Figure 1 Nagasawa

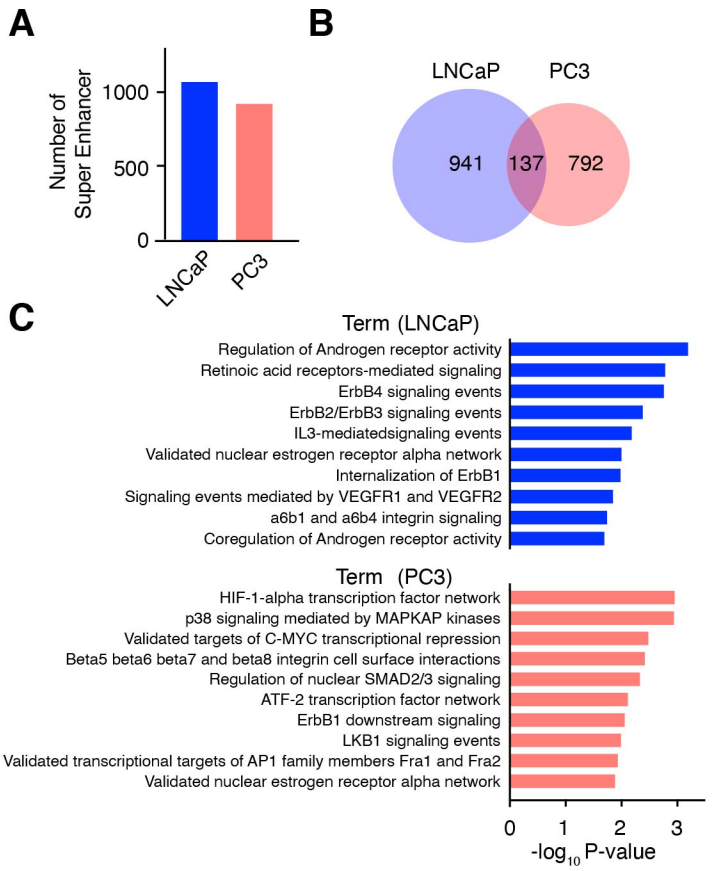

Figure 1. PC3-specific SE-associated genes include genes involved in cell migration and invasion. **(A)** Numbers of SE-associated genes in the indicated cell lines. **(B)** Venn diagram showing the numbers of SE-associated genes in LNCaP and PC3 cells. **(C)** Pathway analysis was performed using the LNCaP- and PC3-specific SE-associated gene sets; the top 10 terms are indicated.

Figure 2 Nagasawa

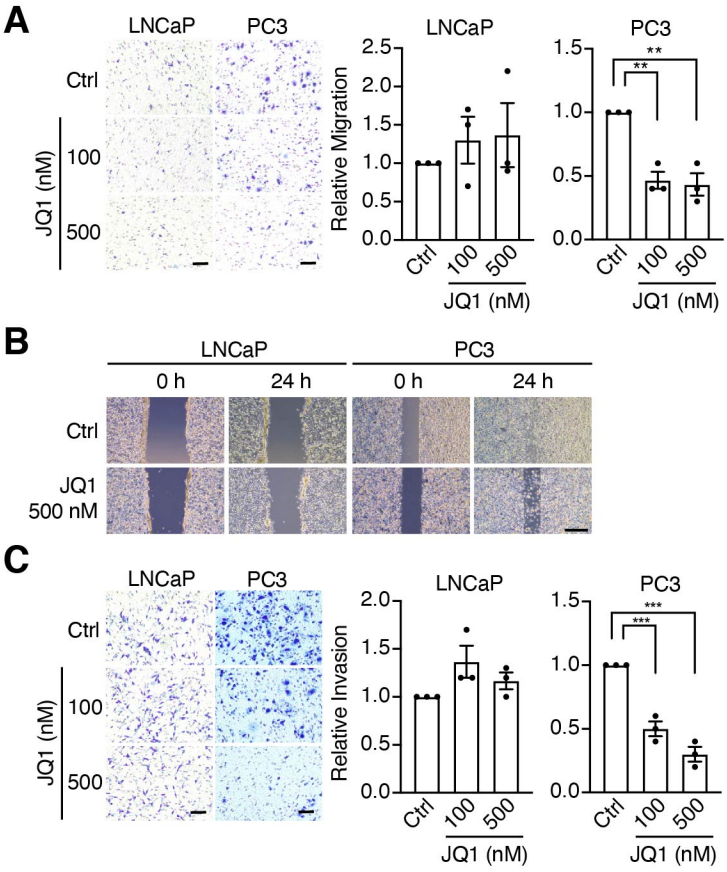

Figure 2. A BETi, JQ1, decreases migration and invasion abilities of PC3 cells.

(A) Migration and **(C)** invasion assays using LNCaP and PC3 cells. Cells were treated with DMSO (Ctrl) or 100 nM or 500 nM JQ1 and incubated in the chamber for 8 h for migration assays and 16 h for invasion assays. Error bars indicate mean ± S.E.M. (n=3 biological replicates). ***P<0.001, **P<0.01, one-way ANOVA. Scale bar, 200 μm. **(B)** Wound healing assay using LNCaP and PC3 cells treated with 500 nM JQ1. Scale bar, 500 μm.

Figure 3 Nagasawa

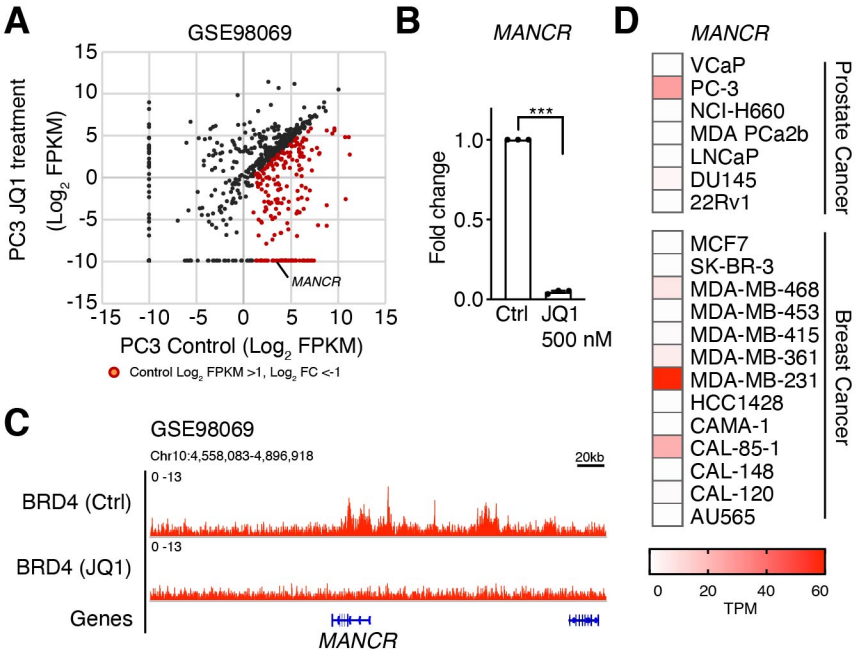

Figure 3. PC3-specific SE-associated lncRNA *MANCR* is down-regulated by JQ1.

(A) Scatter plot comparing Log2 FPKM expression values for PC3-specific SE-associated genes as identified in Figure1B. An RNA-seq dataset for untreated (Ctrl) and JQ1-treated PC3 cells were used (GSE98069). **(B)** RT-qPCR analysis of *MANCR* expression in PC3 cells treated with JQ1. Error bars indicate mean ± S.E.M. (n=3 biological replicates). ****P*<0.001; unpaired t-test. **(C)** Genome browser images of BRD4 ChIP-seq in PC3 cells. ChIP-seq dataset for untreated (Ctrl) and JQ1-treated PC3 cells were used (GSE98069). **(D)** Comparative analysis of *MANCR* expression in several cancer cell lines. Expression data were downloaded from Expression Atlas (http://www.ebi.ac.uk/gxa).

Figure 4 Nagasawa

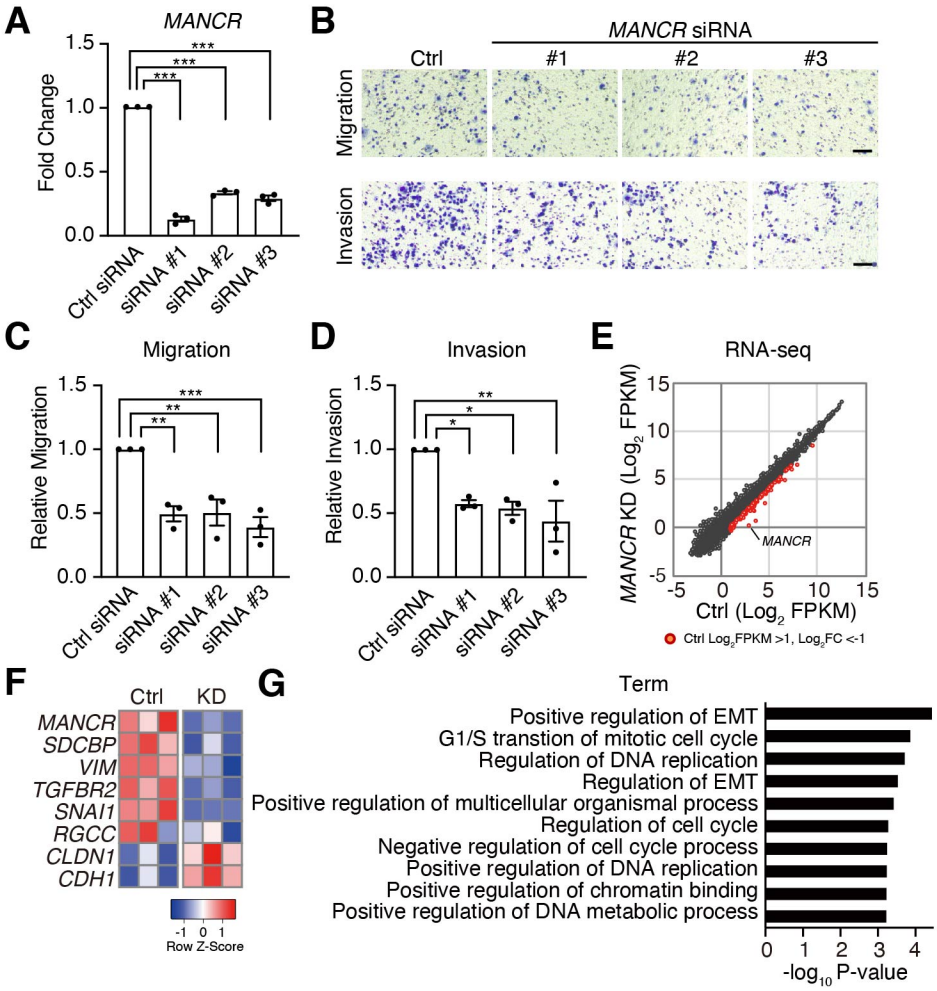

Figure 4. *MANCR* plays a critical role in migration and invasion of PC3 cells.

(A) RT-qPCR analysis of *MANCR* expression in PC3 cells transfected with control or *MANCR*-targeted siRNA. **(B)** Representative images of migration and invasion assays using PC3 cells transfected with the indicated siRNA. Scale bars, 100 μm. **(C, D)** Quantification of the migration (C) and invasion assays (D). **(A, C, D)** Error bars indicate mean ± S.E.M. (n=3 biological replicates). ***P<0.001, **P<0.01, *P<0.05; one-way ANOVA. **(E)** Scatter plot displaying mRNA expression levels in *MANCR*-knocked down PC3 cells compared with the control. Red dots indicate down-regulated genes (Log2 FPKM >1 in Ctrl, Log2 FC <-1 by *MANCR* knockdown). **(F)** Heat map showing expression levels of genes involved in EMT. **(G)** Gene Ontology analysis using the gene set indicated by red dots in **(E)**. Top 10 terms are indicated.