

Supplementary material

Figure S1. Scatter plot showing adjusted variance versus mean gene expression levels. Black dots represent the initial dispersion, which is higher for genes with low counts and decreases for genes with high counts. Blue dots indicate the adjusted dispersion after the Bayesian model is applied, while the red line represents the overall trend.

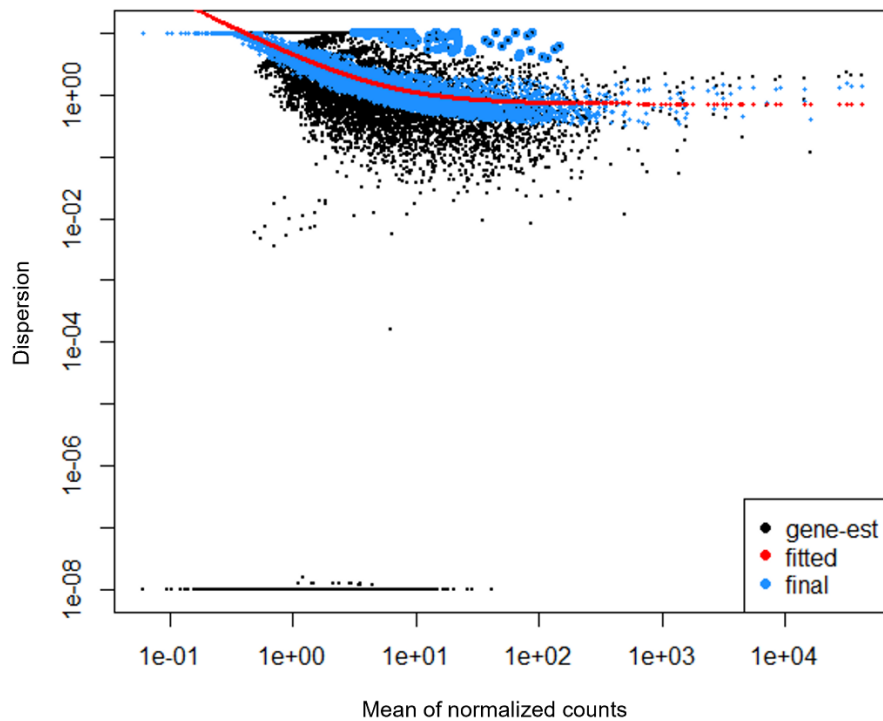


Table S1. Pearson correlation values between two replicates across four developmental stages.

Stage	Pearson value
Pre-pol	0.84
Pol	0.87
Post-pol	0.86
Fer	0.81

Fig. S2. Number of sequences with GO-terms associated with the categories biological process, molecular function, and cellular component.

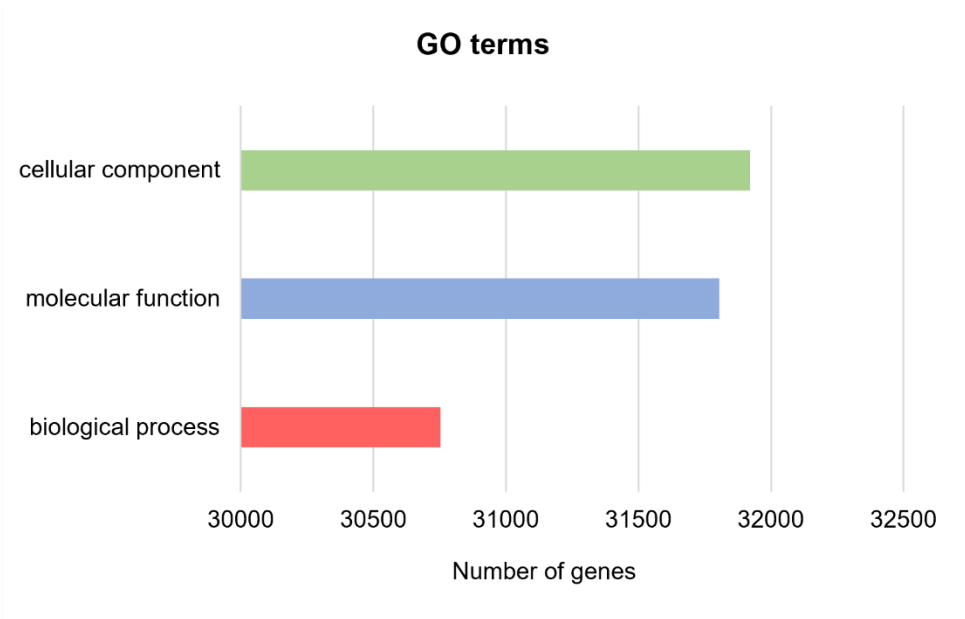


Fig. S3. Number of sequences with GO-terms associated with the biological process category.

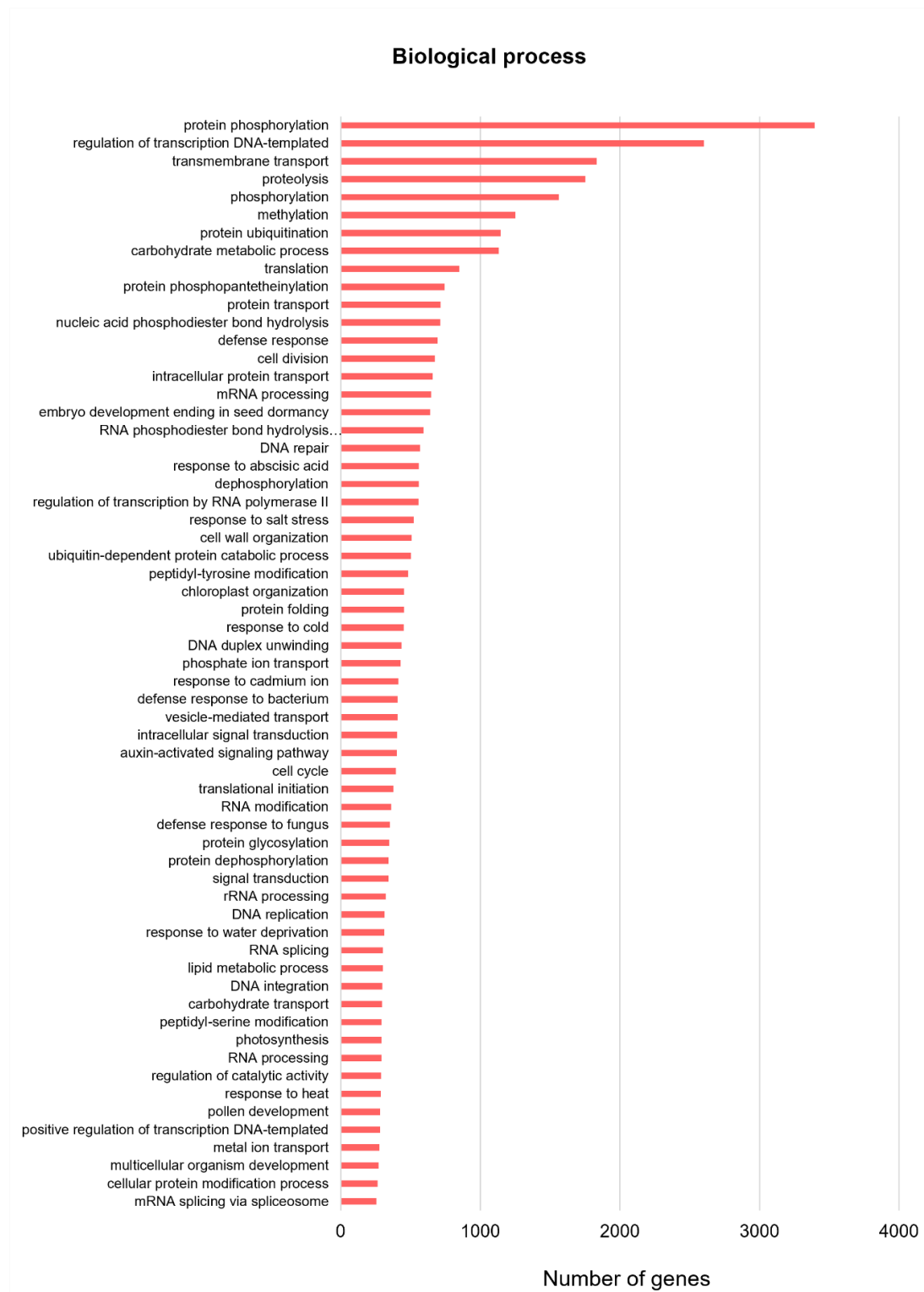


Fig. S4. Number of sequences with GO-terms associated with the molecular function category.

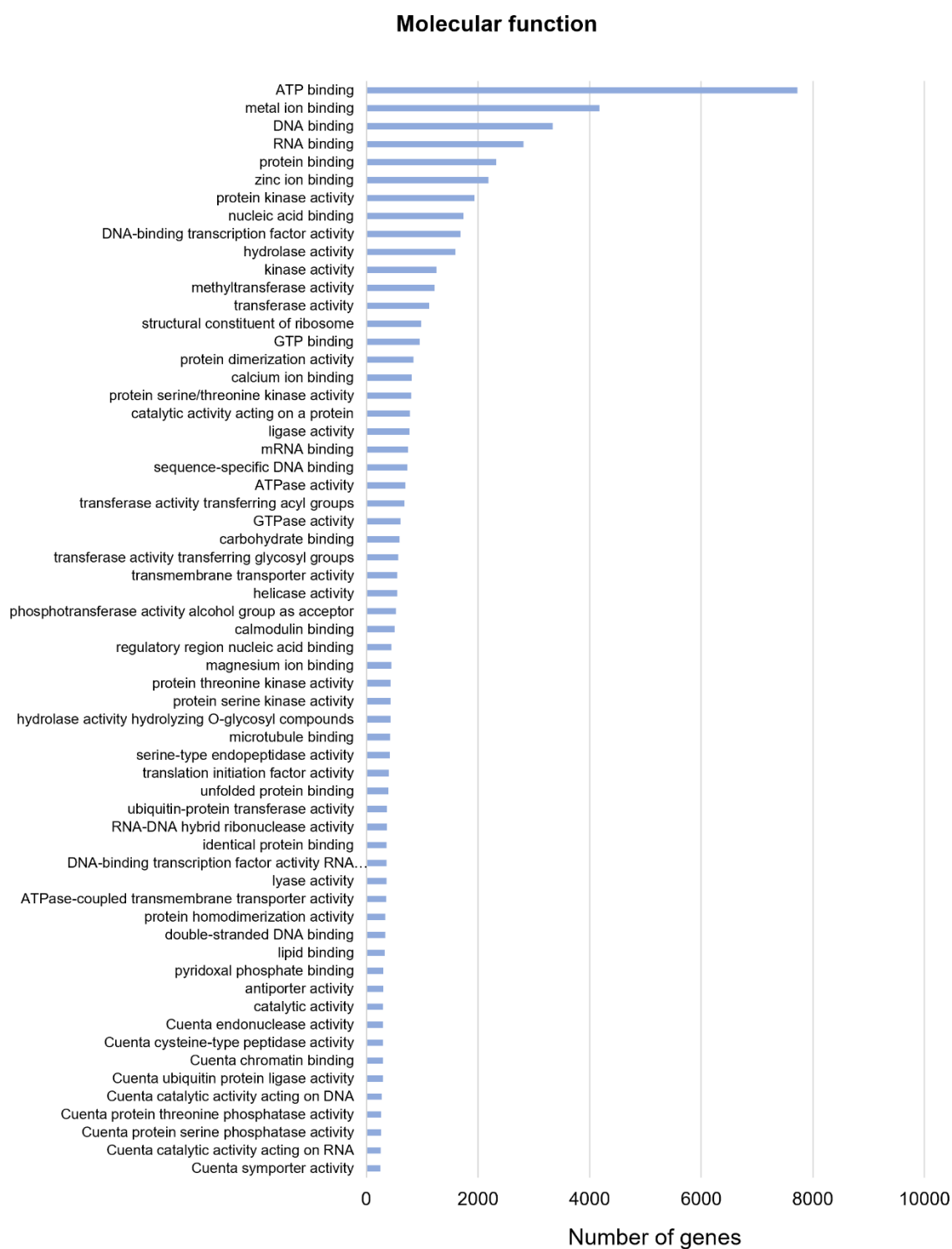


Fig. S5. Number of sequences with GO-terms associated with the cellular component category.

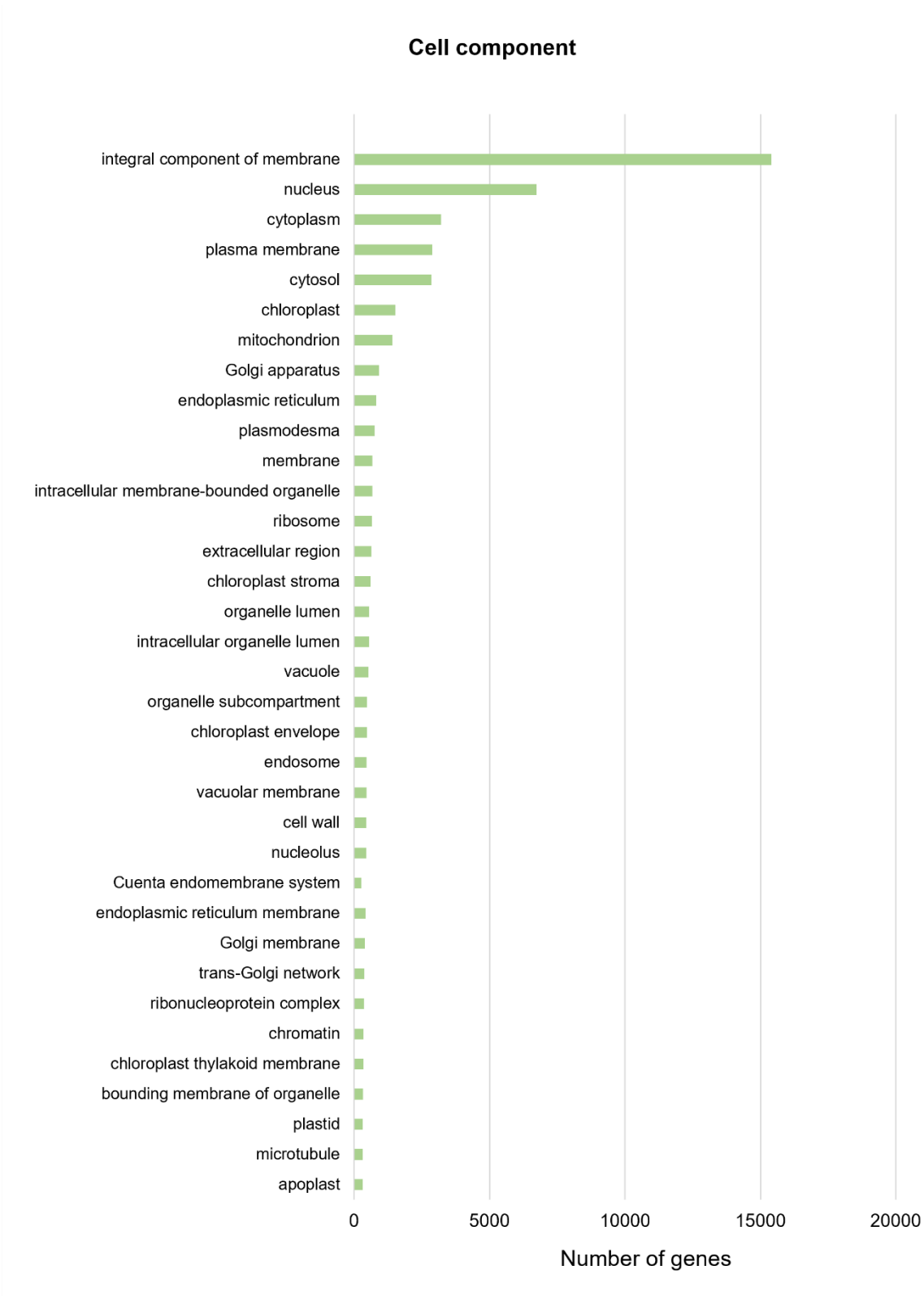


Fig. S6. Volcano plots depicting differential expression between developmental stages.

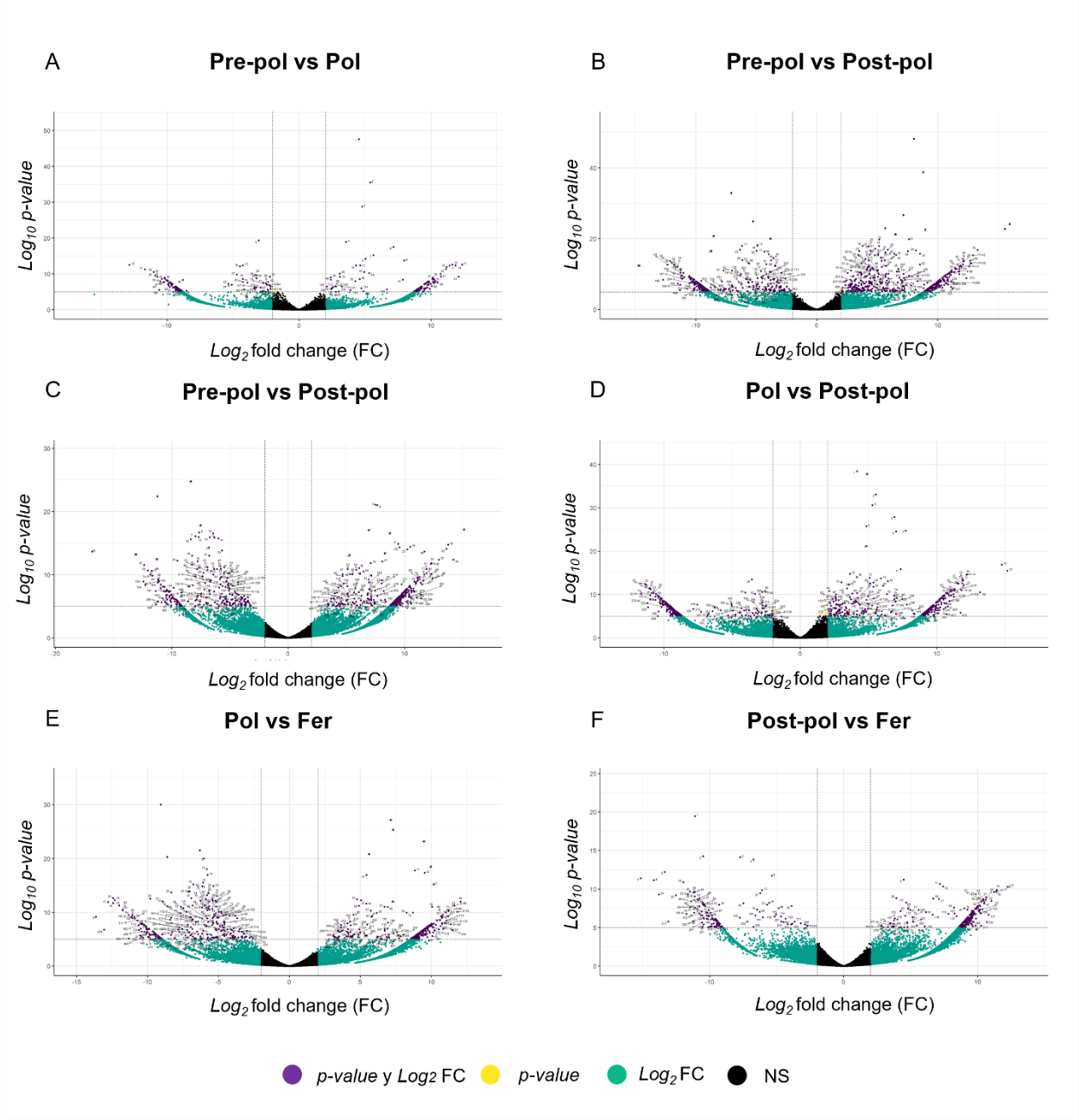


Fig. S7. Number of clusters identified using the cubic clustering criterion of Ward's minimum variance method. The blue dashed line represents the optimal number of clusters according to Ward's minimum variance method.

Cubic clustering criterion (CCC)

