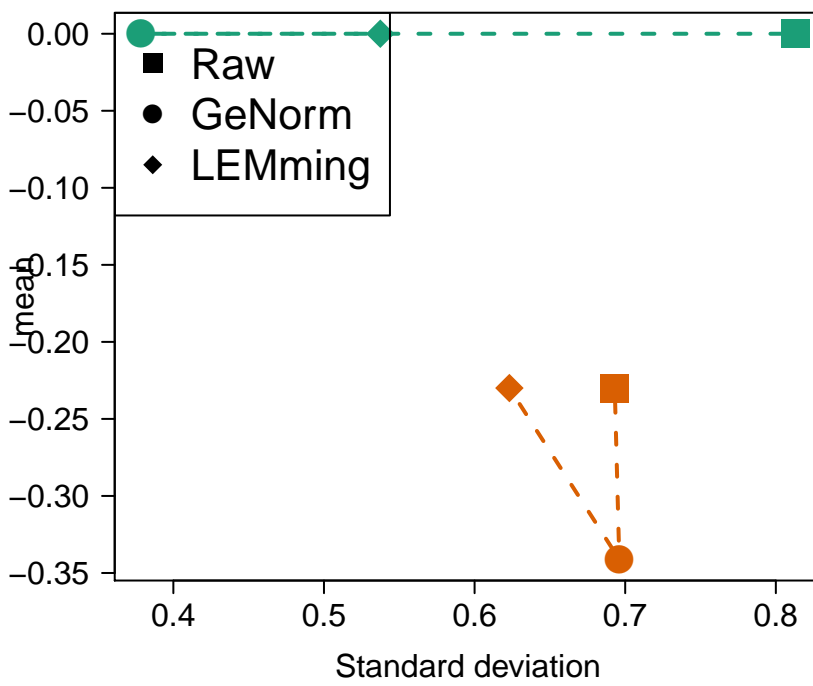


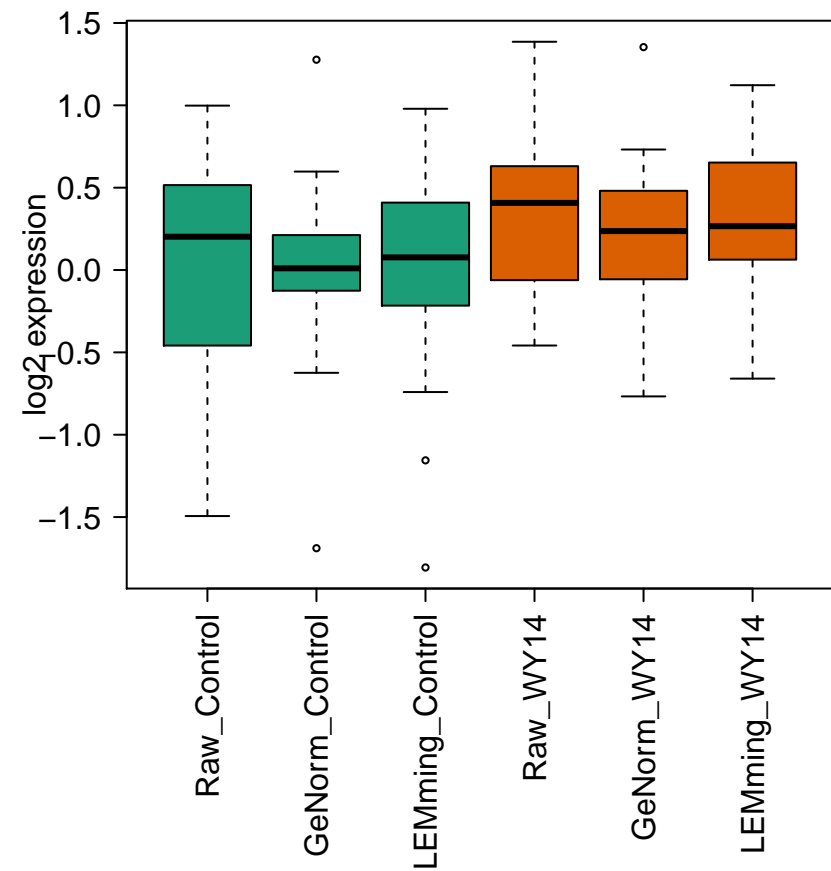
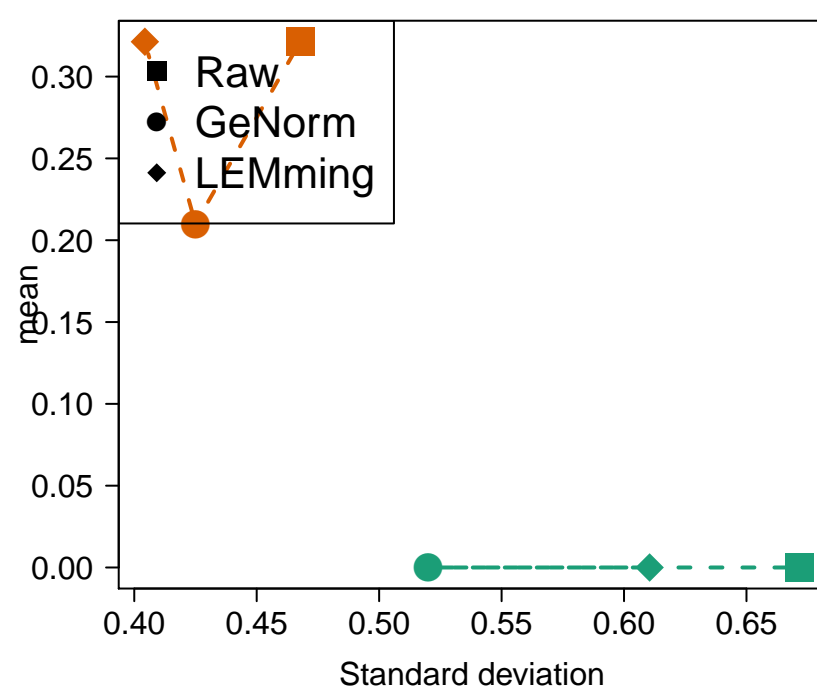
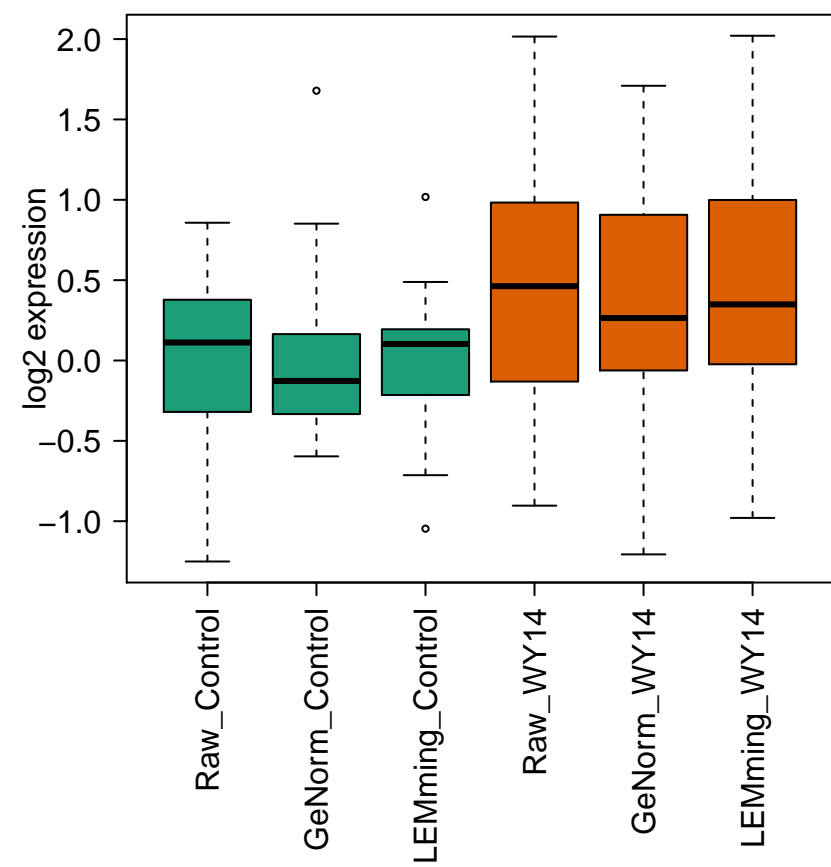
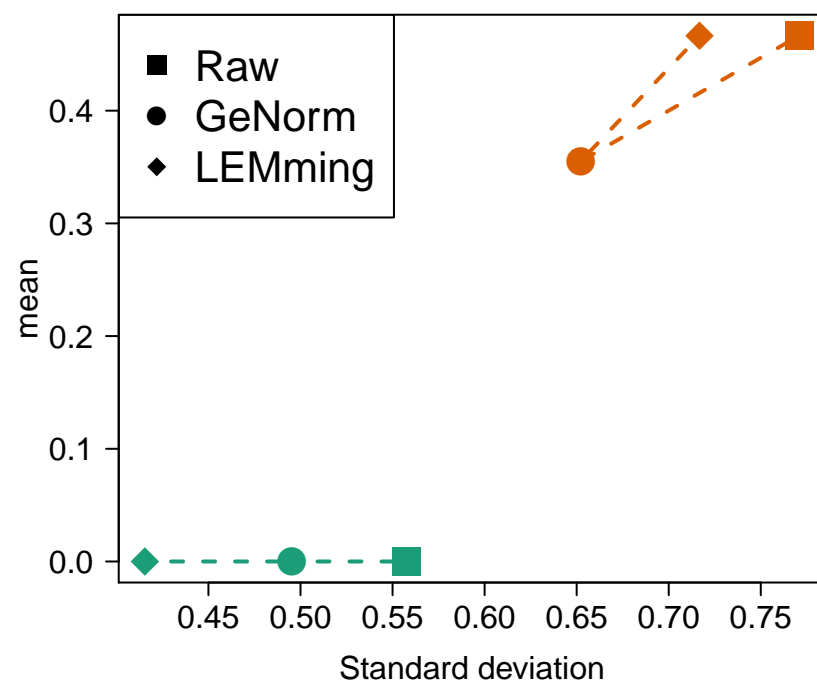
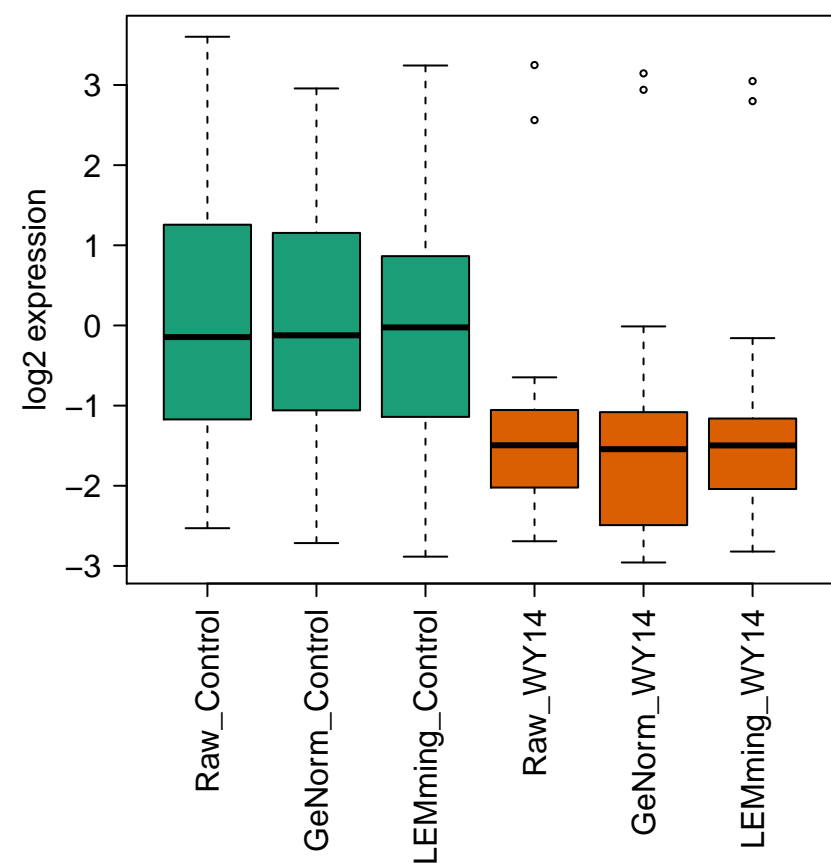
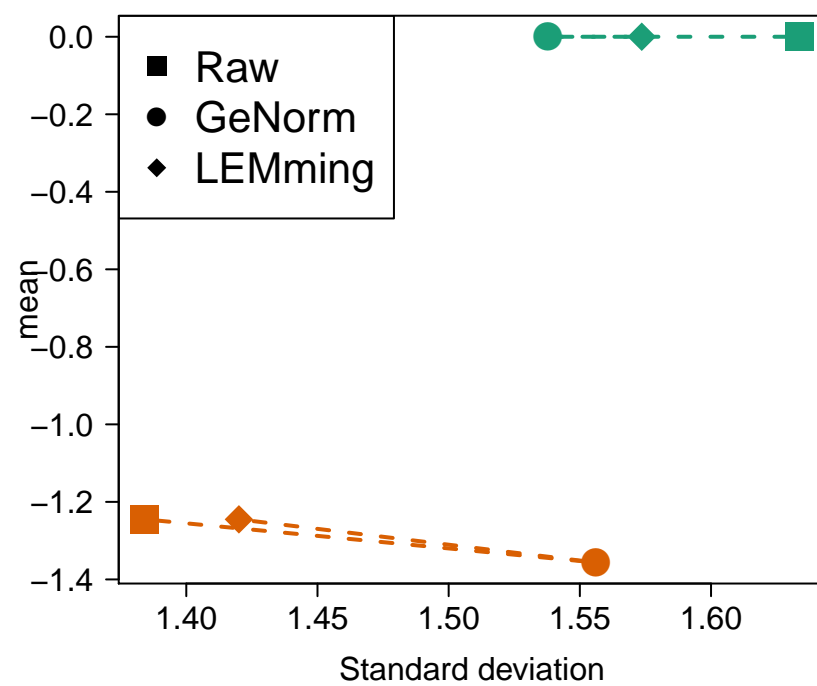
HMBS



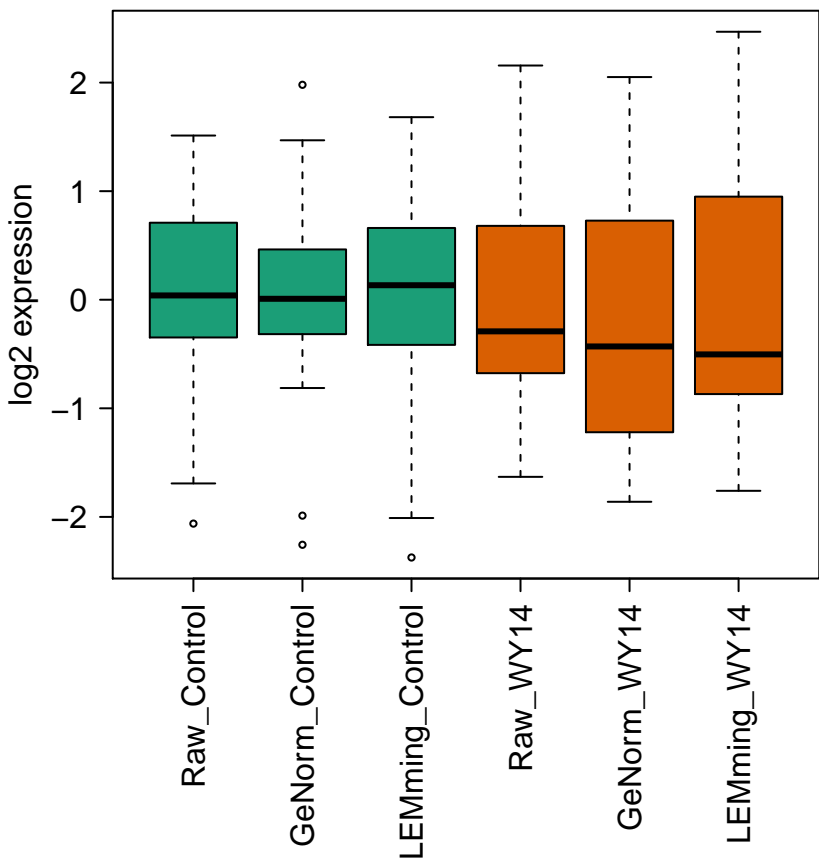
Variance-mean plot



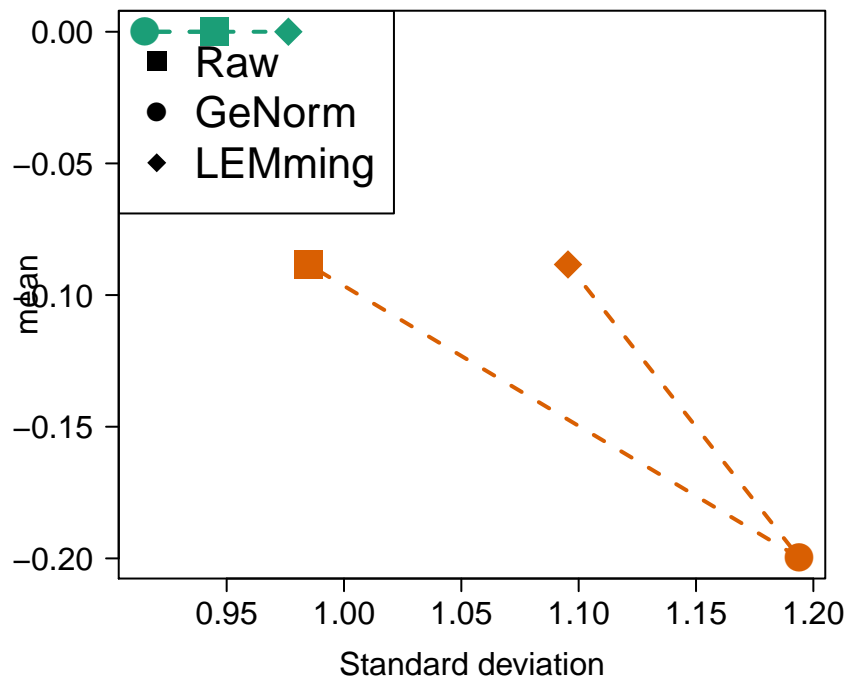
HMGCR**Variance–mean plot****HMGCS2****Variance–mean plot****HMOX1****Variance–mean plot**

HNF1A**Variance–mean plot****HNF4alpha****Variance–mean plot****IL1b****Variance–mean plot**

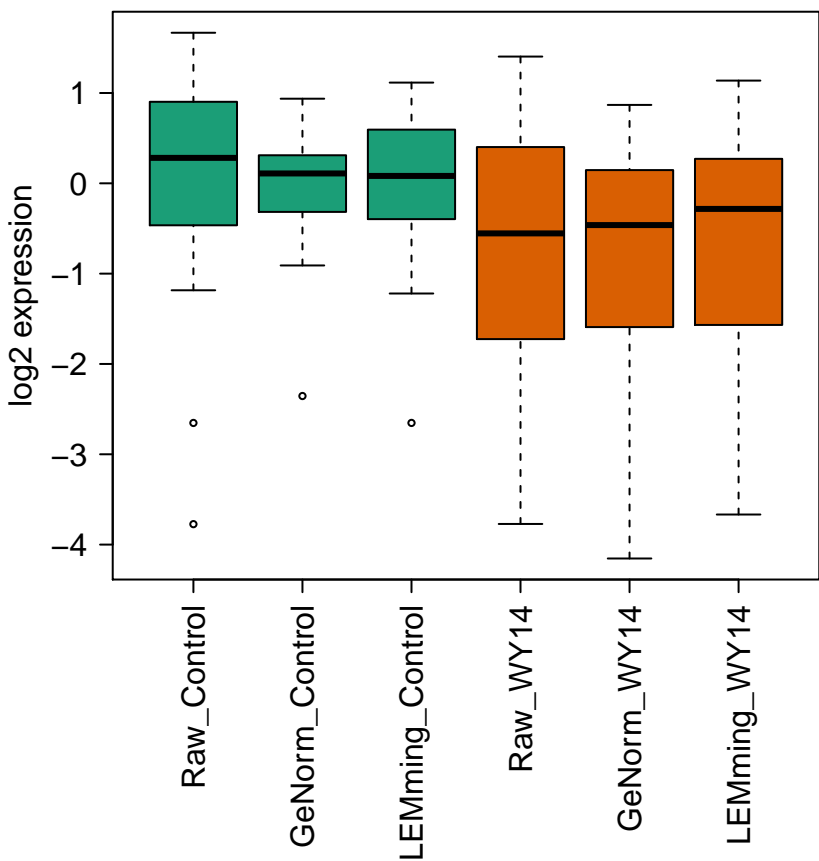
IL6



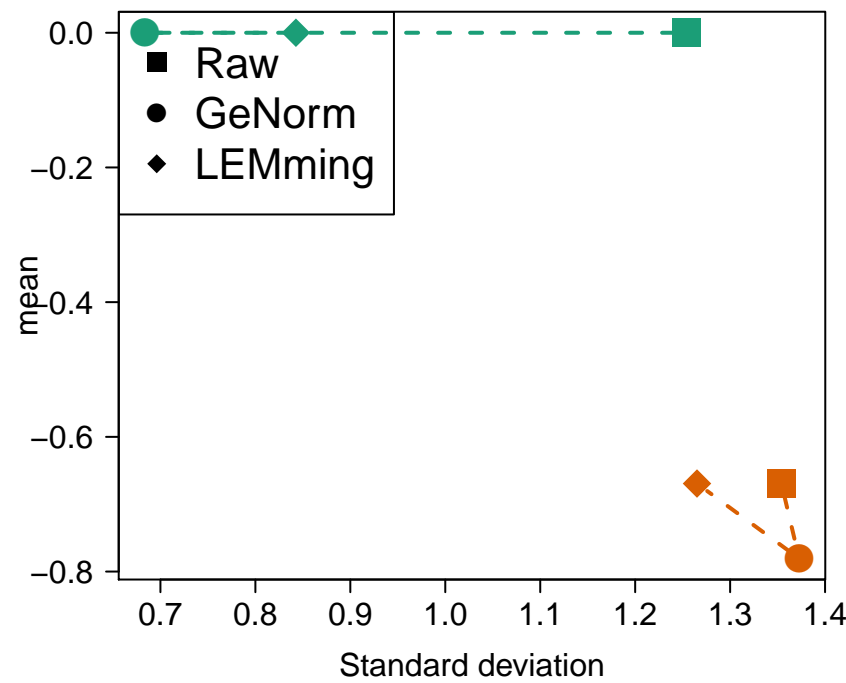
Variance-mean plot



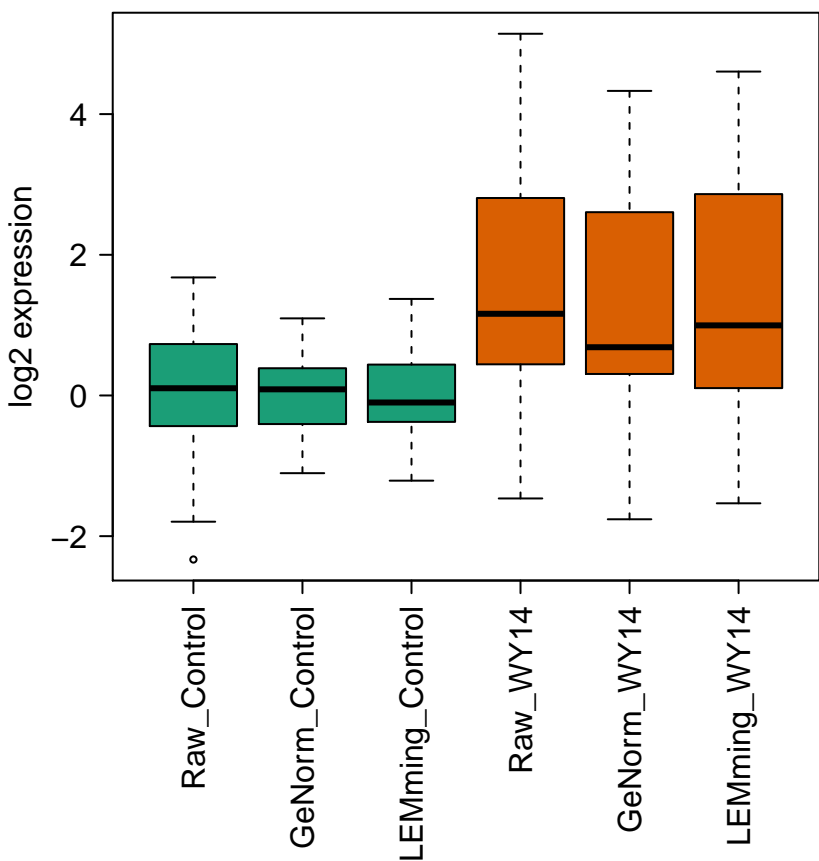
IL8



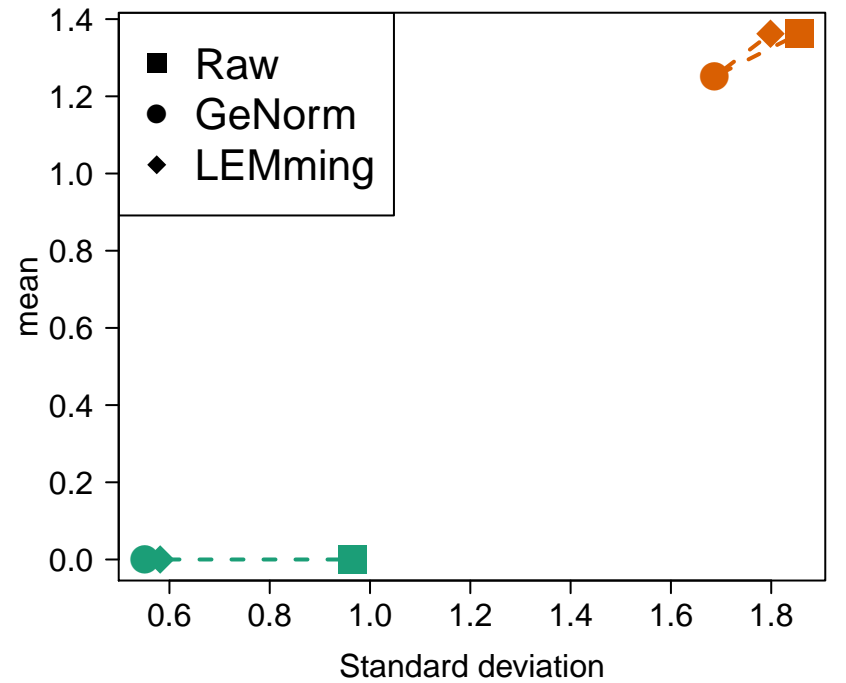
Variance-mean plot

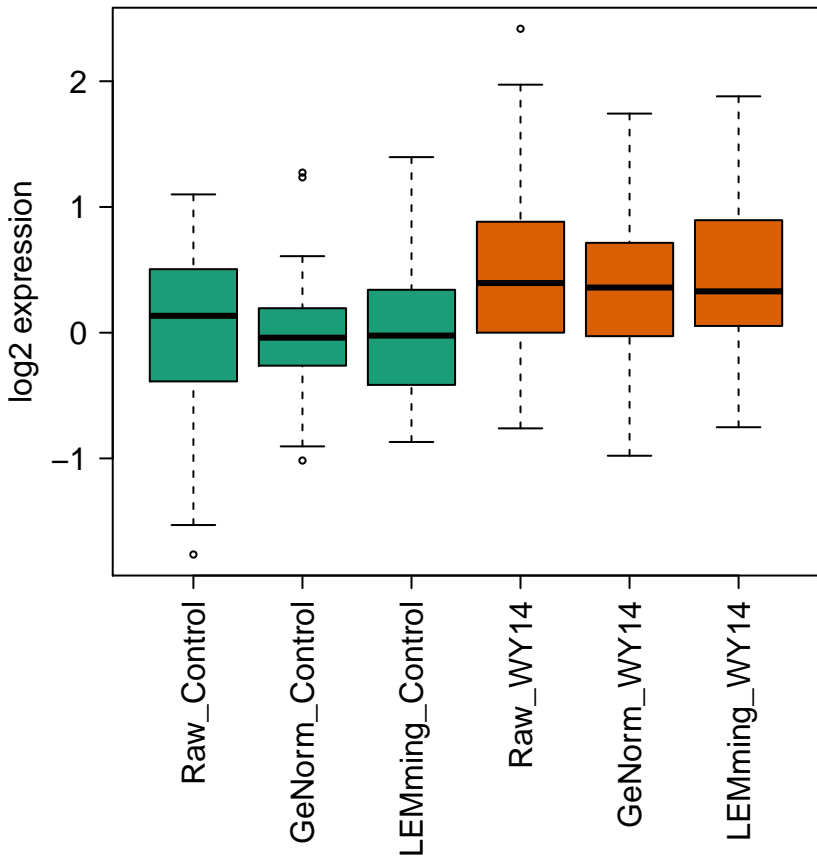
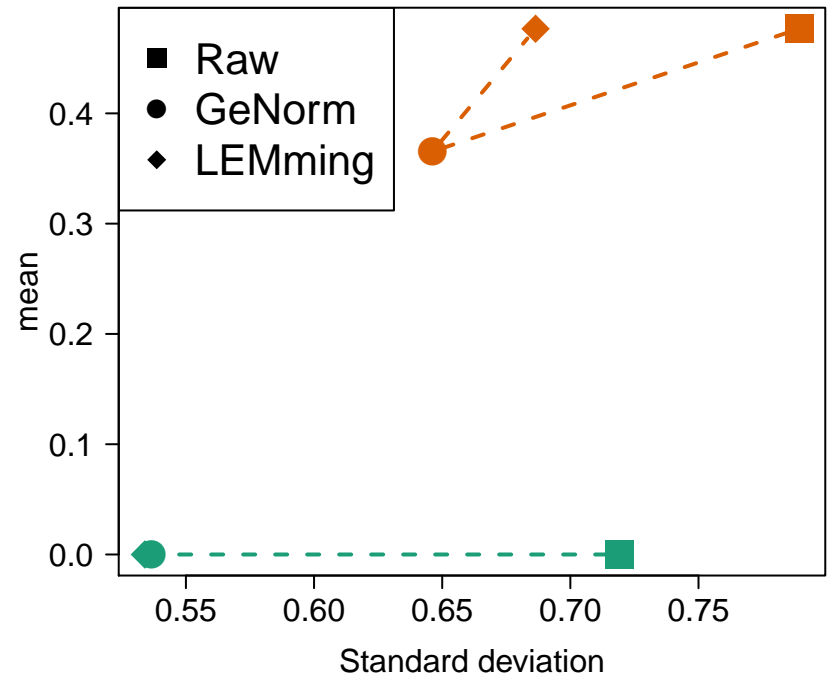
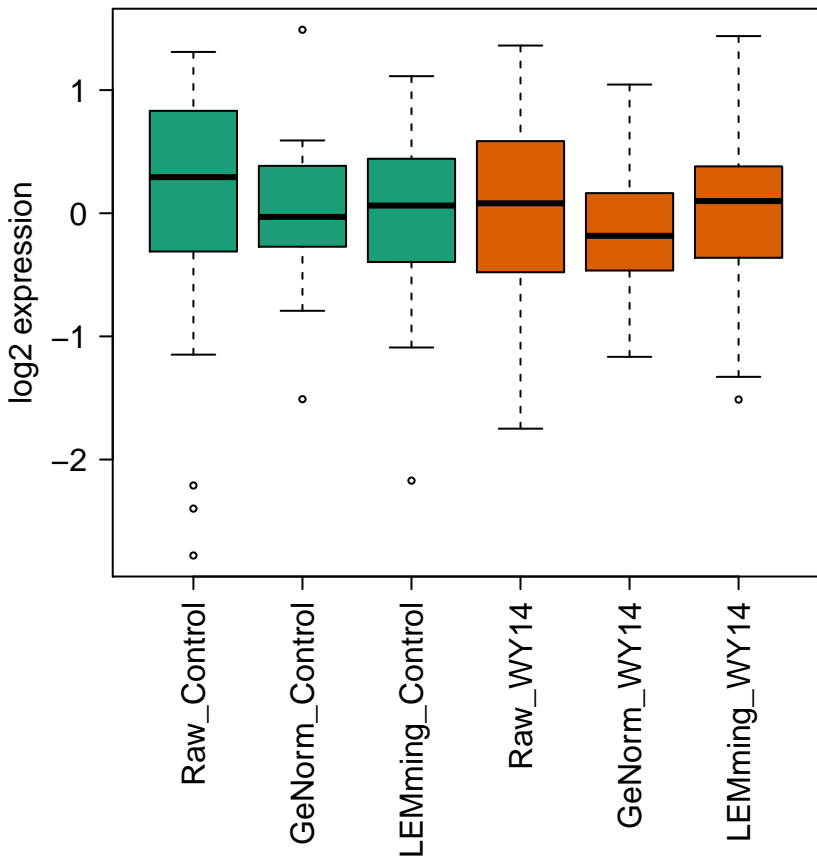


INSIG1



Variance-mean plot



INSIG2**Variance–mean plot****RPLP0****Variance–mean plot**