

# Framework to identify 3' UTRs regulated by SUB1

## I. Data resource: RNA-seq bigwig datasets

- HepG2 WT (cytosolic fraction)
- HepG2 WT (nuclear fraction)
- HepG2 SUB1 KD

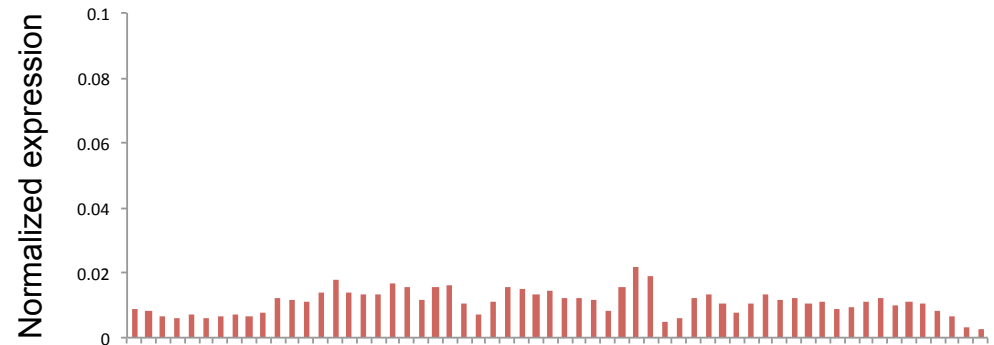
## II. Calculate expression level across 3' UTRs

- Expression level across different datasets are normalized
- Results from two replicates are averaged

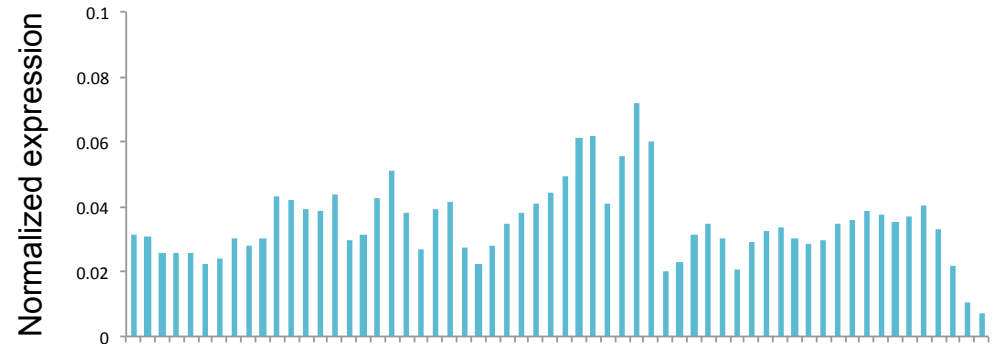
In total, we calculated expression signature across 3' UTRs of 19,639 protein-coding genes and 72,265 transcripts

# Expression across the 3' UTR of TP53: WT vs. SUB1 KD

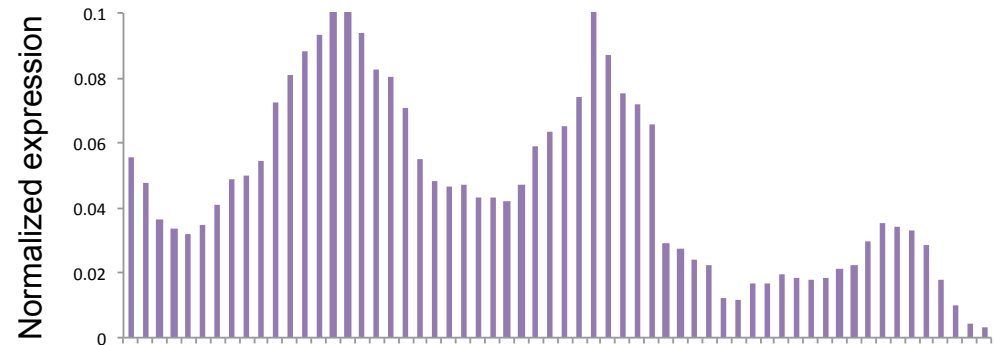
HepG2 WT cytosolic fraction



HepG2 WT nuclear fraction



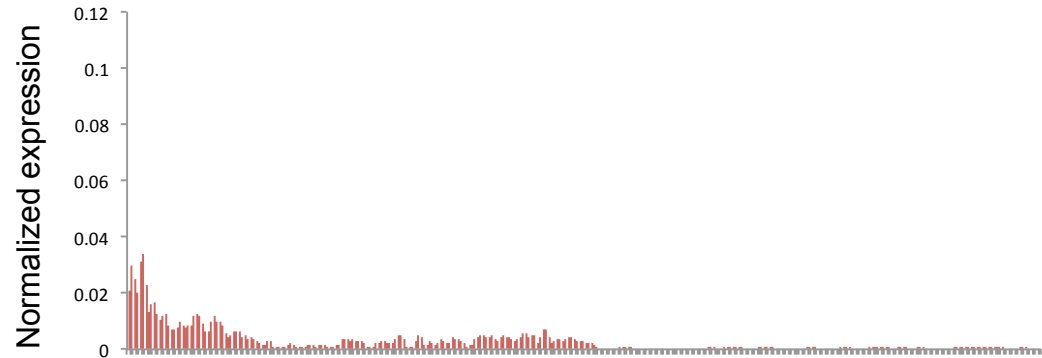
HepG2 SUB1 KD



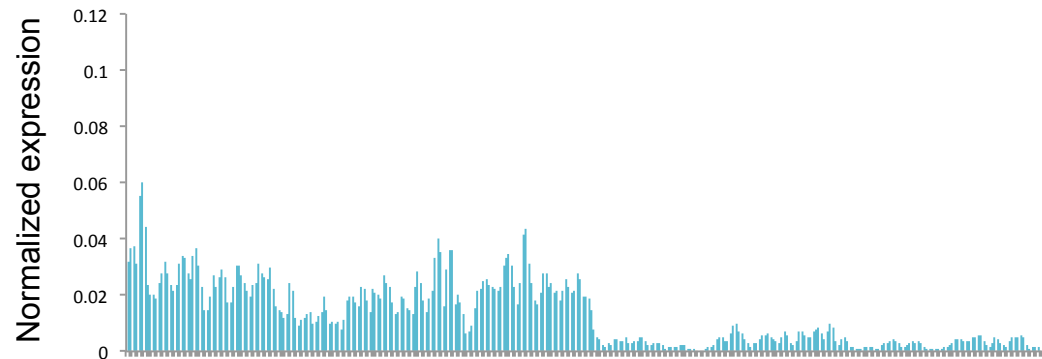
3' UTR index (1,207 bp)

# Expression across the 3' UTR of PTEN: WT vs. SUB1 KD

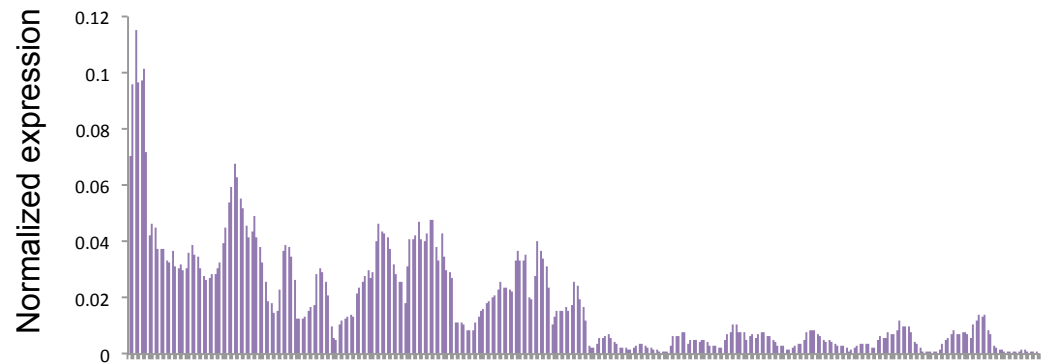
HepG2 WT cytosolic fraction



HepG2 WT nuclear fraction



HepG2 SUB1 KD



3' UTR index (6,457 bp)

# Proposed model

