Genome Biology

AUTHOR CORRECTION Open Access

Author Correction: CRISPRi enables isoform-specific loss-of-function screens and identification of gastric cancer-specific isoform dependencies

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Following publication of the original paper [1], the authors reported an error. In Fig. 1c we have mistakenly mislabeled the sgRNAs. The corrected Fig. 1 is given in this correction article.

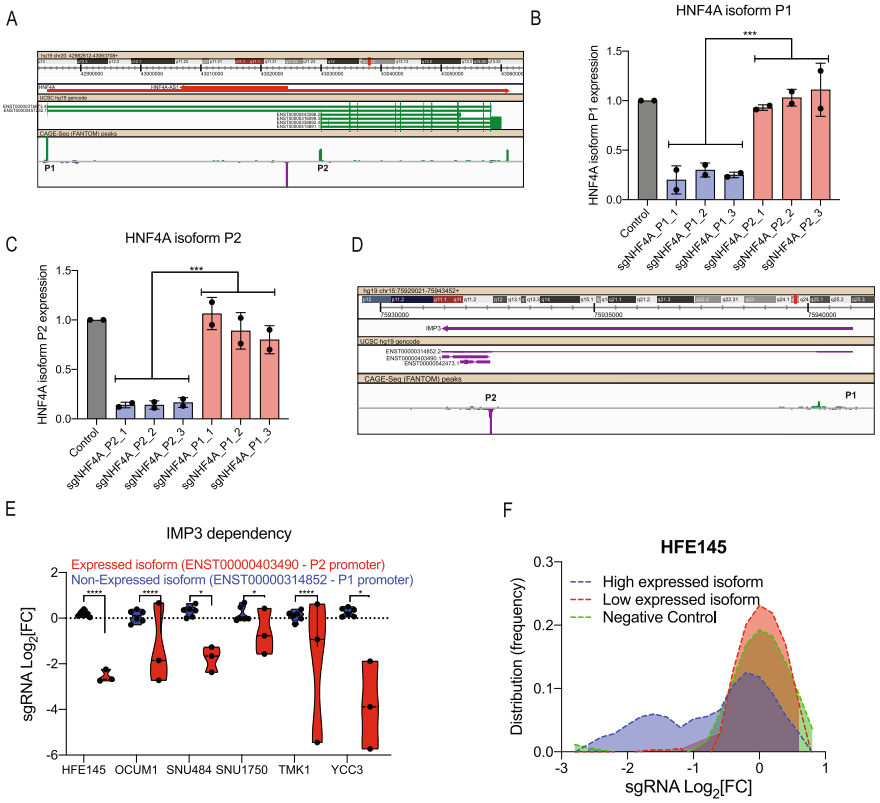

Fig. 1 CRISPRi as a tool for inhibition of specific promoter-driven transcript isoforms. **a** Structure of the *HNF4A* gene. Isoforms P1 and P2 are marked. CAGE-Seq peaks from the FANTOM project [19] are shown in the bottom panel. **b** qRT-PCR quantification of *HNF4A* transcript P1 following CRISPRi-mediated suppression of transcript P1 or P2. Data is shown as mean ± SD, $n = 2$. pValue is calculated using two-tailed unpaired *t* test (***$p \leq 0.001$). **c** qRT-PCR quantification of *HNF4A* transcript P2 following CRISPRi-mediated suppression of transcript P1 or P2. Data is shown as mean ± SD, $n = 2$. pValue is calculated using two-tailed unpaired *t* test (***$p \leq 0.001$). **d** Structure of the *IMP3* gene. Isoforms P1 and P2 are marked. CAGE-Seq peaks from the FANTOM project are shown in the bottom panel. **e** Violin plot showing IMP3 dependency following CRIS PRi-mediated suppression of different isoforms in GC cell lines. Dots represent individual sgRNAs targeting the indicated *IMP3* transcript isoform. pValue is calculated using two-tailed unpaired *t* test (****$p \leq 0.0001$, *$p \leq 0.05$). **f** Distribution of sgRNAs targeting different transcript isoforms of 55 pan cell-essential transcripts. Green, negative control sgRNAs. Purple, sgRNAs targeting the highest expressed (based on RNA-Seq) transcript isoform. Red, sgRNAs targeting the low expressed (based on RNA-Seq) transcript isoform

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