S2 Table Altered proteins in the kidney homogenate among three groups on Day14

| Peak number\(^a\) | N:AA:AA+P (Ratio) | Protein name                                                                 | Molecular mass (Da) | GI number   |
|-------------------|--------------------|------------------------------------------------------------------------------|---------------------|-------------|
| **Glycolysis**    |                    |                                                                              |                     |             |
| 22                | 1:6.56\(^#\):0.87*| Fructose-bisphosphate aldolase B                                            | 39,548              | gi|15723268    |
| 22                | 1:6.56\(^#\):0.87*| Glyoxalase 1                                                                | 20,826              | gi|19354350    |
| 22                | 1:6.56\(^#\):0.87*| Pyruvate dehydrogenase E1 α 1                                              | 43,204              | gi|6679261     |
| 28                | 1:13.40\(^#\):4.06| M2-type pyruvate kinase                                                     | 57,878              | gi|1405933     |
| 32                | 1:39.00\(^#\):1.85*| Triosephosphate isomerase                                                   | 26,679              | gi|54855       |
| 32                | 1:39.00\(^#\):1.85*| Phosphoglycerate kinase                                                     | 59,716              | gi|6679937     |
| 32                | 1:39.00\(^#\):1.85*| Aldose reductase                                                           | 35,725              | gi|786001      |
| **Anti-oxidation**|                    |                                                                              |                     |             |
| 5                 | 1:0.74:1.28*       | Cu/Zn superoxide dismutase                                                 | 15,752              | gi|226471      |
| 14                | 1:0.62\(^#\):0.89  | Catalase                                                                    | 59,697              | gi|442444      |
| 18                | 1:2.22\(^#\):0.67*| Glutaredoxin                                                                | 9,285               | gi|31981830    |
| 20                | 1:0.53\(^#\):0.82*| Glutathione peroxidase                                                      | 22,276              | gi|2673845     |
| 21                | 1:0.47\(^#\):0.80*| Peroxiredoxin V                                                            | 13,309              | gi|7670411     |
| 32                | 1:39.00\(^#\):1.85*| Type II peroxiredoxin 1                                                    | 21,778              | gi|3603241     |
| **ATP synthesis** |                    |                                                                              |                     |             |
| 18                | 1:2.22\(^#\):0.67*| Ubiquinol-cytochrome c reductase                                           | 29,349              | gi|13385168    |
| 18                | 1:2.22\(^#\):0.67*| Electron transferring flavoprotein, alpha polypeptide                        | 35,018              | gi|13097375    |
| 18                | 1:2.22\(^#\):0.67*| Cytochrome c oxidase, subunit VIIa 2                                       | 9,285               | gi|31981830    |
| 22                | 1:6.56\(^#\):0.87*| Cytochrome b-5                                                             | 15,232              | gi|3385268     |
| 30                | 1:3.48:0.12*       | NADH-ubiquinone oxidoreductase B9 subunit                                   | 9,325               | gi|21539587    |
| 37                | 1:1.55:0.32*       | ATP synthase, H+ transporting, mitochondrial F1 complex, α subunit          | 59,716              | gi|6680748     |
| 37                | 1:1.55:0.32*       | Cytochrome b-c1 complex subunit 1                                          | 52,735              | gi|14548301    |
| **Beta oxidation**|                    |                                                                              |                     |             |
| 3                 | 1:0.71\(^#\):0.88  | Apolipoprotein A-I, isoform CRA b                                           | 28,517              | gi|148693731   |
| 28                | 1:13.40\(^#\):4.06| Medium-chain acyl-CoA dehydrogenase                                         | 46,452              | gi|6680618     |

(Cont.)
| Peak number<sup>a</sup> | N:AA:AA+P (Ratio)<sup>b</sup> | Protein name | Molecular mass (Da) | GI number  |
|------------------------|-------------------------------|--------------|---------------------|------------|
| **Apoptosis**          |                               |              |                     |            |
| 14                     | 1:0.62<sup>#</sup>:0.89      | Calreticulin | 47,965              | gi|6680836 |
| 32                     | 1:39.00<sup>*</sup>:1.85      | Heat shock protein 70 cognate | 70,793              | gi|309319 |
| **TCA cycle**          |                               |              |                     |            |
| 10                     | 1:1.33:1.30<sup>*</sup>       | Aconitase 2  | 85,410              | gi|18079339 |
| 37                     | 1:1.55:0.32<sup>*</sup>       | Fumarate hydratase 1 | 54,336              | gi|33859554 |
| 37                     | 1:1.55:0.32<sup>*</sup>       | GTP-specific succinyl-CoA synthetase beta subunit | 43,830 | gi|3766203 |
| **Other**              |                               |              |                     |            |
| 3                      | 1:0.71<sup>#</sup>:0.88      | Nicotinamide phosphoribosyltransferase | 55,346 | gi|10946948 |
| 4                      | 1:1.54:0.07<sup>*</sup>       | Y box-binbing protein | 35,822              | gi|55451 |
| 4                      | 1:1.54:0.07<sup>*</sup>       | Nucleolin    | 76,733              | gi|13529464 |
| 10                     | 1:1.33:1.30                   | Coflin 1     | 18,548              | gi|6680924 |
| 10                     | 1:1.33:1.30                   | AHNAK nucleoprotein isoform 1 | 603,866 | gi|61743961 |
| 14                     | 1:0.62<sup>#</sup>:0.89      | alpha-globin | 15,132              | gi|156257689 |
| 19                     | 1:0.52<sup>#</sup>:0.81      | haemoglobin beta-2 chain | 16,324              | gi|1183933 |
| 19                     | 1:0.52<sup>#</sup>:0.81      | S100 calcium binding protein G | 8,964 | gi|7106263 |
| 19                     | 1:0.52<sup>#</sup>:0.81      | Glyceraldehyde-3-phosphate dehydrogenase | 35,787 | gi|6679937 |
| 22                     | 1:6.56<sup>#</sup>:0.87      | Calmodulin – salmon | 16,696              | gi|71664 |
| 30                     | 1:3.48:0.12<sup>*</sup>       | Tu translation elongation | 49,477 | gi|27370092 |
| 32                     | 1:39.00<sup>#</sup>:1.85    | Glial fibrillary acidic protein | 48,437              | gi|51066 |

<sup>a</sup>The peak numbers correspond to those described in Figure 3. <sup>b</sup>The ratio of AA or AA+P groups to N group showed in the table, and the intensity of N group was regarded as “1”. <sup>#</sup>NCBI processed each consecutive sequence record as GI number, a simple series of digits. N, normal group; AA, aristolochic acid group; AA+P: AA+P: aristolochic acid+prednisolone. *p < 0.05, significantly different from AA group; # p < 0.05, significantly different from N group.