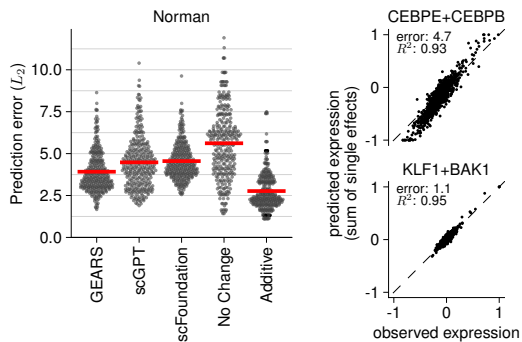
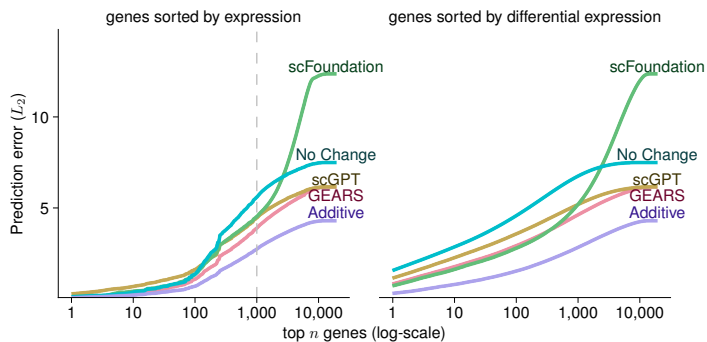
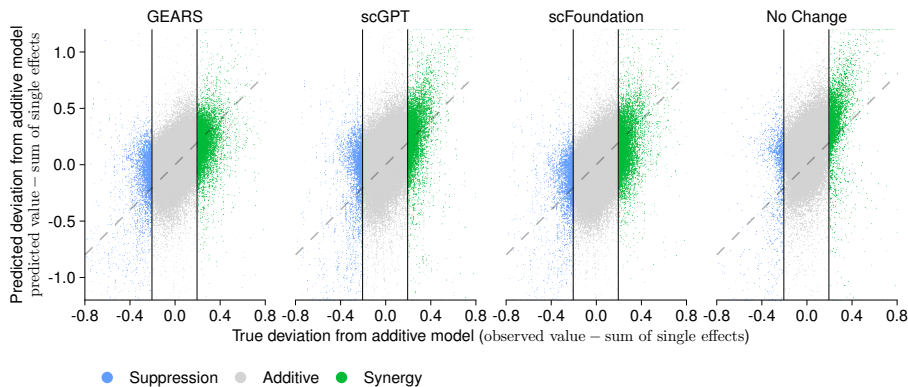


(A) Double perturbation prediction error**(B) Prediction error depends on number of considered genes****(C) Prediction of non-additive perturbation effects****(D) Accuracy of top predictions**