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Figure 2 Research computing versus container-based approaches for differential gene expression analysis of HeLa cells. (\mathbf{a} , \mathbf{b}) Numbers of significantly differentially expressed genes identified using different versions of software packages (\mathbf{a}) and a container-based approach with a defined computing environment (\mathbf{b}). n=3 biological replicates per group (wild-type or double-knockdown HeLa cells).