(B) Prediction error stratified by gene set size (A) Double perturbation prediction error Norman CEBPE+KLF1 genes sorted by expression genes sorted by differential expression 12.5 + error: 5.2 Prediction error (L_2) 5.0 0.5 c.2 scFoundation scFoundation predicted expression (sum of single effects) 10.0 Mean prediction error **GEARS GEARS** 7.5 scGPT scGPT TGFBR2+ETS2

5.0

2.5

Additive

10.000

Number of genes (log-scale)

100

10

1.000

Additive

10.000

100

1,000

(C) Prediction of non-additive perturbation effects

Additive

scFoundation

0.0

GEARS-

scGPT

error: 1.3

observed expression

