

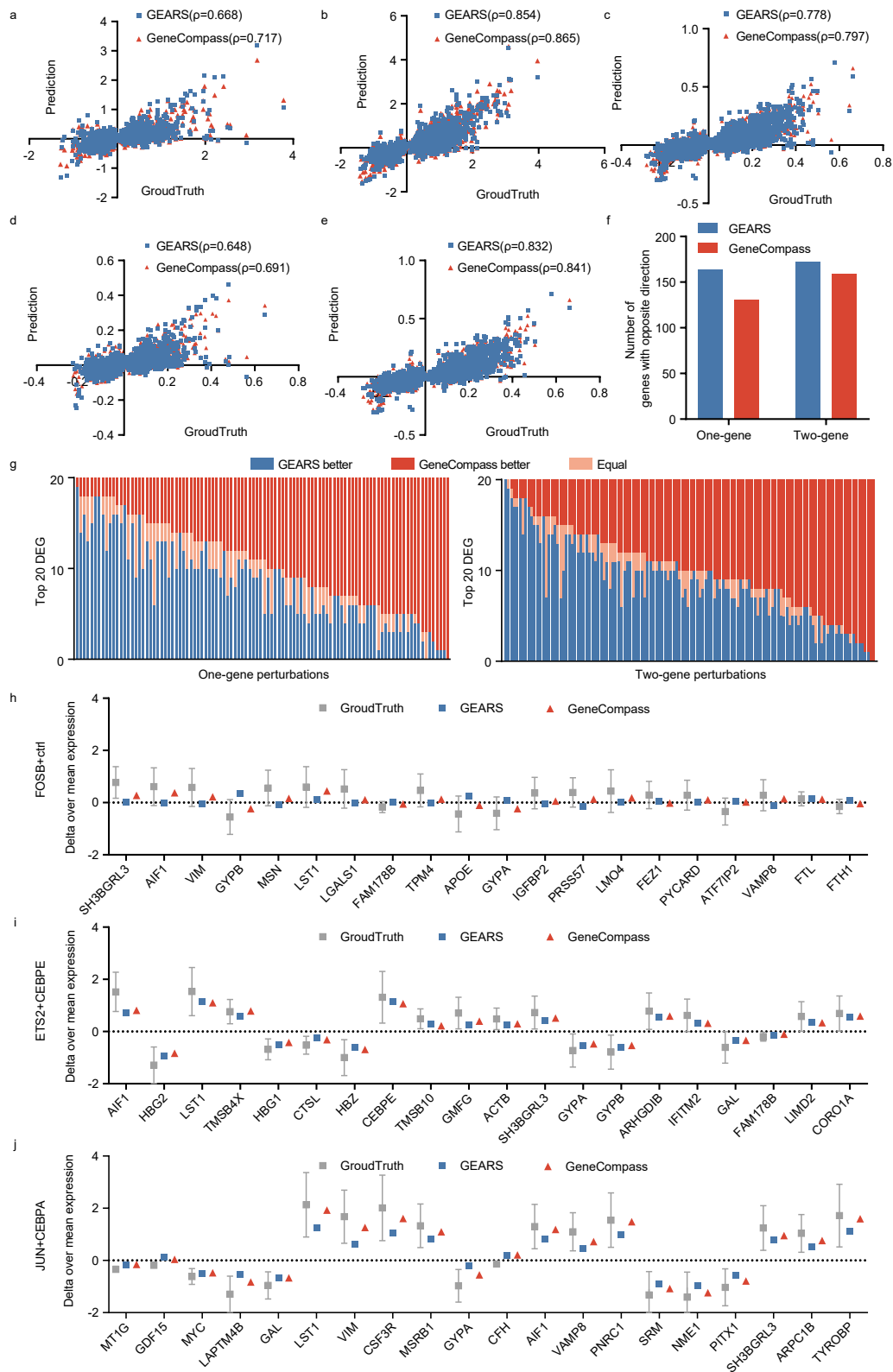


Fig. S9| *In silico* gene perturbation prediction. Scatter plots of the predicted and true changes in gene expression for **a**, one-gene perturbations and **b**, two-gene perturbations. Scatter plots of the predicted and true log fold changes in gene expression for **c**, all perturbations, **d**, one-gene perturbations and **e**, two-gene perturbations. Each dot represents a specific gene, and Spearman's correlation coefficient is marked as " ρ ". **f**, Total number of the top 20 DEGs where the predicted post perturbation differential expression is in the incorrect direction of the ground truth for one-gene and two-gene perturbations. **g**, Comparison between GeneCompass and GEARS for the prediction of the top 20 genes in one-gene perturbations and two-gene perturbations. "GeneCompass better" is defined as GeneCompass having a smaller deviation than GEARS for a specific gene. Expression changes predicted by GeneCompass and GEARS for perturbations of **h**, FOSB+ control, **i**, EST2+CEBPE, **j**, JUN+CEBPA.