Supplementary Material

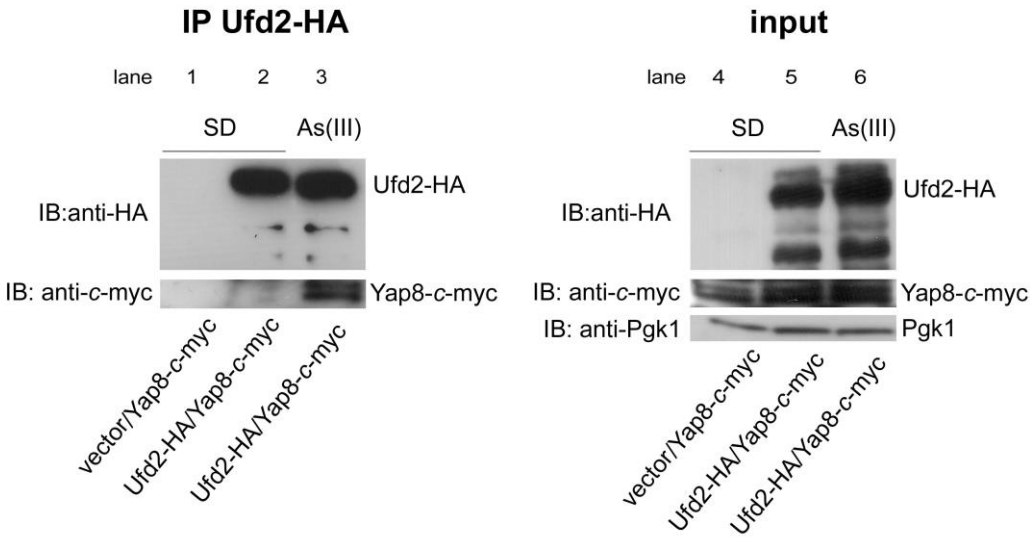

Fig. S1. Reciprocal co-immunoprecipitation assays showing arsenic-mediated interaction between Yap8 and Ufd2. BY4742 cells co-transformed with vector/*YAP8*-*c*-myc (lanes 1 and 4) or *UFD2*-HA/*YAP8*-*c*-myc (lanes 2, 3, 5 and 6) were exposed or not to 1.5 mM As(III) for 90 min and Ufd2-HA was immunoprecipitated with anti-HA antibody. Immunoblotting was performed using anti-HA, anti-*c*-myc and anti-Pgk1 antibodies. A representative experiment is shown. IP – immunoprecipitation; IB – immunoblotting; SD – Synthetic Defined medium, control condition.

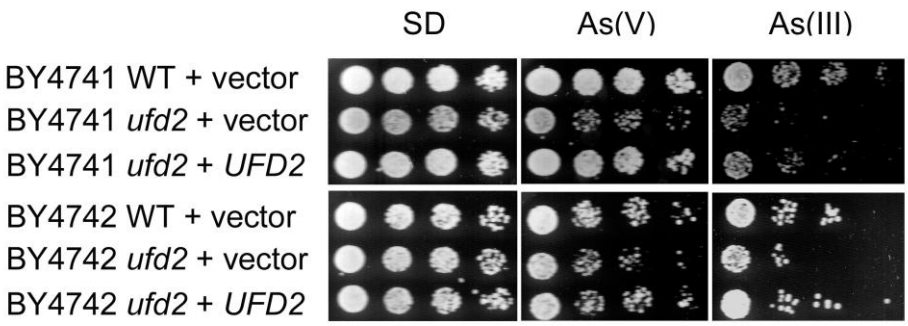

Fig. S2. As(V)- and As(III)-sensitivity phenotypes of *ufd2* are restored by expressing an episomal copy of *UFD2*. Exponential phase BY4741 and BY4742 wild type (WT) and *ufd2* cells expressing an episomal copy of *UFD2* or the respective control vector were serially diluted and spotted onto SD media supplemented or not with 2 mM As(V) or 1.5 mM As(III). Growth was recorded after 2 days incubation at 30ºC. A representative experiment is shown.

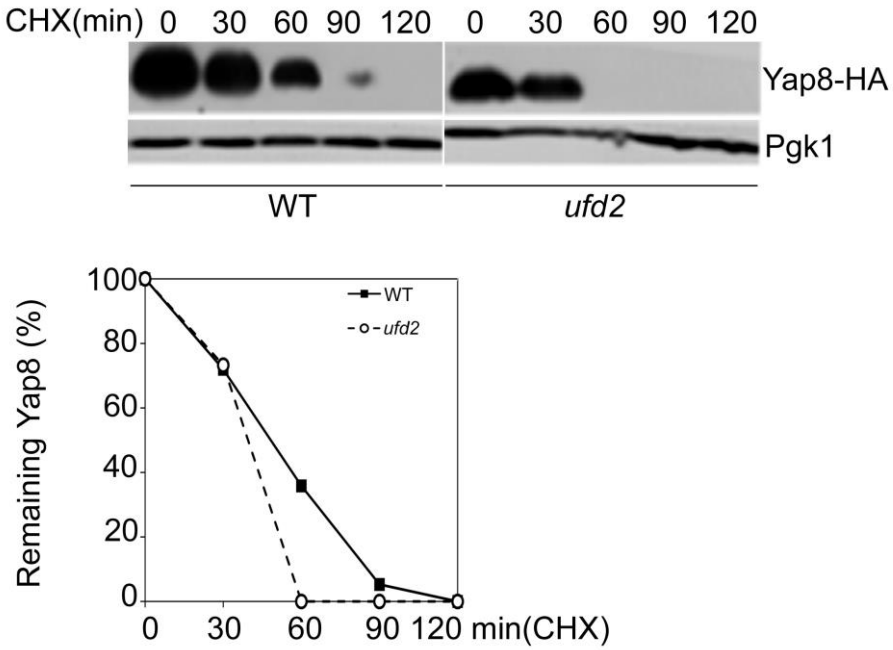

Fig. S3. Ufd2 mediates Yap8 stabilization under As(V) stress conditions. BY4742 wild type (WT) and *ufd2* mutant strains expressing Yap8-HA were pre-treated with 2 mM As(V) for 60 min, washed and subsequently treated with 0.1 mg/mL cycloheximide (CHX) up to 120 min prior to immunoblotting using anti-HA and anti-Pgk1 antibodies. The graph represents the percentage of remaining Yap8 protein after CHX addition. A representative experiment is shown.

Table S1. *Saccharomyces cerevisiae* strains used in this study

Strain	Genotype	Reference or source
BY4742	*MATα his3Δ1 leu2Δ0 lys2Δ0* ura3Δ0	EUROSCARF*
ufd2	*MATα his3Δ1 leu2Δ0* lys2Δ0 *ura3Δ0 YDL190c::kanMX4*	EUROSCARF
yap8	*MATα his3Δ1 leu2Δ0* lys2Δ0 *ura3Δ0 YPR199c::kanMX4*	EUROSCARF
yap8ufd2	*MATα his3Δ1 leu2Δ0* lys2Δ0 *ura3Δ0 YPR199c::kanMX4 YDL190c::HIS3MX4*	This study
ubc4	*MATα his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0 YBR082c::kanMX4*	ATCC**
rad23	*MATα his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0 YEL037c::kanMX4*	EUROSCARF
dsk2	*MATα his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0 YMR276w::kanMX4*	EUROSCARF
Y187	*MATα ura3-52 his3-200 ade2-101 trp1-901 leu2-3 112 gal4Δ met-gal80Δ URA3::GAL1UAS-GAL1TATA-lacZ MEL1*	Clontech Laboratories, Inc.
BY4741	*MATa his3Δ1 leu2Δ0 met15Δ0* ura3Δ0	EUROSCARF
ufd2	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 YDL190C::kanMX4*	EUROSCARF
$Ufd2^{U\text{-}box\Delta}$	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0* $YDL190C^{2568\text{-}2886\ bp}$*::HIS3*	Chang Liu *et al.* (2011)

*EUROpean Saccharomyces Cerevisiae ARchive for Functional analysis

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Table S2. Plasmids used in this study

Name	Features	Reference or source
pRS416	*CEN*, *URA3*	Agilent Technologies
pRS416-*YAP8-HA*		Our unpublished work
pRS416-*YAP8-c-myc*		Amaral et al. (2013)
pRS416-*UFD2-HA*		This study
pGADT7-Rec	2µ, *LEU2, HA*	Clontech
pGADT7-*T-antigen*		Clontech
pGADT7-*UFD2*		This study
pGBKT7	2µ, *TRP1*, *c-myc*	Clontech
pGBKT7-*LamC*		Clontech
pGBKT7-*p53*		Clontech
pGBKT7-*YAP8*		Our unpublished work
YCplac111	*CEN*, *LEU2*	Agilent Technologies
YCplac111-*UFD2-HA*		This study
YEplac181	2µ, *LEU2*	Agilent Technologies
YEplac181-*YAP8-HA*		Our unpublished work
pGal-*MPS1-c-myc*	*Integrative, URA3, GAL1*^{promoter}	Chang Liu et al. (2011)

Table S3. Oligonucleotides used in this study

#	Name	Sequence (5' – 3' UTR)
1	UFD2-HIS-Fw [D]	GGGAAAAGTTAACTTTGAAAGTAGAACCCTCATTCCATAGATCGTAC GCTGCAGG
2	UFD2-HIS-Rv [D]	TTGATTAGGGTCAATTTTGCAATTTATTCTATCACTTATTTTAGGGAG ACCGGCAGAT
3	A1-UFD2[D]	GGCTTGCTGGTACAATATGG
4	A4-UFD2[D]	CCAGAGCTTTGAGAAGAG
5	UFD2 400-Fw*	GAAAGGTAAAGTTGAC
6	UFD2 1300-Fw*	CTTAAACTCAAGGAC
7	UFD2 2200-Fw*	GGTAAATTAGTGCAG
8	UFD2-pGADT7-Fw[C]	ACCGCCATAGAAGATATTTTAC
9	UFD2-pGADT7-Rv[C]	TCACTCGCTTGCTTTATG
10	pRS416-*SmaI*-UFD2-P1000-Fw [C]	GAATTCCTGCAGCCCAATATTCTGTTATTG
11	HA-UFD2-Rv[C]	AGCGTAATCTGGAACATCGTATGGGTACATTCACTTATTCATTCA
12	HA-UFD2-Term500-Fw[C]	ATGTACCCATACGATGTTCCAGATTACGCTTAGAATAAATTGCAA
13	UFD2-Term500-pRS416-*SmaI*-Rv[C]	ACTAGTGGATCCCCCAGTTGGCTGAATTGA
14	UFD2-Fw●	GACTTTCCTGTTGGATGAAG
15	UFD2-Rv●	CTCTTCCTCTCTTGTTGGTG
16	ACR2-Fw●	AGGCAACTCAAGGCCTAAT
17	ACR2-Rv●	GAACATGCCAAGCGTTTGTA
18	ACR3-Fw●	AAGAGGGTCTGGGGAAGAAA
19	ACR3-Rv●	GCAATTGCCAGGGATAGTTC
20	YAP8-Fw●	AACCGCCCACATGTAACACT
21	YAP8-Rv●	TCCAACACACACTGAGAGCAG
22	ACT1-Fw●	CTATTGGTAACGAAAGATTCA
23	ACT1-Rv●	CCTTACGGACATCGACATCA

Fw - forward; Rv - reverse

[D]Gene disruption and mutant confirmation, ∗Sequencing, [C] Cloning, ●qRT-PCR