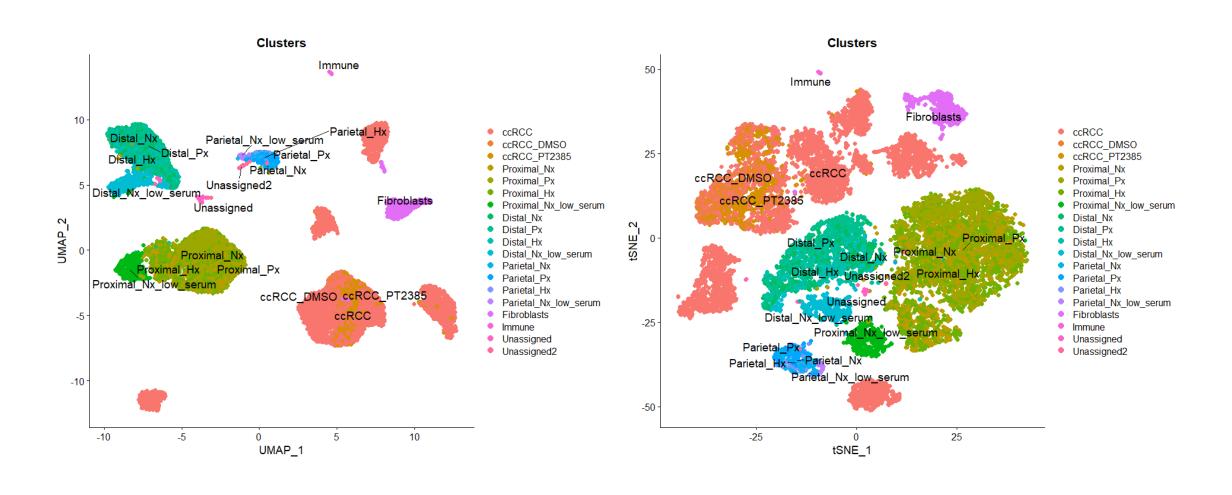
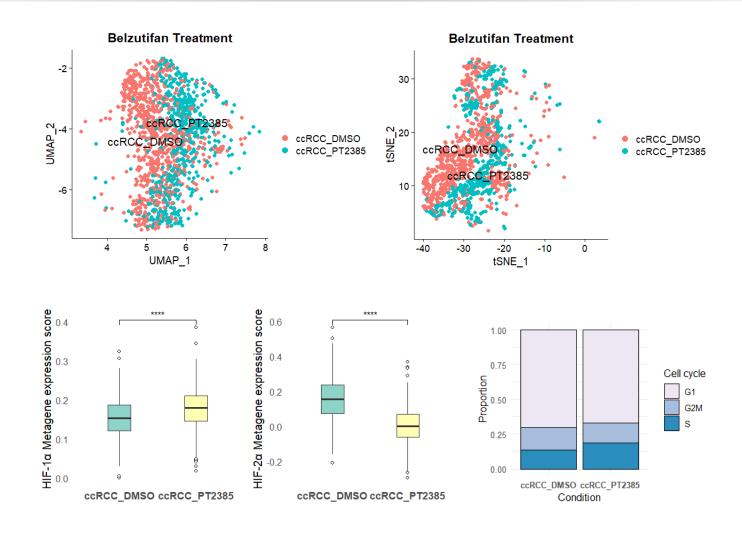
Single-cell RNA-seq using GSE269826

Non-linear dimensionality reduction for all sample

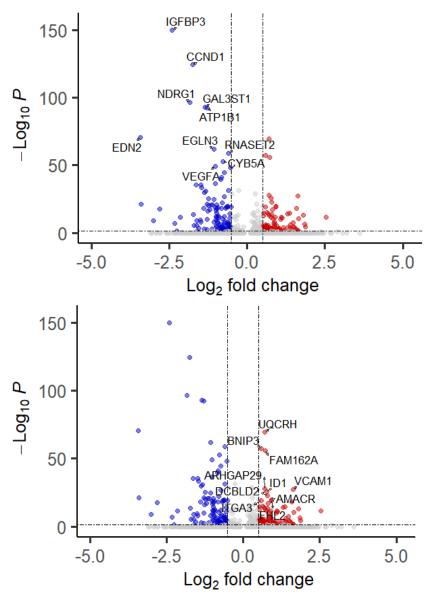


Belzutifan treatment ccRCC vs. ccRCC

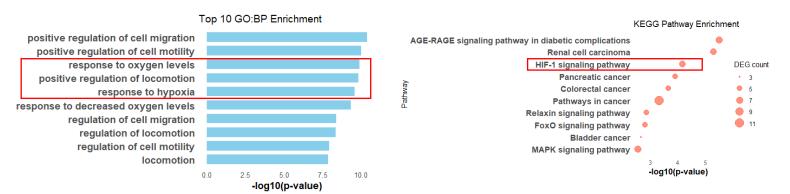


Each target gene expression of HIF-1α and HIF-2α is up-regulated and down-regulated after Belzutifan treatment

HIF-2α target down-regulated & ECM adhesion, inflammation up-regulated

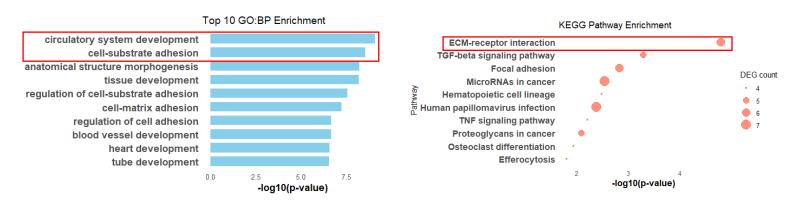


Down-regulated GO & KEGG analysis



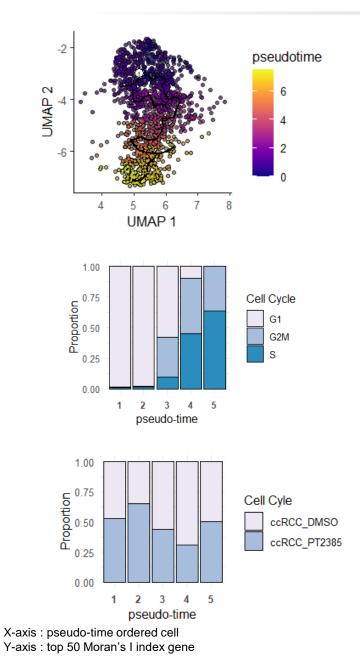
Cell migration down-regulated after Belzutifan treatment

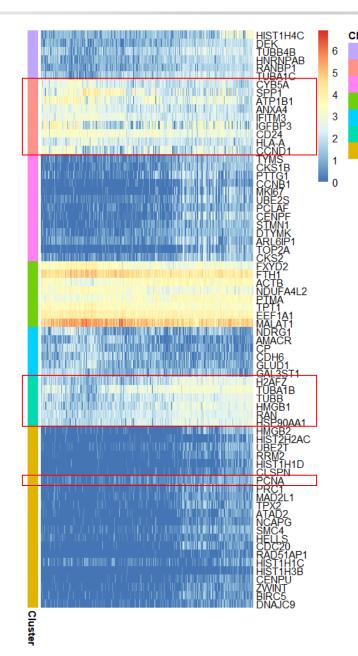
Up-regulated GO & KEGG analysis



Cell-to-cell adhesion up-regulated after Belzutifan treatment

Pseudo-time trajectory analysis using Monocle3





[Down-regulated gene following pseudo-time]

IGFBP3 (insulin-like growth factor binding protein)

CCND1 (cyclin D1)

→ Cells are transitioning into S phase

[**Up-regulated** gene following pseudo-time]

RAN (ras-related nuclear protein)

H2AFZ (H2A.Z Variant Histone 1)

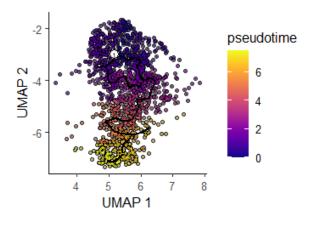
TUBA1B (Tubulin Alpha 1a)

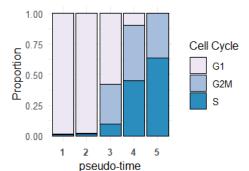
HMGB1 (High mobility group box 1)

PCNA (Proliferating Cell Nuclear Antigen)

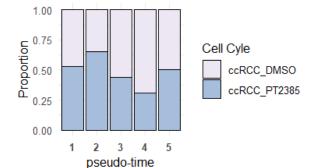
 \rightarrow Cells are transitioning in the direction of the S to G2/M phase

Pseudo-time trajectory analysis using Monocle3

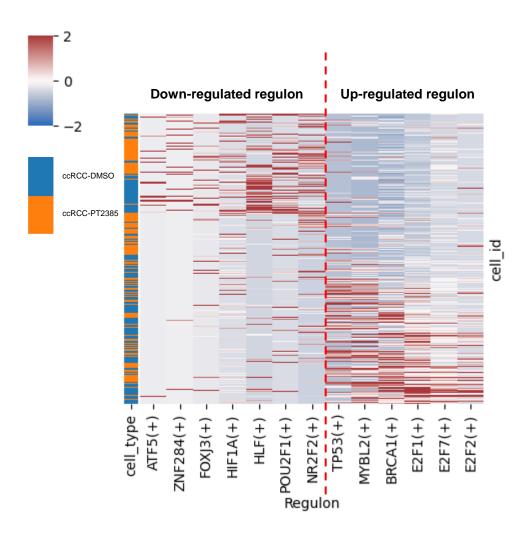




- Due to HIF-2α inhibition, ccRCC cells may bypass the G1 checkpoint or enter the S phase abnormally, choosing a path of forced cell cycle (S \rightarrow G2 \rightarrow M phase) progression
- ✓ ccRCC cells may follow the same differentiation trajectory, but their transcriptional programs could be altered



Alterations of a regulon induced after Belzutifan treatment



- ✓ HIF-2α inhibition suppresses a hypoxia-adaptive transcriptional network
- ✓ HIF-2α inhibition leads to increase in the regulon activity of TP53, MYBL2, BRCA1, and members of the E2F family
- ✓ This suggests that cells undergo a state transition from stress adaptation toward

 DNA repair and cell cycle reprogramming

 Output

 DNA repair and cell cycle reprogramming

 Outp