

## Supplemental Material

**Supplementary Figure S1.** Kidney morphology and function of *Ybx1*-knockout and *wild type* mice.

**Supplementary Figure S2.** The UUO-dependent fibrotic signature and tubular damage differ between wild type and *Ybx1* <sup>$\Delta$ RosaCreERT+TX</sup> animals.

**Supplementary Figure S3.** Immunohistochemistry of Klotho in healthy and diseased kidney tissue of wild type and *Ybx1* <sup>$\Delta$ RosaCreERT+TX</sup> following UUO on day 14.

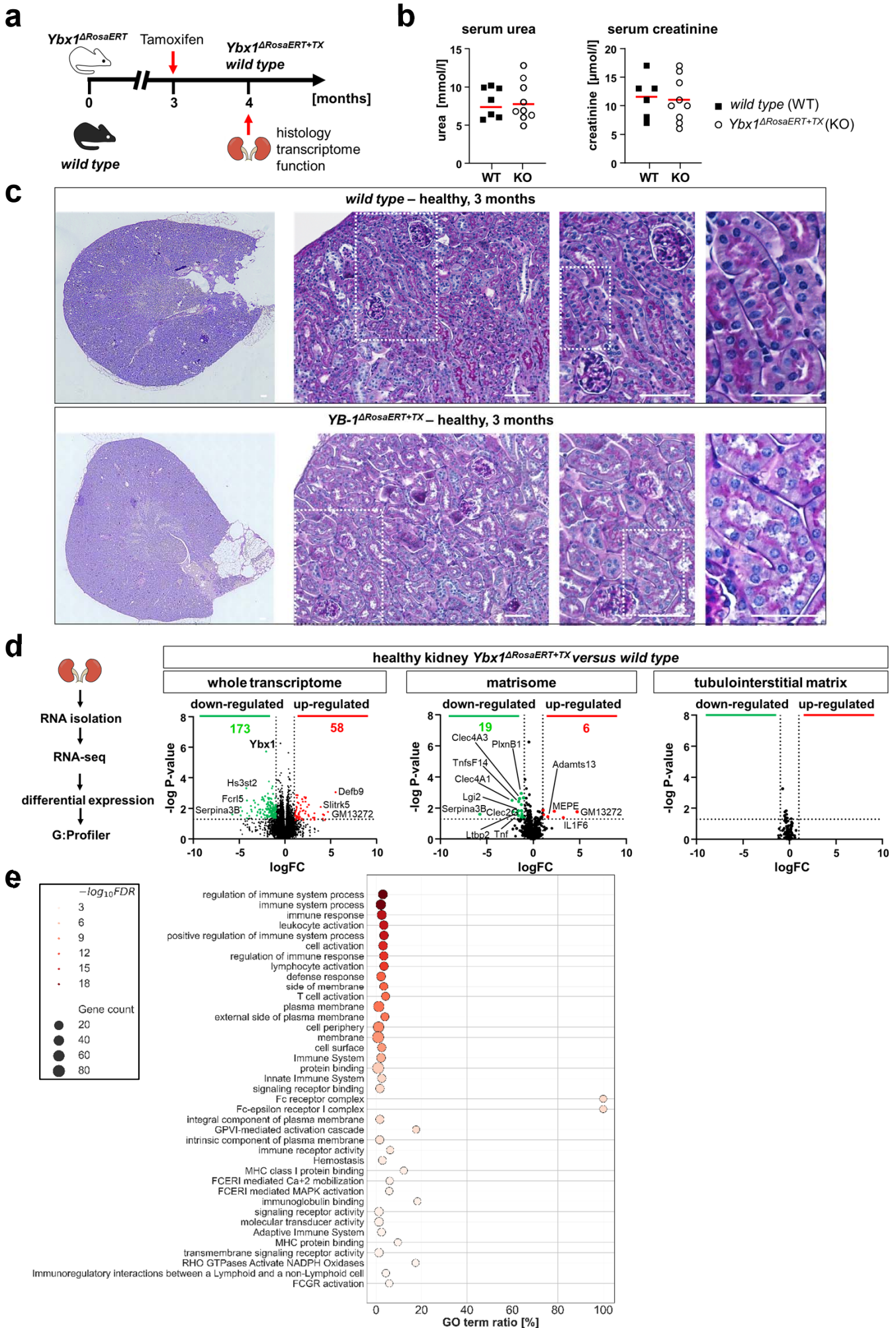
**Supplementary Figure S4.** Sheep IgG deposition within kidney tissue following injection of NTS.

**Supplementary Table S1.** Description of human datasets used in the study.

**Supplementary Table S2.** Matrisome-dependent DEGs identified in samples of patients diagnosed with diabetic kidney disease and IgA nephropathy.

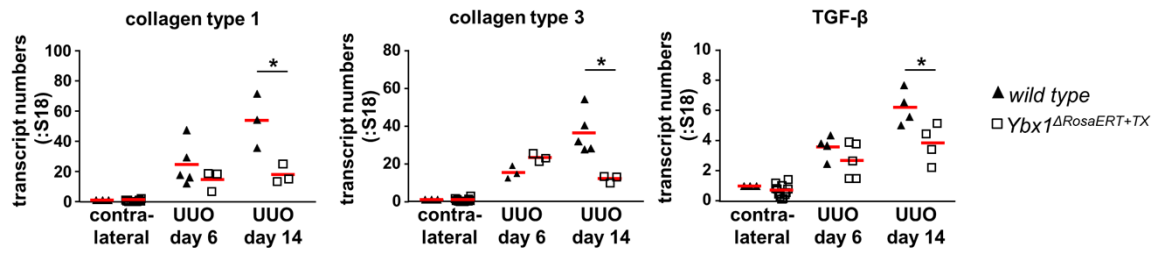
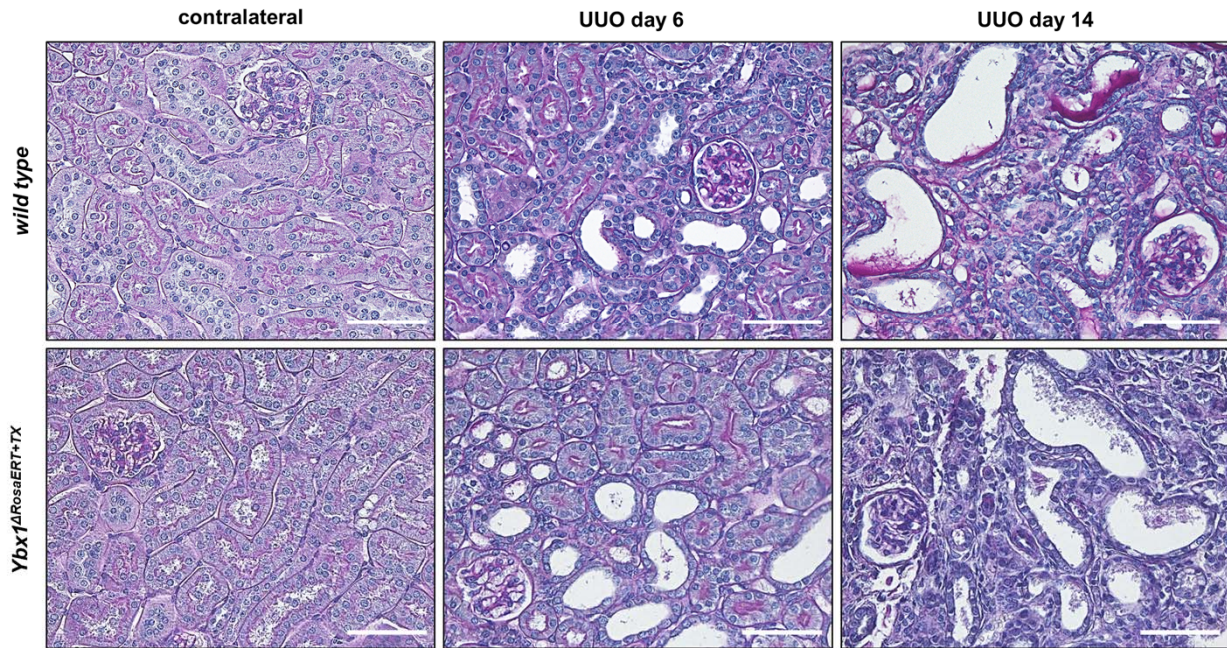
**Supplementary Table S3.** Differential expression genes defining the matrisome in *Ybx1* <sup>$\Delta$ RosaERT+TX</sup> knock out compared to wild type animals following UUO.

**Uncropped Western Blot pictures.**

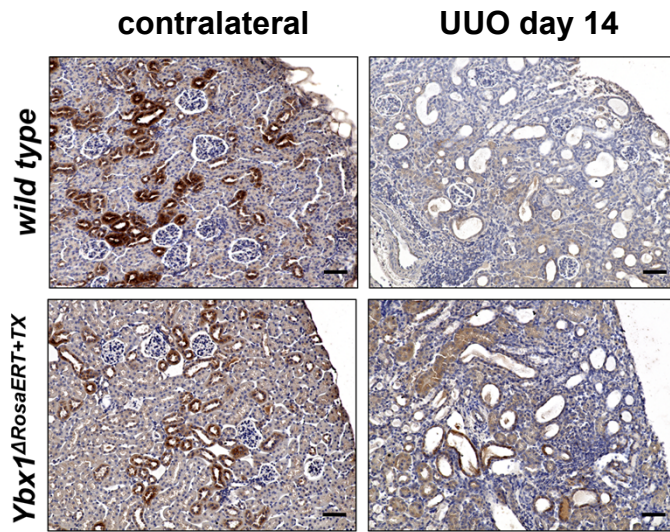
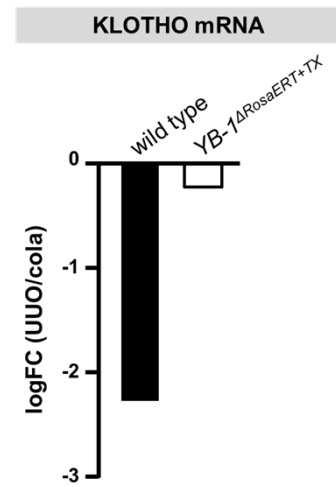


**Supplementary Figure S1. Kidney morphology and function of *Ybx1*-knockout and *wild type* mice.** (A) Tamoxifen was applied in 8 week old mice. 28 days later kidneys of wild type (n=6 and *Ybx1*-knockout (n=8 mice were analyzed. No differences between wild type and *Ybx1*-knockout animals were seen for (B) kidney function (blood urea nitrogen (BUN, serum creatinine and (C) kidney morphology (Periodic Acid-Schiff (PAS staining, scale bars equal 5  $\mu$ m. (D) Volcano plot of differentially expressed genes of *Ybx1*-knockout versus *wild type*. The differences according the whole RNAseq data, to the matrisome relevant genes, and to the tubulointerstitial matrix are depicted. The most significantly upregulated genes in *Ybx1*-knockout mice are shown in red, whereas green represents the significantly downregulated genes. Black dots are genes that are differentially expressed below the cutoff values of log-fold change and  $-\log_1$  of the P-value. Significantly regulated transcripts were those with a  $\log_{FC} \leq \pm 1$  and  $-\log_1$  P-value  $> 1.3$  (dotted lines). (E) Gene enrichment analysis of the differentially expressed genes between healthy *Ybx1*-knockout and wild type kidney tissue. The size of the dots reflects the gene counts for each process and the dot color the P-values, where the most significant result is purple.

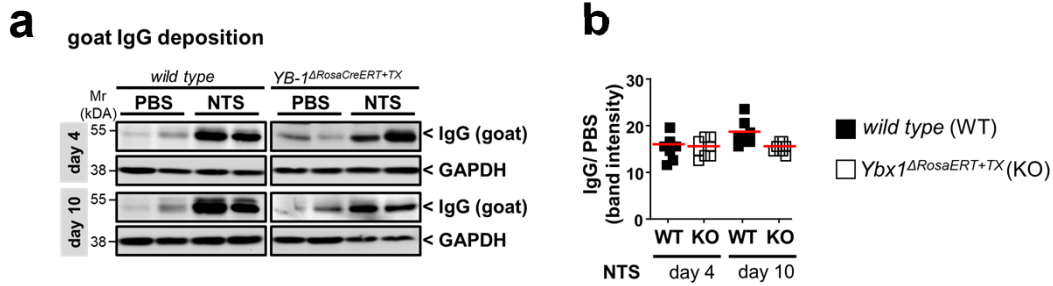


**a****b**

**Supplementary Figure S2. The UUO-dependent fibrotic signature and tubular damage differ between wild type and *Ybx1*<sup>ΔRosaCreERT+TX</sup> animals.** (a) TaqMan analysis of *Col1a1*, *Col1a3*, and *TGFβ* transcript numbers in healthy contralateral and obstructed kidneys. Both wild type and *Ybx1*<sup>ΔRosaCreERT+TX</sup> animals revealed an upregulation of the fibrogenic genes; however to a different degree. (b) Periodic acid-Schiff (PAS) staining of cortical kidney tissue was performed and representative images were taken. The PAS stainings of obstructed kidneys at days 6 and 14 show efficient congestion of the kidneys in both genotypes. Scale bar, 5 μm. (wild type n=3-5; *Ybx1*<sup>ΔRosaCreERT+TX</sup> n=3-5)

**a** Klotho: IHC**b**

**Supplementary Figure S3. KLOTHO is regulated on translational and transcriptional level in a YB-1-dependent manner. (a)** Immunohistochemistry of Klotho in healthy and diseased kidney tissue of wild type and *Ybx1 $\Delta$ RosaCreERT+TX* following UUO on day 14. **(b)** Reduced KLOTHO transcripts in wild type kidney tissue following UUO.



**Supplementary Figure S4. Sheep IgG deposition within kidney tissue following injection of NTS. (a)** Kidney tissue of wild type and *Ybx1 $\Delta$ RosaCreERT+TX* animals was analyzed for sheep IgG deposition following NTS day 4 and day 10. **(b)** Quantification of the IgG band intensity was performed according to PBS injected animals. (wild type n=6; *Ybx1 $\Delta$ RosaCreERT+TX* n=6)

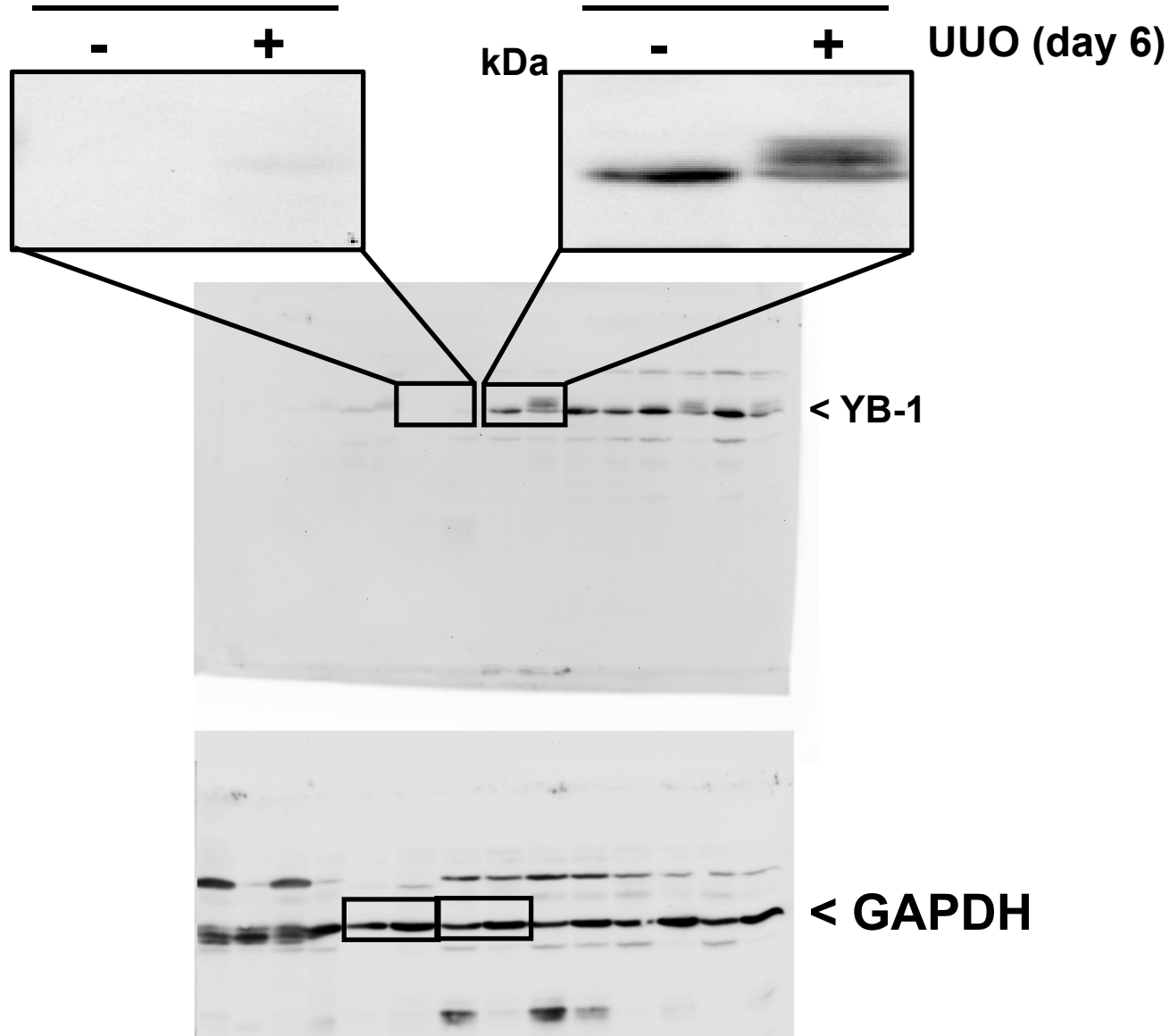
**Supplementary Table S1. Description of human datasets used in the study.**

<b>GEO series</b>	<b>platform</b>	<b>model</b>	<b>Ref.</b>
<b>GSE30122</b>	GPL571 Affymetrix Human Genome U133A 2.0	diabetic kidney disease	35
<b>GSE116626</b>	GPL14951 Illumina HumanHT-12 WG-DASL V4.0 R2	IgA nephropathy	36

35. Woroniecka KI, Park AS, Mohtat D, *et al.* Transcriptome analysis of human diabetic kidney disease. *Diabetes* 2011; **60**: 2354-2369.
36. Cox SN, Chiurlia S, Divella C, *et al.* Formalin-fixed paraffin-embedded renal biopsy tissues: an underexploited biospecimen resource for gene expression profiling in IgA nephropathy. *Scientific reports* 2020; **10**: 15164.

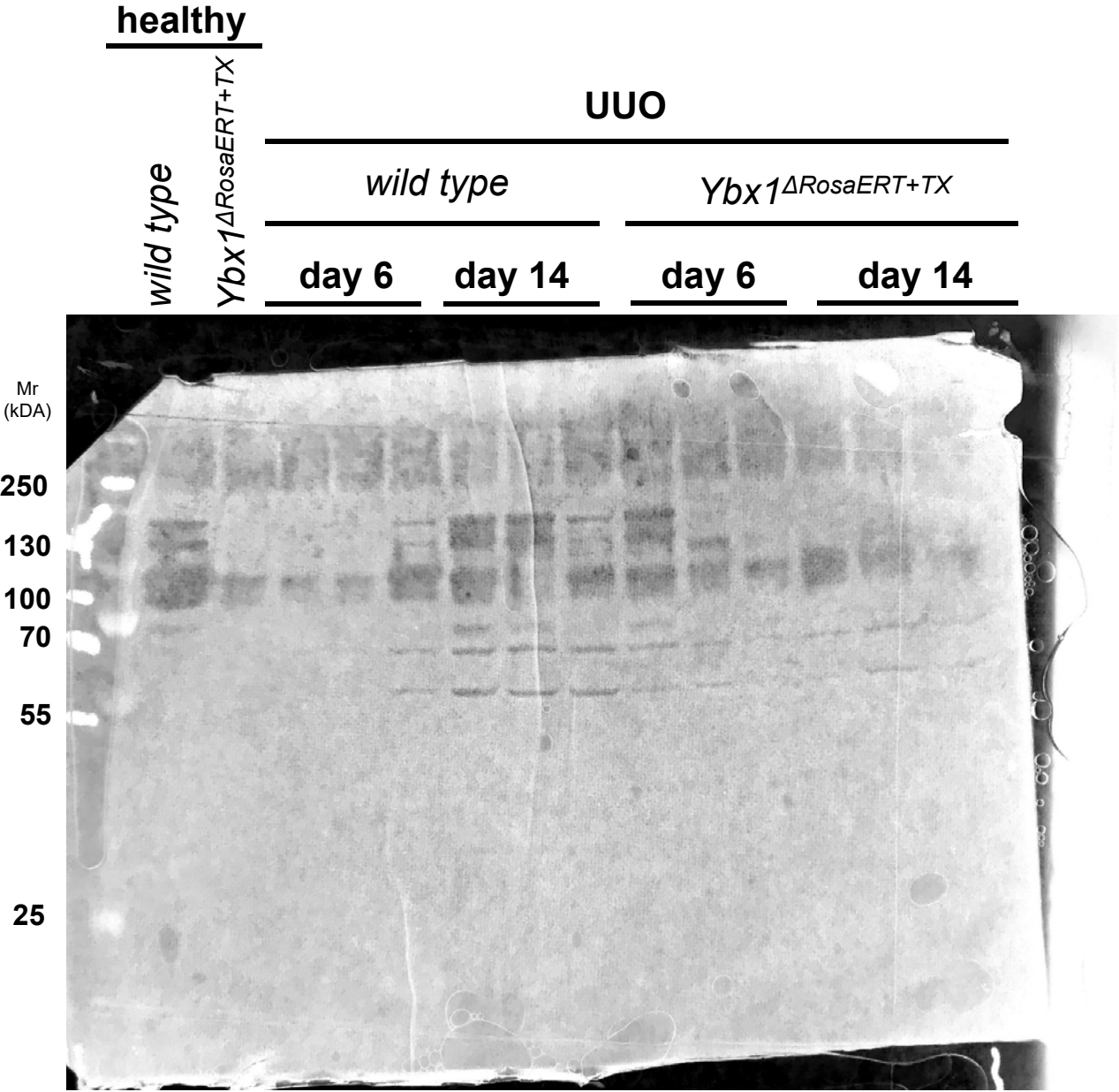
***YB-1* $\Delta$ RosaERT+TX**

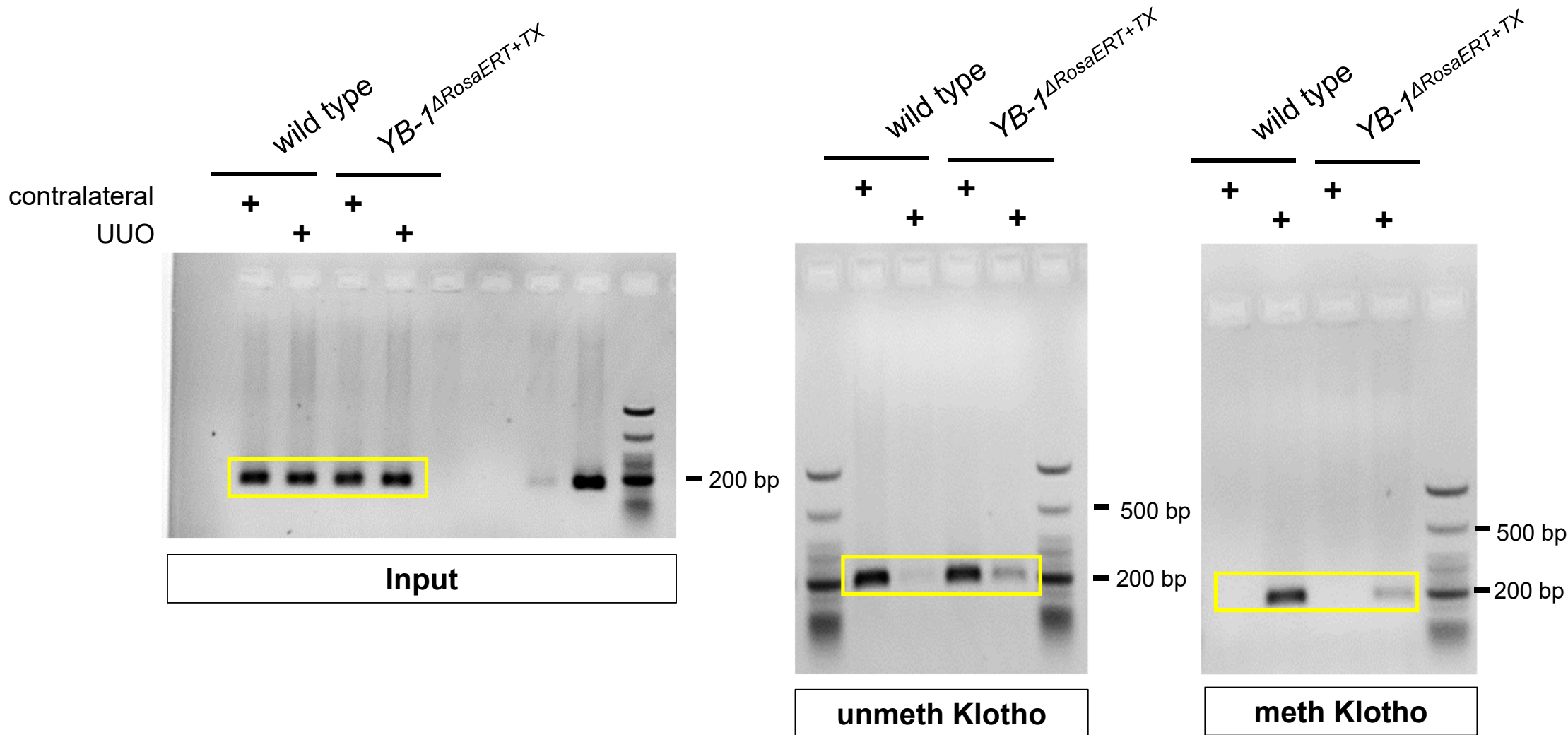
***wild type***

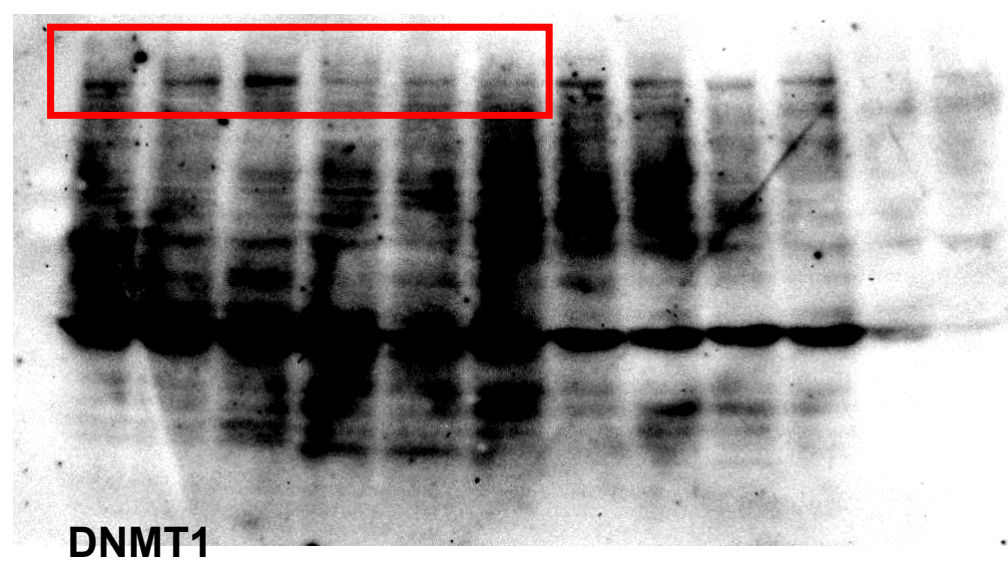
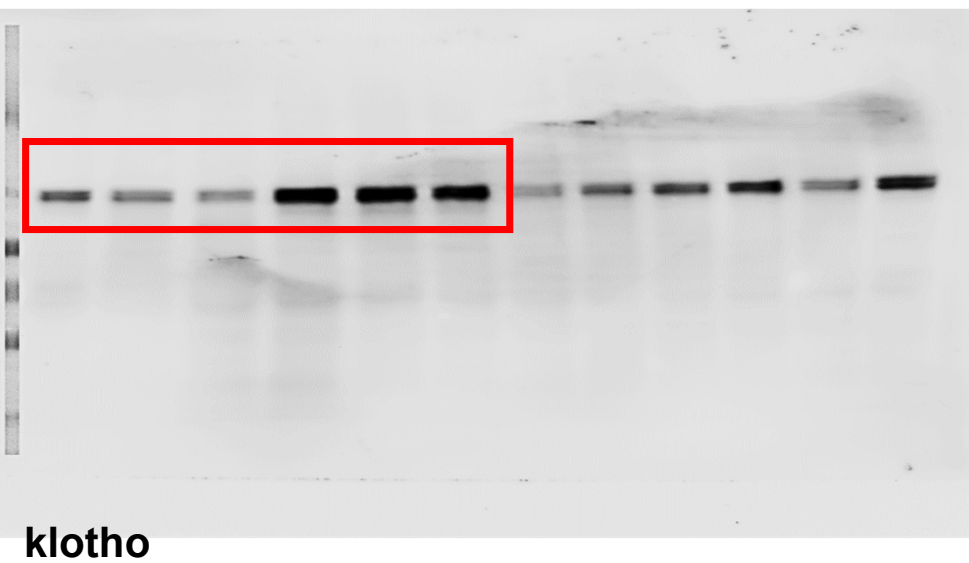
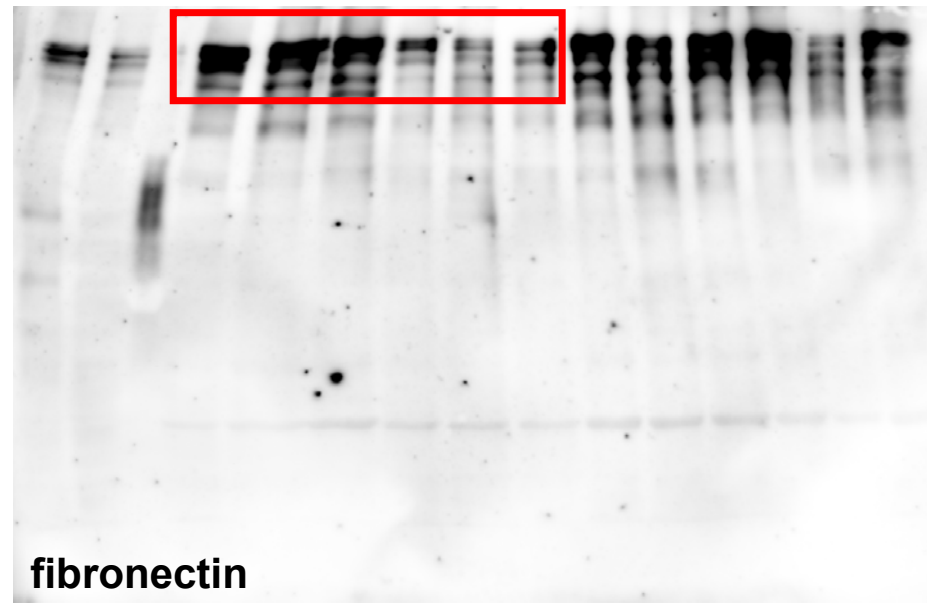


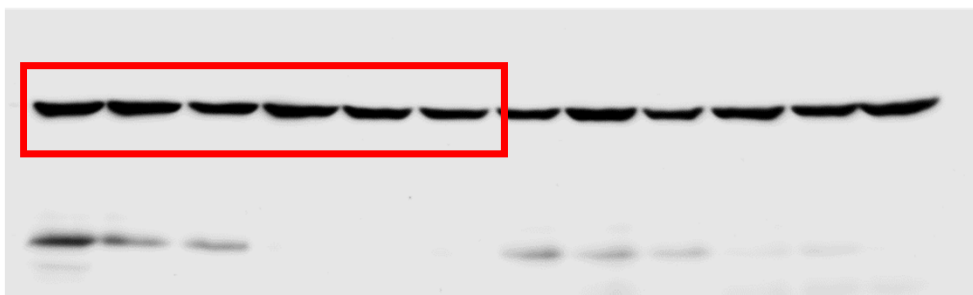


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