Supplementary Figure 1

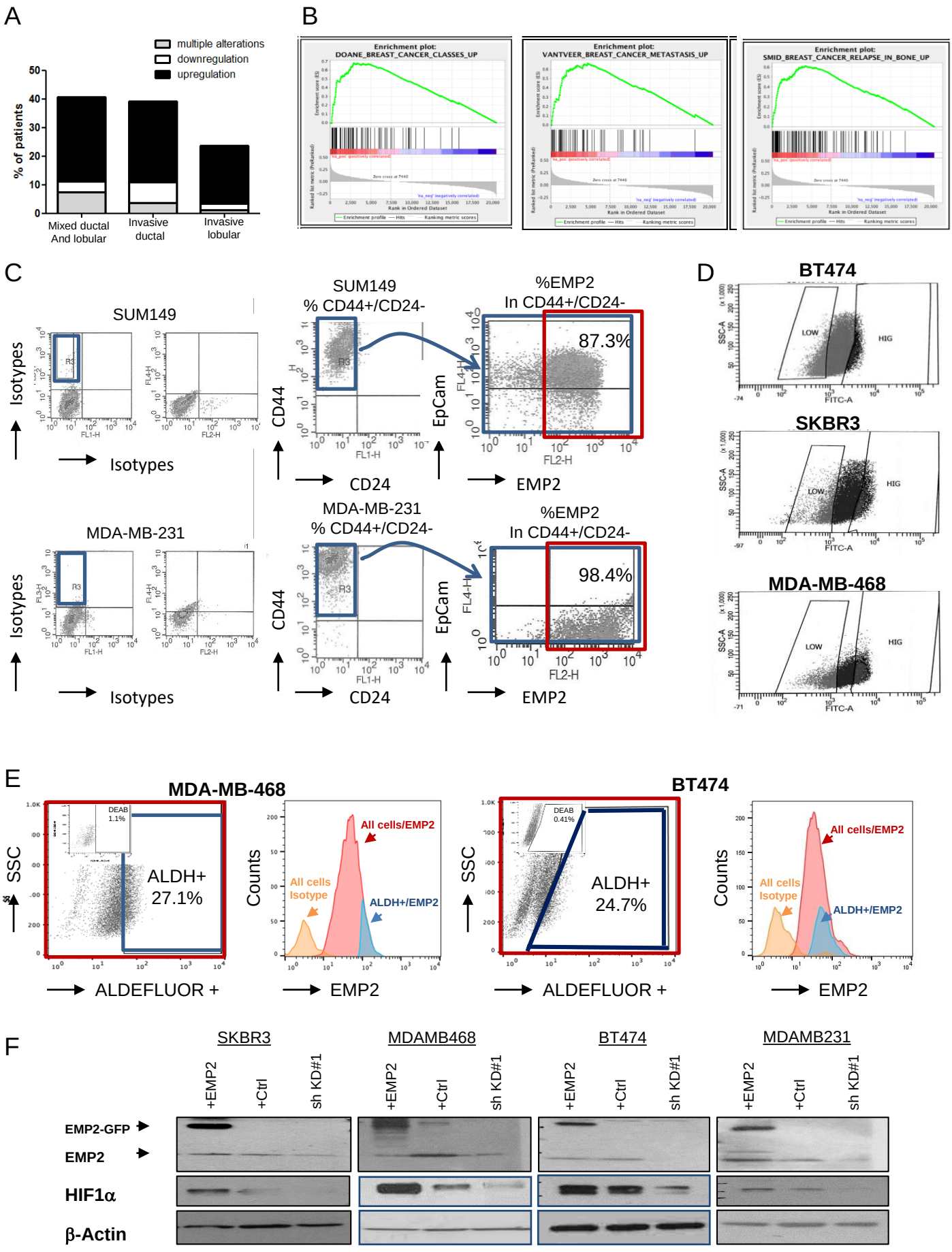

**Fig S1.** Modulation of EMP2 produces transcriptomic changes in breast cancer and markers associated with CSCs. A. *EMP2* mRNA expression was assessed using TCGA (www.cbioportal.com). *EMP2* mRNA is amplified in 36% of women with breast cancer. B. To understand how *EMP2* mRNA may affect tumorigenesis, genes whose expression was enriched by *EMP2* upregulation were sorted and analyzed using GSEA (software.broadinstitute.org/gsea*)*. Elevated *EMP2* in breast cancer patients associated with transcripts involved with all classes of breast cancer as well as those involved with metastasis and cancer relapse to the bone. C. Expression of EMP2 in CD44+/CD24- cells. SUM149 and MDA-MB-231 cells were stained for CD44, CD24, EpCAM, and EMP2 and analyzed using flow cytometry. Live cells were first gated to capture the percentage of CD44+/CD24- cells, after which the percentage of EMP2+ cells in this population was determined. N=3, with a representative example shown. D. Assessment of EMP2 expression in ALDHhigh and ALDHlow cells. ALDH activity was measured in BT474, SKBR3 and MDA-MB-468 cells using the ALDEFLUOR assay, and live cell populations were sorted as indicated for analysis of EMP2 protein levels by western blot. The initial gates were set using diethylaminobenzaldehyde or DEAB, a specific inhibitor of ALDH, as a negative control. E. Assessment of EMP2 expression in ALDHhigh MDA-MB-468 or BT474 cells relative to the entire population. The initial gates were set using DEAB as a negative control as well as using control human mAbs as indicated in the figure. F. Modulation of EMP2 in 4 representative breast cancer cell lines. SKBR3, MDA-MB-468, BT474, and MDA-MB-231 were engineered to overexpress EMP2 (+EMP2), express a vector control (+Ctrl) or knockdown EMP2 levels (sh KD). Representative images are shown.