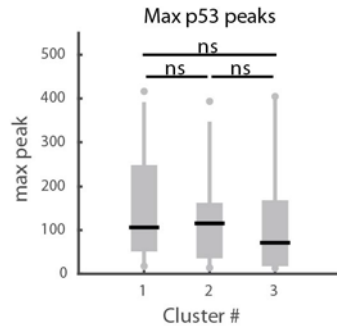


**Supplementary Figure 1**

**Characterization of gene expression clusters shows p53 dependence and enrichment of known p53 target genes among induced genes. (related to Figure 1)**

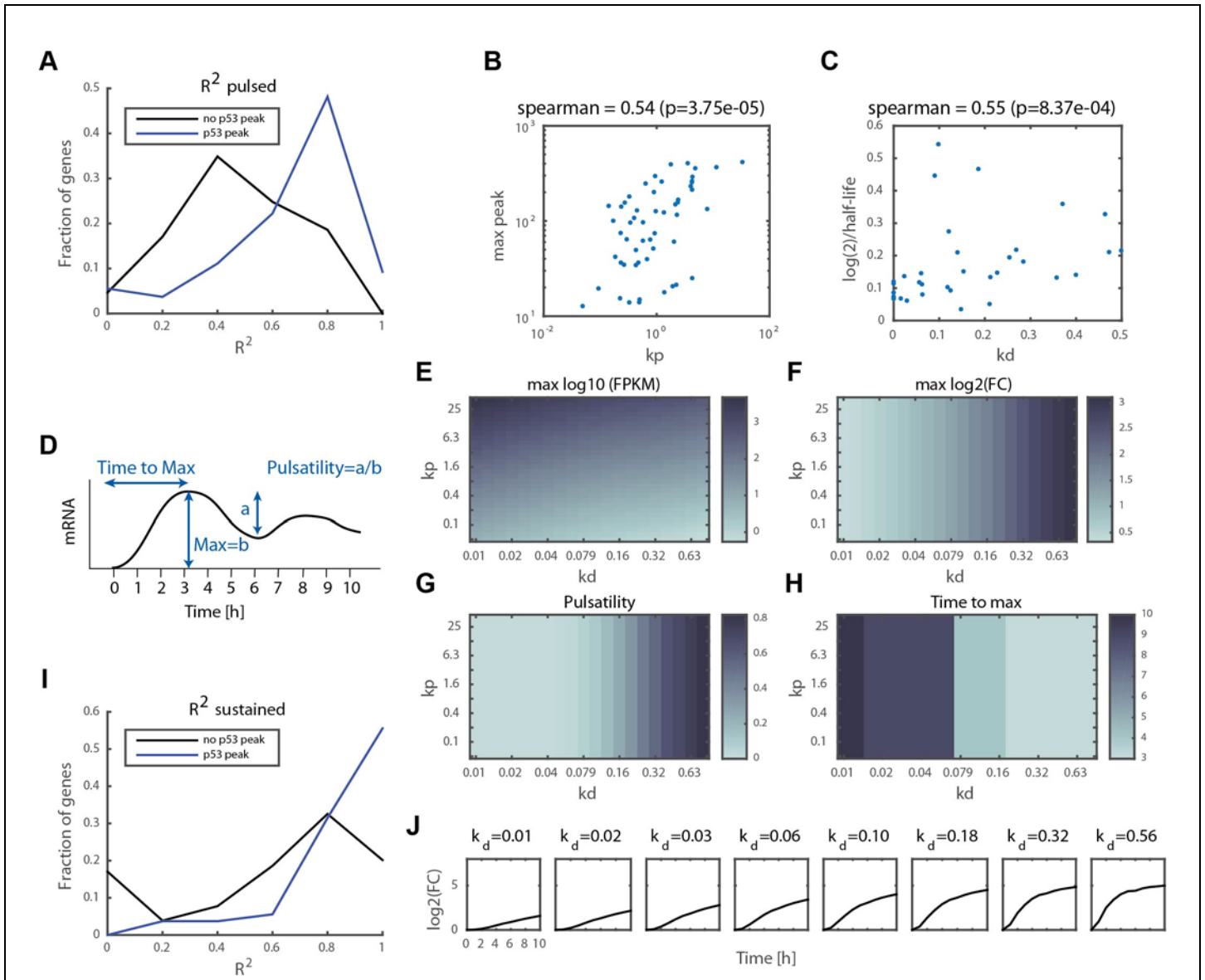
**A.** Quantiles (median in black, shaded area represents the 25% and 75% quantiles) of RNA-Seq data by cluster for MCF7 p53 wild-type cell line (blue) and MCF7 p53-shRNA cell line (gray). **B.** Mapping of the genes in each cluster to known target genes, obtained from Riley et al. 2008<sup>30</sup>. P-values were calculated using the Binomial statistic, \* = p-value<0.01. **C.** Top five enriched GO Biological Process categories in each cluster (FDR<0.05). GO Enrichment analysis was done using Enrichr software<sup>39,40</sup>. Both p-value and FDR are shown.



## Supplementary Figure 2

### Properties of p53 ChIP peaks that map to the induced clusters (related to Figure 3).

Distribution of maximal reads of p53 peaks per cluster. T-test was done to evaluate significance; ns stands for not significant ( $pval > 0.2$  for all comparisons). Black lines indicate the median, and the boxes and whiskers extend to the 25%-75% and the 5%-95% quantiles, respectively.



### Supplementary Figure 3

#### Evaluation of model fit and parameters. (Related to Figures 4 and 5).

**A.** Distribution of  $R^2$  values for the model fit. Comparison between induced genes with p53 ChIP peak and induced genes without a p53 ChIP peak. **B.** Correlation of model derived  $k_p$  values with maximal p53 ChIP peak signal for each gene. The signal from the closest peak was used for genes with multiple p53 ChIP peaks. **C.** Correlation of model derived  $k_d$  values with published mRNA half-life data in MCF7 cells<sup>34</sup>. **D.** Schematic of gene expression dynamical features that were computed for the model stimulation. **E-H.** Simulation of the model (equation 1) for the shown range of  $k_p$  and  $k_d$  values. Heat maps of the gene expression properties derived for each  $k_p$  and  $k_d$  combination. **I.** Distribution of  $R^2$  values for the model fit for sustained data. **J.** Model simulation with p53 sustained input and only varying the  $k_d$  parameter values.