





Supplementary Figure S1. SOS1 depletion rescues LUAD-related pathophysiological parameters in KRAS^{G12D} mutated mice.

a-b, Representative respiratory profiles (**a**) and derived, color-coded graph plot (**b**) illustrating the respiratory rate in surviving, 12-month-old SOS1/2^{WT}/KRAS^{WT}, SOS1/2^{WT}/KRAS^{G12D}, SOS1^{KO}/KRAS^{G12D} and SOS2^{KO}/KRAS^{G12D} mice. Data expressed as mean \pm SD. ** $P=0.0012$ and # $P=0.0439$ vs SOS1^{KO}/KRAS^{G12D}. One-way ANOVA and Tukey's test. $n=3$ independent mice for SOS1/2^{WT}/KRAS^{WT} mice and $n=4$ independent mice for the rest of experimental groups. **c** Representative electrocardiogram (ECG) lead I recordings from 12-month-old mice of the indicated genotypes (SOS1/2^{WT}/KRAS^{WT}, SOS1/2^{WT}/KRAS^{G12D}, SOS1^{KO}/KRAS^{G12D} and SOS2^{KO}/KRAS^{G12D}). Source data are provided as a Source Data file.

Supplementary Figure S2. Impact of SOS1/2 ablation on pulmonary levels of cytokines and chemokines.

a Representative image of membrane arrays used for profiling 40 distinct cytokines and chemokines in lung tumor samples from KRAS^{G12D}-mutated, SOS1/2^{WT}, SOS1^{KO} and SOS2^{KO} mice. **b** Bar chart showing quantitation of the 40 molecular parameters of interest in each of the three color-coded experimental groups. **c**, Bar charts showing detailed quantitations grouped by specific families of cytokines and chemokines. Data shown as mean \pm SD. $n=3$ independent samples per genotype. For MIP-1 (* $P=0.0488$ vs SOS1^{KO} and * $P=0.0431$ vs SOS2^{KO}). For IL-1ra (* $P=0.0234$) vs SOS1/2^{WT}. One-way ANOVA and Tukey's test. C5a: Complement component 5a; CCL: C-C Motif Chemokine Ligand; CXCL: C-X-C motif chemokine; sICAM: Soluble intercellular adhesion molecule; IL: Interleukin; IP: Interferon- γ -Inducible Protein; MCP: Monocyte chemoattractant protein; M-CSF: Macrophage Colony stimulating factor; MIP: Macrophage Inflammatory Proteins; TIMP: TIMP Metallopeptidase Inhibitor; TNF: Tumor Necrosis Factor. TREM-1: triggering receptor expressed on myeloid cells. Source data are provided as a Source Data file.