

Table S1 The histopathology scoring criteria

Pathological	Classification	Describe	Score
Tubulointerstitial and glomerular lesions	No damage	No glomerular injury, no interstitial infiltration	0
	Mild	Mild expansion of the glomerular and mild renal tubular injury (involvement of less than 10% of the cortex)	1
	Moderate	Moderate glomerulonephritis with extensive sclerosis and cell necrosis (involvement of 10-25% of the cortex)	2
	Severe	Severe glomerulonephritis with large area of cell necrosis (involvement of 25-50% of the cortex)	3
	Very severe	Very severe glomerulonephritis (involvement of 50-75% of the cortex)	4
	Extensive damage	Extensive damage of glomerulus and necrosis (involvement of more than 75% of the cortex)	5

Table S2 Primer sequence of the target genes for RT-PCR analysis

Target gene	forward primer (5' to 3')	reverse primer (5' to 3')
<i>TNF-α</i>	GCTCCCTCTCATCAGTTCCA	GCTTGGTGGTTTGCTACGAC
<i>Il-β</i>	GCCAACAAGTGGTATTCTCCA	TGCCGTCTTTCATCACACAG
<i>Il-6</i>	AGTTGCCTTCTTGGGACTGA	CAGAATTGCCATTGCACAAC
<i>NF-κB</i>	GAGGCATGTTCGGTAGTGGC	TGCAATCCCACCGTAAGCAG
<i>S100a9</i>	TCAAAGAGCTGGTGCGAAAA	AACTCCTCGAAGCTCAGCTG
<i>Hk3</i>	TGTTGTGTATTTATTACGGGAAGCC	ACATTCCGGAGTTCTTCCATATAGC
<i>Casp-3</i>	GGATTGAGACGGACAGTG	TTCGCCAGGAATAGTAACC
<i>Bax</i>	CAAGAAGCTGAGCGAGTGTCT	GGTTCTGATCAGCTCGGGCAC
<i>GAPDH</i>	AGTGCCAGCCTCGTCTCATA	GATGGTGATGGGTTTCCCGT

Table S3 Metabolic pathways of differential metabolites in FGL-vs-GLS group

Pathway name	Raw p	Impact	UP	Down
Galactose metabolism	0.49471	0.70379	Stachyose Galactose 1-phosphate	Raffinose Glucose 1-phosphate
Arginine and proline metabolism	0.53133	0.63238	Hydroxyproline, Ornithine L-Arginine, L-Glutamic acid L-Proline	4-Guanidinobutanoate
Valine, leucine and isoleucine biosynthesis	0.59176	0.52466	L-Valine L-Isoleucine L-Leucine	

Glycine, serine and threonine metabolism	0.66826	0.40308	L-Serine, Glycine L-Threonine, L-Homoserine 5-Aminolevulinic acid	
Valine, leucine and isoleucine degradation	0.68725	0.37506	L-Valine L-Isoleucine L-Leucine	
Pentose and glucuronate interconversions	0.75517	0.28081	D-Xylitol	Glucose 1-phosphate
Tyrosine metabolism	0.79814	0.22547	L-Tyrosine	3,4-Dihydroxymandelate 3,4-Dihydroxyphenylacetaldehyde
Lysine biosynthesis	0.79814	0.22547	L-Homoserine L-Lysine	Amino adipic acid

Phenylalanine metabolism	0.80969	0.2111	L-Phenylalanine	
Fructose and mannose metabolism	0.90241	0.10268		Sorbitol Mannose 6-phosphate
Amino sugar and nucleotide sugar metabolism	0.90981	0.09453	Galactose 1-phosphate	Glucose 1-phosphate Mannose 6-phosphate
Pentose phosphate pathway	0.91954	0.083883	D-Ribose	Glucose 1-phosphate
Starch and sucrose metabolism	0.91954	0.08388		D-Maltose Glucose 1-phosphate
Cysteine and methionine metabolism	0.9414	0.06039	5'-Methylthioadenosine L-Serine L-Methionine L-Homoserine	

Alanine, aspartate and glutamate metabolism	0.94569	0.05584	L-Glutamine L-Glutamic acid	
Phenylalanine, tyrosine and tryptophan biosynthesis	0.96365	0.03703	L-Tyrosine L-Phenylalanine	
Pantothenate and CoA biosynthesis	0.97796	0.02228	L-Valine	
Butanoate metabolism	0.98269	0.01747	L-Glutamic acid	
Citrate cycle	0.99162	0.00842	cis-Aconitic acid	
Glycolysis or Gluconeogenesis	0.99683	0.00317		Glucose 1-phosphate
Tryptophan metabolism	0.99848	0.00153		3-Hydroxyanthranilic acid
Fatty acid metabolism	0.99881	0.00119		Palmitic acid
Biosynthesis of unsaturated fatty	0.99952	0.00048		Palmitic acid

acids				Stearic acid
Fatty acid biosynthesis	0.99987	0.00013		Palmitic acid

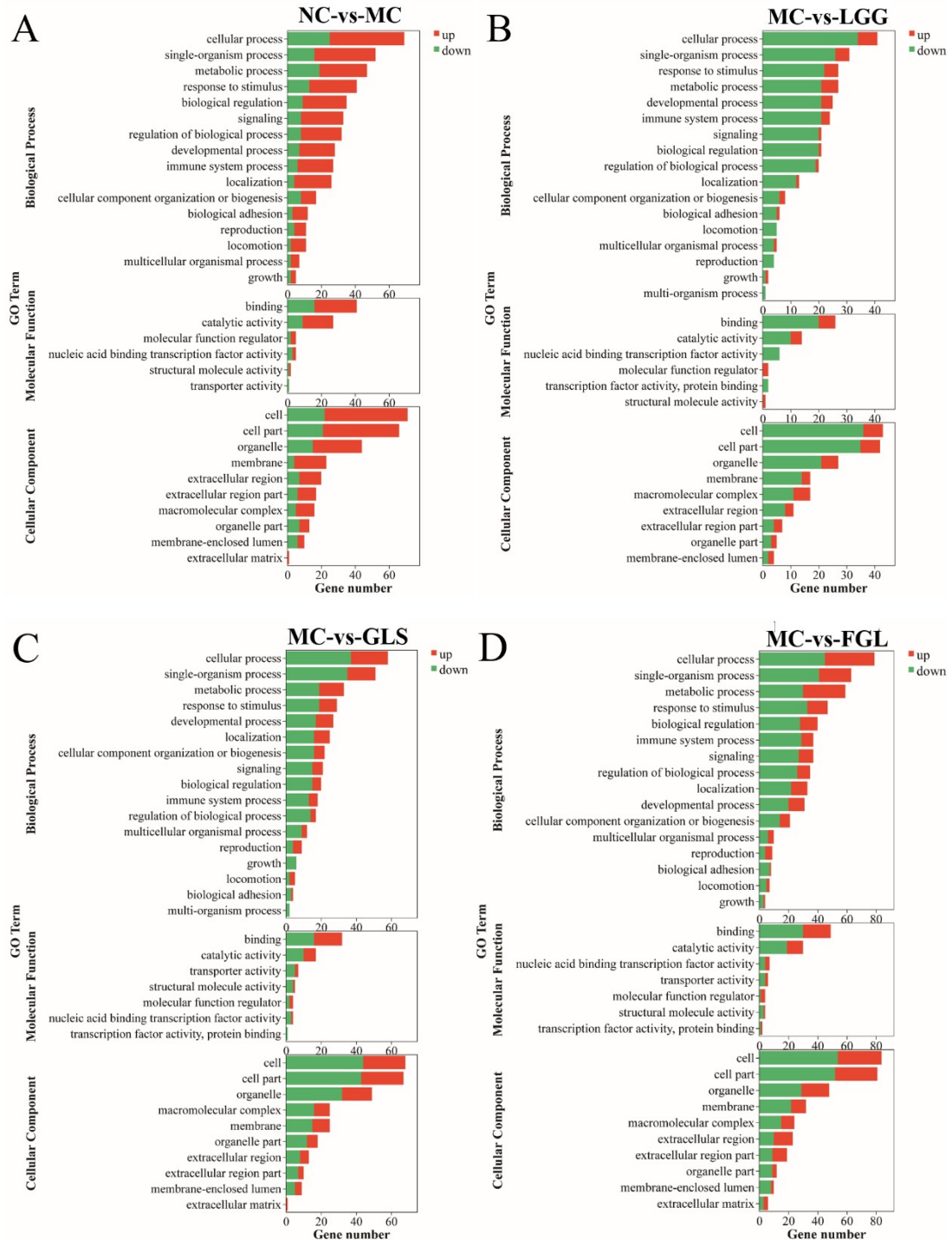


Fig. S1. Gene Ontology analysis of differentially expressed genes in the kidney tissue. (A) NC-vs-MC: normal control group versus model control group; (B) MC-vs-LGG: model control group versus *Lactobacillus rhamnosus* intervention group; (C) MC-vs-GLS: model control group versus ground *Ganoderma lucidum* slice powder mixed with water group; (D) MC-vs-FGL: model control group versus *Lactobacillus*

rhamnoses-fermented *G. lucidum* solution.