

# Supplementary Material for

## A Novel Rabbit Anti-Myoglobin Monoclonal Antibody's Potential Application in Rhabdomyolysis Associated Acute Kidney Injury

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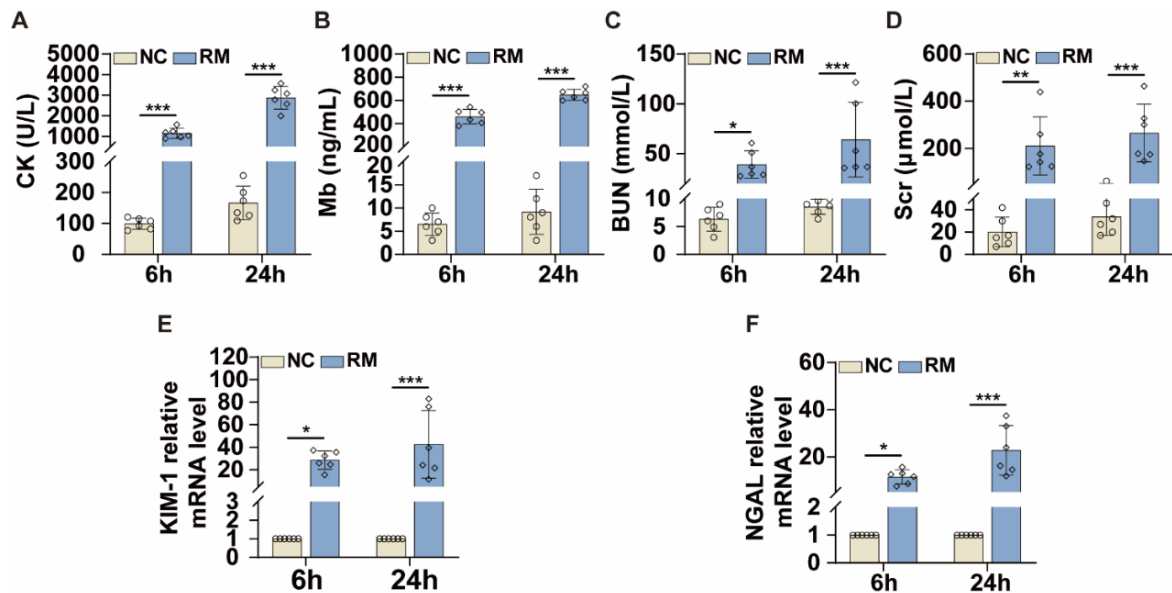
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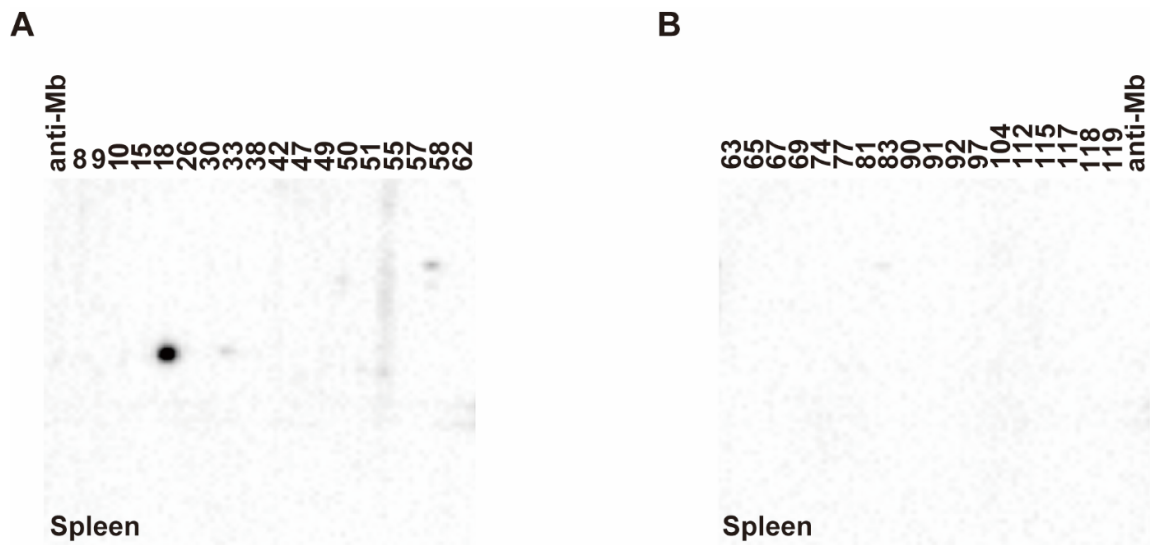
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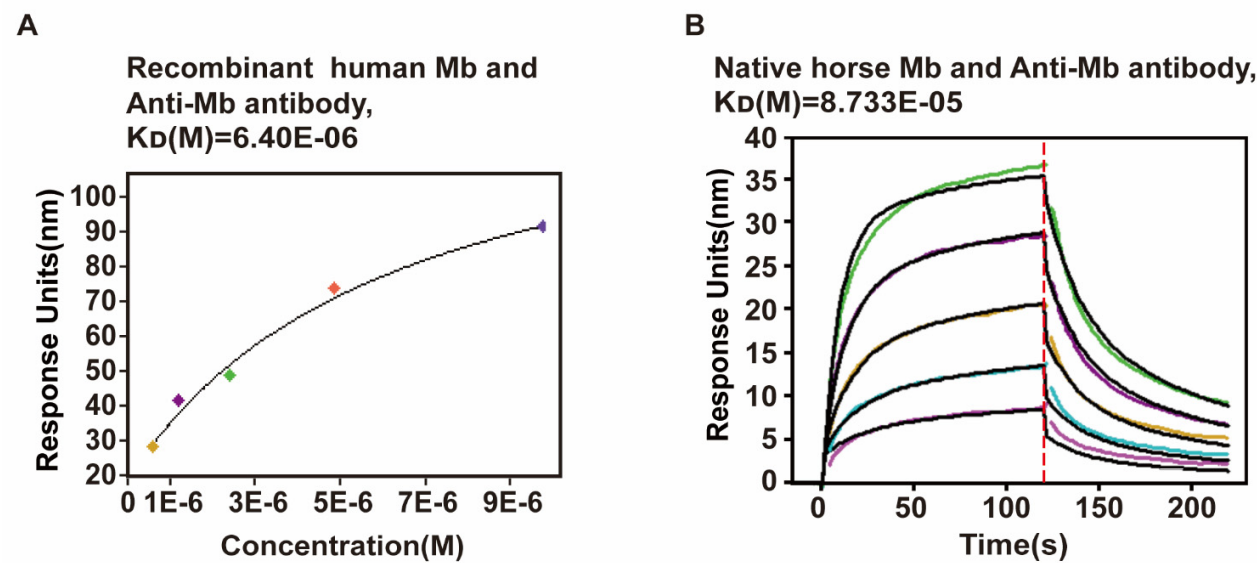
### 1 Supplementary Figures



**Figure S1.** Validation of successful establishment of the mice RM-AKI model. (A-D) Biochemical indicator detection of CK, Mb, BUN and Scr concentration in the serum. (E-F) qPCR analysis the mRNA expression level changes of KIM-1 and NGAL in the kidney of RM-AKI mice in 6h and 24h, respectively ( $n = 6$ ; \*,  $p < 0.05$ ; \*\*,  $p < 0.01$ ; \*\*\*,  $p < 0.001$ ).



**Figure S2.** Negative exclude screening of hybridoma-derived rabbit anti-Mb monoclonal antibody. (A-B) WB analysis the reactivity of 36 positive hybridoma supernatants (screening from Fig. 3A-D) with rat spleen tissue protein. Commercial anti-Mb antibody as control.



**Figure S3.** SPR sensorgrams of recombinant anti-Mb monoclonal antibody to the recombinant human Mb protein (A) and native horse Mb protein (B) immobilized sensor chip. The raw data is shown as a colourful line, the calculated fit is shown as a black line.

2 Supplementary Tables

**Table S1. Binding kinetic information form Fortebio detection.**

| Sample ID | Conc. (nM) | $K_D$ (M)             | $K_D$ Error            | $K_{on}(1/Ms)$     | $K_{on}$ Error     | $K_{dis}(1/s)$        | Full $R^2$ |
|-----------|------------|-----------------------|------------------------|--------------------|--------------------|-----------------------|------------|
| Number 9  | 534.8      | $1.60 \times 10^{-6}$ | $4.35 \times 10^{-11}$ | $2.52 \times 10^4$ | $5.06 \times 10^1$ | $4.04 \times 10^{-4}$ | 0.9979     |

|                   |       |                       |                        |                    |                    |                       |        |
|-------------------|-------|-----------------------|------------------------|--------------------|--------------------|-----------------------|--------|
| <b>Number 42</b>  | 534.8 | $3.44 \times 10^{-8}$ | $1.09 \times 10^{-10}$ | $2.84 \times 10^4$ | $8.16 \times 10^1$ | $9.75 \times 10^{-4}$ | 0.9983 |
| <b>Number 49</b>  | 534.8 | $1.36 \times 10^{-7}$ | $1.63 \times 10^{-8}$  | $7.54 \times 10^4$ | $8.55 \times 10^3$ | $1.02 \times 10^{-2}$ | 0.884  |
| <b>Number 81</b>  | 534.8 | $5.16 \times 10^{-8}$ | $1.29 \times 10^{-9}$  | $3.46 \times 10^4$ | $8.19 \times 10^2$ | $1.79 \times 10^{-3}$ | 0.9488 |
| <b>Number 115</b> | 534.8 | $4.53 \times 10^{-8}$ | $1.95 \times 10^{-10}$ | $2.78 \times 10^4$ | $1.11 \times 10^2$ | $1.26 \times 10^{-3}$ | 0.9976 |
| <b>Number 118</b> | 534.8 | $2.50 \times 10^{-7}$ | $1.13 \times 10^{-8}$  | $2.45 \times 10^4$ | $1.05 \times 10^3$ | $6.12 \times 10^{-3}$ | 0.964  |

**Table S2. Binding kinetic information form SPR detection.**

| <b>Sample</b>   | <b>K<sub>D</sub> (M)</b> | <b>K<sub>on</sub> (1/Ms)</b> | <b>K<sub>off</sub> (1/s)</b> | <b>R<sub>max</sub> (RU)</b> |
|-----------------|--------------------------|------------------------------|------------------------------|-----------------------------|
| <b>H: L=1:1</b> | $5.94 \times 10^{-9}$    | $5.00 \times 10^4$           | $2.97 \times 10^{-4}$        | 0.9979                      |
| <b>H: L=1:2</b> | $1.21 \times 10^{-12}$   | $1.66 \times 10^5$           | $2.01 \times 10^{-7}$        | 0.0532                      |
| <b>H: L=1:3</b> | $7.12 \times 10^{-10}$   | $1.63 \times 10^5$           | $1.16 \times 10^{-4}$        | 0.0473                      |
| <b>H: L=1:4</b> | $1.17 \times 10^{-9}$    | $2.11 \times 10^5$           | $2.46 \times 10^{-4}$        | 0.0686                      |

**Table S3. The list of primers used in this study.**

| <b>Gene names</b> | <b>Forward primer (5'-3')</b> | <b>Reverse primer (5'-3')</b> |
|-------------------|-------------------------------|-------------------------------|
| <b>NGAL</b>       | TGGCCCTGAGTGTTCATGTG          | CTCTTGTAGCTCATAGATGGTGC       |
| <b>KIM-1</b>      | GGTCTGTATTGTTGCCGAGTGGAG      | GCCTTGTGGTTGTGGGTCTTGTAG      |
| <b>GAPDH</b>      | AGGTCGGTGTGAACGGATTTG         | TGTAGACCATGTAGTTGAGGTCA       |