

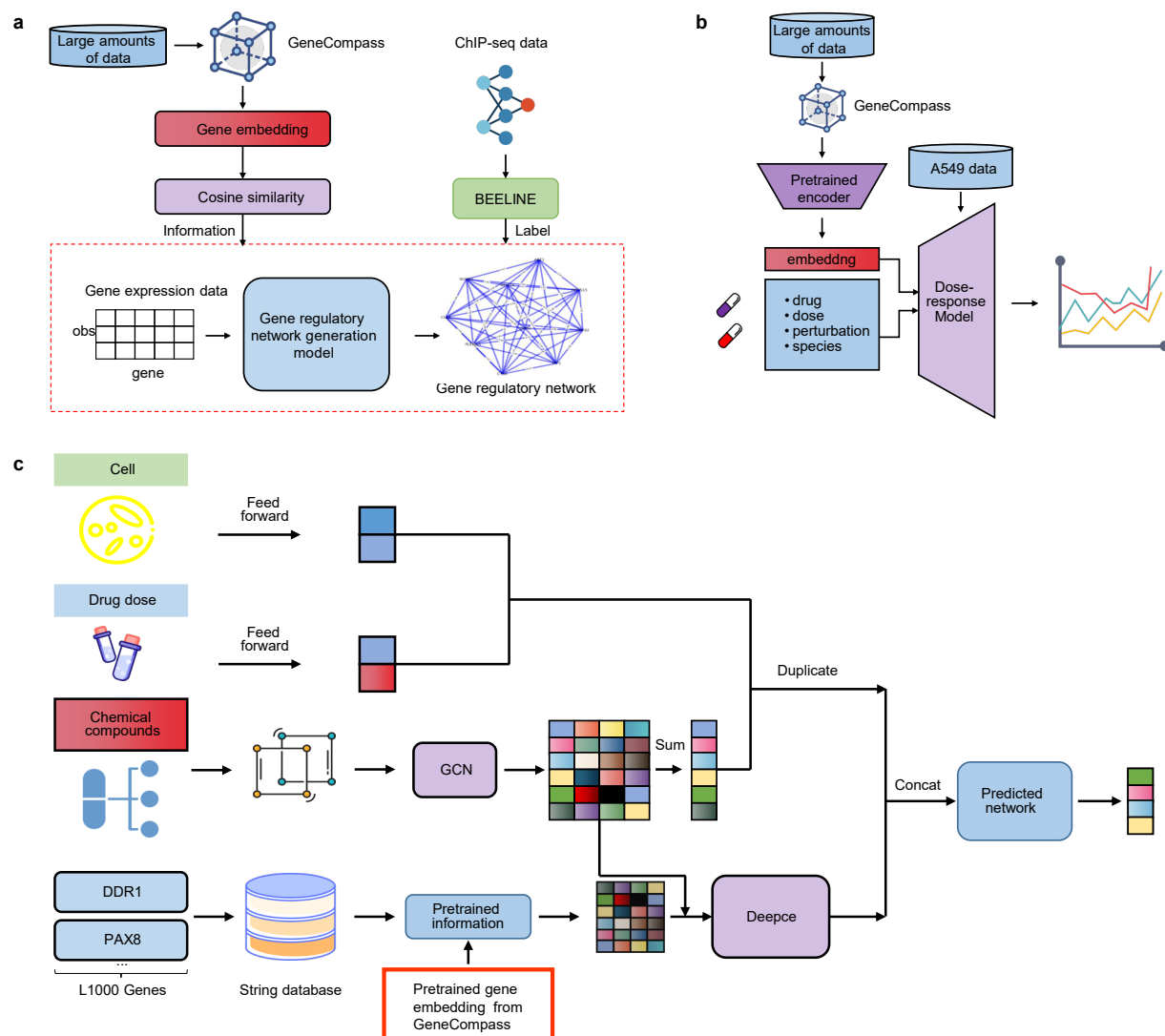


Fig. S6| Workflows of three downstream tasks. a, GRN inference, gene-gene relationship information captured by GeneCompass is used, and the ground truth comes from ChIP-Seq data. **b**, The detailed process of drug dose response prediction task. **c**, Gene expression profile prediction. Combined features of cell, drug, chemical compounds and genes are used to predict gene expression.