

Table S1. Sample sizes in publically available data sets

| GSE#     | Plished Jornal       | STA Sample | CAI Sample (CADI>4) | Total Samples |
|----------|----------------------|------------|---------------------|---------------|
| GSE12187 | Kurian, PlosOne 2009 | 26         | 22                  | 48            |
| GSE25902 | Neasens, KI 2010     | 48         | 25                  | 73            |
| GSE44131 | Hayde, cJASN 2013    | 12         | 17                  | 29            |
| GSE9493  | Rodder, AJT 2009     | 20         | 18                  | 38            |
| GSE22459 | Park, JASN 2010      | 25         | 40                  | 65            |
| GSE74313 | GoCAR data           | 16         | 6                   | 22            |

CADI  $\geq$  4, #Moderate-Sever IF/TA. STA = stable. N<sub>samples</sub>=275.

Table S2. *Hck* expression has strong correlation with CADI, IFTA, ci, cg ct scores.

| GSE25902 dataset        | IFTA       | cadi      |
|-------------------------|------------|-----------|
| correlation coefficient | 0.37011455 | 0.40987   |
| P value                 | 0.001269   | 0.0003169 |

| GoCAR dataset           | CADI    | ci      | cg      | ct      |
|-------------------------|---------|---------|---------|---------|
| Correlation coefficient | 0.66606 | 0.57560 | 0.48846 | 0.44518 |
| P value                 | 0.0007  | 0.0051  | 0.0211  | 0.0379  |

Table S3. Meta analysis information for the 23 genes interacted with *HCK*

| GeneID | Symbol   | MetaEffectFoldChange | FDR(Meta-EffectSize) |
|--------|----------|----------------------|----------------------|
| 8945   | BTRC     | -1.01                | 1.66E-02             |
| 841    | CASP8    | 1.13                 | 4.46E-02             |
| 867    | CBL      | 1.1                  | 2.85E-02             |
| 915    | CD3D     | 1.64                 | 4.92E-02             |
| 51363  | CHST15   | 1.47                 | 4.34E-02             |
| 2533   | FYB      | 1.37                 | 1.13E-03             |
| 3055   | HCK      | 1.39                 | 1.45E-02             |
| 3313   | HSPA9    | -1.13                | 4.63E-02             |
| 10261  | IGSF6    | 1.7                  | 2.83E-02             |
| 3575   | IL7R     | 1.66                 | 3.79E-02             |
| 3718   | JAK3     | 1.05                 | 2.57E-02             |
| 4069   | LYZ      | 1.58                 | 2.01E-02             |
| 4170   | MCL1     | 1.05                 | 0.00E+00             |
| 2206   | MS4A2    | 1.26                 | 3.19E-02             |
| 9111   | NMI      | 1.26                 | 7.46E-03             |
| 5788   | PTPRC    | 1.37                 | 1.82E-02             |
| 5791   | PTPRE    | 1.14                 | 9.11E-03             |
| 64407  | RGS18    | 1.41                 | 1.45E-02             |
| 1901   | S1PR1    | 1.1                  | 3.59E-02             |
| 25939  | SAMHD1   | 1.37                 | 9.87E-03             |
| 6402   | SELL     | 1.55                 | 2.80E-02             |
| 7068   | THRB     | -1.16                | 1.06E-02             |
| 10673  | TNFSF13B | 1.5                  | 1.53E-02             |

Table S4. *Src* and *Hck* transcription level in different kidney diseases in Nephromine database

|            | Woroniecka<br>Diabetes |        | Reich IgA<br>Nephropathy |        | Ju Podocyte IgA<br>Nephropathy |        | Ju Podocyte<br>Lupus Nephritis |        | Hodgin Diabetes<br>Mouse |        | Flechner<br>Transplant AR |        |
|------------|------------------------|--------|--------------------------|--------|--------------------------------|--------|--------------------------------|--------|--------------------------|--------|---------------------------|--------|
| Gene       | p value                | FC     | p value                  | FC     | p value                        | FC     | p value                        | FC     | p value                  | FC     | p value                   | FC     |
| <i>Src</i> | 0.0497                 | 1.1740 | 0.0428                   | 1.0687 | 0.0060                         | 1.1506 | 0.0020                         | 1.1546 | 0.2697                   | 1.0815 | 0.0000                    | 1.5090 |
| <i>Hck</i> | 0.0088                 | 1.6806 | 0.0000                   | 3.7287 | 0.0000                         | 2.4849 | 0.0000                         | 5.8143 | 0.0128                   | 1.8969 | 0.0348                    | 2.2248 |

Table S5. Dasatinib binding affinity for *HCK* and *SRC*

| InhibitorCAS | Kinase | BindingScore | Name      | TargetGroup |
|--------------|--------|--------------|-----------|-------------|
| 302962-49-8  | HCK    | 0.79         | Dasatinib | TK          |
| 302962-49-8  | c-SRC  | 3.52         | Dasatinib | TK          |

Figure S6. Western blots confirming *HCK* over-expression and knock-down in HEK-Blue™ TGF- $\beta$  cells.

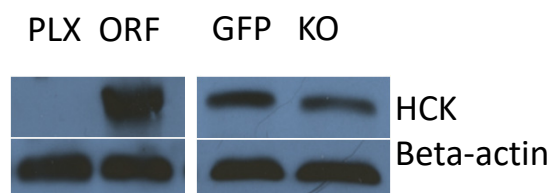


Figure S7. mRNA-levels of pro-fibrotic and inflammatory markers at 3-days post-UUO by RT-PCR (normalized to GAPDH), from whole cortices of control and UUO kidneys of dasatinib and PBS-fed animals.

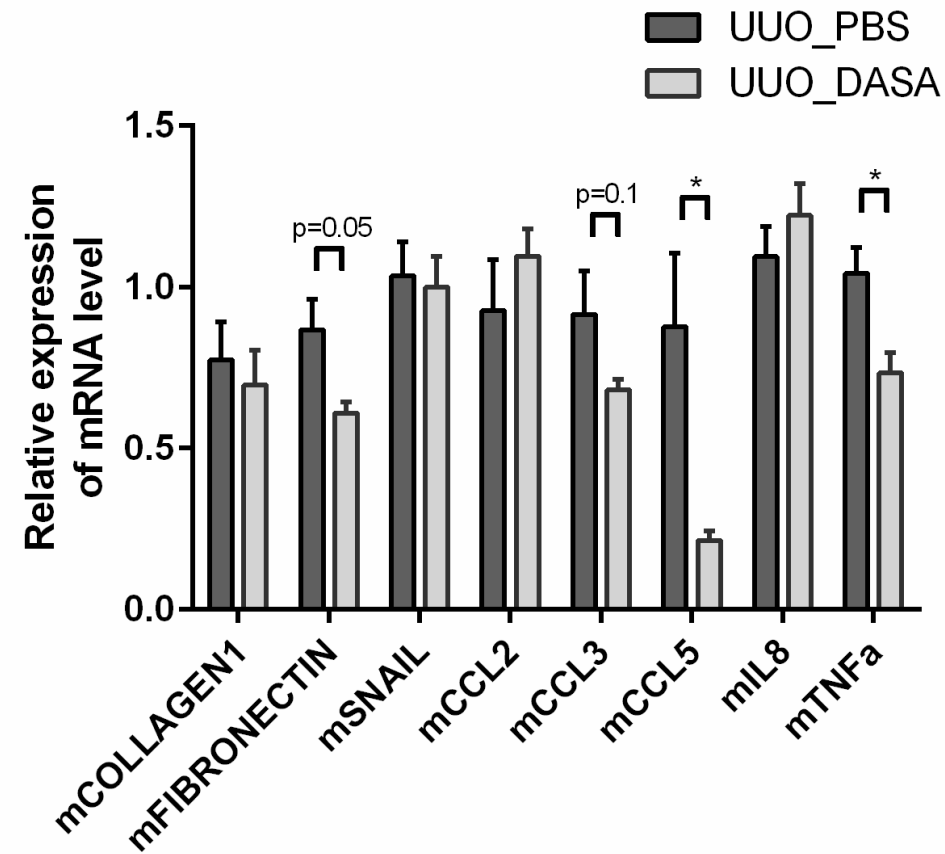


Figure S8. Immunohistochemistry for CD3 shown T cell infiltration in UUO kidney

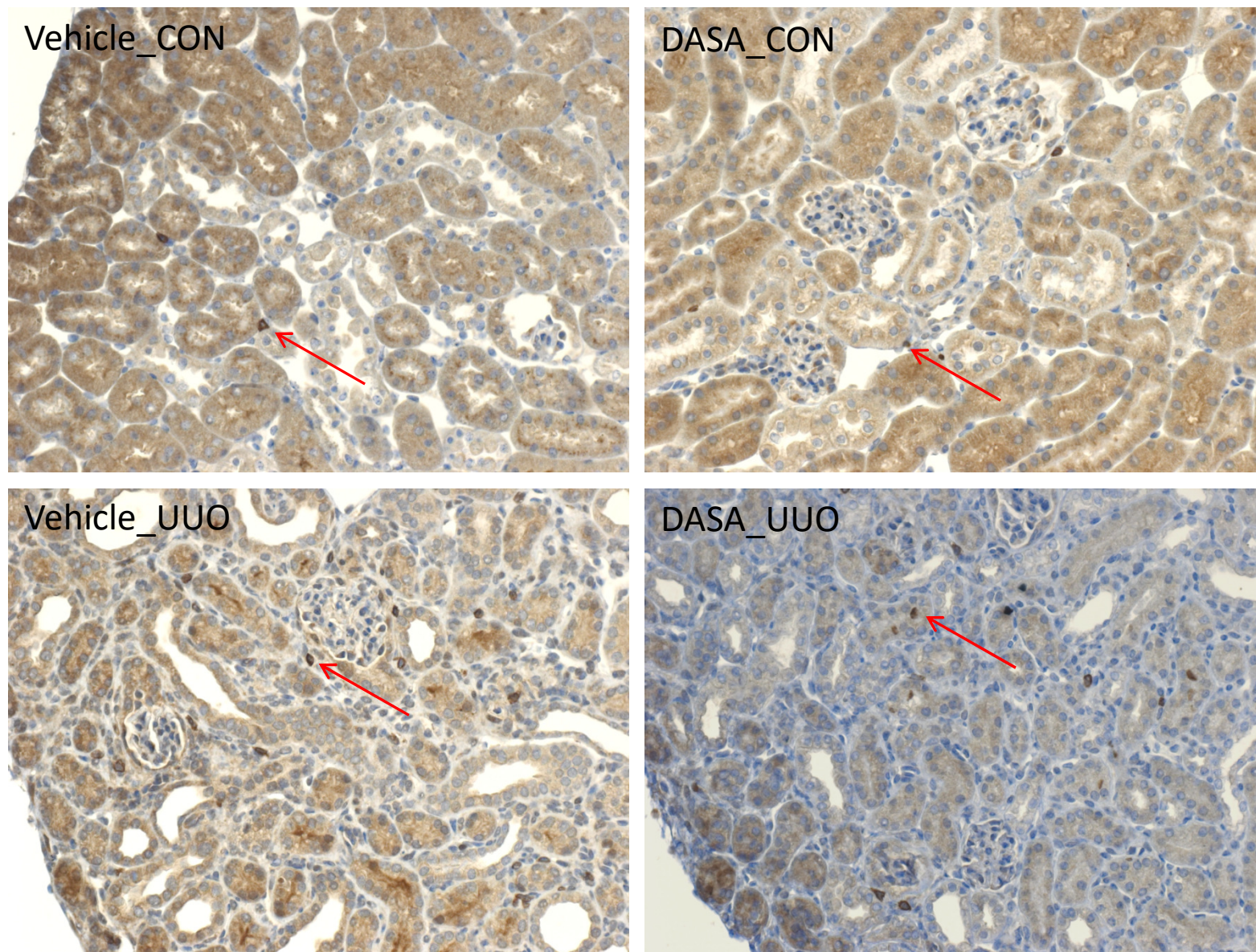




Figure S9. Immunohistochemistry for CD45R shown very few B cell in control and UUO kidney

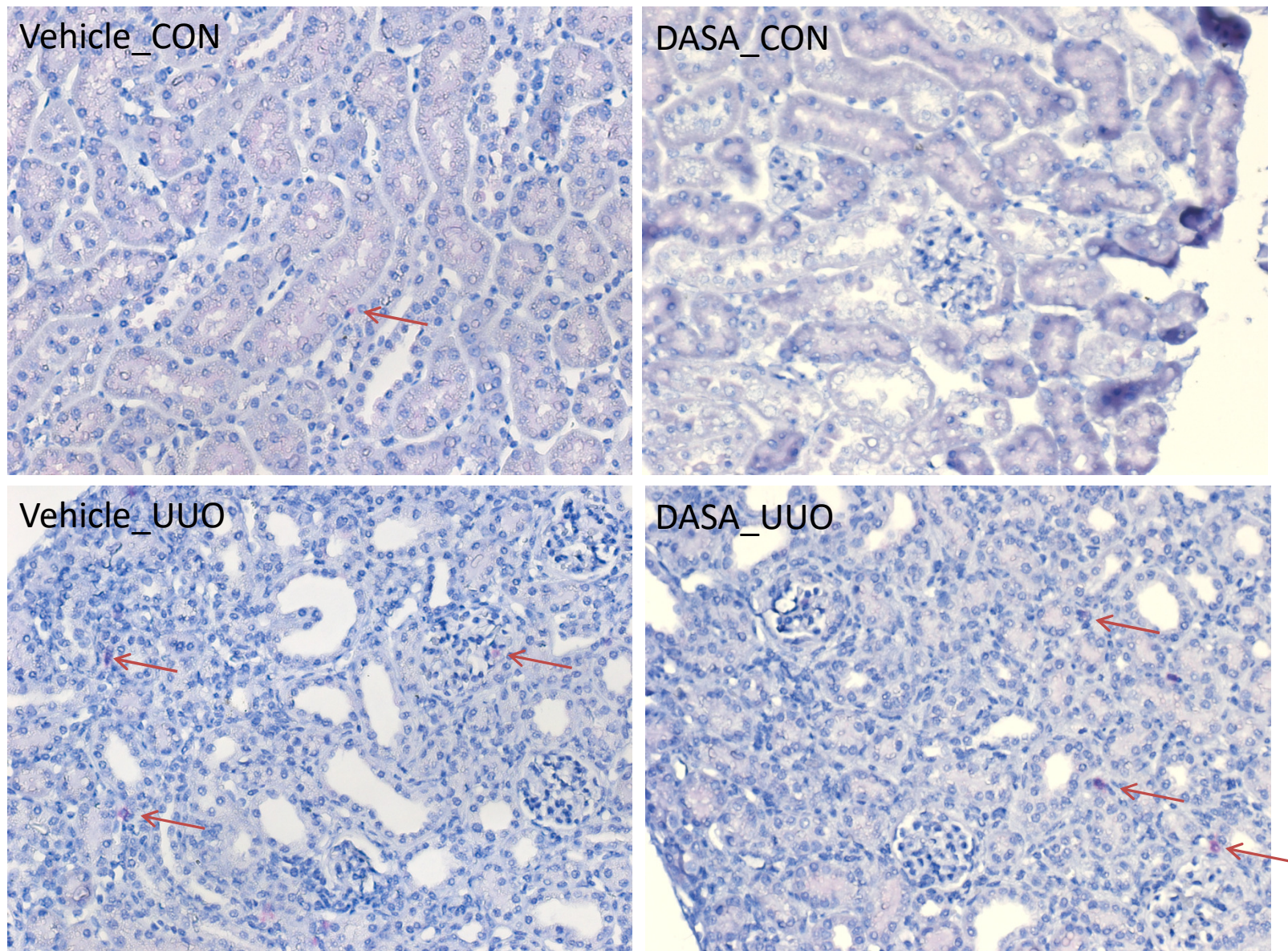




Figure S10. Immunohistochemistry for Mac2 shown Macrophage cell infiltration in UUO kidney

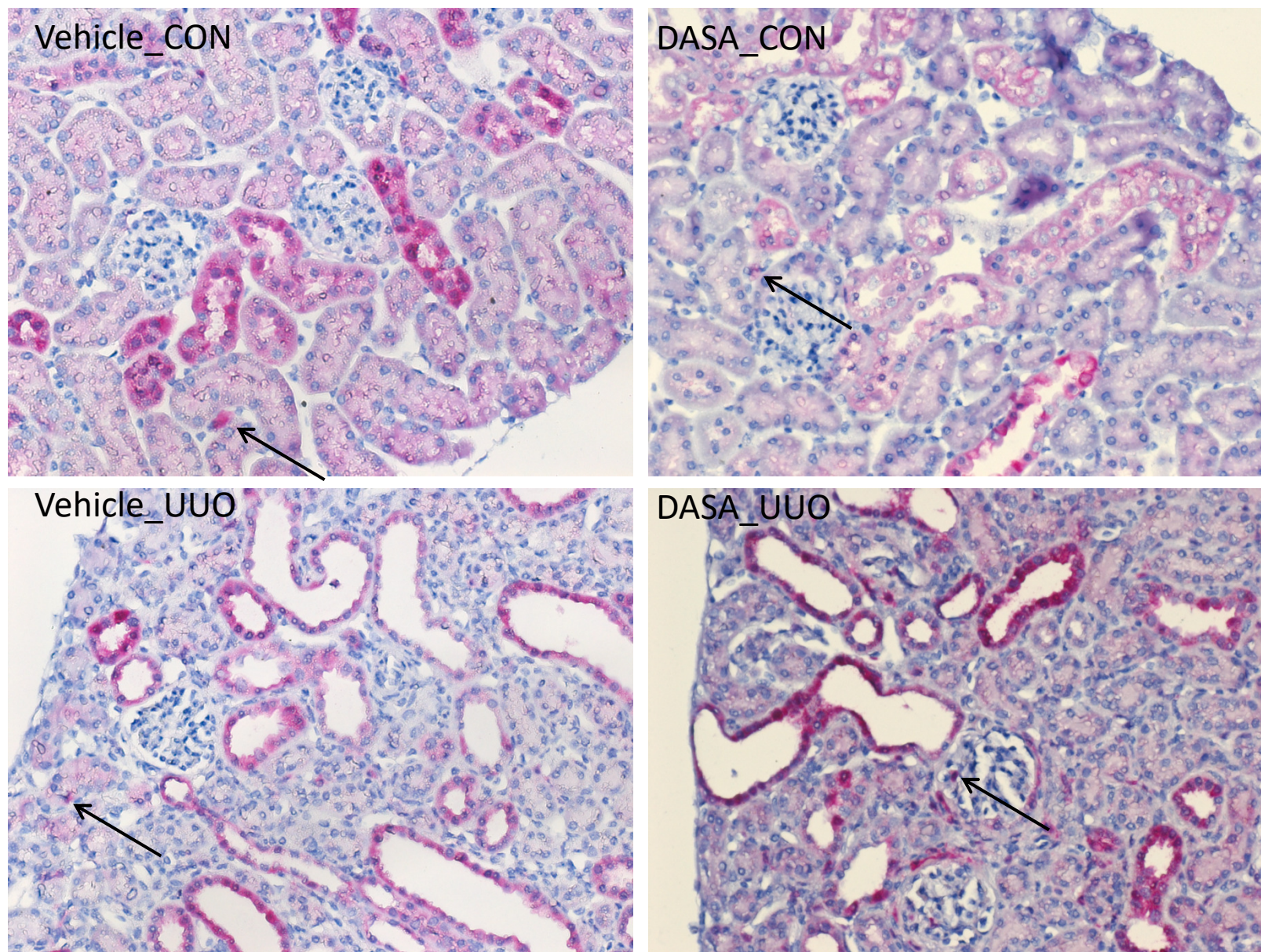
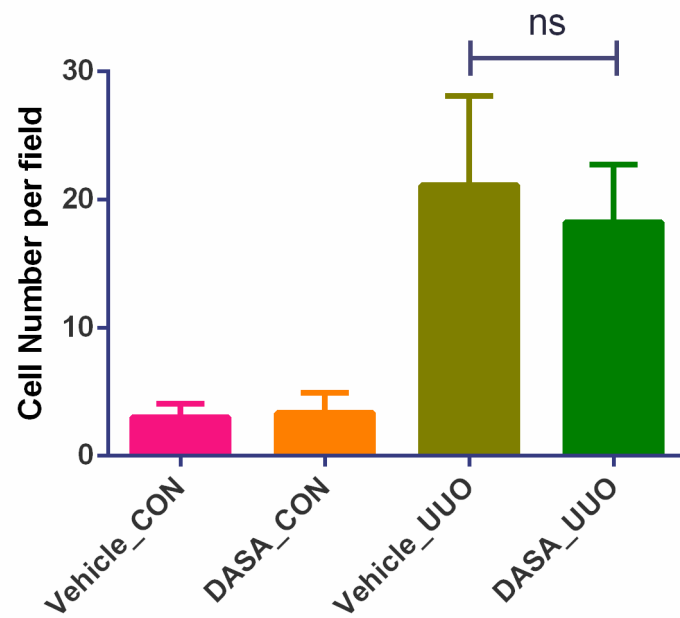


Figure S11. Quantification of T cells(A) and macrophage cells(B) per field in control and UUO kidney (n=3)

A



B

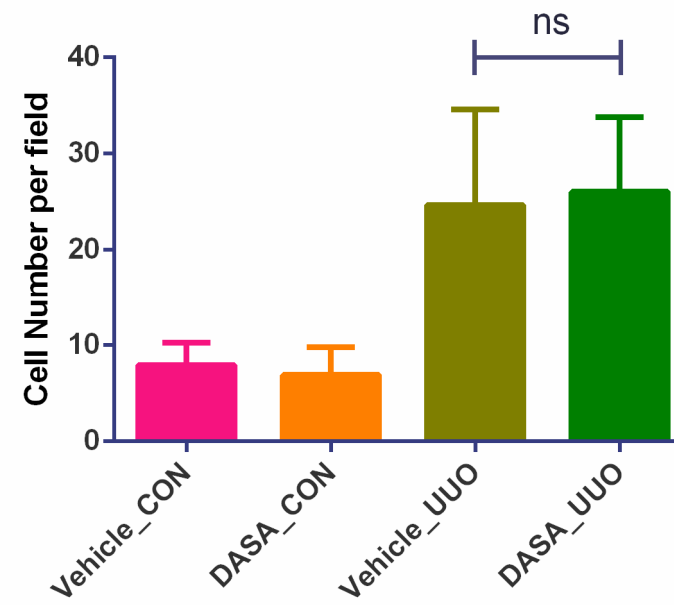




Figure S12. Immunohistochemistry for CD3 shown T cell infiltration in lupus kidney

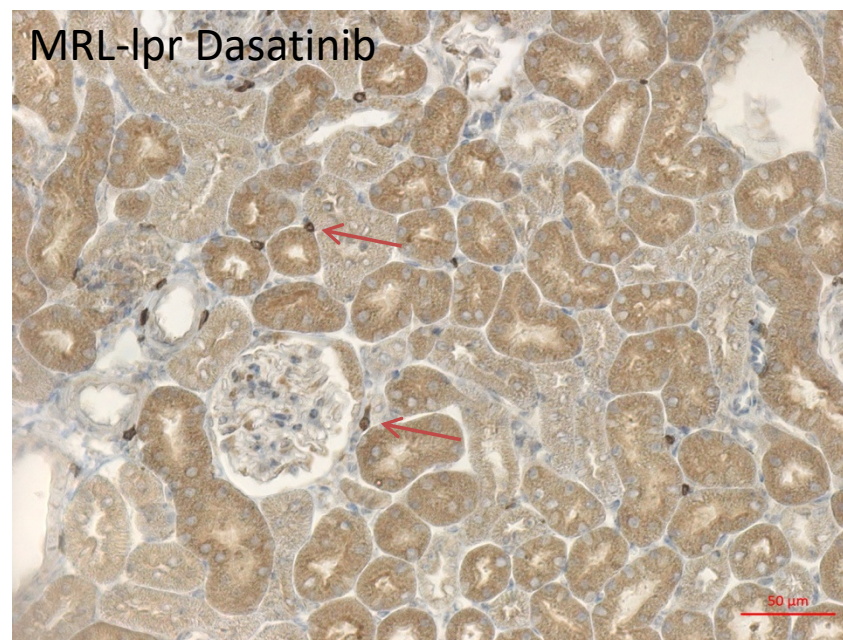
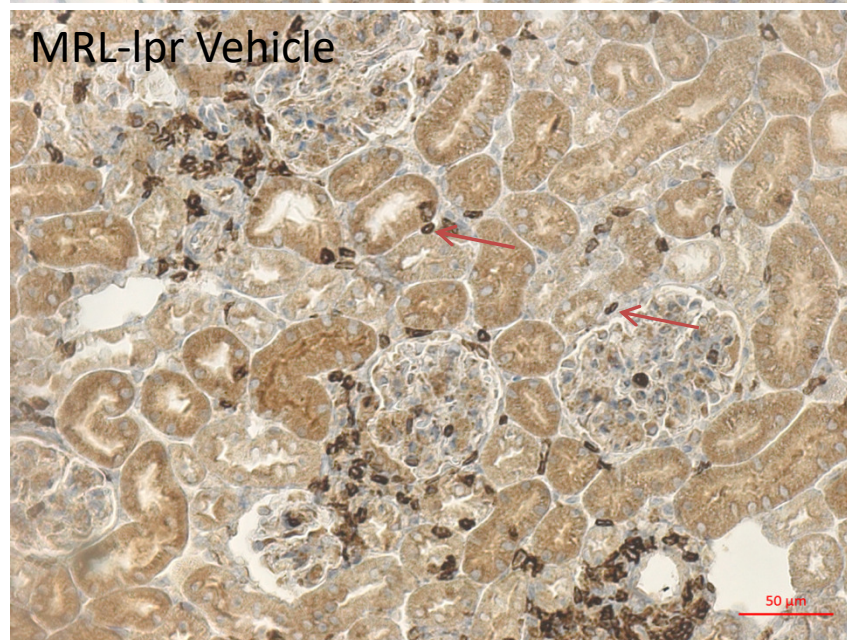
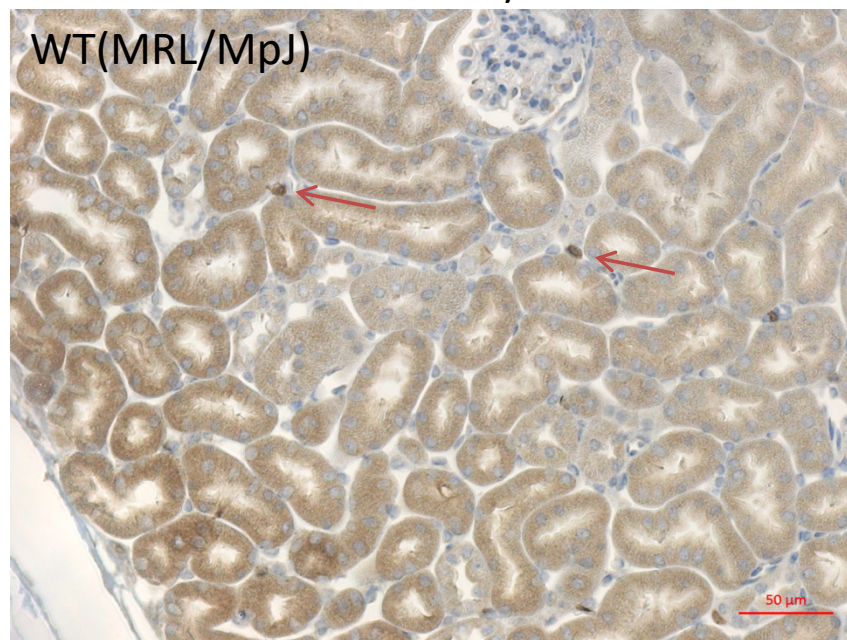




Figure S13. Immunohistochemistry for CD45R shown very few B cell in control and lupus kidney

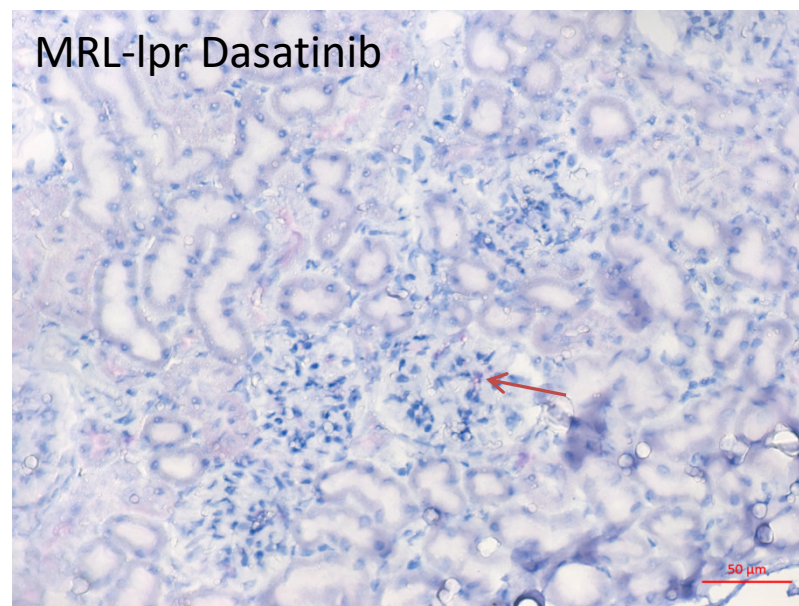
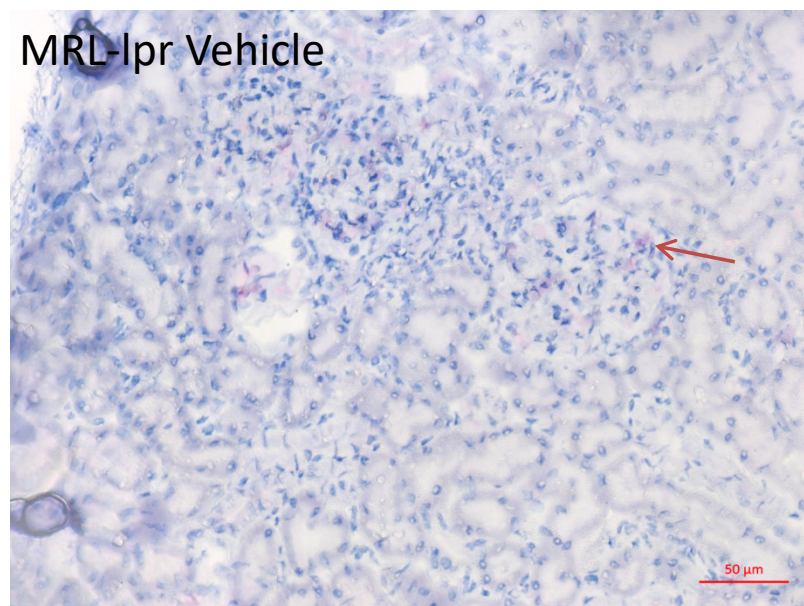
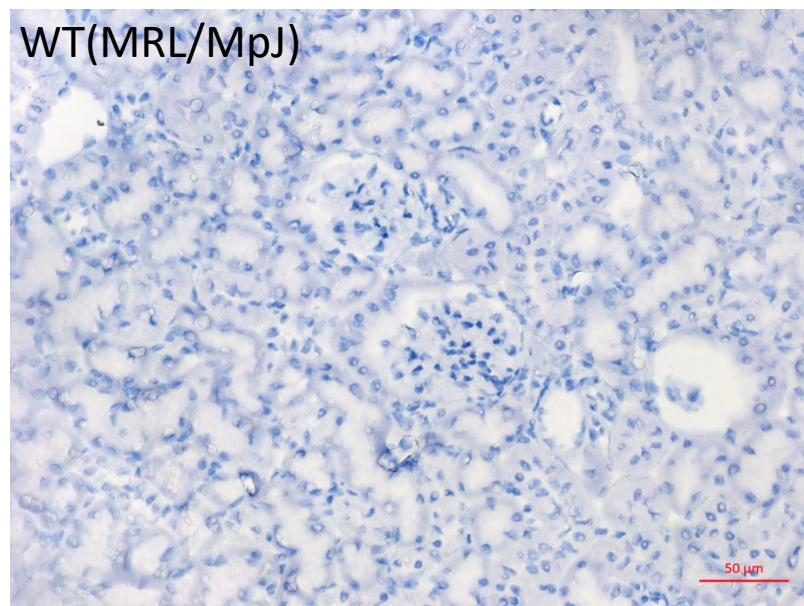




Figure S14. Immunohistochemistry for Mac2 Macrophage cell infiltration in lupus kidney

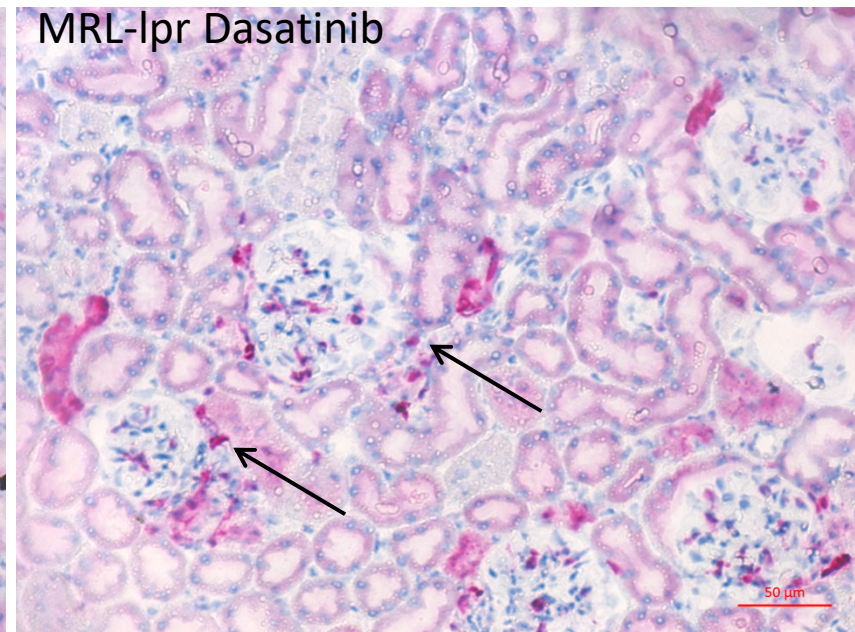
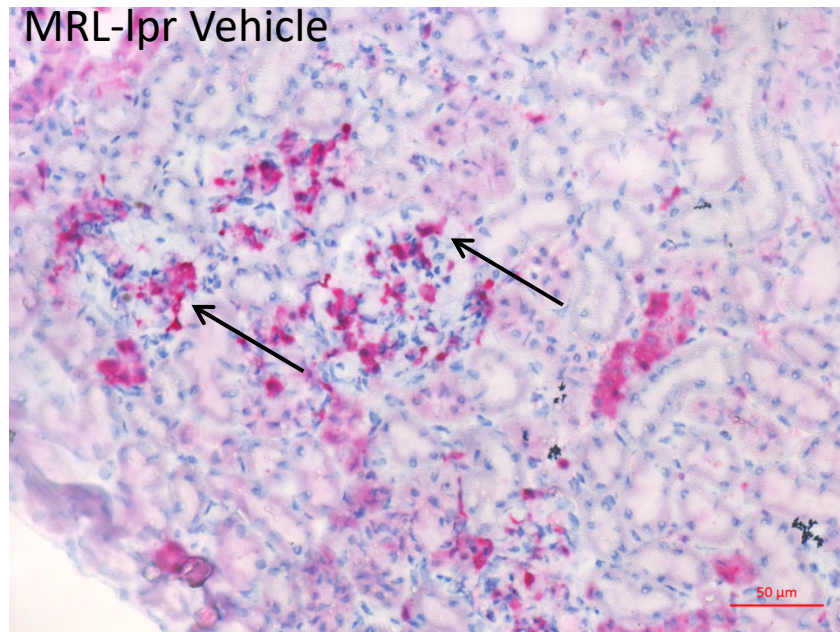
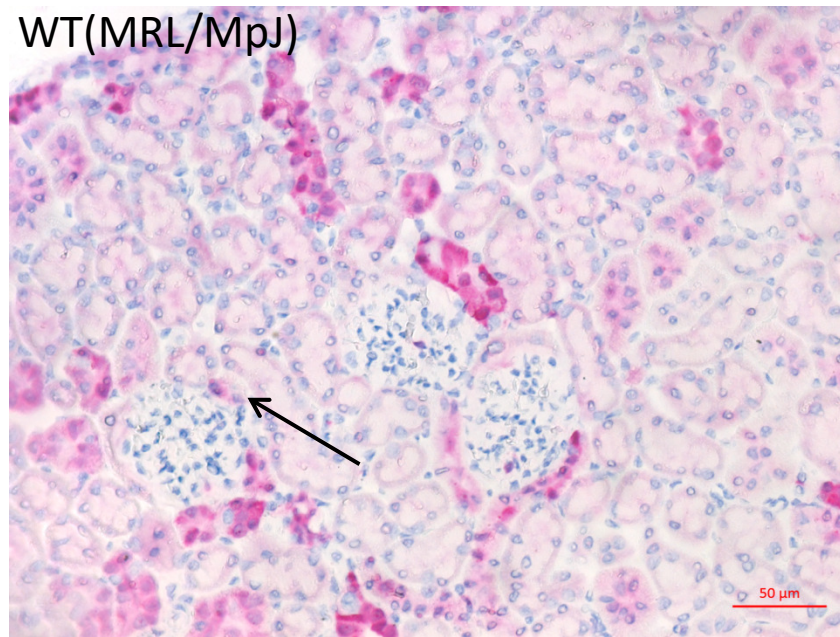


Figure S15. Quantification of T cells(A) and macrophage cells(B) per field in control and lupus kidney(\*\*P<0.001, n=3)

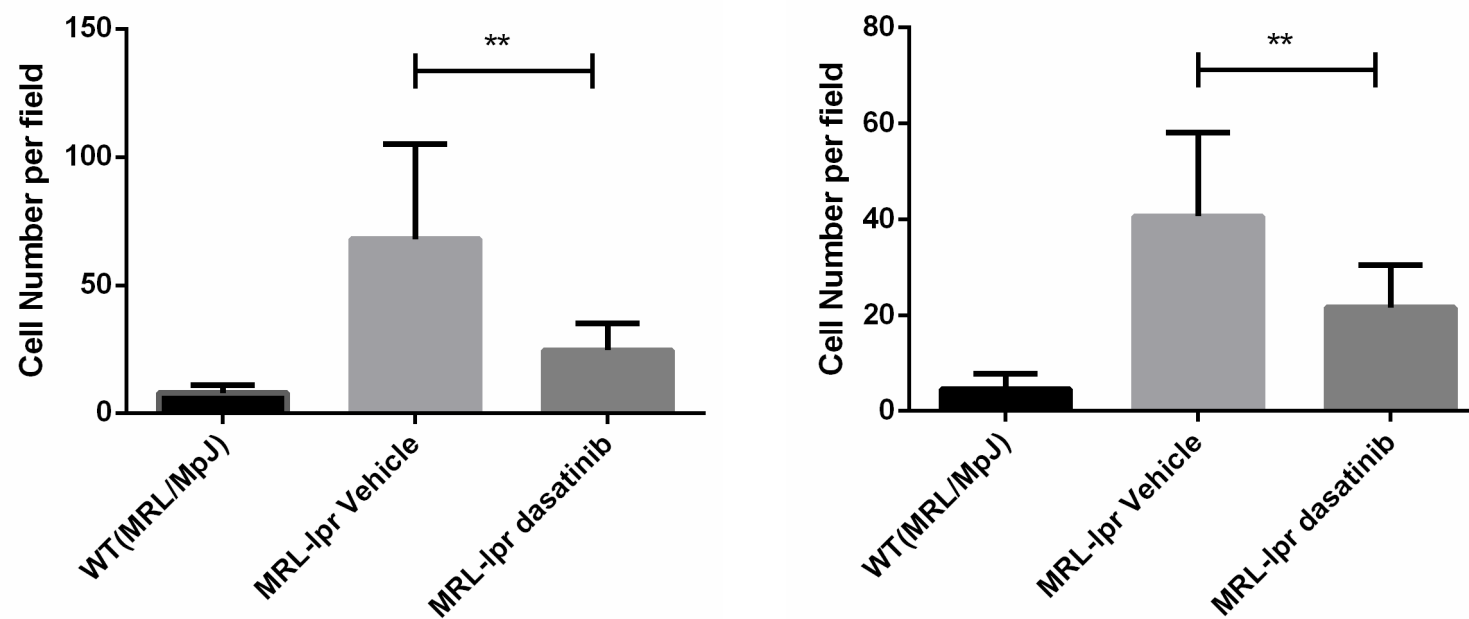
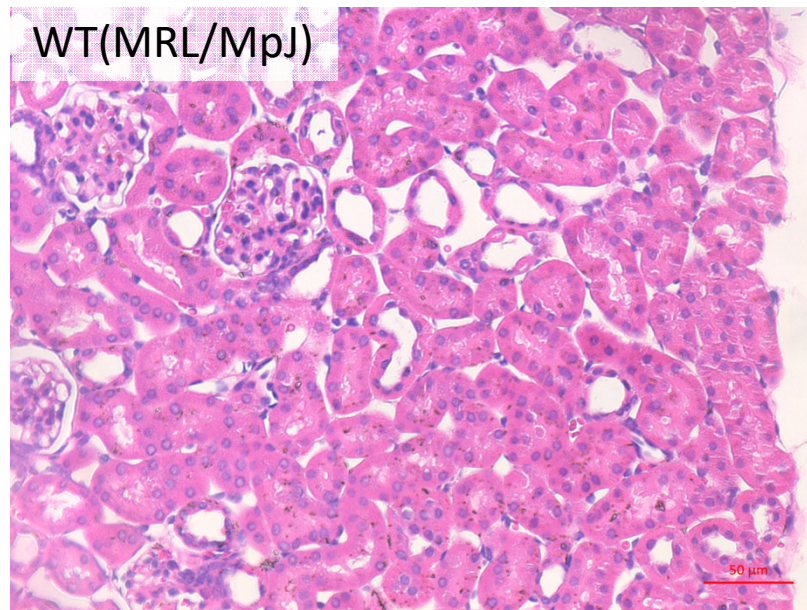




Figure S16. H&E staining for lupus kidney section(A) and quantification of lupus nephritis(B-F)(n=4)



A

