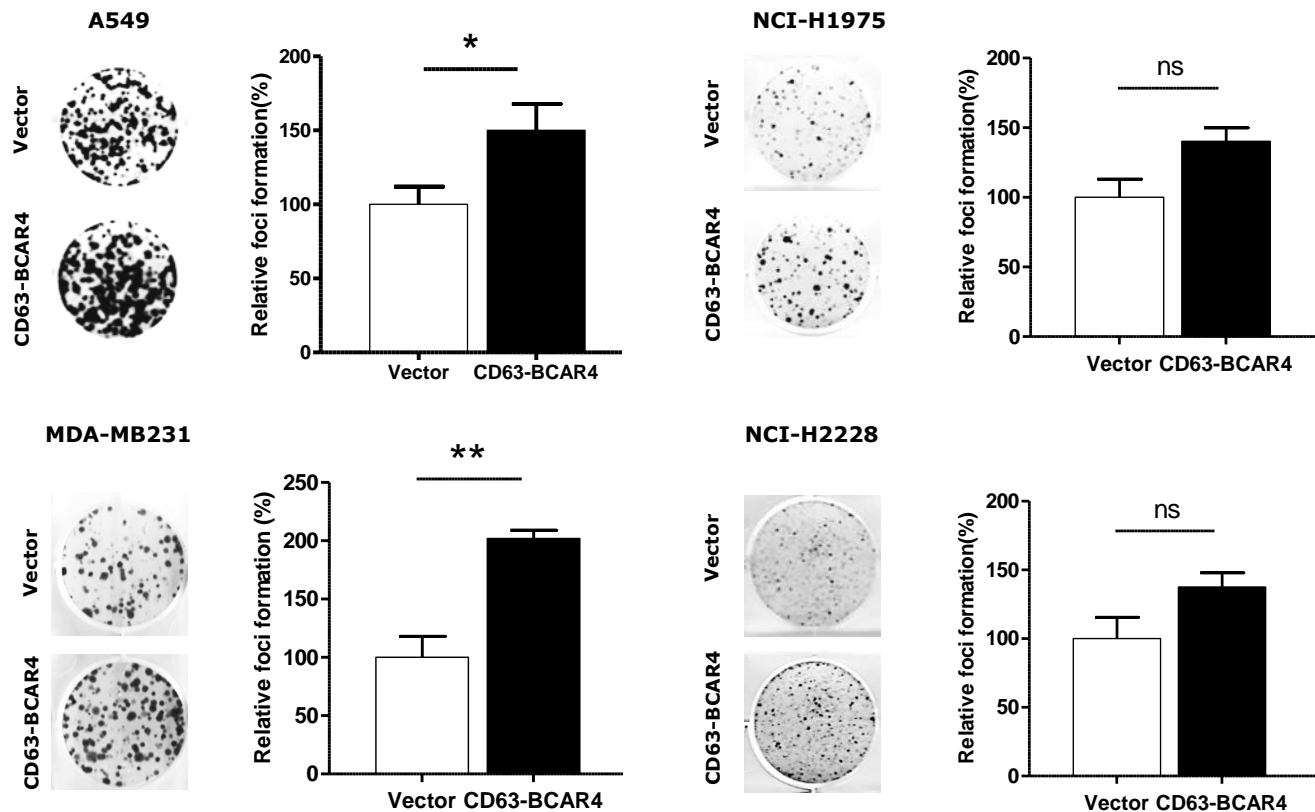
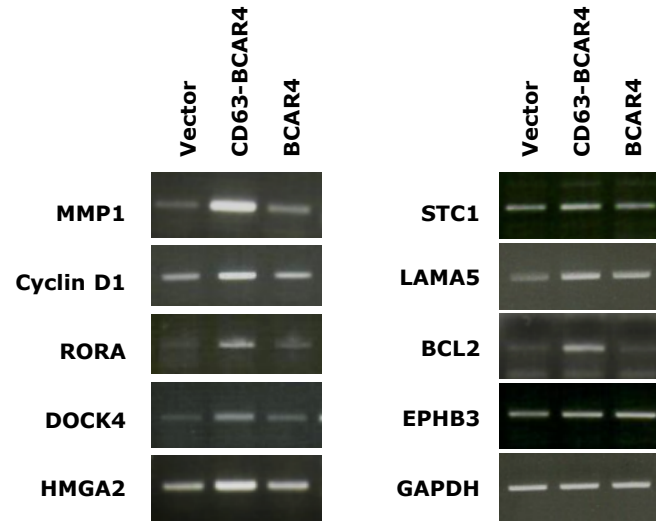


**Supplementary Fig.1 BCAR4 fusions that discovered in lung adenocarcinomas. A.** *CD63-BCAR4* fusion detected in a patient (NCCLUAD-010) in the present study. **B.** *ERBB3-BCAR4* fusion occurred in one TCGA patient

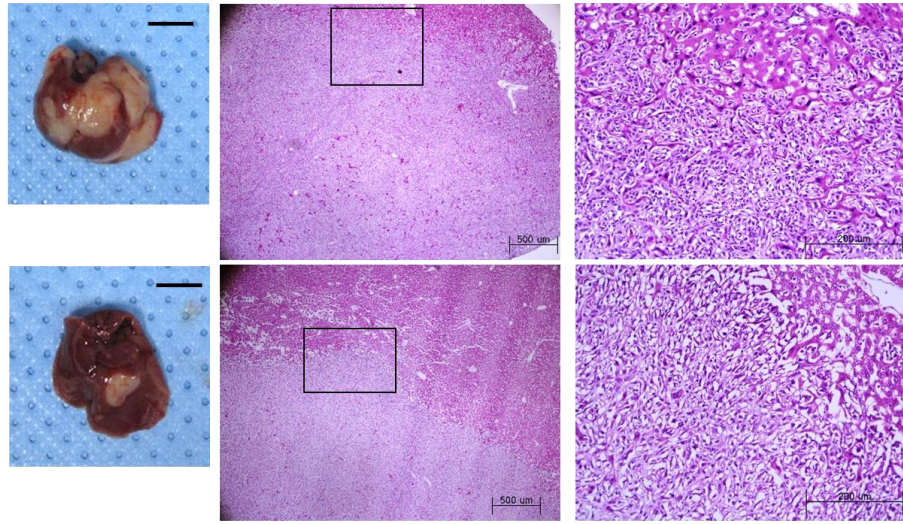


**Supplementary Fig.2 Colony forming assay in lung and breast cancer cells overexpressing CD63-BCAR4.** Colony-forming ability was measured for two weeks after 100 cells/well were seeded into 6-well plates. The number of colonies was counted after staining with 0.5% crystal violet solution. All experiments were performed in triplicate. Representative colonies and relative colony-forming activity of CD63-BCAR4 or empty vector-expressing cells. The statistical significances are marked with \* ( $p < 0.05$ ), \*\* ( $p < 0.005$ ), or ns (not significant).

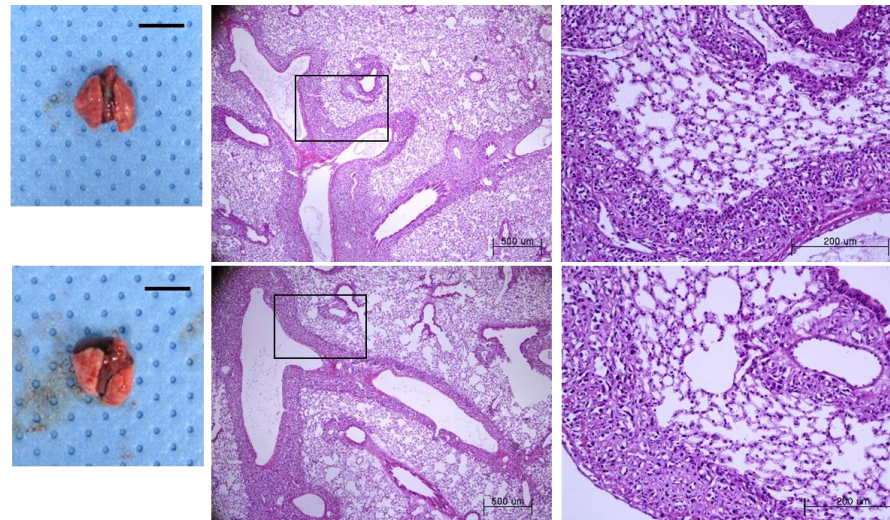


**Supplementary Fig.3** *Gene expression in BEAS-2B cells overexpressing CD63-BCAR4 and BCAR4.* Semi-quantitative RT-PCR was performed to compare mRNA expression of genes that demonstrated differential expression in microarray.

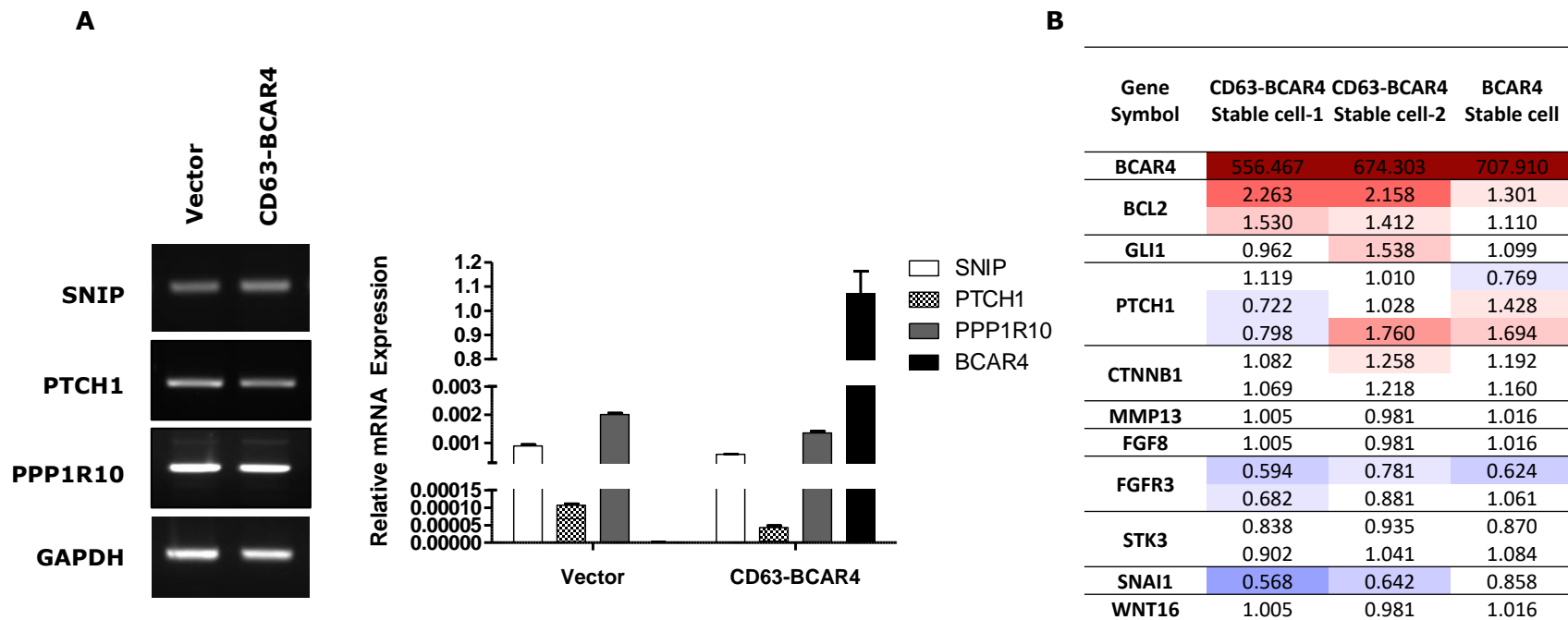
### Liver



### Lung



**Supplementary Fig.4 Tumor formation in liver and lung after intravenous injection in NOG mice.** CD63-BCAR4 overexpressing BEAS-2B cells ( $2 \times 10^5$ ) were injected into tail vein of NOG mice (n=3). Mice were housed under pathogen-free condition in the animal facility and monitored two times a week. Mice were sacrificed at three months after intravenous injection of cells to evaluate tumor growth in organs. Tissue sections of liver and lung were stained with H&E. All animal experiments were performed under the approval of the ethical committee (IACUC) of our institute (NCC-15-271 and KU17167).



**Supplementary Fig.5 Gene expression of SNIP, PTCH1, and PPP1R10 in CD63-BCAR4 overexpressed cells.** **A.** RT-PCR (left) and quantitative real-time RT-PCR (right) were used to compare mRNA expression of *SNIP*, *PTCH1*, and *PPP1R10* between control vector and CD3-BCAR4 overexpressed cells. **B.** Expression level of GLI2-target genes was examined by microarray.