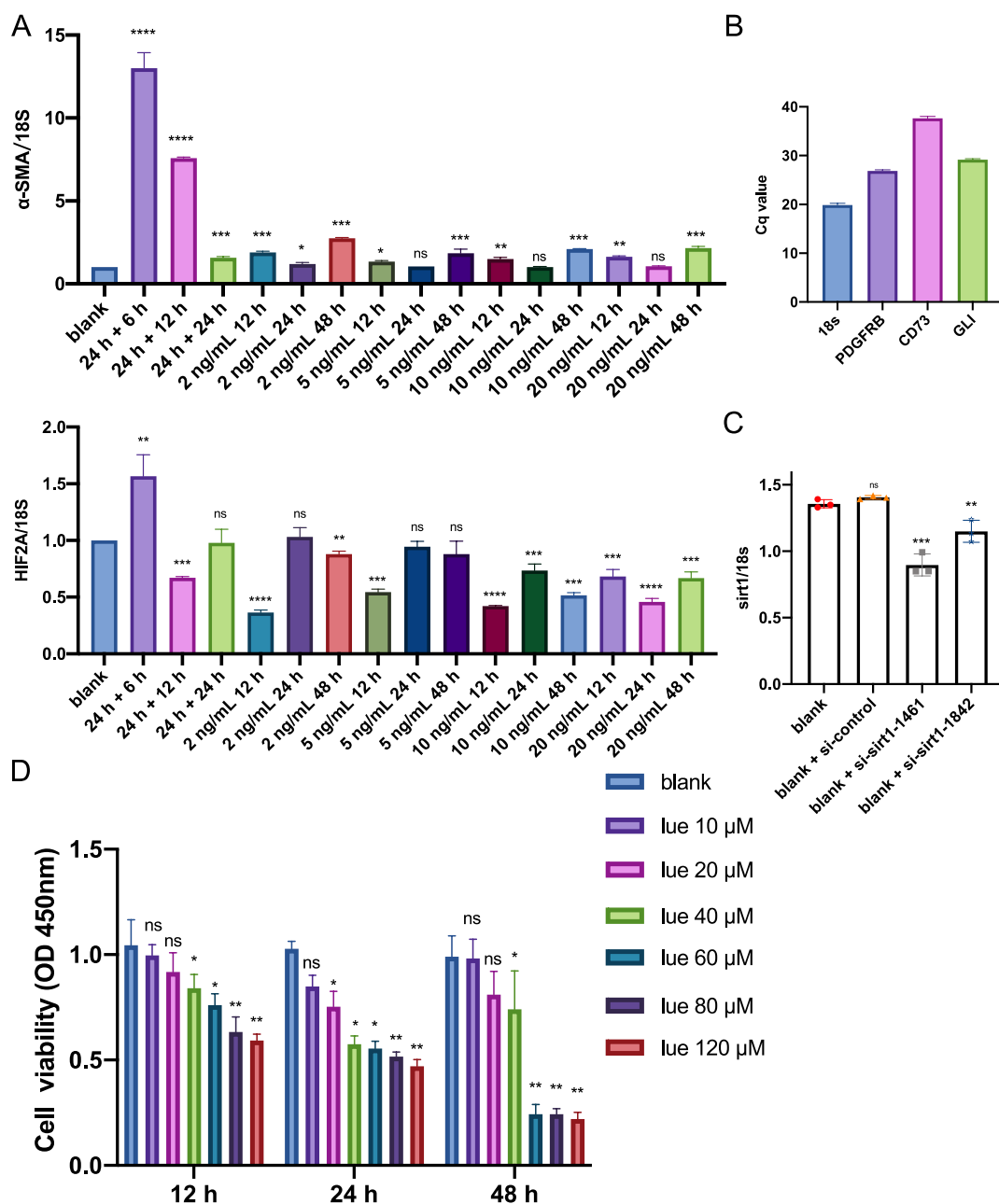**Figure Legends**

Fig. S1 A RT-qPCR detection of *α-SMA* and *HIF2A* mRNA expression in hypoxia-reoxygenation and TGFβ1-induced NRK49F myofibrosis-induced renal anaemia model. B RT-qPCR method to identify the REPs properties of NRK-49F. C SIRT1-siRNA transfection efficiency was detected by RT-qPCR. * represents comparison with blank group, ns represents P > 0.05. D Proliferation and toxicity of luteolin on NRK49F. The Y axis represents the OD value of cell viability at wavelength = 450 nm by the microplate reader. n = 5, represents 5 replicate wells per group, * represents comparison with blank group, ns represents P > 0.05.
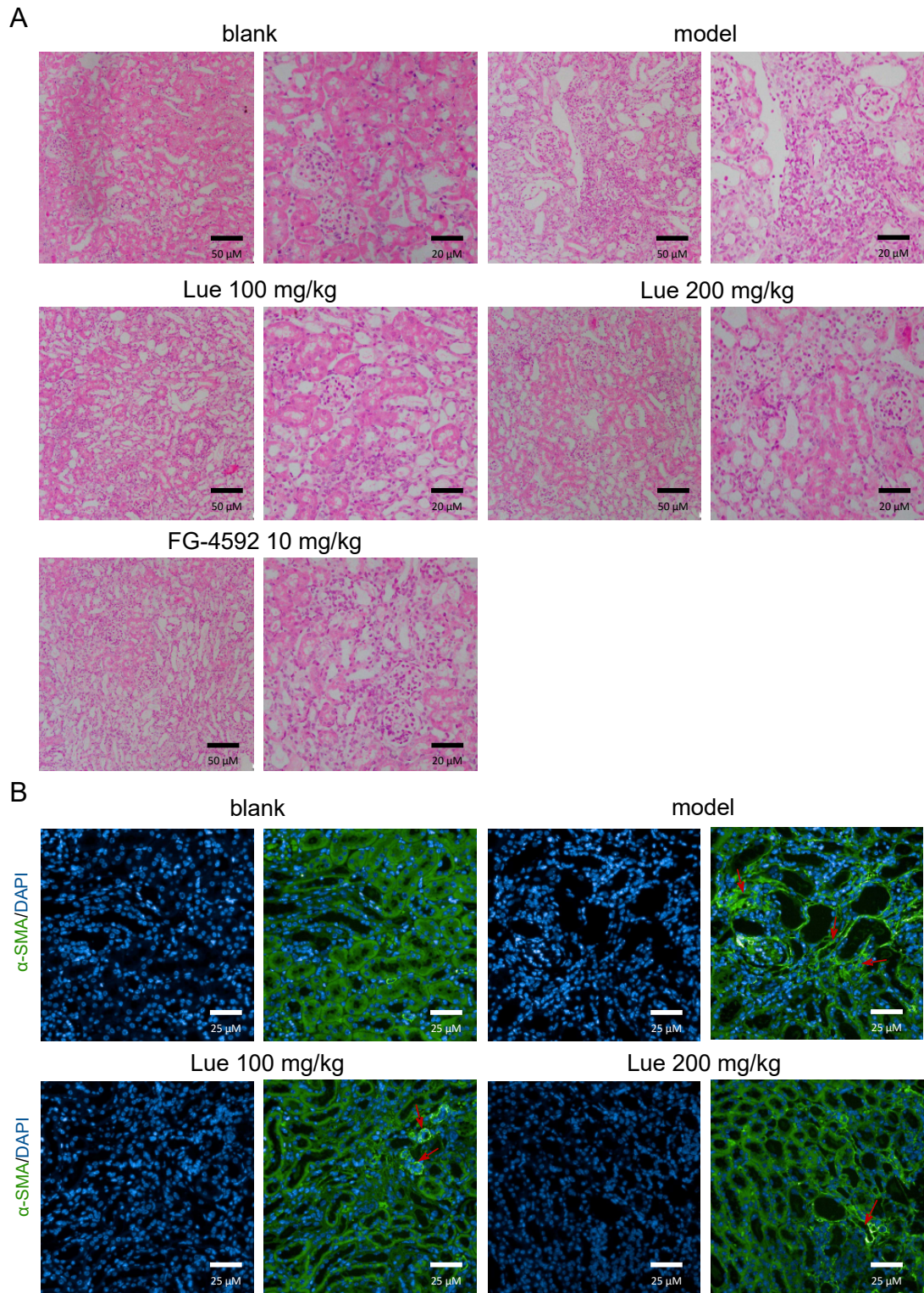
Fig. S2 A Kidney HE staining results of each group *in vivo*, Scale bar = 50 μM & 20 μM. B Immunofluorescence expression of α-SMA in kidney tissue of various groups of mice. Green fluorescence indicates α-SMA, blue fluorescence indicates the nucleus, and red arrows represent the site of α-SMA expression, Scale bar = 25 μM.

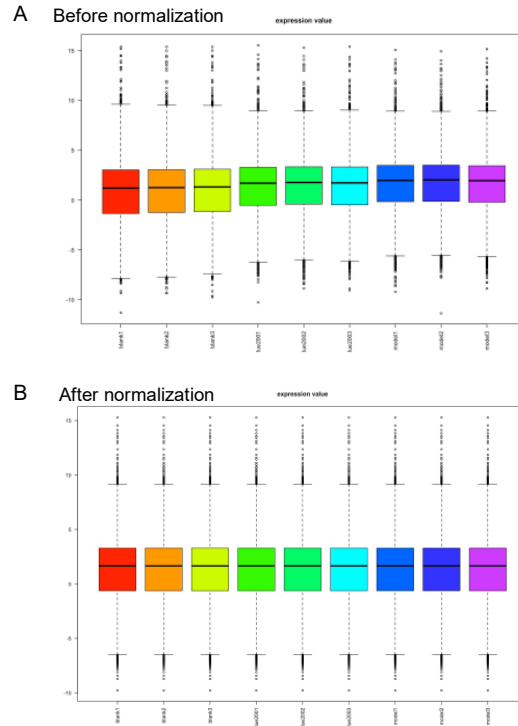**Fig. S3** Box plots of three groups of animal samples before and after normalization of FPKM data. A Box plots of three groups of samples before normalization; B Box plots of three groups of samples after normalization.
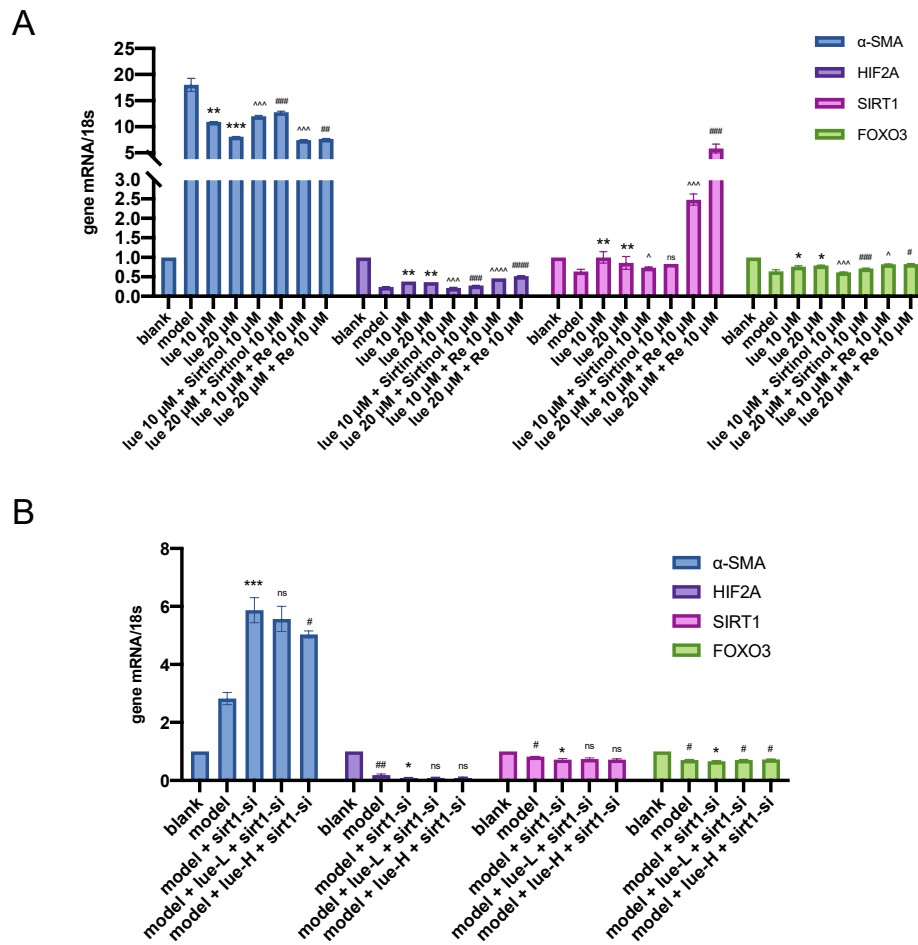
Fig. S4 A After administration of SIRT1 activator and inhibitor, *α-SMA*, *HIF2A*, *SIRT1* and *FOXO3* mRNA expression levels were measured by RT-qPCR in each group of cells. n= 3, [*] represents comparison with model group, [^] represents comparison with Lue 10 µM group, [#] represents comparison with Lue 20 µM group, [ns] represents P > 0.05. B After administration of SIRT1-siRNA intervention, *α-SMA*, *HIF2A*, *SIRT1* and *FOXO3* mRNA expression levels were measured by RT-qPCR in each group of cells. n = 3, [*] represents comparison with model group, [#] represents comparison with model + sirt1-si group, [ns] represents P > 0.05.

Table S1 RT-qPCR Primer Sequences.

Gene name	Forward sequence(5'to 3')	Reverse sequence (5' to 3')	Product size (bp)
18S	GTAACCCGTTGAACCCCATT	CCATCCAACGGTAGTAGCG	150
Mice EPO	TGGGAGCTCAGAAGGAATTGA	TCCACTGTGAGTGTTCGGAG	73
Mice HIF2A	TCCTTCGGACACATAAGCTCC	GACAGAAAGATCATGTCACCGT	148
Mice α-SMA	CCCAGACATCAGGGAGTAATGG	TCTATCGGATACTTCAGCGTCA	104
Mice Collagen I	TAAGGGTCCCCAATGGTGAGA	GGGTCCCTCGACTCCTACAT	203
Mice Fibronectin	ACAAGGTTCGGGAAGAGGTT	CCGTGTAAGGGTCAAAGCAT	93
Mice SIRT1	ATGACGCTGTGGCAGATTGTT	CCGCAAGGCGAGCATAGAT	202
Mice FOXO3	GCTAAGCAGGCCTCATCTCA	TTCCGTCAGTTTGAGGGTCT	92
Rat PDGFRB	GTCAATGTCCCTGTCCGTGT	GTGTGGGTGACAGTTTTCGC	157
Rat CD73	CTCTGCACCAAGTGTCGAGT	ATCCGTCCTTCAACTGCTGG	215
Rat Gli	TGAAGACACACCTTCGGTCG	TCGATGTCGTTTGGTCACGT	242
Rat EPO	TCACAATGGGCTGTGCAGAA	ACCCGAAGCAGTGAAGTGAG	259
Rat HIF2A	GATGCCTGACAAGACCGTCA	CCCTTTTGAGCTCCTGGAGG	207
Rat α-SMA	ACCATCGGGAATGAACGCTT	CTGTCAGCAATGCCTGGGTA	191
Rat Collagen I	CCCAGCGGTGGTTATGACTT	TCTCCGCTCTTCCAGTCAGA	245
Rat Fibronectin	TCCACCTGTACACGCTCAAC	AGGGGATCCAGGCTTCTCAT	188
Rat SIRT1	TATGTGCCTGTGCAGTGGAAG	GCTGTTGCAAAGGAACCATGAC	198
Rat FOXO3	CTCCCTGCGAGTGTCTATAACTTT	TACCTCGGCTCCTTCCCTTCA	219
Rat SIRT1-siRNA-1842	GCAGAUUAGUAAGCGUCUUTT	AAGACGCUUACUAAUCUGCTT	-
Rat SIRT1-siRNA-1461	CCCUGUAAAGCUUUCAGAATT	UUCUGAAAGCUUUACAGGGTT	-
control-siRNA	UUCUCCGAACGUGUCACGUTT	ACGUGACACGUUCGGAGAATT	-

Table S2 GO-BP and KEGG analysis results of differentially expressed genes in model group compared with blank group.

ID	Description	NES	p.adjust	qvalues
GO:0001837	epithelial to mesenchymal transition	-1.519249529	0.019241347	0.012953674
GO:0048762	mesenchymal cell differentiation	-1.470766065	0.023500184	0.015820812
GO:0010257	NADH dehydrogenase complex assembly	1.885553324	0.013724482	0.009239606
GO:0009060	aerobic respiration	1.824333874	0.014083269	0.009481149
GO:0038065	collagen-activated signaling	-1.733708223	0.009467815	0.006373929

	pathway			
GO:0030097	hemopoiesis	-2.340186288	0.009467815	0.006373929
GO:0032905	transforming growth factor beta1 production	-1.738118032	0.016448773	0.011073655
GO:0045445	myoblast differentiation	-1.762729176	0.009467815	0.006373929
GO:0048659	smooth muscle cell proliferation	-1.781186718	0.009467815	0.006373929
GO:0048144	fibroblast proliferation	-1.833216376	0.009467815	0.006373929
mmu04151	PI3K-Akt signaling pathway	-1.54744084	0.006770203	0.003498478
mmu04010	MAPK signaling pathway	-1.667391483	0.006770203	0.003498478
mmu04370	VEGF signaling pathway	-1.694635121	0.008911693	0.004605085
mmu04218	Cellular senescence	-1.707798709	0.006770203	0.003498478
mmu04630	JAK-STAT signaling pathway	-1.945581178	0.006770203	0.003498478
mmu04621	NOD-like receptor signaling pathway	-2.308817127	0.006770203	0.003498478
mmu04620	Toll-like receptor signaling pathway	-2.376118318	0.006770203	0.003498478
mmu04064	NF-kappa B signaling pathway	-2.416432	0.006770203	0.003498478
mmu04640	Hematopoietic cell lineage	-2.541799609	0.006770203	0.003498478

Description represents the name of this GO-ID; NES represents the normalized enrichment score; P.adjust represents the P value, which characterizes the confidence of the enrichment results; qvalues represent the q value, which is the P value after correction for multiple hypothesis testing.

Table S3 GO-BP and KEGG analysis results of differentially expressed genes in lue group compared with model group.

ID	Description	NES	p.adjust	qvalues
GO:0038065	collagen-activated signaling pathway	1.756224839	0.014870134	0.009072282
GO:1903706	regulation of hemopoiesis	2.376743276	0.00859736	0.005245257
GO:0001837	epithelial to mesenchymal transition	1.876447466	0.00859736	0.005245257
GO:0048762	mesenchymal cell differentiation	1.996126515	0.00859736	0.005245257
GO:0007568	aging	1.37444252	0.053107412	0.03240088
GO:0001666	response to hypoxia	1.313970554	0.072676395	0.044339934
GO:0070482	response to oxygen levels	1.266294441	0.132029266	0.080551175
GO:0032905	transforming growth factor beta1 production	1.632523628	0.030416142	0.018556916
GO:0048144	fibroblast proliferation	2.106615903	0.00859736	0.005245257
GO:0045445	myoblast differentiation	1.938722004	0.00859736	0.005245257
GO:0048659	smooth muscle cell proliferation	1.770546001	0.00859736	0.005245257
mmu04640	Hematopoietic cell lineage	2.506992483	0.006840796	0.003120363
mmu04064	NF-kappa B signaling pathway	2.369092984	0.006840796	0.003120363
mmu04620	Toll-like receptor signaling pathway	2.208029091	0.006840796	0.003120363
mmu04621	NOD-like receptor signaling pathway	2.004542887	0.006840796	0.003120363

mmu04010	MAPK signaling pathway	1.885521472	0.006840796	0.003120363
mmu04218	Cellular senescence	1.868056261	0.006840796	0.003120363
mmu04630	JAK-STAT signaling pathway	1.865676493	0.008506032	0.003879944
mmu04151	PI3K-Akt signaling pathway	1.828879397	0.006840796	0.003120363
mmu04370	VEGF signaling pathway	1.744036596	0.012254902	0.005589955

Description indicates the name of the KEGG pathway; NES represents the normalized enrichment score; P.adjust represents the P value, which characterizes the confidence of the enrichment results; qvalues represent the q value, which is the P value after correction for multiple hypothesis testing.

Table S4 Molecular Docking Binding Energy of Luteolin and SIRT1.

mode	lue-5btr-affinity (kcal/mol)	lue-4i5i-affinity (kcal/mol)
1	-7.9	-9.6
2	-7.8	-9.1
3	-7.7	-9
4	-7.6	-8.8
5	-7.6	-8.1
6	-7.5	-7.5
7	-7.5	-7.4
8	-7.5	-7.3
9	-7.4	-7.3
10	-7.4	-7.1
11	-7.4	-7.1
12	-7.4	-7.1
13	-7.4	-7
14	-7.3	-7
15	-7.3	-7
16	-7.3	-7
17	-7.2	-6.9
18	-7.2	-6.9
19	-7.1	-6.8
20	-7.1	-6.8