Supplemental Figure Legend

Supplementary Figure 1S: Principal component analysis (PCA) of the 44 experimental samples analyzed by array. The top 500 highly expressed genes across samples were considered for the analysis.

Supplementary Figure 2S: TCGA validation of up-regulated RCC associated genes. Boxplots show expression level of each gene in 72 kidney normal samples and 533 kidney renal clear cell carcinoma samples. The significance of differential expression is measured by unpaired t-test.

Supplementary Figure 3S: TCGA validation of down-regulated RCC associated genes. Boxplots show expression level of each gene in 72 kidney normal samples and 533 kidney renal clear cell carcinoma samples. The significance of differential expression is measured by unpaired t-test.

Supplementary Figure 4S: Oncomine (https://www.oncomine.com) analysis of RCC associated genes. Heatmap shows expression pattern of up-regulated [upper panel] and down-regulated [lower panel] RCC genes in published Beroukhim RCC study, consisting renal cortex (n=10), renal tissue (n=1) and non-hereditary clear cell renal cell carcinoma samples (n=27)(1).

Supplementary Figure 5S: Oncomine analysis of RCC associated genes. Heatmap shows expression pattern of up-regulated [upper panel] and down-regulated [lower panel] RCC genes in published Jones Renal Study, consisting normal kidney (n=23) and clear cell renal cell carcinoma (n=23) samples(2).

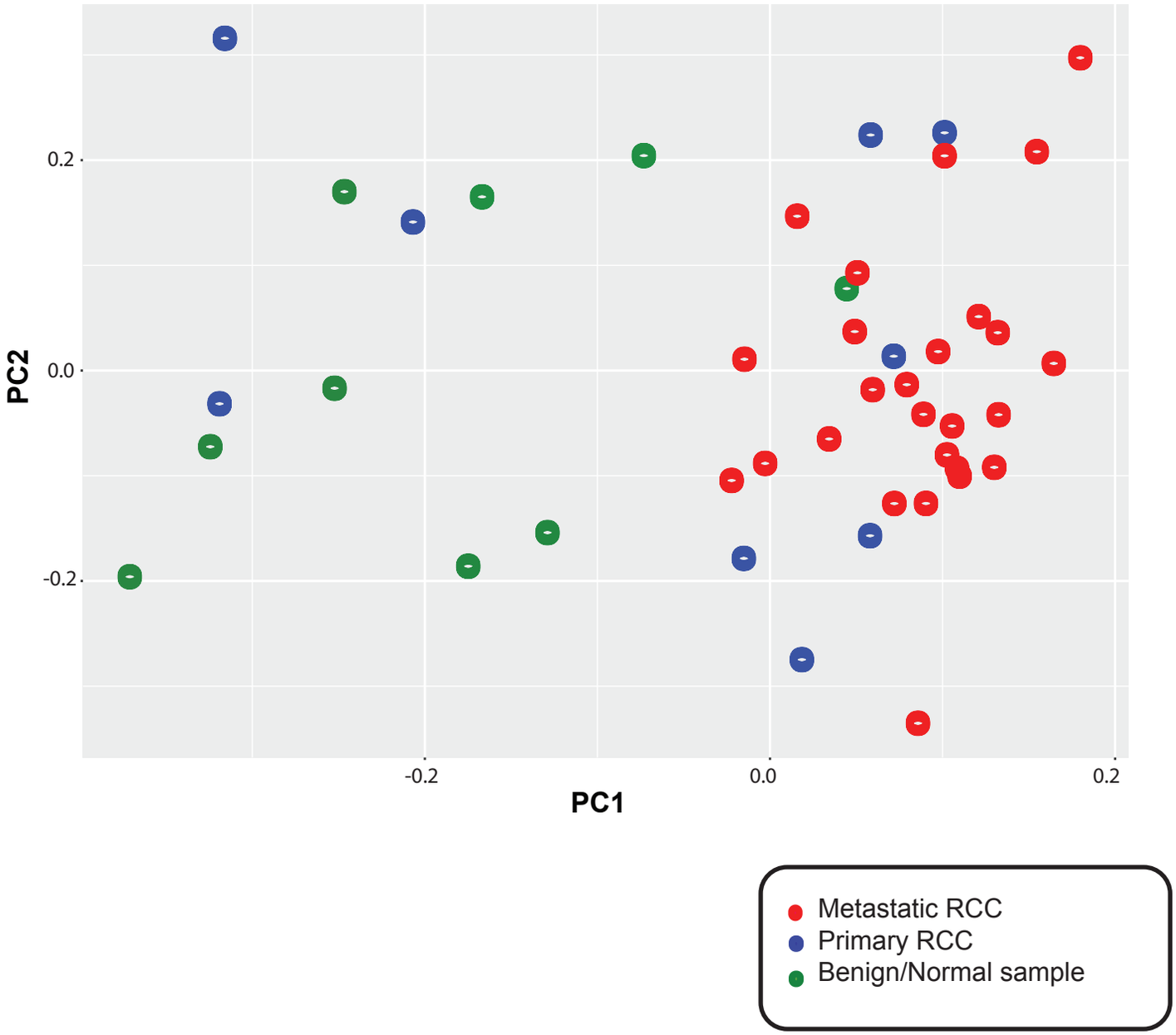
Supplementary Figure 6S: Oncomine analysis of RCC associated genes. Heatmap shows expression pattern of up-regulated [upper panel] and down-regulated [lower panel] RCC genes in published Gumz Renal Study, consisting normal kidney (n=10) and clear cell renal cell carcinoma (n=10) samples(3).

Supplementary Figure 7S: Kaplan meier plots showing effect of gene expression level on overall survival of kidney renal clear cell carcinoma patients. The survival plots were obtained from UALCAN, which uses level 3 RNA-seq data and survival information from TCGA kidney renal clear cell carcinoma[KIRC] patients (n=533). The significance of difference between survival curves were obtained by log rank test.

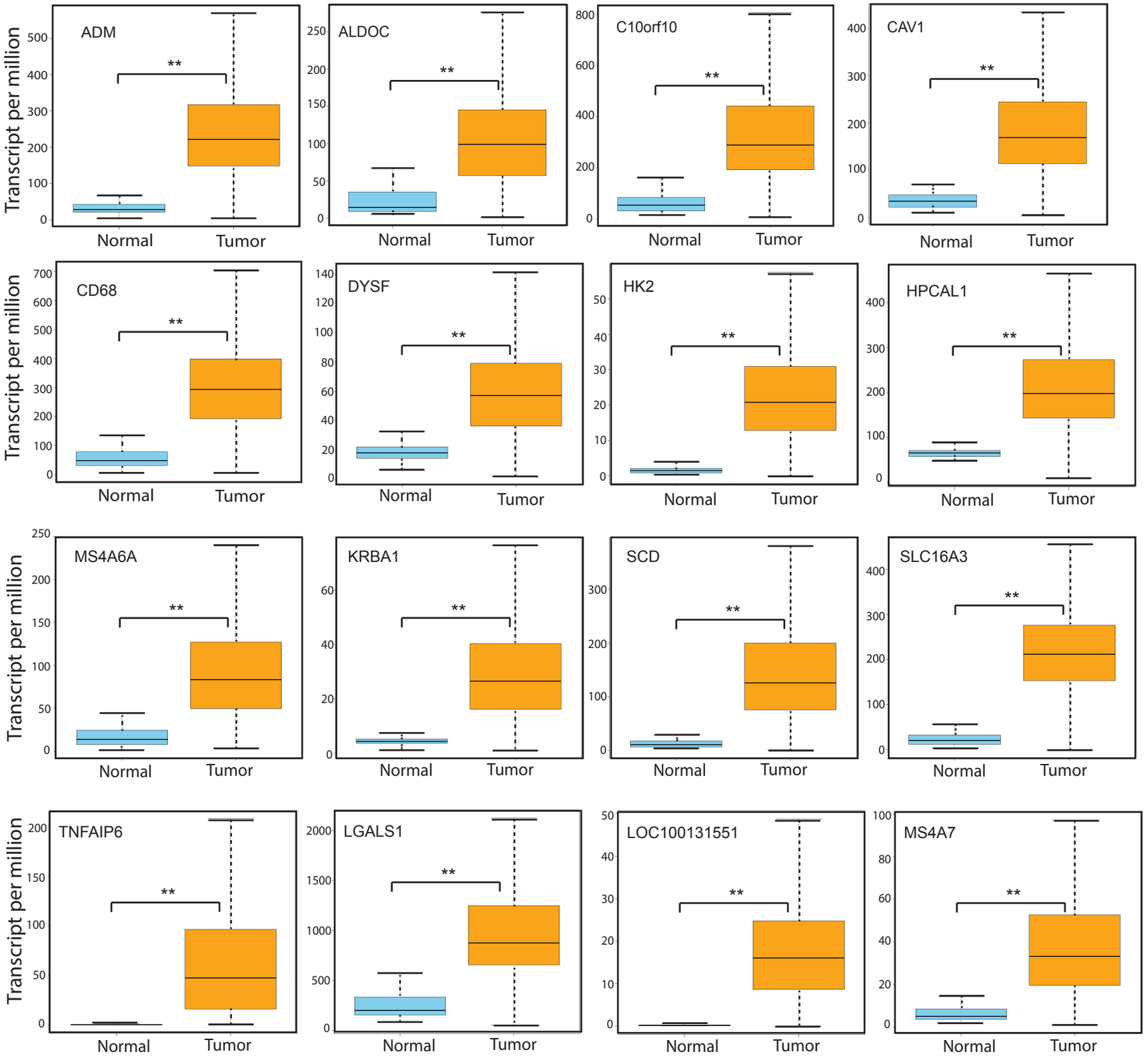
References for Supplemental Figures

1. Beroukhim R, Brunet JP, Di Napoli A, Mertz KD, Seeley A, Pires MM, et al. Patterns of gene expression and copy-number alterations in von-hippel lindau disease-associated and sporadic clear cell carcinoma of the kidney. Cancer research. 2009;69(11):4674-81.
2. Jones J, Otu H, Spentzos D, Kolia S, Inan M, Beecken WD, et al. Gene signatures of progression and metastasis in renal cell cancer. Clin Cancer Res. 2005;11(16):5730-9.
3. Gumz ML, Zou H, Kreinest PA, Childs AC, Belmonte LS, LeGrand SN, et al. Secreted frizzled-related protein 1 loss contributes to tumor phenotype of clear cell renal cell carcinoma. Clin Cancer Res. 2007;13(16):4740-9.

Supplementary Figure 1S

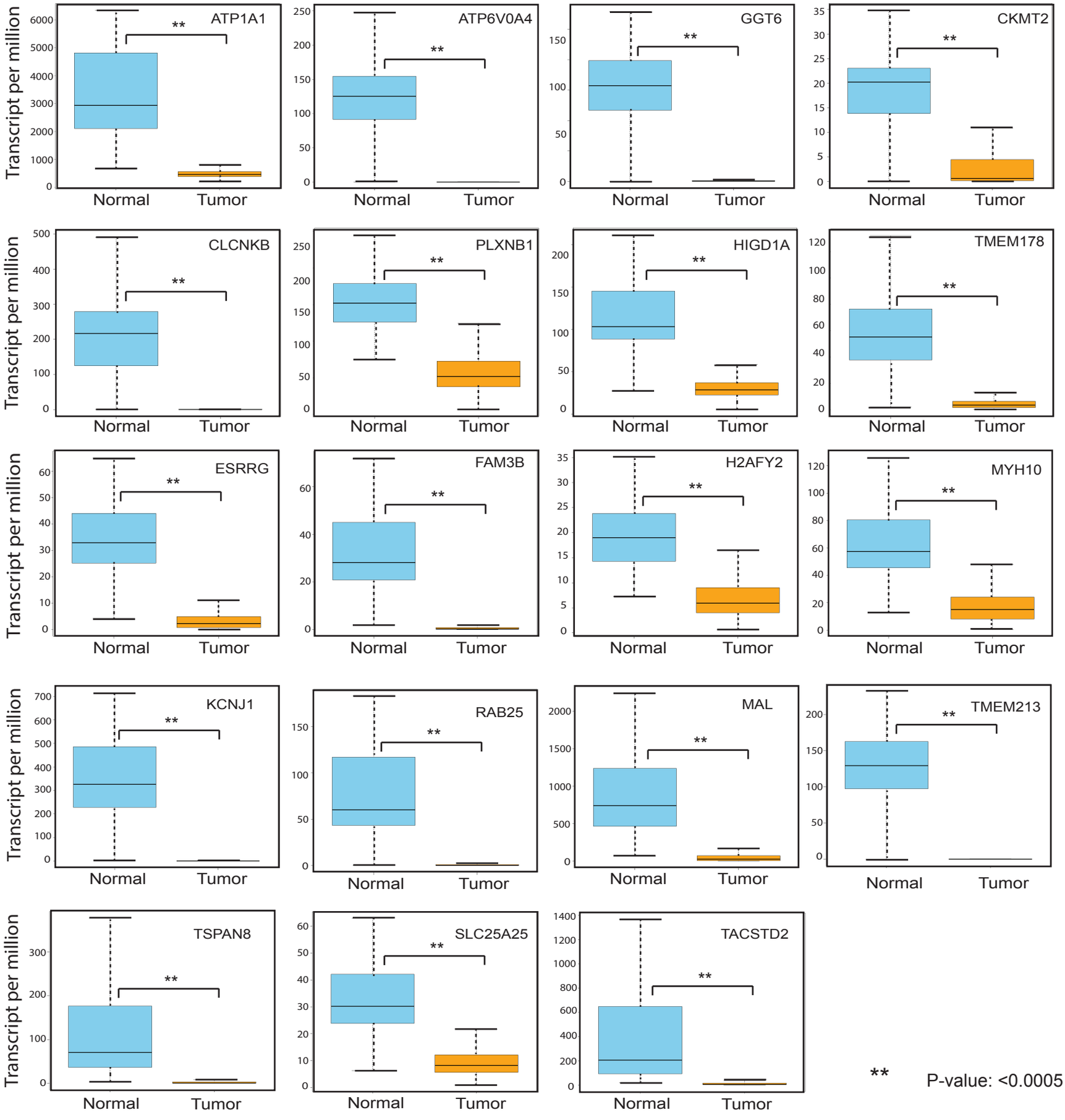


Supplementary Figure 2S

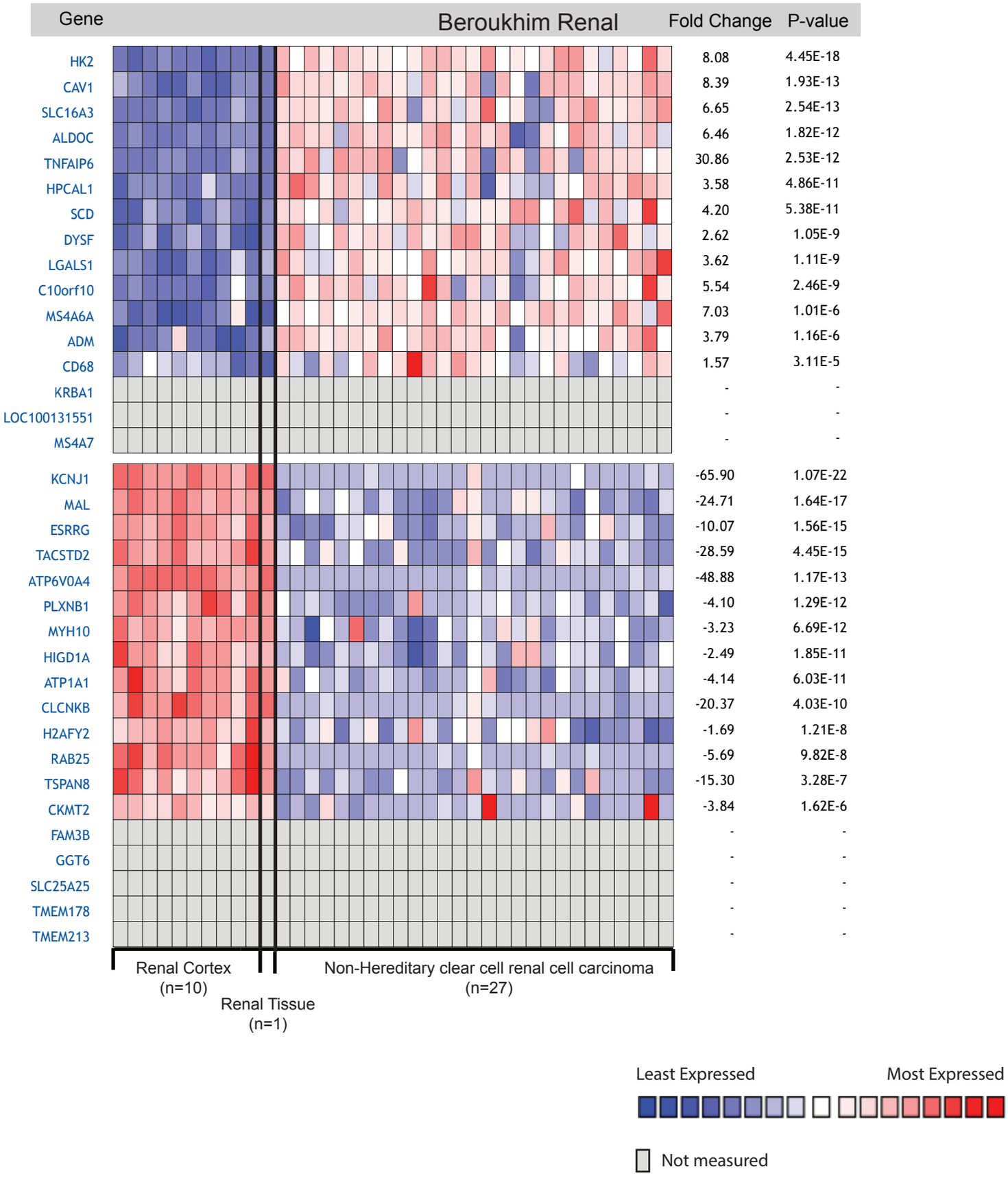


** P-value: <0.0005

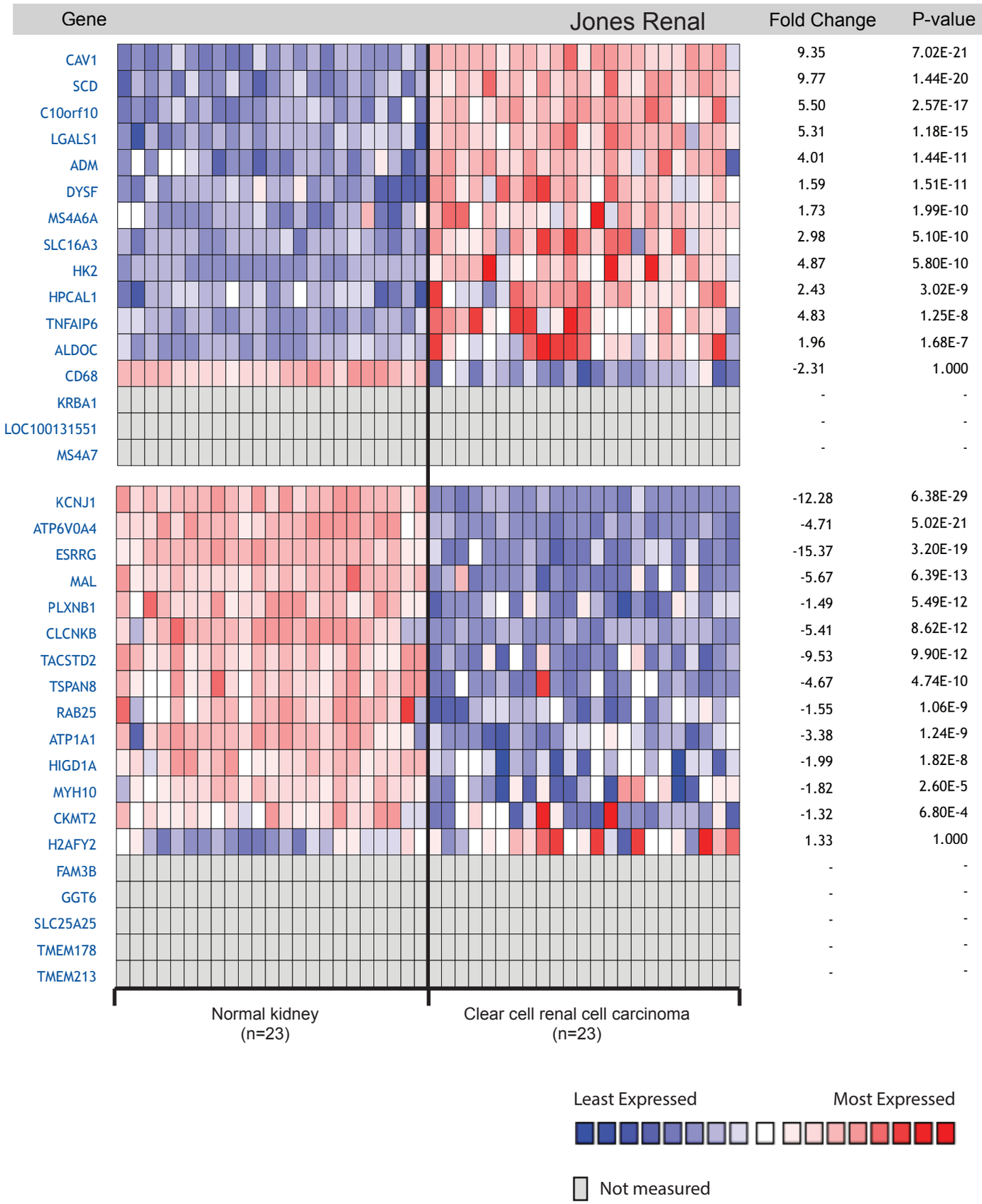
Supplementary Figure 3S



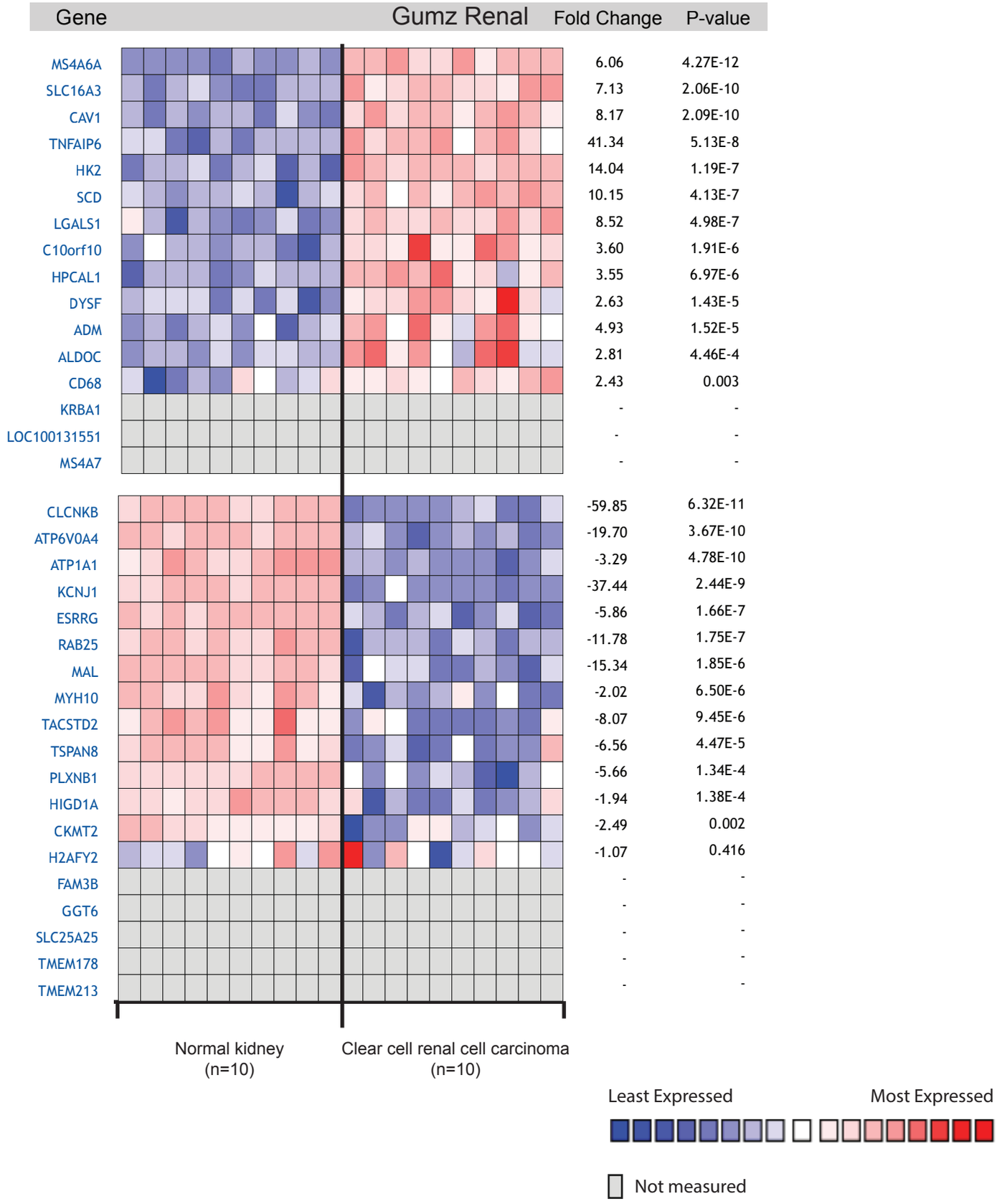
Supplementary Figure 4S



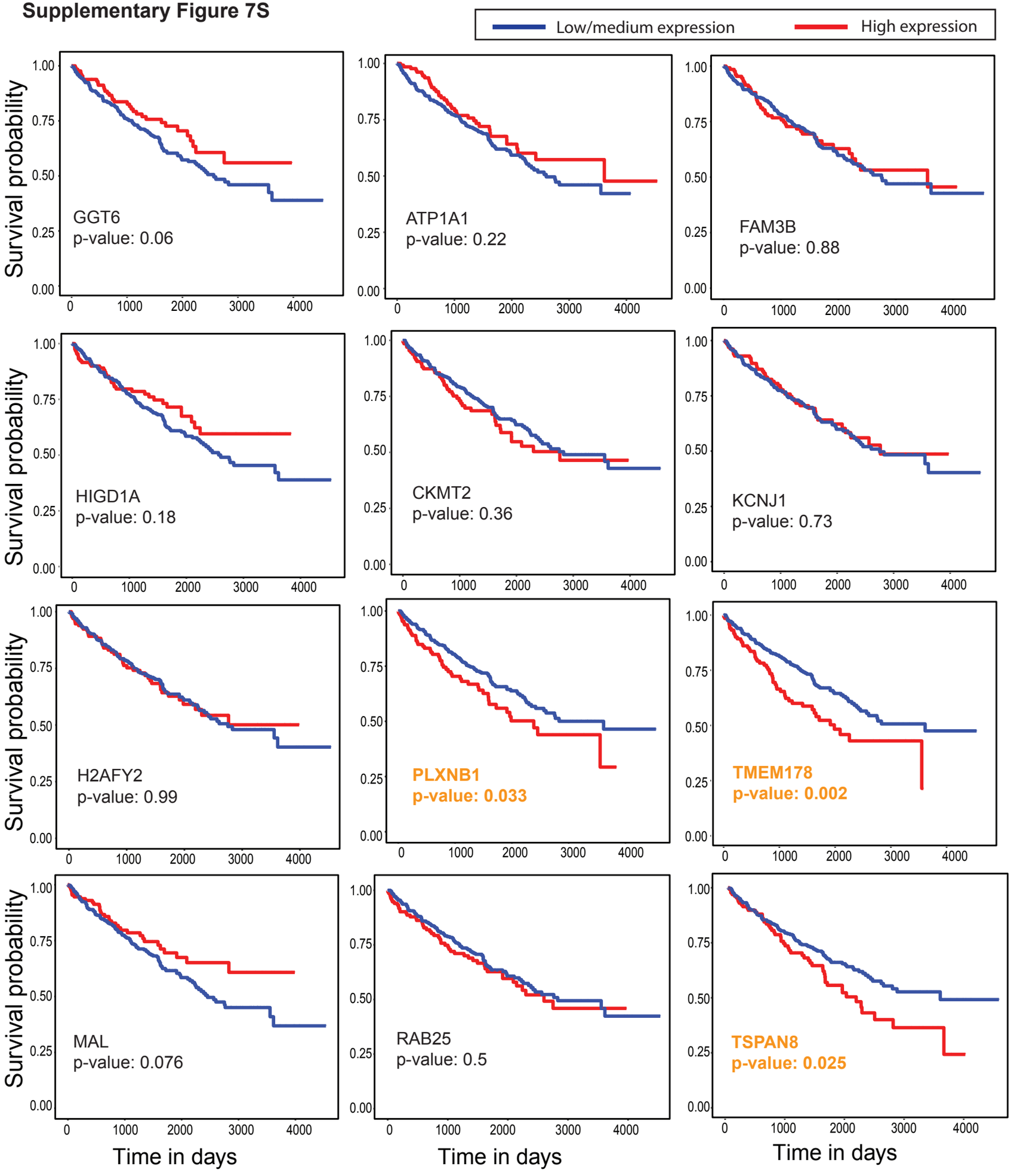
Supplementary Figure 5S

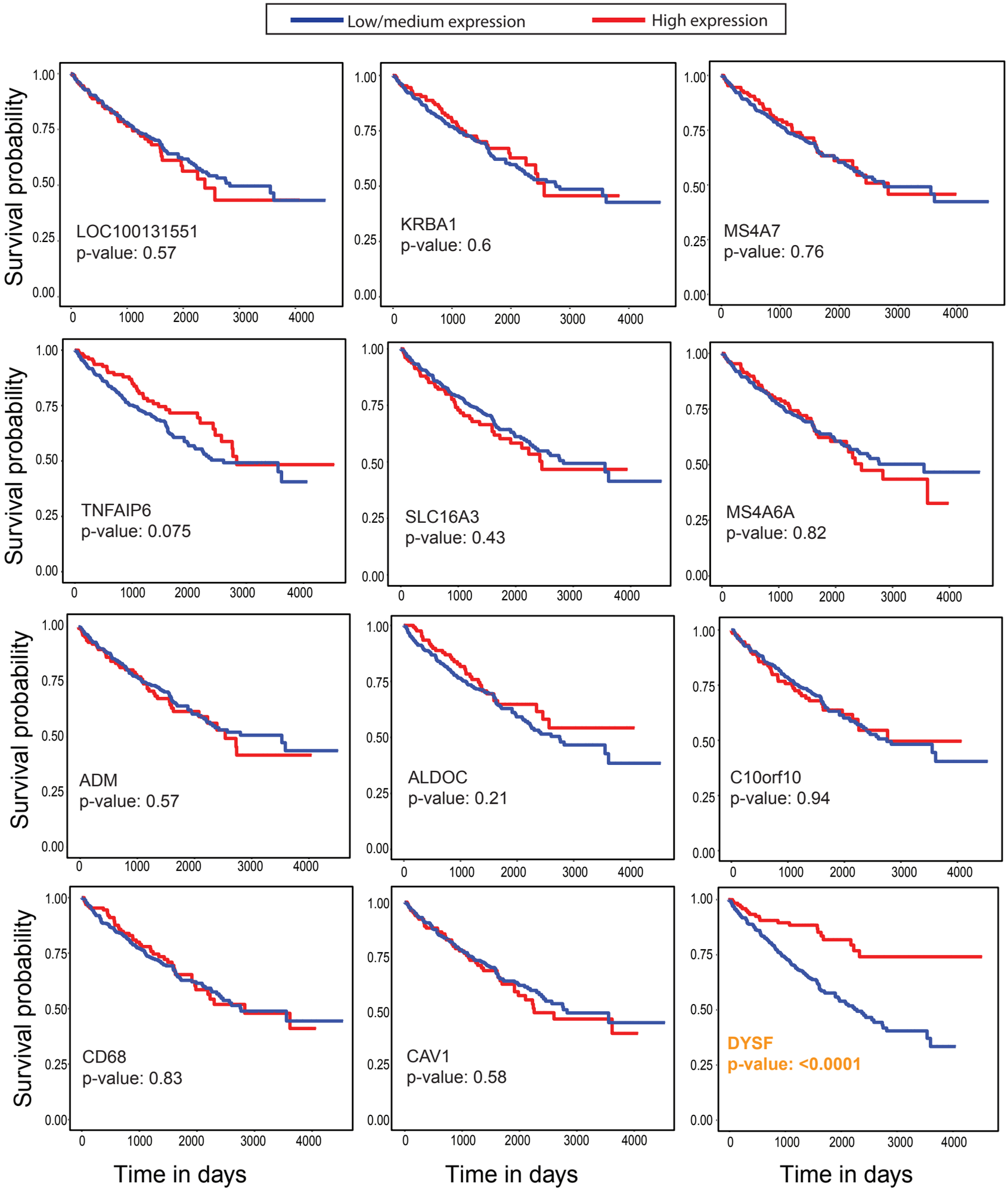


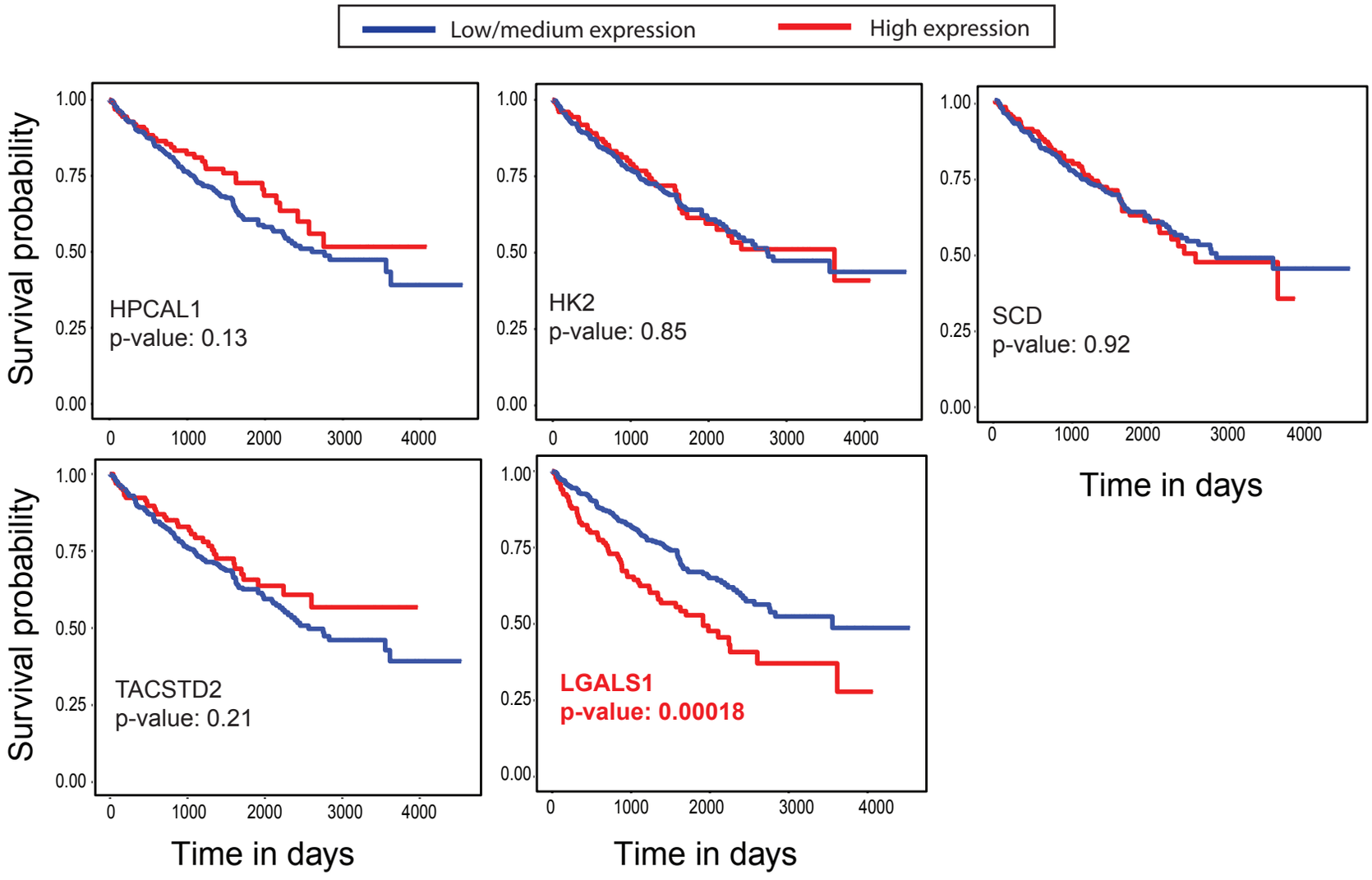
Supplementary Figure 6S



Supplementary Figure 7S




Low/medium expression
High expression
Survival probability
LOC100131551
p-value: 0.57
KRBA1
p-value: 0.6
MS4A7
p-value: 0.76
TNFAIP6
p-value: 0.075
SLC16A3
p-value: 0.43
MS4A6A
p-value: 0.82
ADM
p-value: 0.57
ALDOC
p-value: 0.21
C10orf10
p-value: 0.94
CD68
p-value: 0.83
CAV1
p-value: 0.58
DYSF
p-value: <0.0001
Time in days
Time in days
Time in days


Low/medium expression
High expression
Survival probability
1.00
0.75
0.50
0.25
0.00
0
1000
2000
3000
4000
HPCAL1
p-value: 0.13
HK2
p-value: 0.85
SCD
p-value: 0.92
Time in days
TACSTD2
p-value: 0.21
LGALS1
p-value: 0.00018
Time in days
Time in days