

Supplementary information

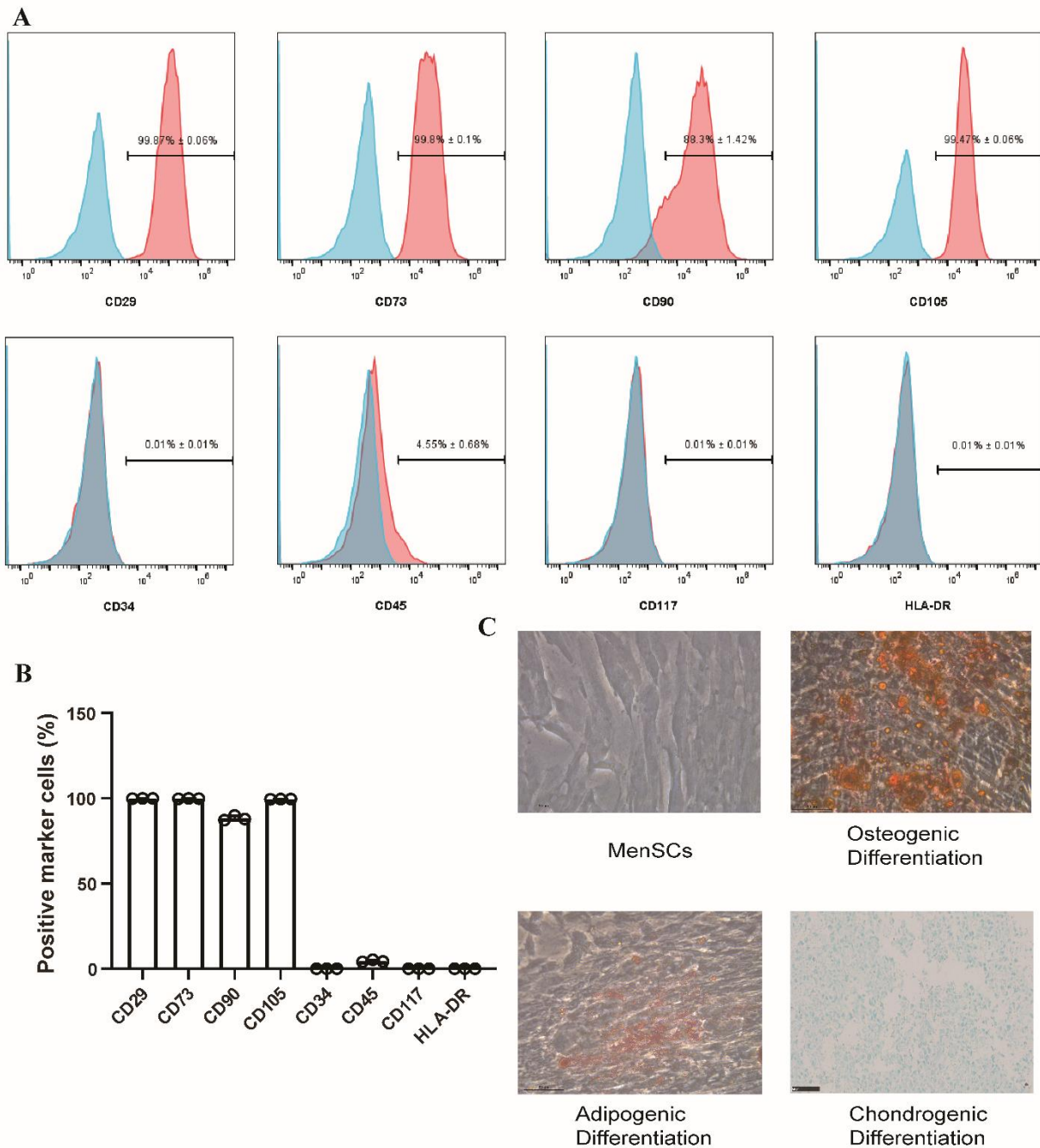


Fig. S1 Identification of MenSCs. A-B, Surface markers of MenSCs (five to seven passages; red) and isotype controls (blue) as indicated by flow cytometry (n = 3 per stain). C, Representative graphs showing the morphology of MenSCs and osteogenic, chondrogenic, and adipogenic differentiation potential. Scale bar 50 μ m (n = 3 per group).

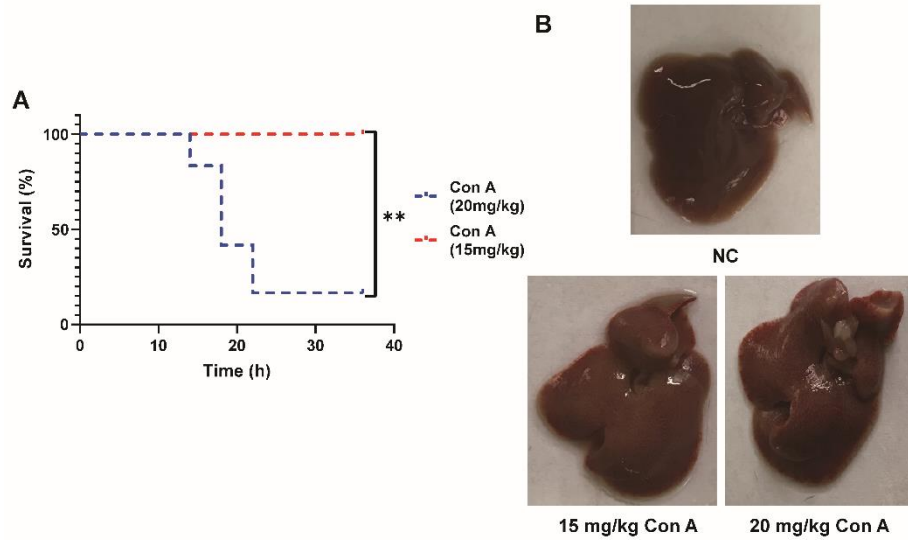


Fig. S2 Con A mouse model establishment. A, Survival rate of Con A (dosage: 20 mg/kg) compared with Con A (dosage: 15 mg/kg) ($n = 12$ in 20 mg/kg dosage and $n = 10$ in 15 mg/kg dosage, $**p < .01$). B, The liver morphology of Con A (dosage: 15 mg/kg), Con A (dosage: 20 mg/kg), and NC groups at 24 h.

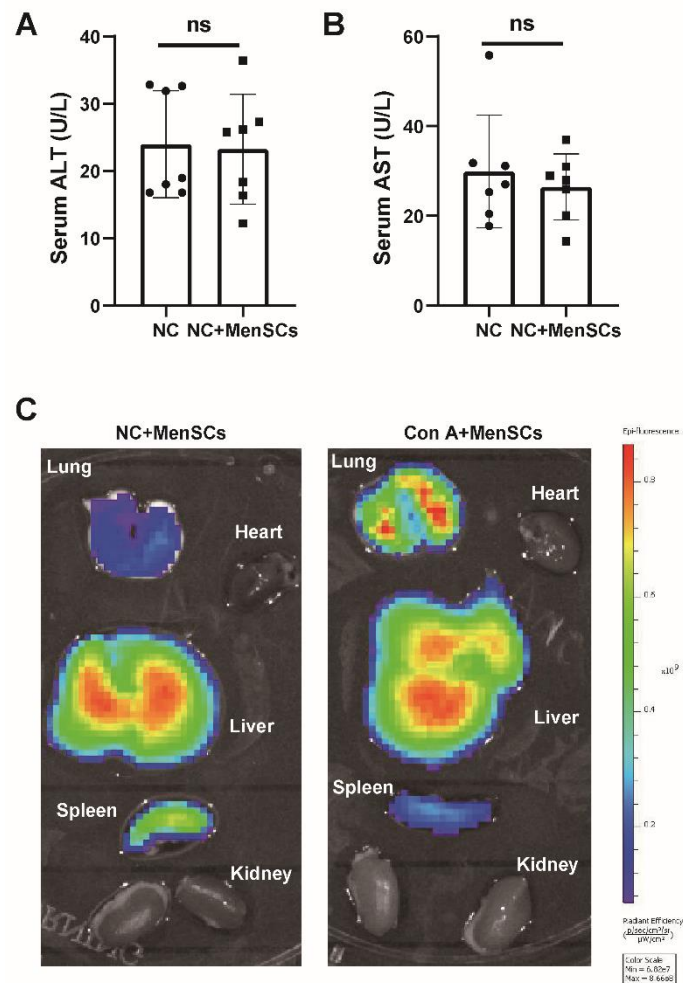


Fig. S3 MenSCs transplantation and distribution in vivo. A-B, Serum ALT and AST levels of NC+MenSCs and NC groups at

24 h (n = 7 per group). C, DiR-marked MenSCs distribution in vivo of NC and Con A groups after transplantation (n = 3 per group).

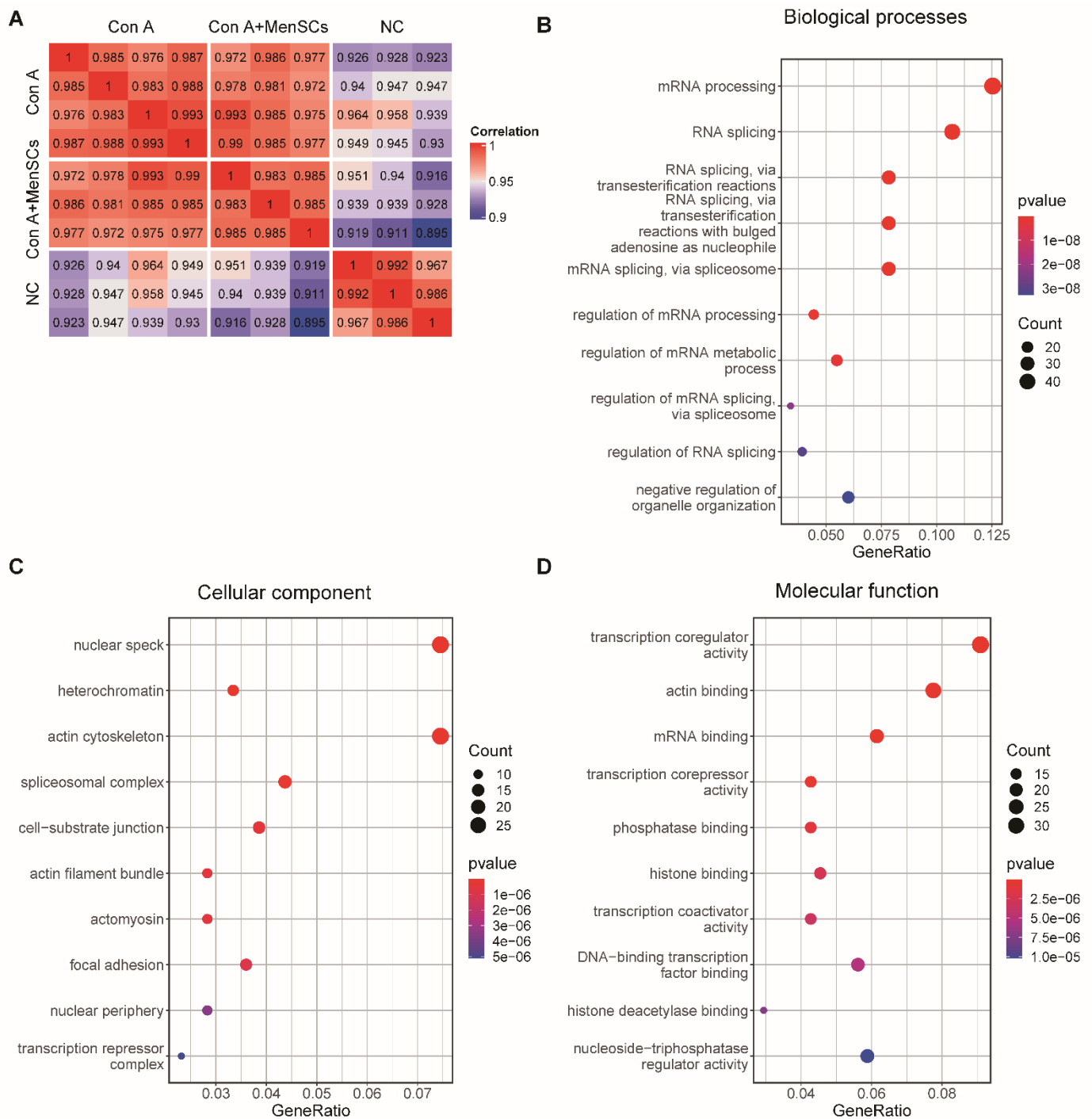


Fig. S4 Properties of Phosphoproteomic among NC group and Con A, Con A+MenSCs groups at 12h. A, Correlation analysis of phosphoproteome. B-D, Bubble diagram represents the top ten enriched BP, CC, MF pathways in the phosphoproteome among three groups, separately. (n = 3 per group of NC, Con A+MenSCs, n = 4 of Con A group).

Supplemental Table 1 GO analysis of Con A and Con A+MenSCs groups at 12 h

GO.ID	Term	Annotated	Significant	Expected	KS
GO:0006351	transcription, DNA-templated	1908	41	52.05	< 1e-30
GO:0006366	transcription from RNA polymerase II promoter	954	28	26.02	< 1e-30
GO:0000278	mitotic cell cycle	329	5	8.97	< 1e-30
GO:0001501	skeletal system development	177	5	4.83	< 1e-30
GO:0001525	angiogenesis	167	12	4.56	< 1e-30
GO:0001101	response to acid chemical	244	18	6.66	< 1e-30
GO:0001649	osteoblast differentiation	100	2	2.73	< 1e-30
GO:0000165	MAPK cascade	347	15	9.47	< 1e-30
GO:0002237	response to molecule of bacterial origin	251	10	6.85	< 1e-30
GO:0001503	ossification	227	7	6.19	< 1e-30
GO:0000082	G1/S transition of mitotic cell cycle	59	1	1.61	< 1e-30
GO:0001819	positive regulation of cytokine production	145	8	3.96	< 1e-30
GO:0000398	mRNA splicing, via spliceosome	72	4	1.96	< 1e-30
GO:0001932	regulation of protein phosphorylation	606	29	16.53	< 1e-30
GO:0003002	regionalization	149	4	4.06	< 1e-30
GO:0000423	mitophagy	63	2	1.72	< 1e-30
GO:0001934	positive regulation of protein phosphorylation	351	19	9.57	< 1e-30
GO:0001666	response to hypoxia	72	1	1.96	< 1e-30
GO:0000302	response to reactive oxygen species	149	4	4.06	< 1e-30
GO:0003006	developmental process involved in reproduction	242	10	6.6	< 1e-30
GO:0006412	translation	181	3	4.94	< 1e-30
GO:0008284	positive regulation of cell proliferation	230	11	6.27	< 1e-30
GO:0001818	negative regulation of cytokine production	83	5	2.26	< 1e-30
GO:0006259	DNA metabolic process	251	12	6.85	< 1e-30

GO.ID	Biological processes ID of GO term;
Term	Function description of GO term;
Annotated	The number of Genes annotated to the GO term;
Significant	The number of differentially expressed genes annotated to the GO term;
Expected	The expected value of the number of differential genes annotated to the GO term;
KS	The statistical significance of the enrichment of the GO term, the smaller the KS value, the more significant the enrichment