Framework to identify 3' UTRs regulated by SUB1

Data resource: RNA-seq bigwig datasets

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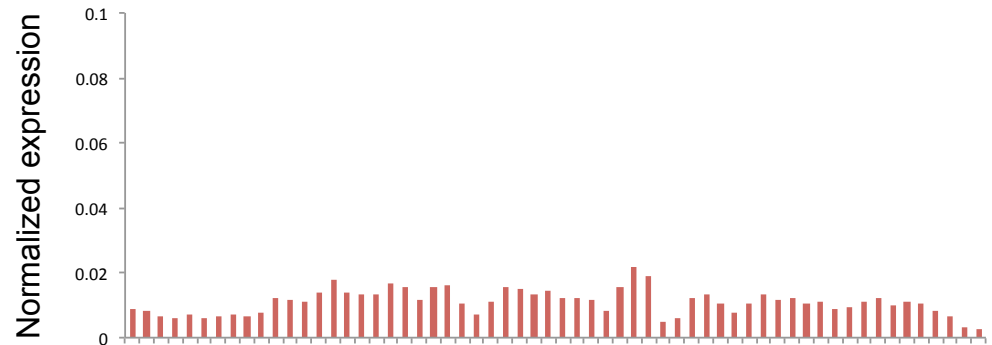
- HepG2 WT (nuclear fraction)

- HepG2 SUB1 KD

Calculate expression level across 3' UTRs

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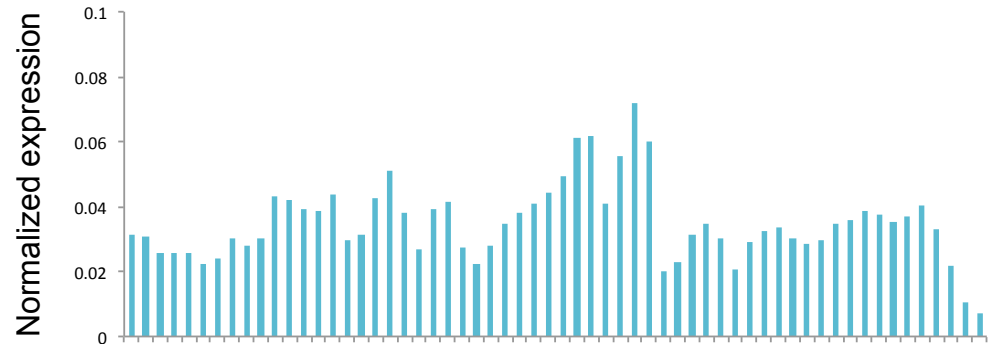
- Results from two replicates are averaged

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

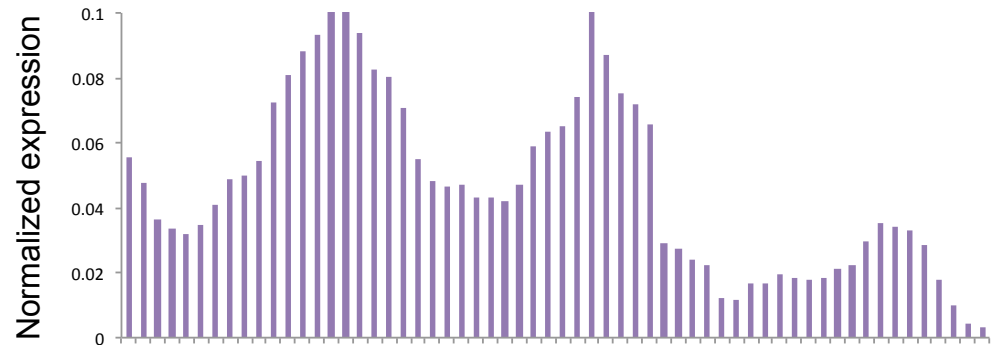# Expression across the 3' UTR of TP53: WT vs. SUB1 KD

HepG2 WT cytosolic fraction
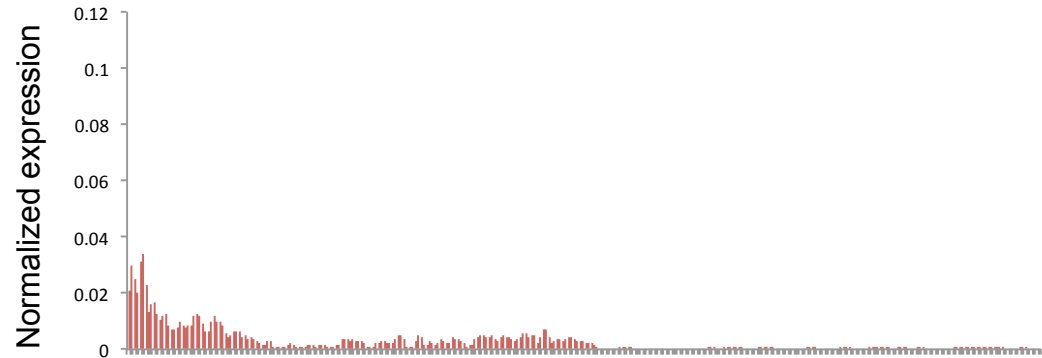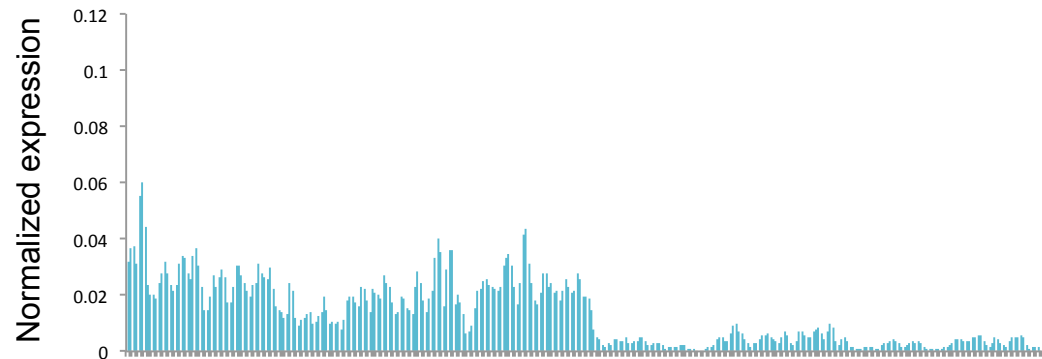
HepG2 WT nuclear fraction

HepG2 SUB1 KD

3' UTR index (1,207 bp)
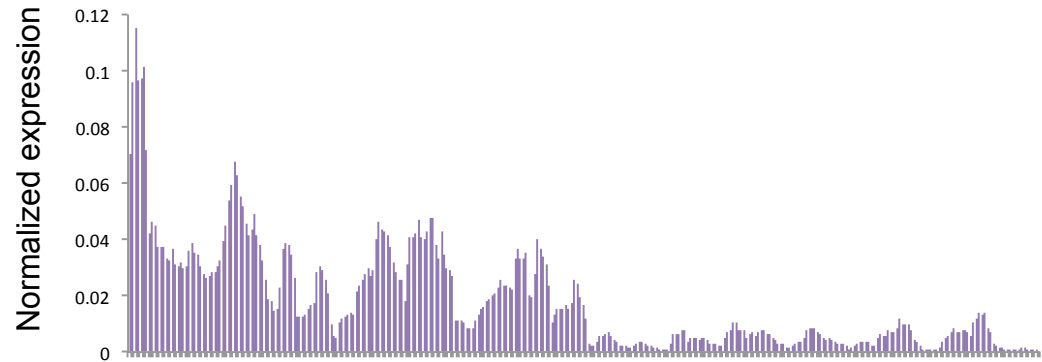
Expression across the 3' UTR of PTEN: WT vs. SUB1 KD

HepG2 WT cytosolic fraction

HepG2 WT nuclear fraction

HepG2 SUB1 KD

3' UTR index (6,457 bp)

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Proposed model

SUB1 KD

Our analysis here

PTEN 3' UTR expression ↑

Need experimental validation

PTEN stability/expression ↑

(2013) Akiyama-Abe et al.
(2013) Zhang et al.
(2017) Li et al.
et al.

(2016) Chakravarthi et al.

Cancer proliferation, invasion and migration ↓

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