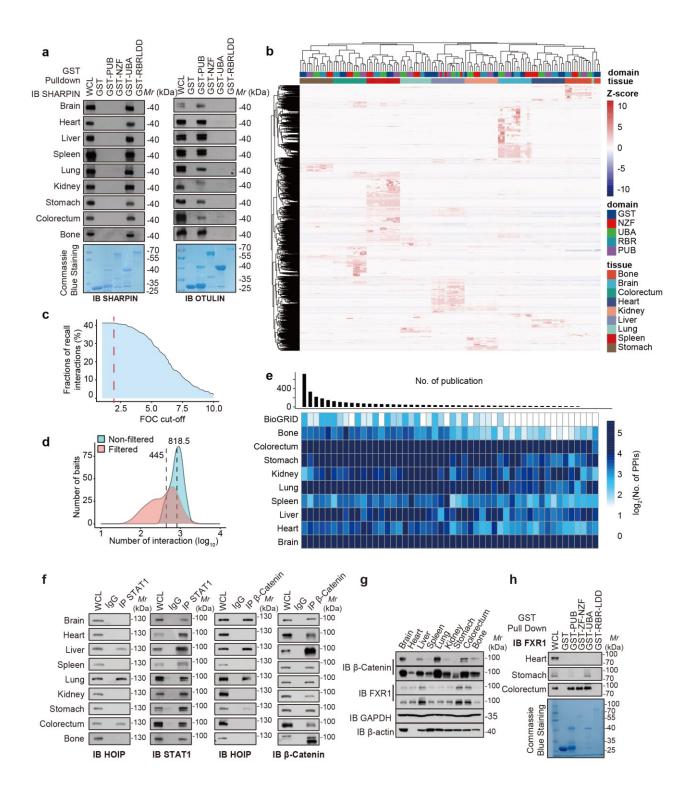
Supplementary Information File

Systematic HOIP Interactome Profiling Reveals Critical Roles of Linear Ubiquitination in Tissue Homeostasis

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The PDF file includes: Supplementary Figures 1–9 Unprocessed blots for Supplementary Figures



Supplemental Fig. 1 Data filtering and detection of known interactions, related to Fig. 1.

a Immunoprecipitation analysis of canonical interactions, such as OTULIN and SHARPIN between four HOIP domains in various tissues.

b Global visualization of HOIP interacting proteins across domains and tissues. Protein abundance is calculated by iBAQ and homogenized by z-score.

c Positive discovery rate of the known HOIP interacting proteins with different fold of change (FOC)

cut-offs.

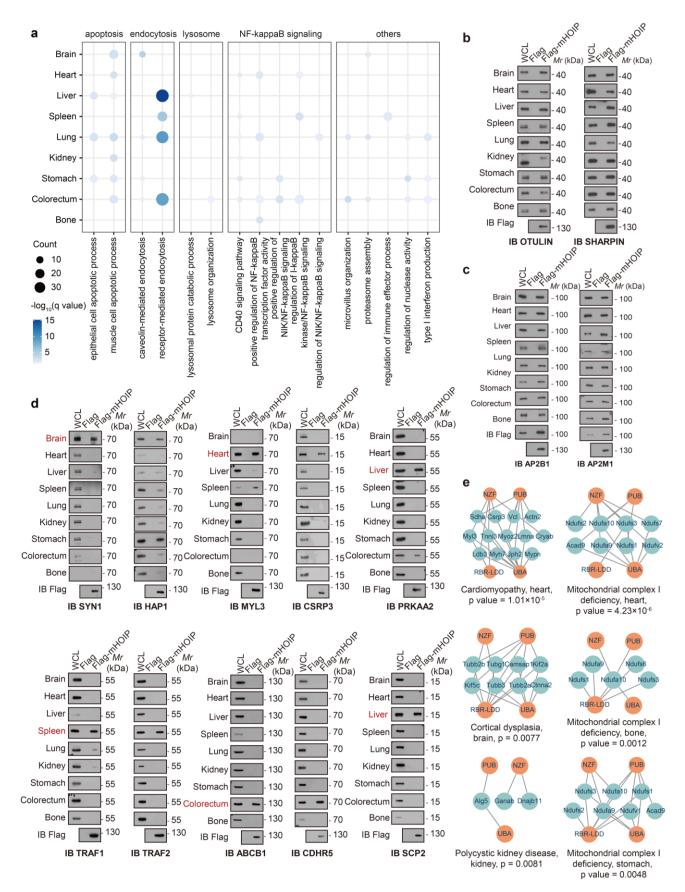
d Histograms depicting the number of HOIP interactions before and after filtering.

e Number of interactions between proteins binned by number of publications. Histogram shows the median number of publications.

f Endogenous immunoprecipitation analysis of STAT1 (or β -Catenin) and HOIP across tissues.

g Immunoblot analysis of HOIP, β -Catenin and FXR1 across tissues.

h Immunoprecipitation analysis of the known β -Catenin-interacting protein FXR1 between four HOIP domains in heart, stomach and colorectum.



Supplemental Fig. 2 Identification of tissue-specific HOIP PPIs, related to Fig. 2.

a Functional enrichment analysis of HOIP PPIs identifies a number of Gene Ontology (GO) terms

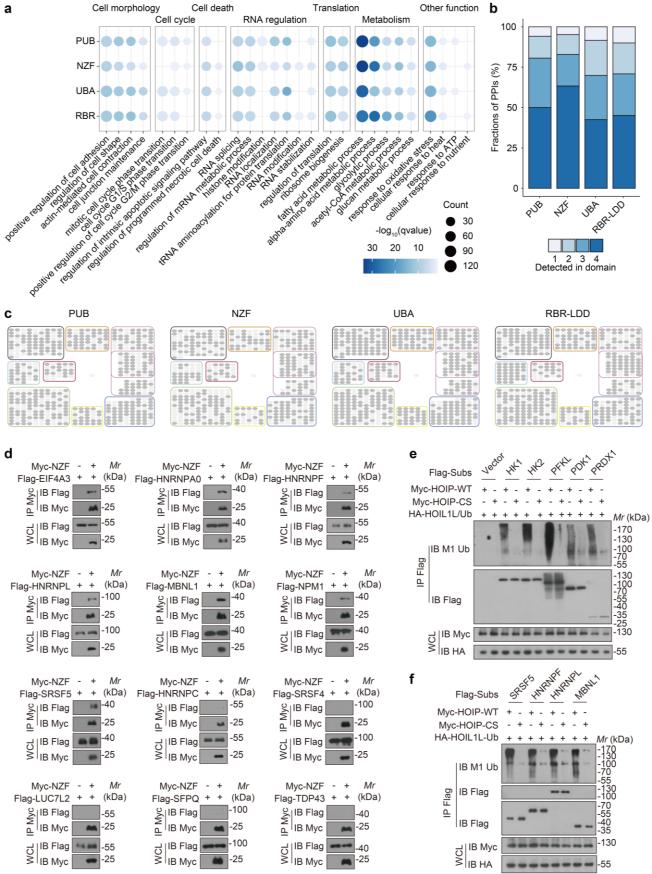
associated with the known functions of HOIP. q value is calculated by Benjamini-Hochberg method.

b Immunoprecipitation of ectopic expressed HOIP from HEK293T cells in different tissues and immunoblot with the antibodies of OTULIN and SHARPIN. The ectopically expressed Flag-tagged only peptide was a negative control.

c Immunoprecipitation of ectopic expressed HOIP from HEK293T cells in different tissues and immunoblot with the antibodies of AP2B1 and AP2M1. The ectopically expressed Flag-tagged only peptide was a negative control.

d Immunoprecipitation of ectopic expressed HOIP from HEK293T cells in different tissues and immunoblot with the antibodies of tissue-specific proteins. The ectopically expressed Flag-tagged only peptide was a negative control.

e HOIP interaction modules, in which interactors with the same disease term are present at a statistically significant frequency, are shown. p values are from the Fisher exact test.



Supplemental Fig. 3 Functional landscape of proteins included in the HOIP interaction network,

related to Fig. 3.

a Functional enrichment analysis of HOIP PPIs identifies a number of Gene Ontology (GO) terms associated with the fundamental cellular functions. q value is calculated by Benjamini–Hochberg method.

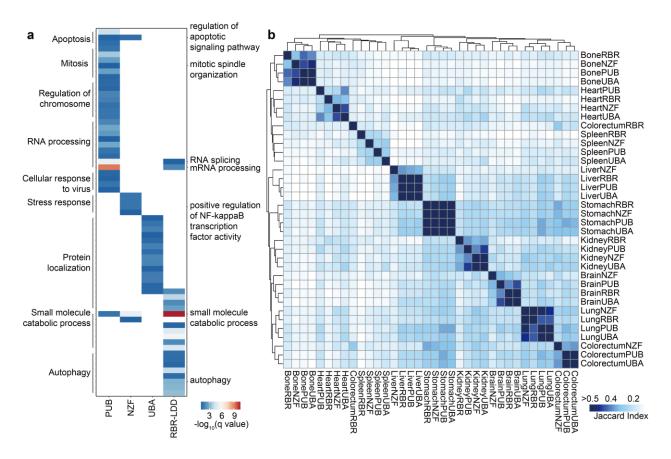
b Distribution of the fraction of HOIP PPIs quantified in each domain.

c Individual diagrams of domain-dependent interactors. Domain-dependent nodes are shown in gray, whereas domain-independent interactors are depicted in white.

d Immunoprecipitation of ectopic expressed Myc-tagged HOIP NZF in lysates from HEK293T cells transfected with indicate Flag-tagged proteins, and immunoblot with the corresponding antibodies. The Myc-tagged vector was a negative control.

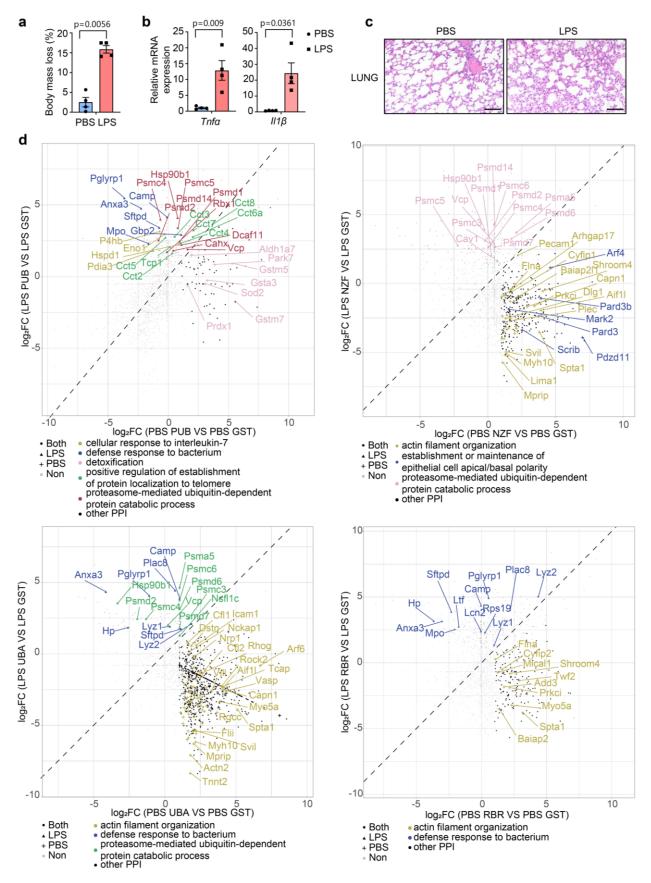
e Immunoprecipitates of HK1, HK2, PFKL, PDK1 and PRDX1 to detect the linear ubiquitination in HEK293T cells transfected with Myc-tagged HOIP WT or CS (a HOIP inactivate mutant).

f Immunoprecipitates of SRSF5, HNRNPF, HNRNPL and MBNL1 to detect the linear ubiquitination in HEK293T cells transfected with Myc-tagged HOIP WT or CS (a HOIP inactivate mutant).



Supplemental Fig. 4 Functional enrichment of domain-specific HOIP PPIs across tissues, related to Fig. 3.

a Functional enrichment analysis of HOIP PPIs identifies a number of Gene Ontology (GO) terms associated with the domain-specific PPIs. q value is calculated by Benjamini–Hochberg method.
b Jaccard index of HOIP PPIs detected by various tissues and domains to show protein coverage between different tissues and domains.



Supplemental Fig. 5 Functional landscape of HOIP interaction network in lungs from LPSinduced sepsis models, related to Fig. 3.

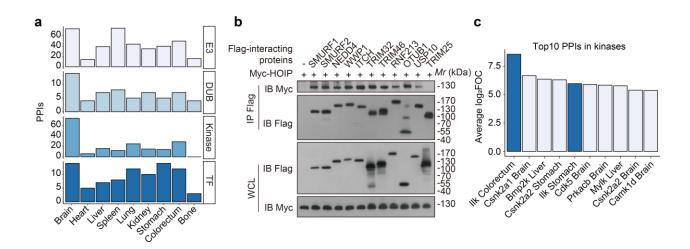
a Weight monitoring of mice i.p. injection with or without LPS (12 mg/kg body weight in saline). n = 4 per group.

b Quantitative RT-PCR analysis of *Tnfa* and *IL1β* mRNA levels in lungs from LPS-induced sepsis models. n = 4 per group.

c H&E staining of lungs from LPS-induced sepsis models. Scale bars, 100 $\mu m.$

d Correlation plot of log₂FC (HOIP domains/GST) for lungs with or without LPS injection.

Data are shown as the mean \pm SEM; p values are from the unpaired two-sided t-test.

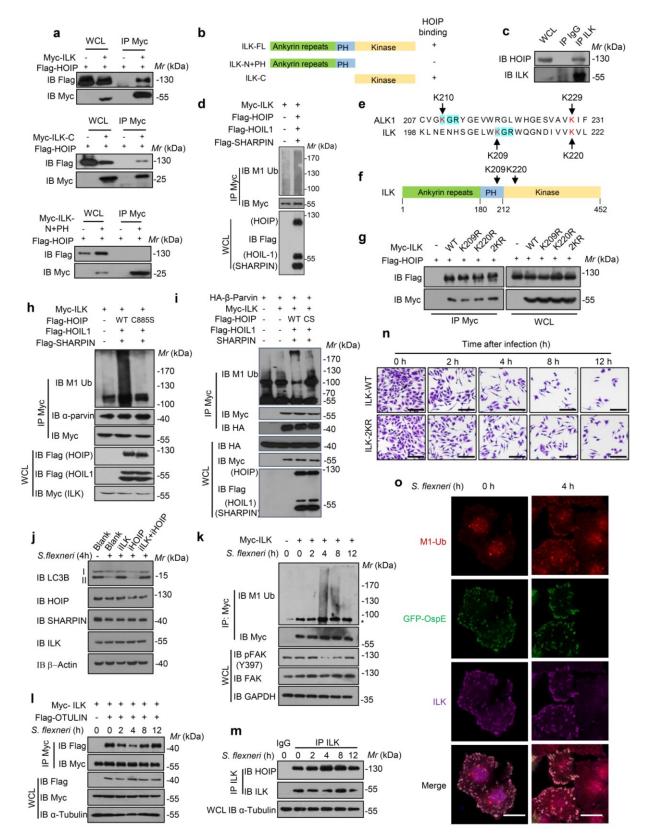


Supplemental Fig. 6 Functional analysis of HOIP PPIs associated with kinases, E3 ligases, deubiquitinases and transcriptional factors, related to Fig. 4.

a Barchart with the numbers of HOIP PPIs associated with kinases, E3 ligases, deubiquitinases and transcriptional factors.

b Immunoprecipitation of ectopic expressed NEDD4-1, WWP1, ITCH, SMURF1, SMURF2, TRIM32, TRIM46, RNF213, OTUB1 and USP10 in HEK293T cells transfected with Myc-tagged HOIP and immunoblot with indicated antibodies.

c Representable top 10 HOIP PPIs in the kinases.



Supplemental Fig. 7 Linearly ubiquitinated ILK is dynamically regulated during *Shigella flexner* infection, related to Fig. 4.

a HEK293T cells were transfected with Flag-tagged HOIP and Myc-tagged ILK (or ILK truncations), and then immunoprecipitated with the Myc antibody, followed by immunoblotting with the indicated

antibodies.

b Schematic representative of the ILK truncations.

c Immunoprecipitation of ILK in HEK293T cells and immunoblot with indicated antibodies.

d Immunoprecipitation of ILK linear ubiquitination in HEK293T cells transfected with Flag-tagged

HOIP, Flag-tagged HOIL1, Flag-tagged SHARPIN and immunoblot with indicated antibodies.

e Distribution diagram of potential linear ubiquitination sites of ILK.

f Sequence alignment of ILK and ALK1. The horizontal line represents a conservative sequence, arrows indicate linear ubiquitination sites of ALK1 and predicted potential linear ubiquitination sites of ILK.

g Immunoprecipitation of ILK and its mutants in HEK293T cells transfected with Myc-tagged ILK wild type (WT) or its mutants K209R, K220R or 2KR (K209R/K220R) and Flag-tagged HOIP, followed by immunoblotting with indicated antibodies.

h Cell lysates from HEK293T cells transfected with Myc-tagged ILK, Flag-tagged HOIL-1, Flag-tagged SHARPIN and Flag-tagged HOIP wild type or its catalytically inactivated mutant were immunoprecipitated with the Myc antibody, followed by immunoblotting with indicated antibodies.

i Cell lysates from HEK293T cells transfected with HA-tagged β -Parvin, Myc-tagged ILK, Flagtagged HOIL-1, Flag-tagged SHARPIN and Flag-tagged HOIP wild type or its catalytically inactivated mutant were immunoprecipitated with the Myc antibody, followed by immunoblotting with indicated antibodies.

j Immunoblot analysis of the LC3B in *Shigella flexner* infected Hela cells with 2 μ M ILK inhibitor ILK-IN-3 and 20 μ M HOIP inhibitor HOIPin-8.

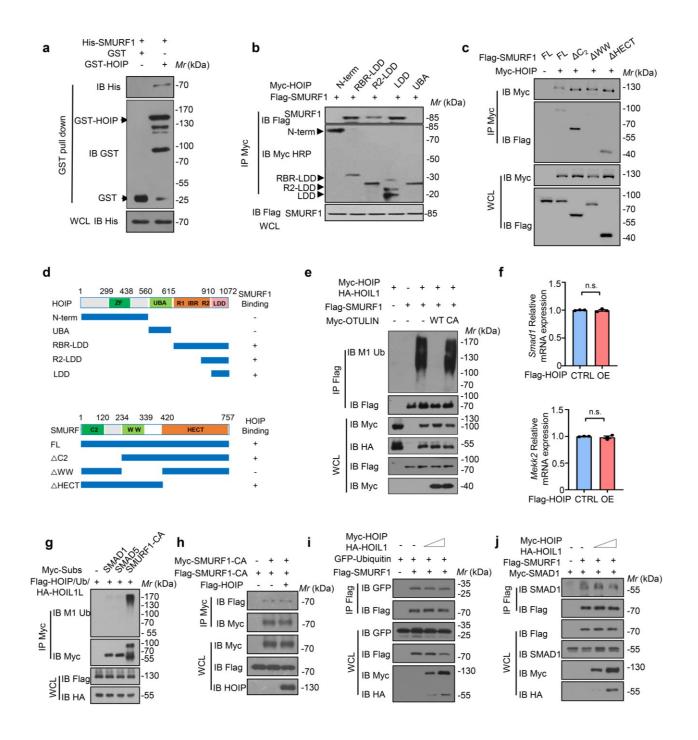
k Immunoprecipitation of ILK linear ubiquitination in Myc-tagged ILK overexpressed HeLa cells, infected with *Shigella flexner* for 0 h, 2 h, 4 h, 8 h and 12 h respectively. And immunoblot with indicated antibodies.

I Immunoprecipitation of ILK in HeLa cells transfected with Flag-tagged OTULIN and Myc-tagged ILK after *Shigella flexner* infection and immunoblot with indicated antibodies.

m Immunoprecipitation analysis of interactions between ILK and HOIP after *Shigella flexner* infection in HeLa cells.

n Representative images showing the attached cells of control and ILK-2KR groups infected with *Shigella flexner* for indicated time points, Scale bars, 10 µm.

o HeLa cells were infected with or without *Shigella flexner* for 4h, then the cells were collected for immunofluorescence with indicated antibodies. Scale bars, 20 μm.



Supplemental Fig. 8 SMURF1 is a HOIP-interacting protein, related to Fig. 5.

a In vitro binding assay of purified GST-tagged HOIP and His-tagged SMURF1.

b Immunoprecipitates of HOIP and its truncations in HEK293T cells transfected with Flag-tagged SMURF1 and immunoblot with the indicated antibodies.

c Immunoprecipitates of SMURF1 and its truncations in HEK293T cells transfected with Myc-tagged HOIP and immunoblot with the indicated antibodies.

d Schematic representative of the HOIP-interacting region in SMURF1 and the SMURF1-interacting region in HOIP.

e Immunoprecipitates of SMURF1 linear ubiquitination in HEK293T cells transfected with LUBAC and OTULIN mutants.

f Analysis of *Smad1* and *Mekk2* genes expression by qPCR in HOIP stably over-expressed (OE) BMSCs.

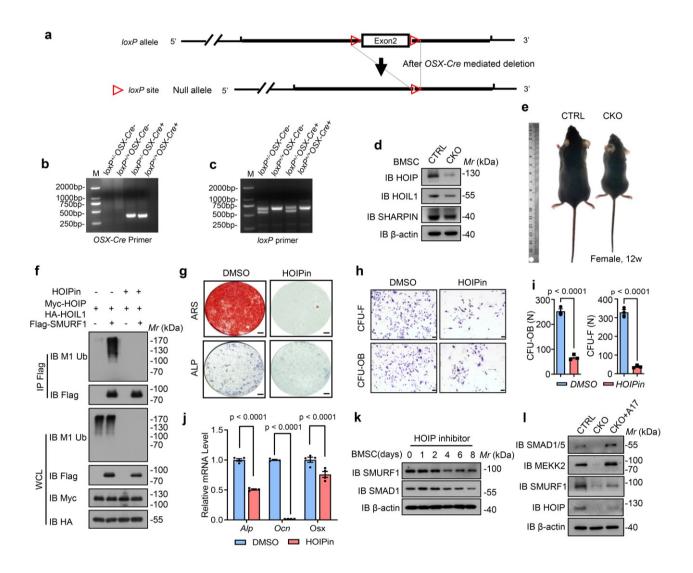
g Immunoprecipitates of SMAD1, SMAD5 and SMURF1-C699A's linear ubiquitination in HEK293T cells transfected with LUBAC

h Immunoblot analysis of the interaction between Myc-tagged SMURF1-C699A and Flag-tagged SMURF1-C699A in HEK293T cells transfected with Myc-tagged HOIP.

i Immunoblot analysis of the interaction between SMURF1 and ubiquitin in HEK293T cells transfected with LUBAC.

j Immunoblot analysis of the interaction between SMURF1 and its substrate SMAD1 in HEK293T cells transfected with LUBAC.

Data are shown as the mean \pm SEM; n = 3 per group, p values are from the unpaired two-sided t-test. n.s., no significant.



Supplemental Fig. 9 Targeted disruption of the murine *Hoip* gene, related to Fig. 6.

a Diagram of Hoip osteoblast specific knockout strategy.

b, **c** PCR analysis of HOIP CTRL and CKO mice tails.

d Immunoblot analysis of HOIP, HOIL1 and SHARPIN protein levels in BMSCs from HOIP CTRL and CKO mice.

e Representative image of 8-week-old female HOIP CTRL and CKO mice.

f Immunoprecipitates of SMURF1 linear ubiquitination in HEK293T cells transfected with LUBAC with or without HOIP inhibitor HOIPin-8.

g Representative images of ALP and ARS staining of BMSCs with or without HOIP inhibitor treatment after cultured in osteogenic medium for 14 and 28 days. Scale bars, 2 mm.

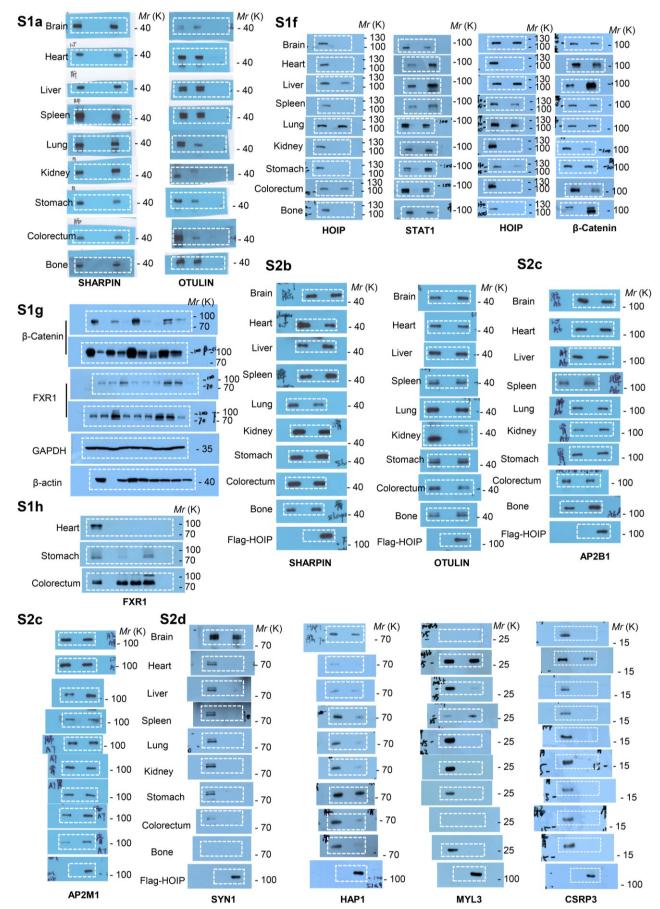
h, **i** Representative images and quantification of CFU-OB and CFU-F of BMSCs with or without HOIP inhibitor treatment. Scale bars, 50 μ m. n = 3 per group.

j Immunoblot of SMURF1 in BMSCs with HOIP inhibitor treatment.

k Quantitative RT-PCR analysis of osteogenesis genes mRNA levels in BMSCs with or without HOIP inhibitor treatment. n = 3 per group.

I Immunoblot of SMURF1 and its substrate SMAD1/5, MEKK2 in BMSCs from CTRL, CKO and CKO treated with SMURF1 inhibitor A17 groups for 28 days.

Data are shown as the mean \pm SEM; p values are from the unpaired two-sided t-test and the two-way ANOVA (Sidak's multiple comparisons test).



Uncropped blots for Supplementary Figures

