Supplemental Figure Legends

Fig. S1 Bioinformatic analysis of *Hsp* mRNA from the publicly available data for mouse KI/R (GSE172042).

A. Heatmap of 29 *Hsps* mRNA levels in kidneys of sham and KI/R mice.

B. mRNA levels of 29 *Hsps* in sham kidneys. Note that *Hspa12a* mRNA showed the highest level among these 29 *Hsps* in normal kidneys.

C. Effects of KI/R on mRNA levels of 29 *Hsps* in kidneys. Data are mean ± SD, **P* < 0.05 and ***P* < 0.01 by Student's two-tailed unpaired *t*- test or Mann–Whitney U test. *n* = 2-3.

Fig. S2 Identification of the isolated primary TEC.

The primary TEC that isolated from mouse kidneys were immunostained with the epithelial marker CK-18 (red). DAPI was used to counter stain nuclei. Scale bar = 50 μm.

Fig. S3 HSPA12A increases nuclear abundance of c-Myc in TEC after H/R.

Nuclear fractions were prepared from H/R-treated TEC. c-Myc protein expression was examined by immunoblotting. Blots for H3 served as loading controls. Data are mean ± SD, **P* < 0.05 by Student's two-tailed unpaired *t*- test. *n* = 4.

Fig. S4 Knockdown of c-Myc in TEC after H/R.

c-Myc knockdown in TEC was confirmed by immunoblotting. $^{**}P < 0.01$ by Mann–Whitney U test. $n = 5$/group.

Fig. S5 C646 reverses the HSPA12A-increased c-Myc nuclear abundance in TEC.

Nuclear fractions were prepared from H/R-treated TEC in the presence or absence of C646. c-Myc protein in nuclear fraction was examined by immunoblotting. Blots for H3 served as loading controls. Data are mean ± SD, $^{**}P < 0.01$ by one-way ANOVA followed by Tukey's test. $n = 4$.

Fig. S6 Effects of HSPA12A on expression of glycolysis-related genes in primary TEC.

A. ATP production rate was analyzed by the seahorse assay in primary TEC following H/R. Data are mean ± SD, $^{*}P < 0.05$ by Student's two-tailed unpaired *t*- test $n = 4$.

B. Expression of the indicated genes were examined by immunoblotting in primary TEC following H/R. Blots for GAPDH served as loading controls. Data are mean ± SD, $^{**}P < 0.01$ by two-way ANOVA followed by Tukey's test. $n = 3$.

Fig. S7 Effects of HSPA12A on expression of glycolysis-related genes in mouse kidneys following KI/R.

A. Lactate contents were analyzed in serum of mice following KI/R. Data are mean ± SD, $^{**}P < 0.01$ by Mann–Whitney U test. $n = 5$.

B. Protein expressions of glycolysis-related genes were determined by immunoblotting in KI/R kidneys of mice. Data are mean ± SD, $^{**}P < 0.01$ by Student's two-tailed unpaired *t*- test. $n = 5$ for GLUT1 groups and $n = 6$ for the other groups.

Fig. S8 2-DG abolishes the HSPA12A-increaseed lactate generation and proliferation of TEC after H/R.

A. The brief diagram of glycolysis pathway. 2-DG was used to block lactate generation.

B. Lactate contents in culture medium of H/R-treated TEC were measured in the presence or absence of 2-DG. Data are mean ± SD, $^{**}P < 0.01$ by one-way ANOVA followed by Brown-Forsythe and Welch test. $n = 5$.

C. Cell proliferation in H/R-treated TEC was indicated by EdU incorporation in the presence or absence of 2-DG. Data are mean ± SD, $^{**}P < 0.01$ by one-way ANOVA followed by Tukey's test. $n = 3$. Scale bar = 50 μm.

Fig. S9 Effect of HSPA12A on nuclear abundance of Hif1α in KI/R kidney.

A. Experimental setting of primary TEC.

B. Anti-Flag-HSPA12A immunoprecipitates prepared from H/R-treated TEC were immunoblotted with Hif1α. Input or IgG-immunoprecipitates served as positive or negative controls. Note that Hif1α was not recovered in Flag-tagged HSPA12A immunoprecipitates.

C. Experimental setting of mouse kidneys.

D. Following KI/R, nuclear fraction was prepared from kidneys for immunoblotting

against Hif1α. Blots for LaminA/C served as loading controls. Data are mean ± SD, $^{**}P < 0.01$ by Student's two-tailed unpaired *t*- test. $n = 5$.

Fig. S10 Hif1α inhibition diminishes the HSPA12A-induced increase of proliferation of TEC after H/R.

Cell proliferation was examined by EdU incorporation in H/R-treated *Hspa12a*$^{O/E}$ TEC in the presence or absence of YC-1. Data are mean ± SD, $^{**}P < 0.01$ by one-way ANOVA followed by Tukey's test. $n = 3$. Scale bar = 50 μm.