# FGFR1 governs iron metabolism via regulating post-translational modification of IRP2 in prostate cancer cells

Hui Lin[1#], Liuhong Shi[2], Dongyan Zhou[1], Shuangya Chen[1], Ping He[1], Xiaolu Zheng[1,3], Feng Qiu[1], Yuying Yuan[1], Shuaijun Lin[1], Xiaokun Li[1*], Fen Wang[4*], Cong Wang[1*]

**Supplemental table 1.**

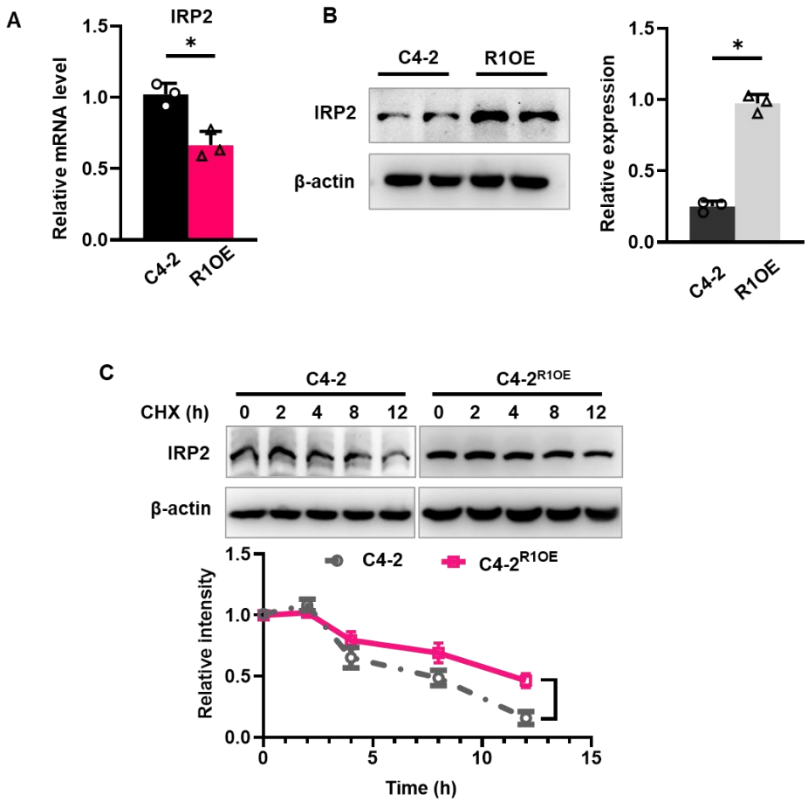
**Supplemental figure 1.**

## Supplemental table.

**Table 1 Primer sequences for quantitative real time PCR**

| Name/Symbol | Forward primers | Reverse primers |
|---|---|---|
| *FGFR1/FGFR1* | CCCGTAGCTCCATATTGGACA | TTTGCCATTTTTCAACCAGCG |
| *TFR1/TFRC* | ACCATTGTCATATACCCGGTTCA | CAATAGCCCAAGTAGCCAATCAT |
| *DMT1/SLC11A2* | TGGAGATCATGGGGAGTCTG | AAGAAAACCTGGTCCGGTGAA |
| *IRP1/ACO1* | AACCCATTCGCACACCTTG | ATGGTAAGCGCCCATATCTTG |
| *IRP2/IREB2* | TCGATGTATCTAAACTTGGCACC | GCCATCACAATTTCGTACAGCAG |
| *P53/TP53* | CAGCACATGACGGAGGTTGT | TCATCCAAATACTCCACACGC |
| *cMyc/MYC* | GGCTCCTGGCAAAAGGTCA | CTGCGTAGTTGTGCTGATGT |
| *β-actin/actb* | CATGTACGTTGCTATCCAGGC | CTCCTTAATGTCACGCACGAT |

**Supplemental figure 1.**




**Supplemental figure 1. Overexpression of FGFR1 retarded the degradation of IRP2 in C4-2 PCa cell.**

**A.** Relative mRNA expression of IRP2 in C4-2 and C4-2$^{R1OE}$ cells. **B.** Western blotting analysis of IRP2 and the quantitative analyses with Image J. **C.** Western blotting analysis of IRP2 in C4-2 and C4-2$^{\Delta R1OE}$ cells treated with CHX for 0, 2, 4, 8 or 12 hours. Bottom panel, Western blot analysis was quantitated by Image J software. R1OE/C4-2$^{R1OE}$, C4-2 overexpressed with FGFR1. *, $P < 0.05$.