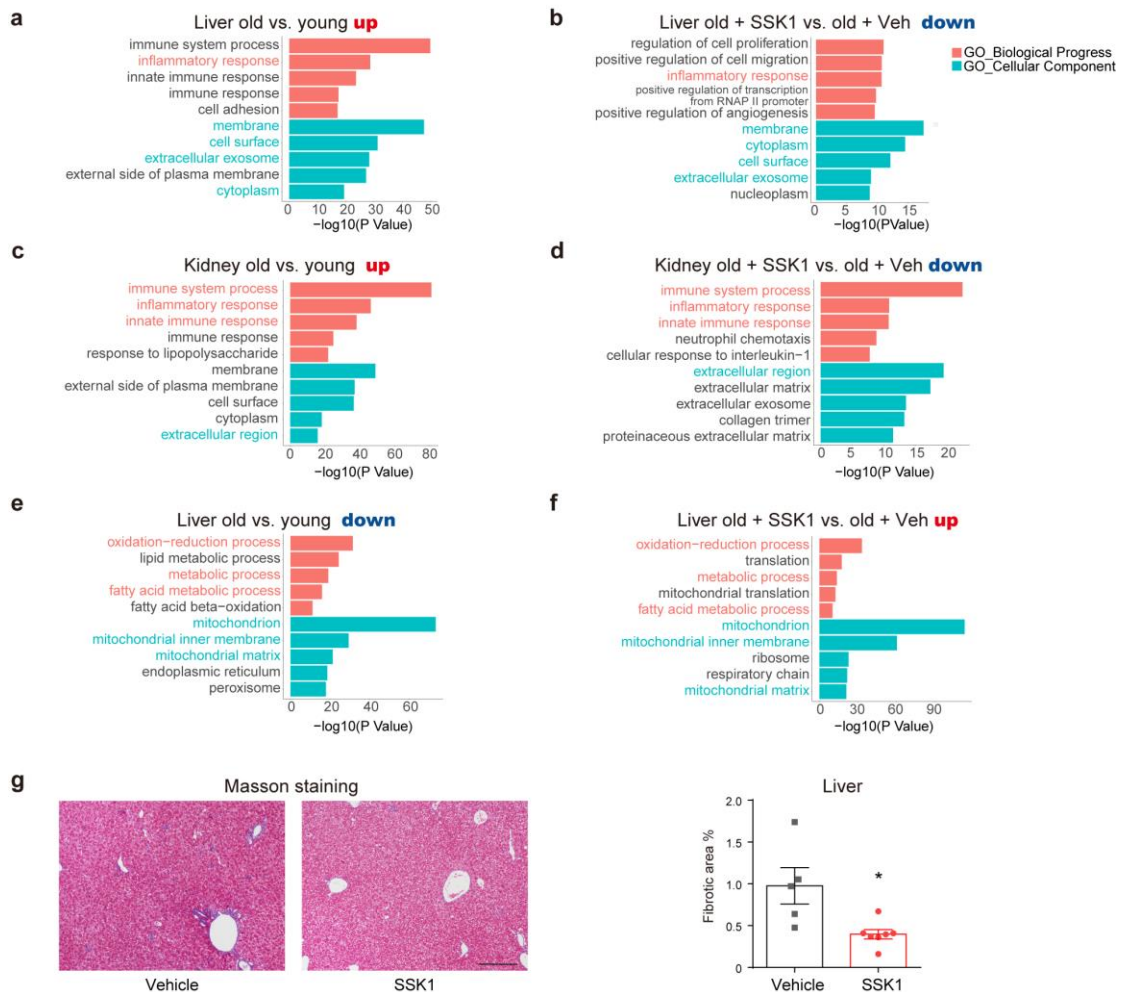


Supplementary information, Figure S7



Supplementary information Fig. 7: Gene ontology analysis of SSK1 treatment.

a-d GO Terms of up-regulated genes in the livers (**a**) and kidneys (**c**) of old mice compared with young mice; And GO terms for down-regulated genes in the livers (**b**) and kidneys (**d**) of SSK1-treated old mice relative to vehicle-treated old mice. **e, f** GO Terms of down-regulated genes in the livers of old mice compared with young mice (**e**) and GO terms for up-regulated genes of SSK1-treated old mice relative to vehicle-treated old mice (**f**). Terms both in **a** and **b** (**c** and **d**; **e** and **f**) are in red or cyan. Details of GO analysis shown in Table S3. **g** Representative Masson fibrosis staining (**left**) and quantification of the proportion of fibrosis (**right**) of liver paraffin sections from old mice treated with vehicle or SSK1 (Vehicle-treated, $n = 5$; SSK1-treated, $n = 7$). Scale bar, 200

μm. Each data point represents an individual mouse. '*n*' represents number of mice. Data are presented as means ± SEM. Unpaired two-tailed *t*-test, **P* < 0.05.