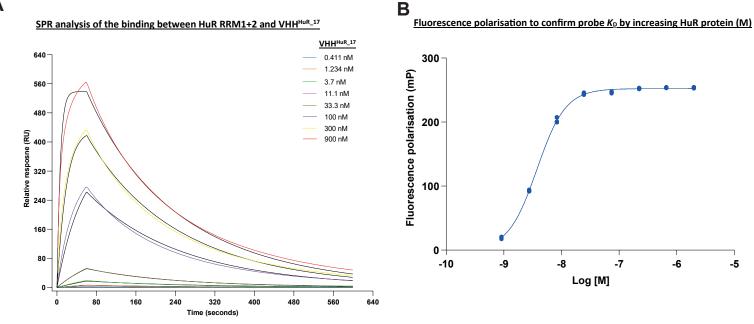
Supplementary Information





Supplementary Figure 1. Characterisation of a lead VHHHuR which binds and inhibits HuR. A) Representative example of SPR analysis showing the binding between HuR RRM1+2 and VHHHuR_17 at a range of concentrations. B) Graph of fluorescence polarisation to confirm probe K_D by increasing HuR protein (x-axis) when incubated with 10 nM Msi1-FITC labelled RNA probe (n=1; four technical repeats per concentration, line = non-linear curve fit). Source data are provided as a Source Data file.

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Supplementary Figure 2 NHOR TO THE CO THE TO THE CO - XARBCUHHAS - The Carther P = 0.0046Mod Haldebill В P = 0.0130 1.6 JHH^{GR} Relative HuR protein expression (kDa) HuR 30 ▶ 42 ▶ НА 0.0 T2/EBCC-JHH WHY IN THE CC VHHING TO RECC T21RECC.JHHI 15 36 ▶ HHW TY TROC anot transledion P = 0.0017 D C P = 0.0012 Relative HuR protein expression (kDa) HuR 30 0.8 42 НΑ TARRECT WHITE Takeecc. WHite Mocktransfection WHY TO RECC WHY TA TEECC 15 GAPDH F HCT116 E Mock transfection VHH^{HuR} T21RBCC-VHHHuR VHHHuR-T21RBCC P = 0.000252 P < 0.0001 10000 HuF Total HuR intensity 5000 HA

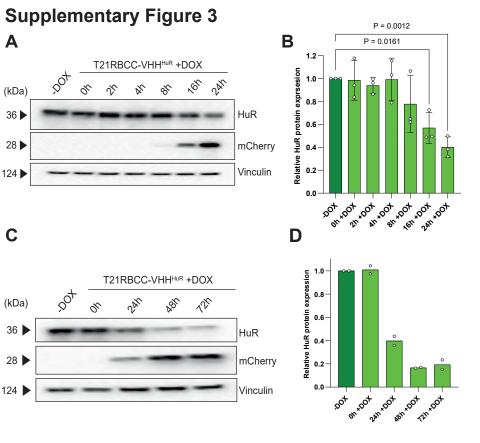
Supplementary Figure 2. T21RBCC-VHHHuR bioPROTACs degrade HuR in multiple cell lines. Representative immunoblot and associated densitometry following mRNA transfection of HA-tagged bioPROTAC constructs in the A549 (A-B) or U2OS (C-D) cell lines for 18 hours. (E-F) Representative images and quantification of immunofluorescence of total HuR intensity in HCT116 cells 18 hours posttransfection with HA-tagged bioPROTAC constructs followed by staining with HuR (green), HA (red) and DAPI (blue) (n=3). Blots shown in (A) and (C) are representative from n=3 biologically independent samples per group. Data in (B), (D) and (F) show the mean and standard deviation from n=3 biologically independent samples per group. Statistical significance was calculated using a one-way ANOVA and post-hoc test. Source data are provided as a Source Data file.

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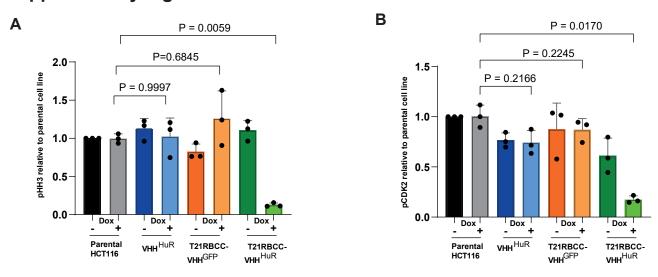
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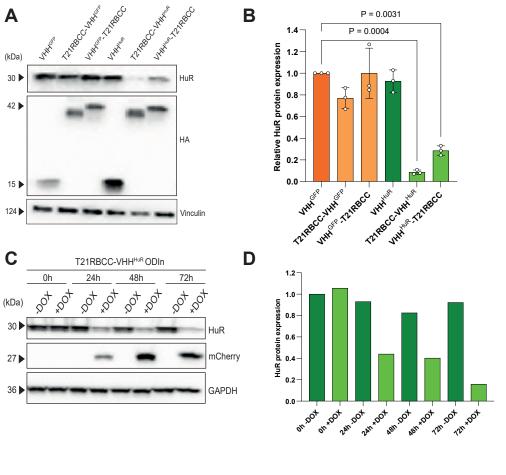
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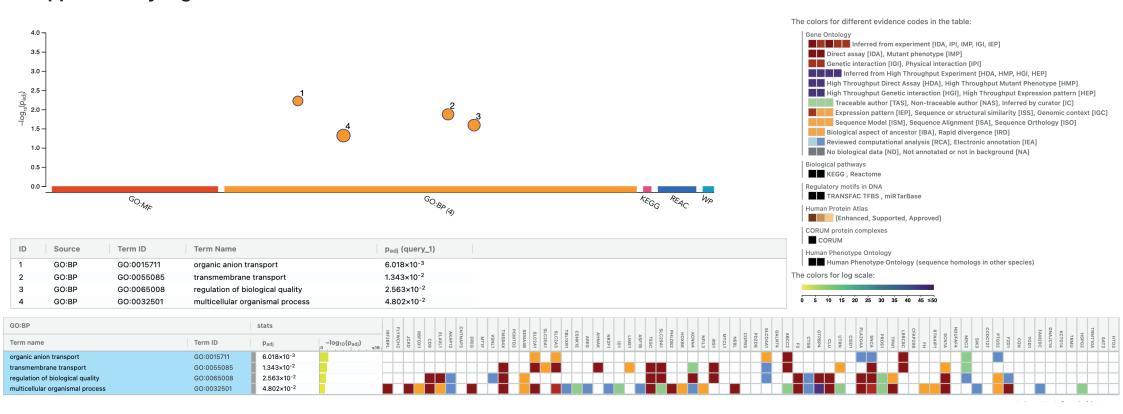
Supplementary Figure 3. BioPROTAC expression and HuR degradation in the T21RBCC-VHH^{HuR} **ODIn cell line.** Representative immunoblot and associated densitometry following doxycycline induction of the HCT116-ODIn T21RBCC-VHH^{HuR} cell line between 0-24 hours (A-B) or 0-72 hours (C-D) post-doxycycline induction. Blots shown in (A) and (C) are representative from n=3 (A) or n=2 (C) biologically independent samples per group. Data in (B) shows the mean and standard deviation, and in (D) mean alone, for densitometry measurements. Statistical significance was calculated using a one-way ANOVA and post-hoc test. Source data are provided as a Source Data file.



Supplementary Figure 4. BioPROTAC expression and HuR degradation leads to a reduction in cell cycle markers pHH3 and pCDK2 in ODIn cell lines. Densitometry, (A) pHH3 and (B) pCDK2, following doxycycline induction of the HCT116-ODIn T21RBCC-VHHHuR cell line (dark and light green) and related controls (parental cells, black and grey; VHHHUR alone cells, dark and light blue; T21RBCC-VHHGFP cells dark and light orange). Data in (A) and (B) show the mean and standard deviation from n=3 replicates of immunoblot of samples described in Fig. 2A and 2B. Statistical significance was calculated using a one-way ANOVA and post-hoc test. Source data are provided as a Source Data file.



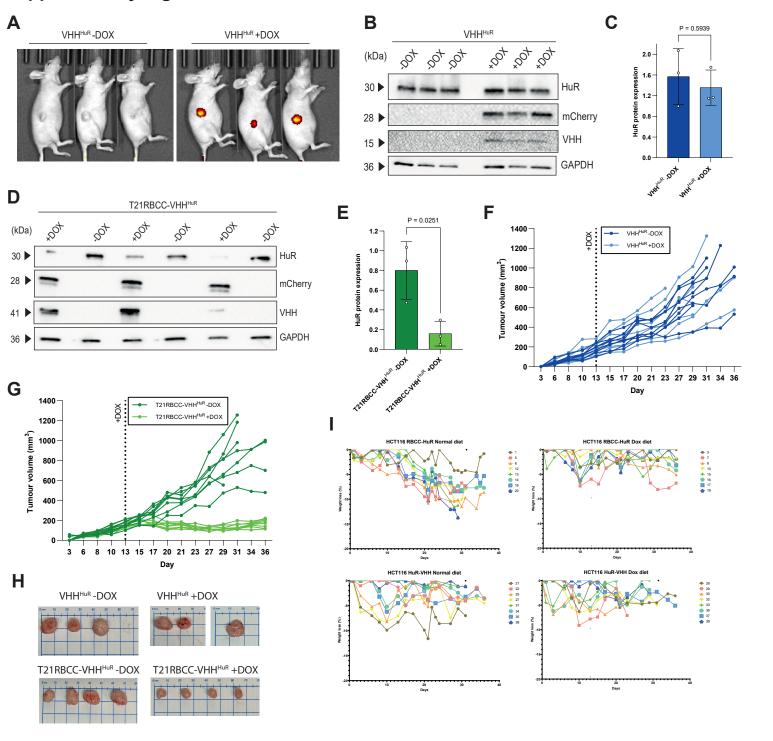
Supplementary Figure 5. Confirmation of HuR degradation in samples prepared for mass spectrometry. (A-B) Representative immunoblot and associated densitometry following mRNA transfection of bioPROTAC constructs in the HCT116 cell line for 18 hours. Blot shown in (A) is representative from n=3 biologically independent samples per group. Data in (B) shows the mean and standard deviation from n=3 biologically independent samples per group. Statistical significance was calculated using a one-way ANOVA and post-hoc test. (C-D) Immunoblot and associated densitometry of the HCT116-ODIn T21RBCC-VHHHuR cell line at 0-72 hours post-doxycycline (n=1). Source data are provided as a Source Data file.



Supplementary Figure 6. GO, KEGG, Reactome and WikiPathways enrichment analysis. Analysis for the 71 significantly (Fisher's one-sided test) down- and up-regulated proteins at both 48-72 hours due to T21RBCC-VHH^{HuR} expression using g:Profiler (https://biit.cs.ut.ee/gprofiler/gost) (Raudvere, U., et al., 2019).

Supplementary Figure 7 C В T21RBCC-VHH^{HuR} +DOX (kDa) Relative HuR 36 IGF2BP3 47▶ EIF4A2 TNFRSF6B 33▶ D Ε 48▶ TFAP4 28▶ mCherry Vinculin K G H T21RBCC-VHH^{HuR} -DOX T21RBCC-VHH^{Huf} TFAP4 protein 6 L M N VHH^{HuR} T21RBCC-VHHHuR (kDa) IGF2BP3 protein expression 36 HuR HuR protein expression IGF2BP3 EIF4A2 TIRBECHHI PROOT Tr. Reecc. Harris Dox WHY FOOT Takeccaruman and 33 TNFRSF6B 48▶ TFAP4 Q 0 28▶ mCherry EIF4A2 protein expression Vinculin 0

Supplementary Figure 7. T21RBCC-VHHHuR decreases the expression of proteins of interest. Representative immunoblots and associated densitometry (A-F) or protein expression intensity from mass spectrometry-based measurements (G-K) for HuR, IGF2BP3, EIF4A2, TNFRSF6B and TFAP4 in the HCT116-ODIn T21RBCC-VHHHuR cell line at 0-72 hours post-induction. Representative immunoblots and associated densitometry for HuR, IGF2BP3, EIF4A2, TNFRSF6B and TFAP4 in the T21RBCC-VHHHuR from mouse xenograft tumours (L-Q). Blots shown in (A) and (L) are representative from n=2 biologically independent samples per group. Data in (B-F) and (M-Q) show the mean and individual data points from n=2 biologically independent samples per group. Mass spectrometry data (G-K) shows technical repeats for each timepoint from one biologically independent sample with line showing mean value. Source data are provided as a Source Data file.



Supplementary Figure 8. Validation and evaluation of mouse xenograft models - T21RBCC-VHH^{HuR} arrests tumour growth *in vivo*. (A) Confirmation of mCherry fluorescence in mice with VHH^{HuR} xenografts receiving a standard or doxycycline-containing diet. Representative immunoblot and associated densitometry of lysates from VHH^{HuR} (B-C) or T21RBCC-VHH^{HuR} (D-E) xenografts in mice receiving a standard or doxycycline-containing diet. Line graph of tumour volumes (mm³) from day 3-36 of VHH^{HuR} (F) or T21RBCC-VHH^{HuR} (G) xenografts in mice receiving a standard or doxycycline-containing diet (n=8 – data for individual mice displayed). (H) Representative images of tumours resected from VHH^{HuR} or T21RBCC-VHH^{HuR} xenografts. (I) Graphs of individual mouse weight for each group for the duration of the *in vivo* study. Blots shown in (B) and (D) are representative from n=3 biologically independent samples per group. Data in (C) and (E) show the mean and standard deviation from n=3 biologically independent samples per group. Statistical significance was calculated using an unpaired two-tailed t-test. Source data are provided as a Source Data file.