

Appendix

Time-series transcriptomics and proteomics reveal alternative modes to decode p53 oscillations

Alba Jimenez^{*.1}, Dan Lu^{*.1}, Marian Kalocsay^{1,2}, Matthew J. Berberich^{2,3}, Petra Balbi¹, Ashwini Jambhekar^{**1}, Galit Lahav^{**1}

*=authors with equal contributions

**= co-corresponding authors

- 1 Department of Systems Biology, Blavatnik Institute at Harvard Medical School, Boston, MA 02115, USA
- 2 Laboratory of Systems Pharmacology, Blavatnik Institute at Harvard Medical School, Boston, MA 02115, USA
- 3 Center for Protein Degradation, Dana-Farber Cancer Institute, Boston, MA 02115

Correspondence: galit@hms.harvard.edu / ashwini_jambhekar@hms.harvard.edu

Table of content

Appendix Figure S1. Flowcharts detailing the different data sets and filters used in the study.

Appendix Figure S2. mRNA and protein profiles of house-keeping genes GAPDH and TUBB, and p53 targets E2F7 and XPC.

Appendix Figure S3. mRNA and protein profiles of all targets classified into the 11 categories of dynamical responses.

Appendix Figure S1

A

Data sets

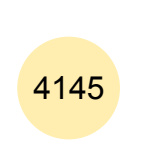
RNASeq
p53 pulsatile

RNASeq
p53 rising

TMT Mass-Spec
p53 pulsatile

TMT Mass-Spec
p53 rising

Chip-seq p53
bound targets



Filters

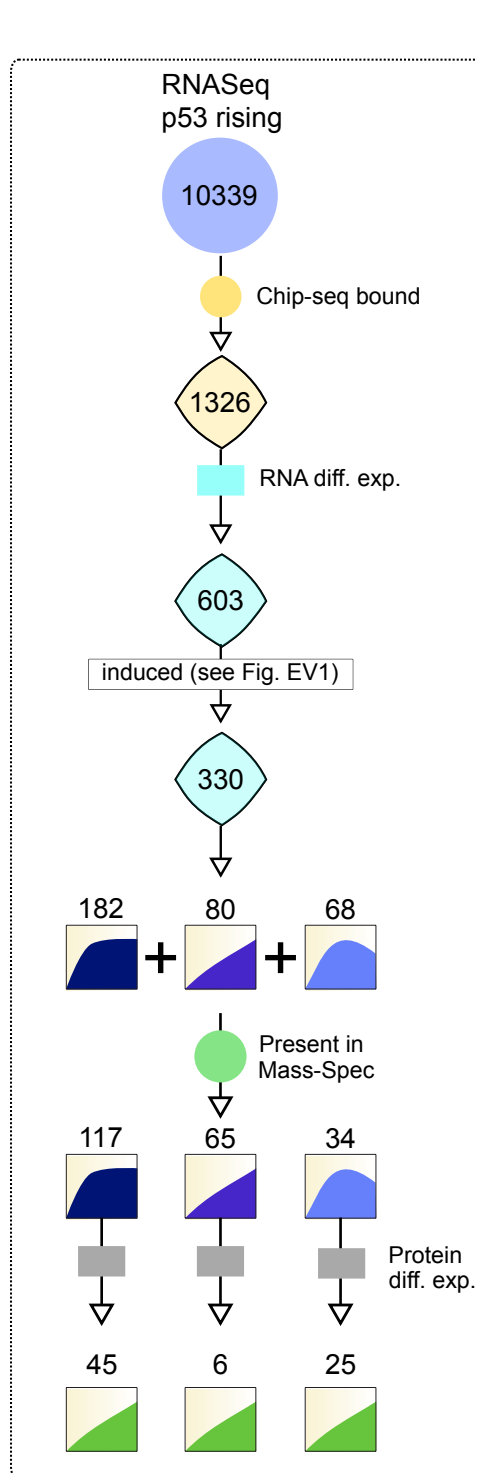
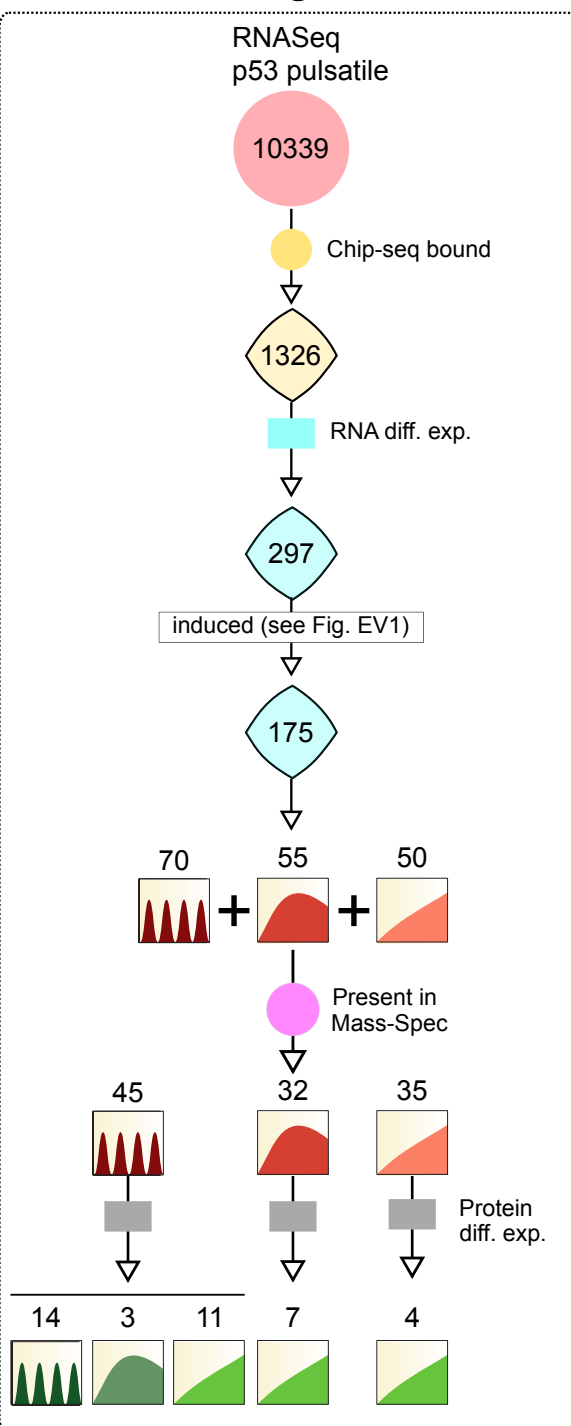
Differential mRNA expression:
Fold change > 1.5,
FDR < 0.2 and
Pearson corr. between replicates > 0.5

Differential Protein expression:
Fold change > 1.15,
FDR < 0.2 and
Pearson corr. between replicates > 0.5

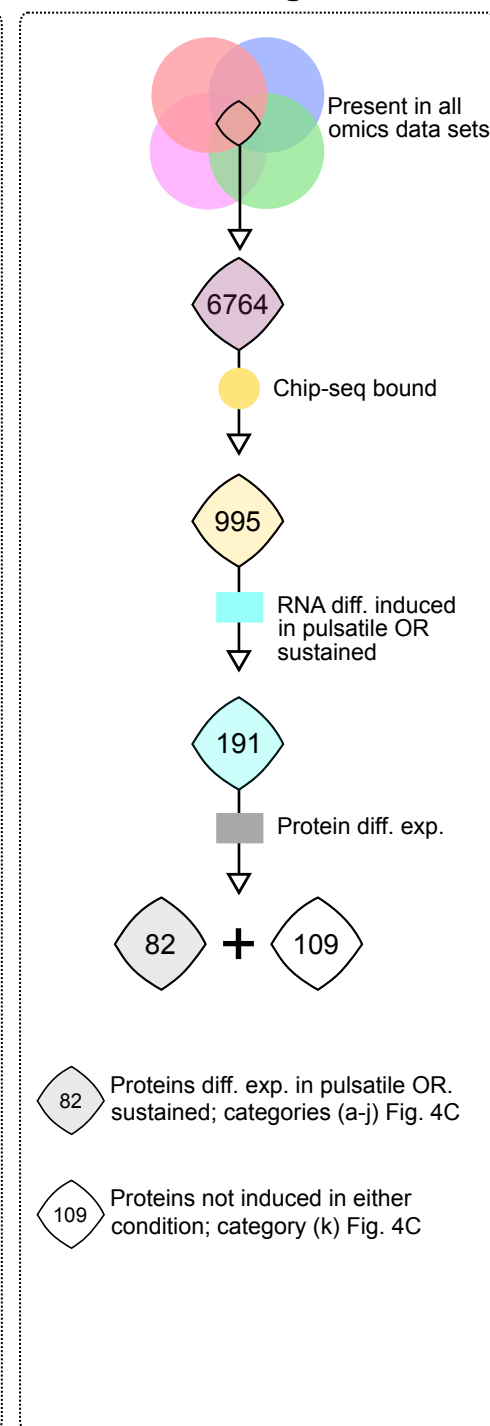
Legend

- RNASeq pulsatile
- RNASeq rising
- Mass-Spec pulsatile
- Mass-Spec rising
- Chip-seq
- Diff. exp. mRNA
- Diff. exp. protein

B Flowchart Figures 2-3

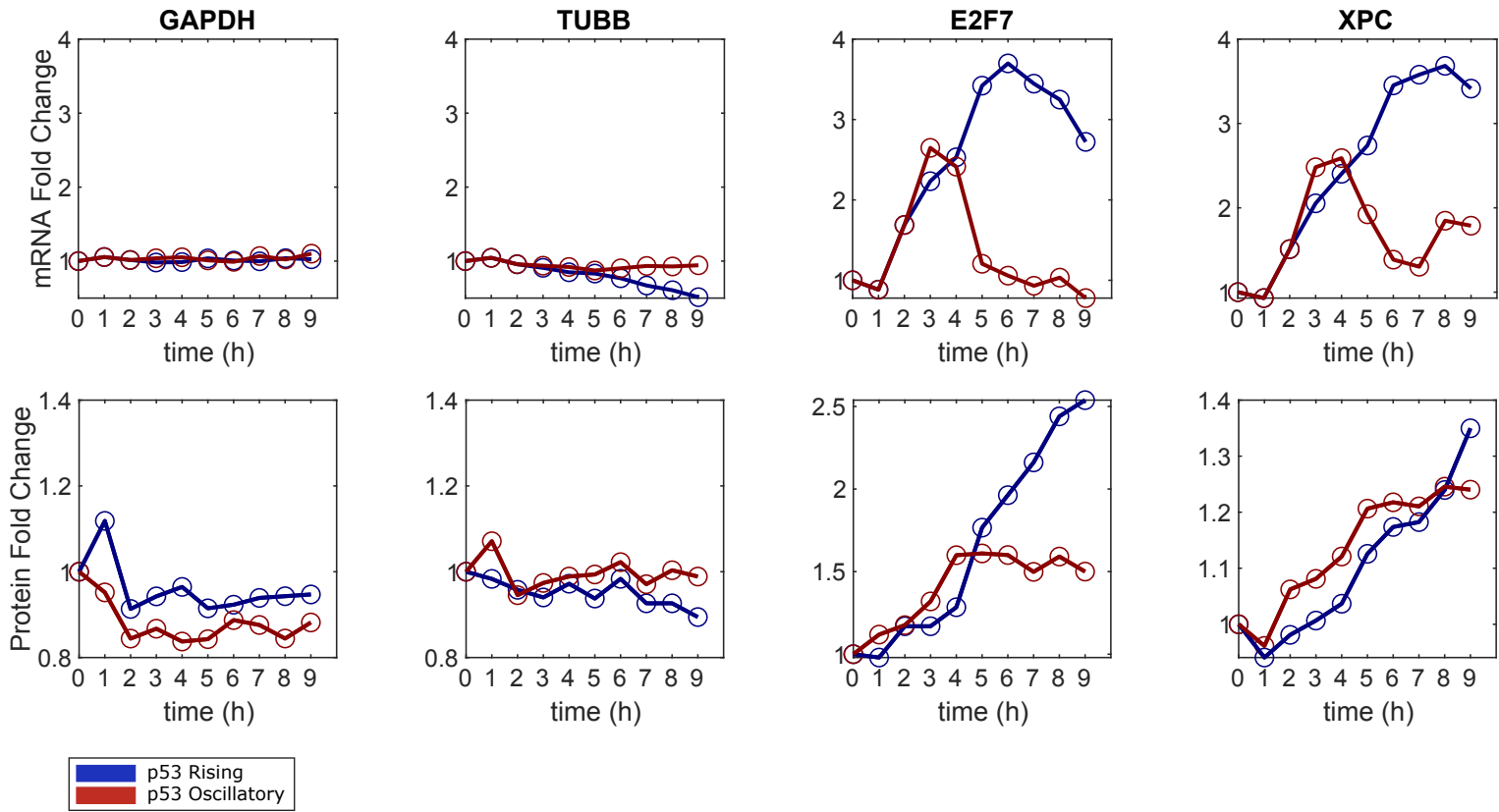


C Flowchart Figure 4



Appendix Figure S1: Flowcharts detailing (A) The different data sets and filters used in the study (B) Flowcharts for Figures 2 and 3 (C) Flowchart for Figure 4.

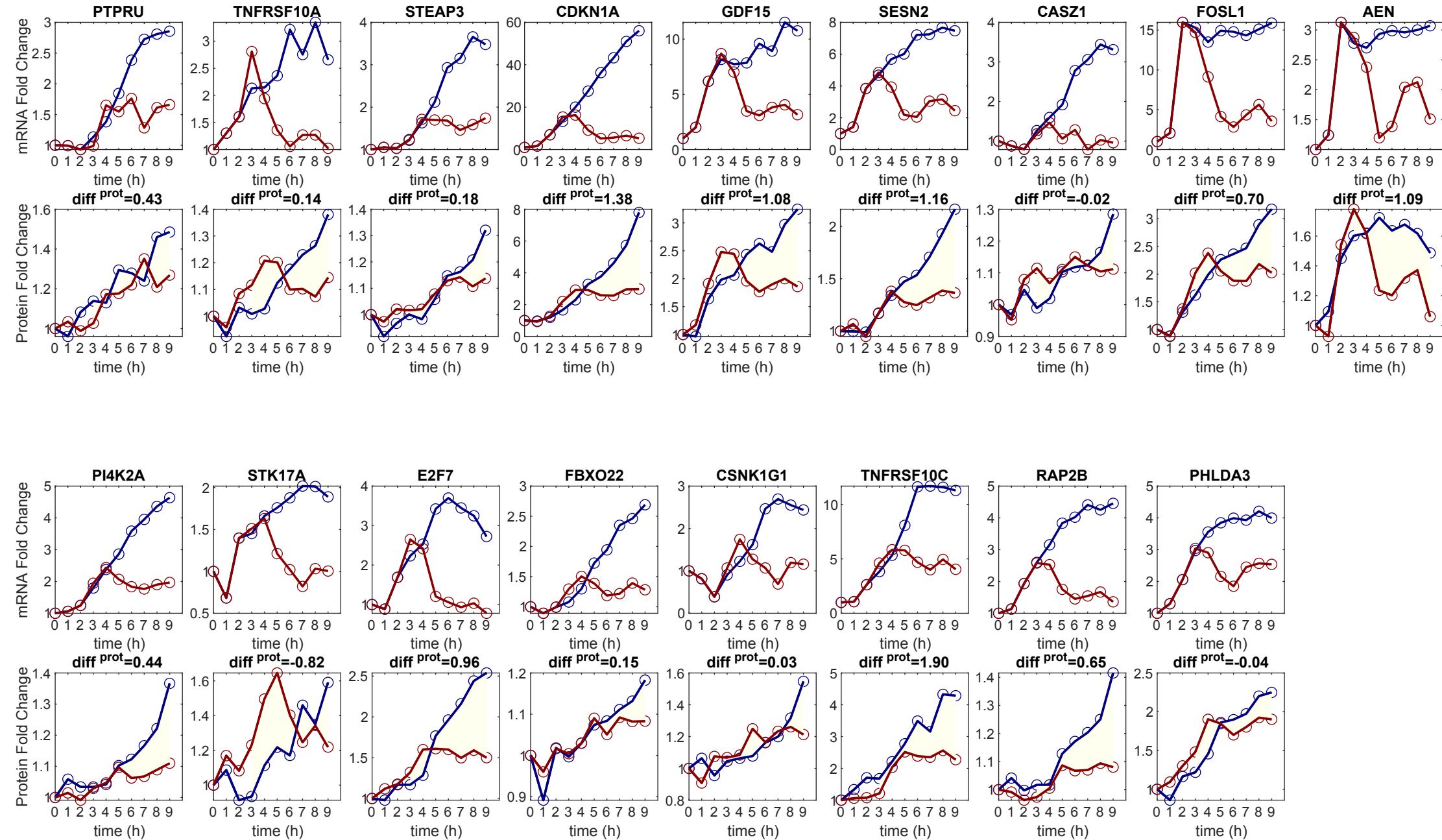
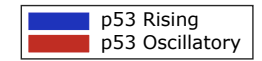
Appendix Figure S2



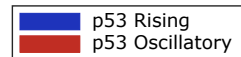
Appendix Figure S2: mRNA and protein profiles of house-keeping genes GAPDH and TUBB, as well as two p53 targets E2F7 and XPC.

Appendix Figure S3

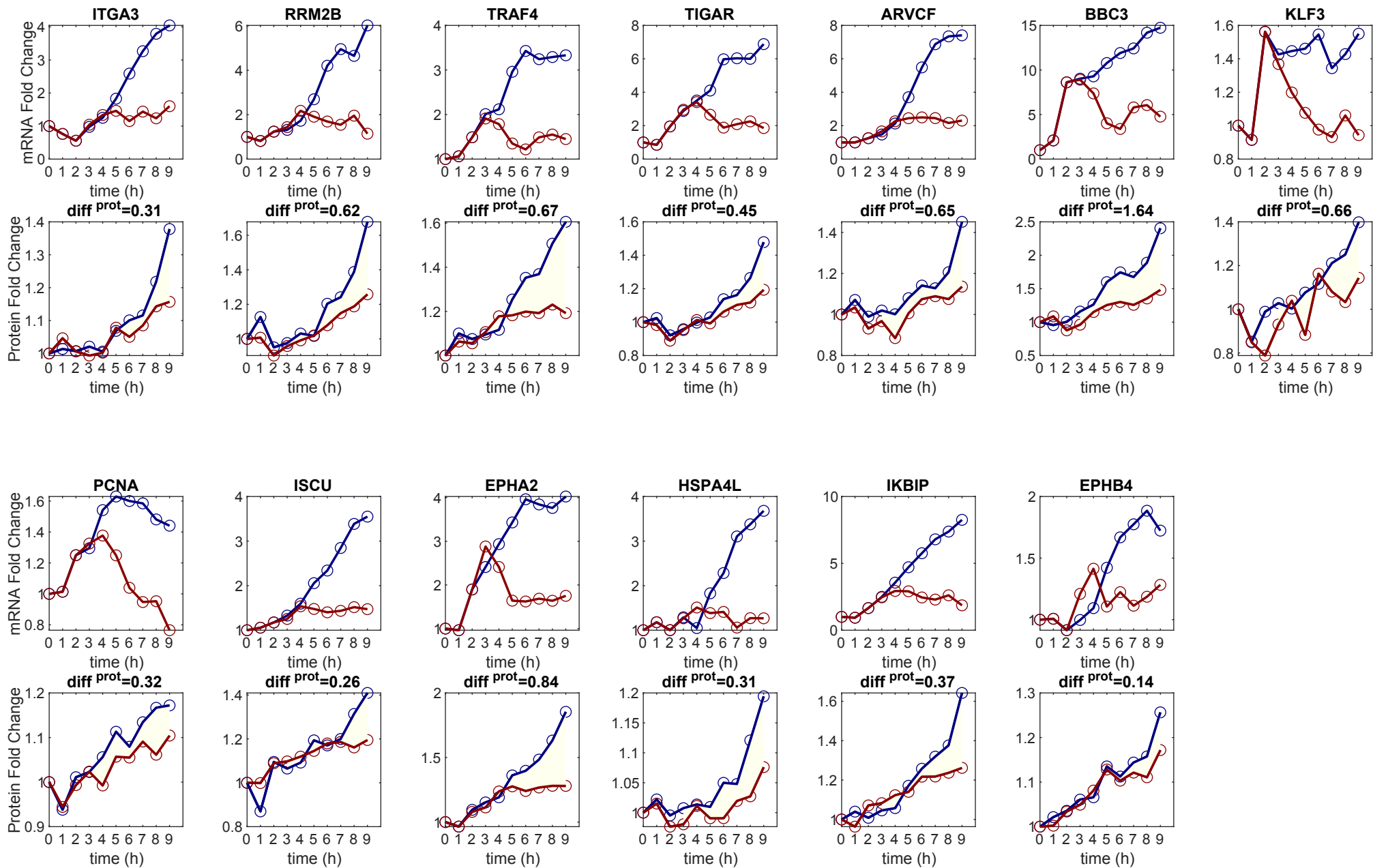
category (a)

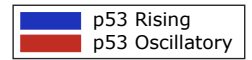


Appendix Figure S3: mRNA and protein profiles of all targets classified into 11 categories (a-k) of dynamical responses as defined in Figure 4.

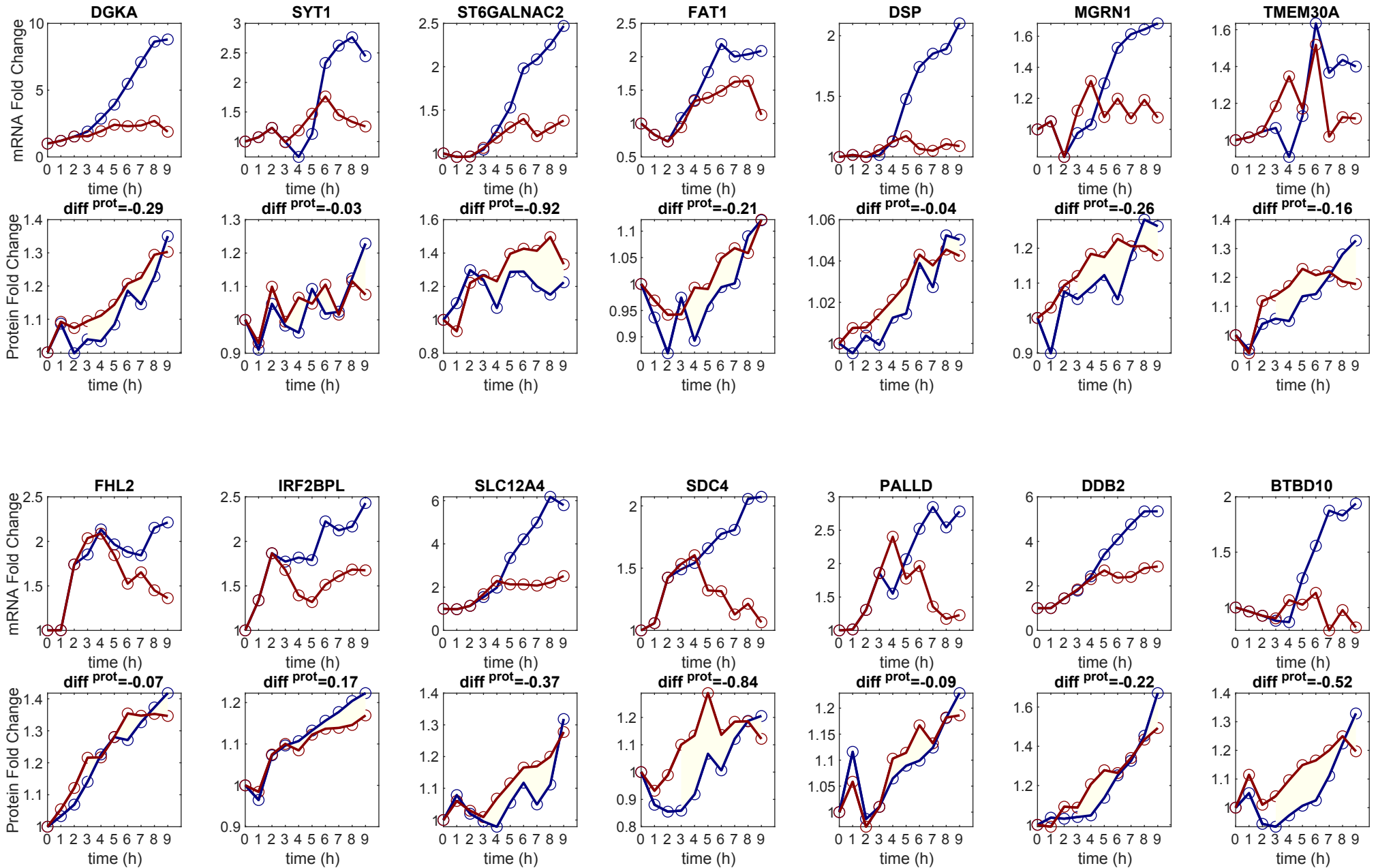


category (b)



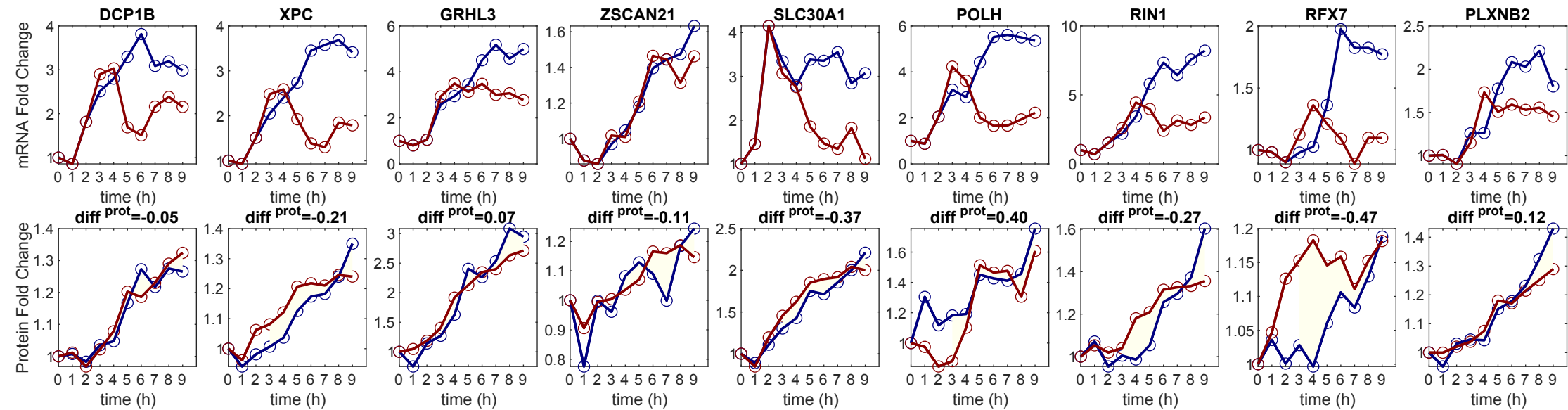


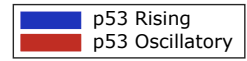
category (c)-page1



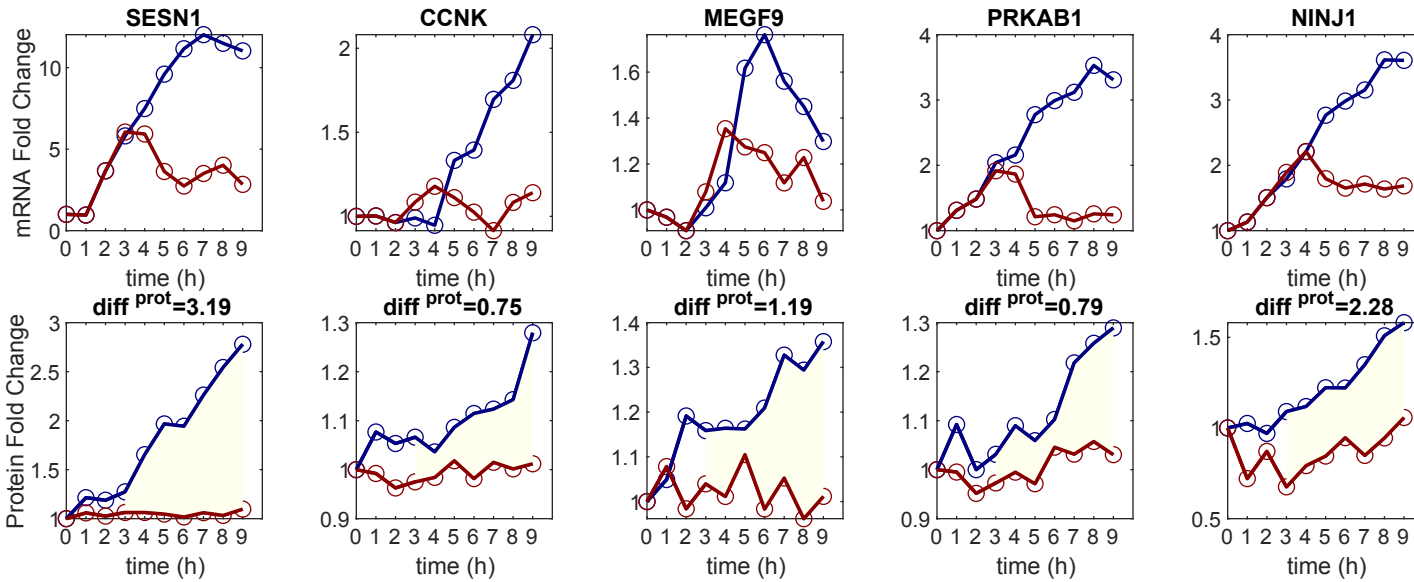


category (c)-page2

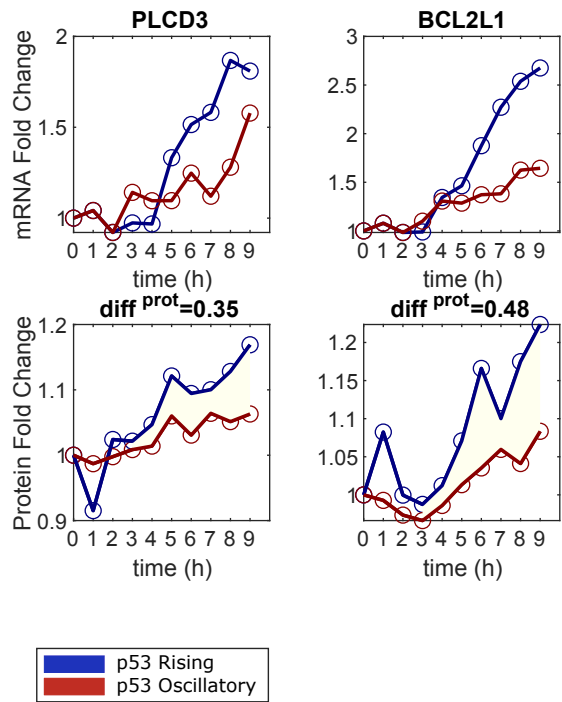


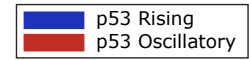


category (d)

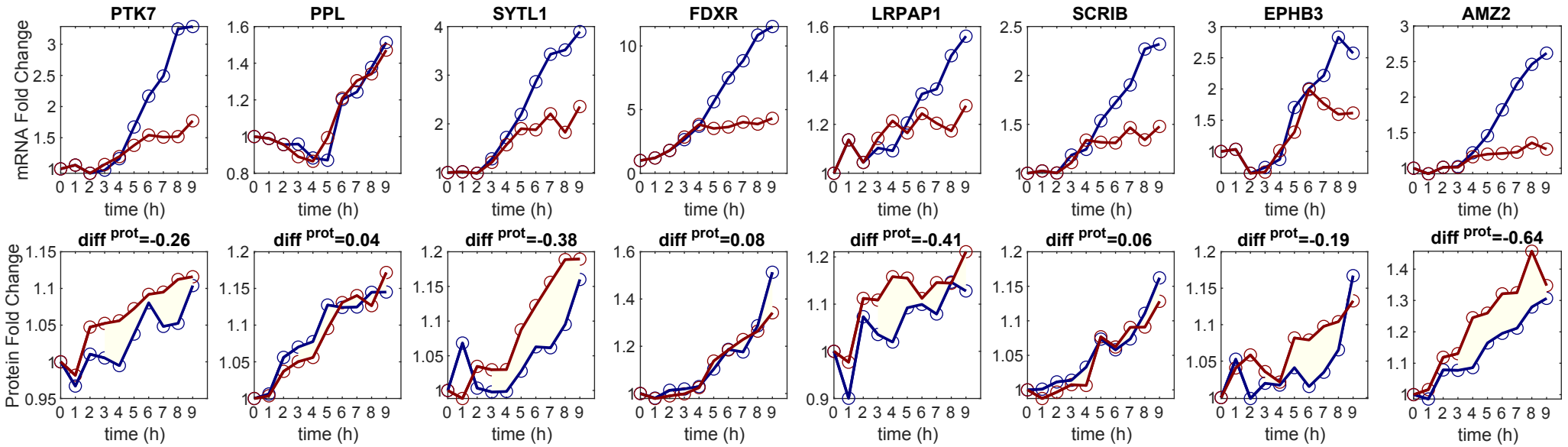


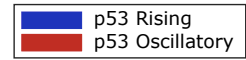
category (e)



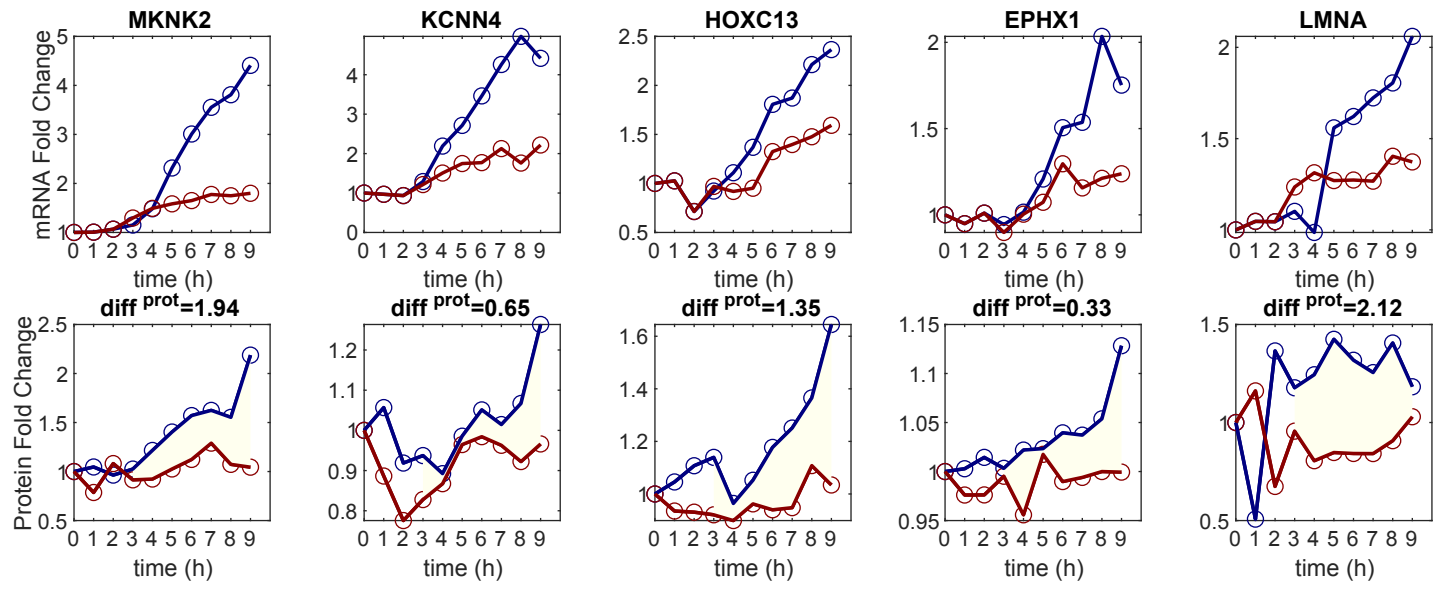


category (f)

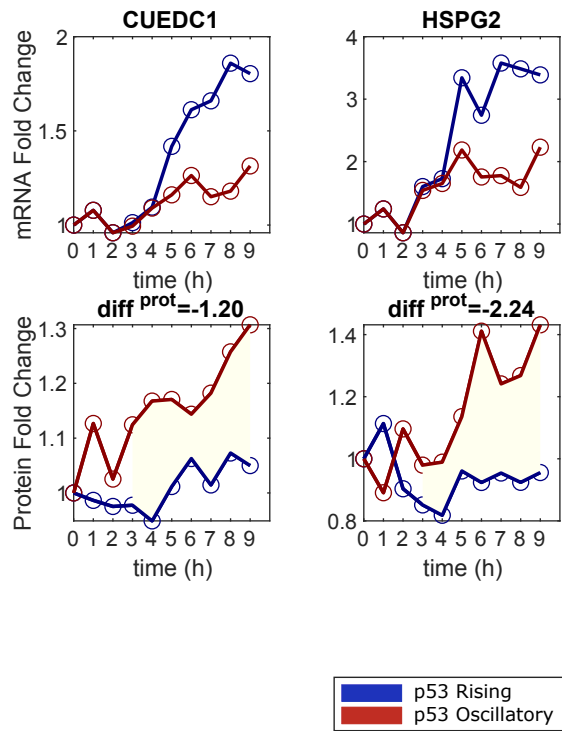




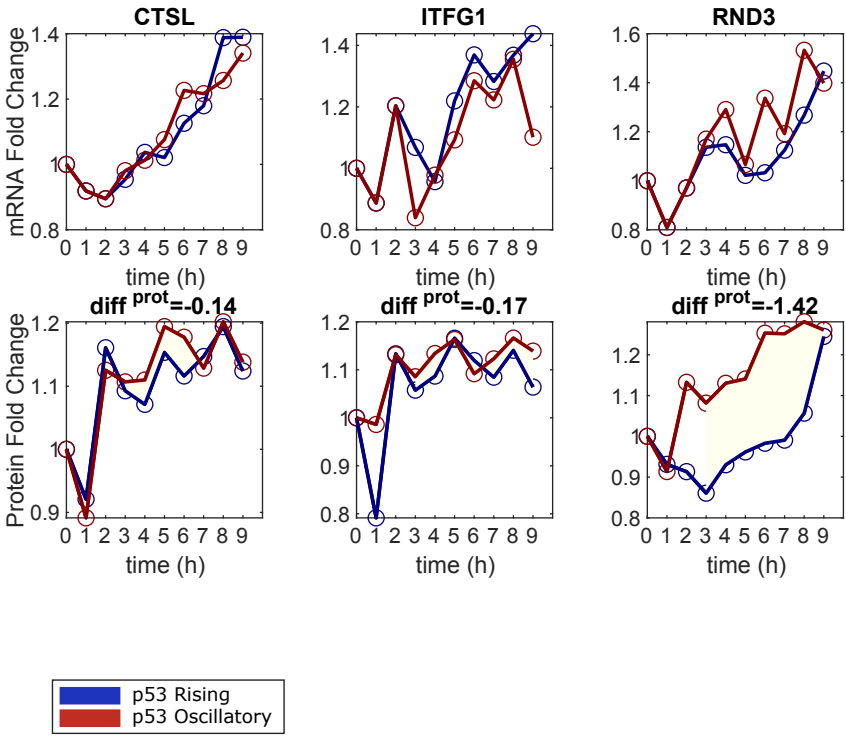
category (g)



category (h)



category (i)



category (j)

