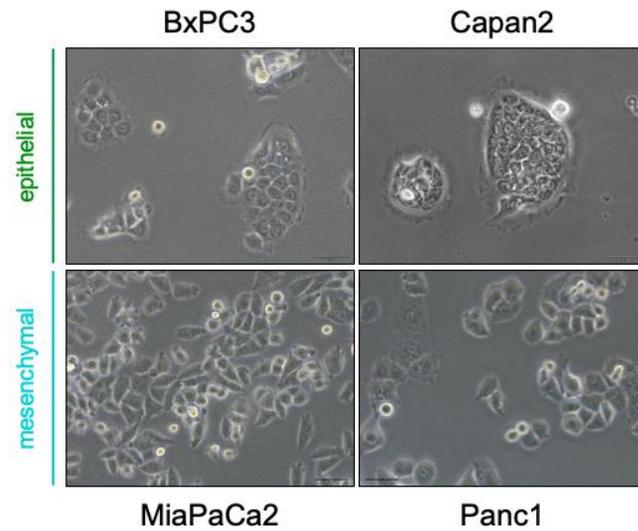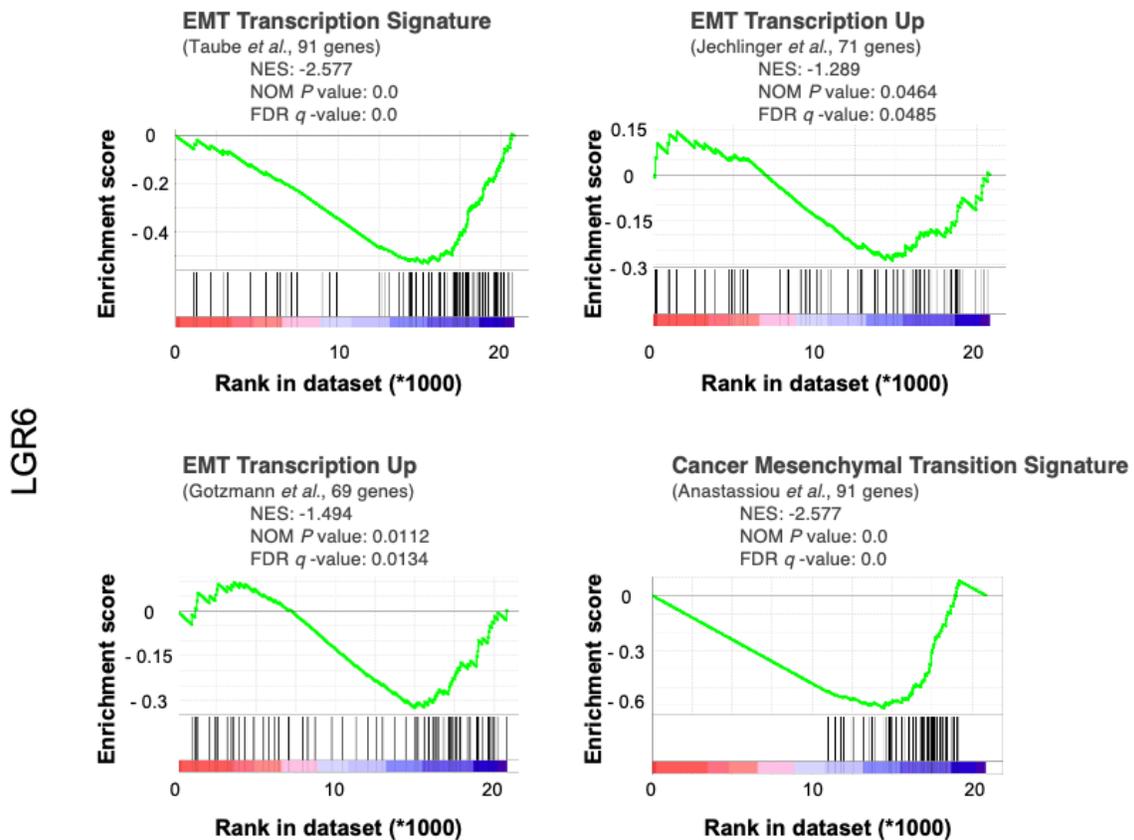## Morphology of all PDAC cell lines used in this study in 2D



**Supplementary Figure 1. 2D-Morphology of PDAC cell lines used in this study.** Grouping according to epithelial (green; BxPC3, Capan2) or mesenchymal (blue; MiaPaCa2, Panc1) phenotype.

# Prediction of inverse correlation between LGR6 and EMT signatures in PDAC



**EMT Transcription Signature**
(Taube *et al.*, 91 genes)
NES: -2.577
NOM *P* value: 0.0
FDR *q* -value: 0.0

**EMT Transcription Up**
(Jechlinger *et al.*, 71 genes)
NES: -1.289
NOM *P* value: 0.0464
FDR *q* -value: 0.0485

**EMT Transcription Up**
(Gotzmann *et al.*, 69 genes)
NES: -1.494
NOM *P* value: 0.0112
FDR *q* -value: 0.0134

**Cancer Mesenchymal Transition Signature**
(Anastassiou *et al.*, 91 genes)
NES: -2.577
NOM *P* value: 0.0
FDR *q* -value: 0.0

**Supplementary Figure 2. GSEA analysis of typical EMT signatures in TCGA data (PDAC).**

## VENN Diagram LGR6high vs. LGR6low TCGA and CCLE Overlap
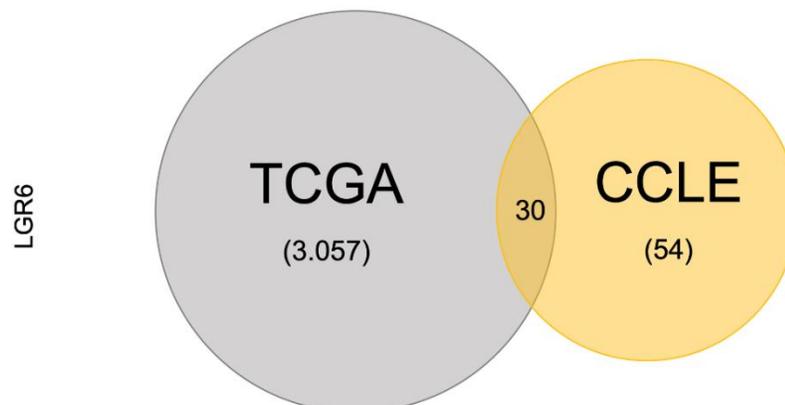


**Supplementary Figure 3. VENN diagram of overlap analysis (TCGA in grey and CCLE in yellow); comparison of LGR6high to LGR6low expression (overlapping genes are listed in Supplementary Table 2).**
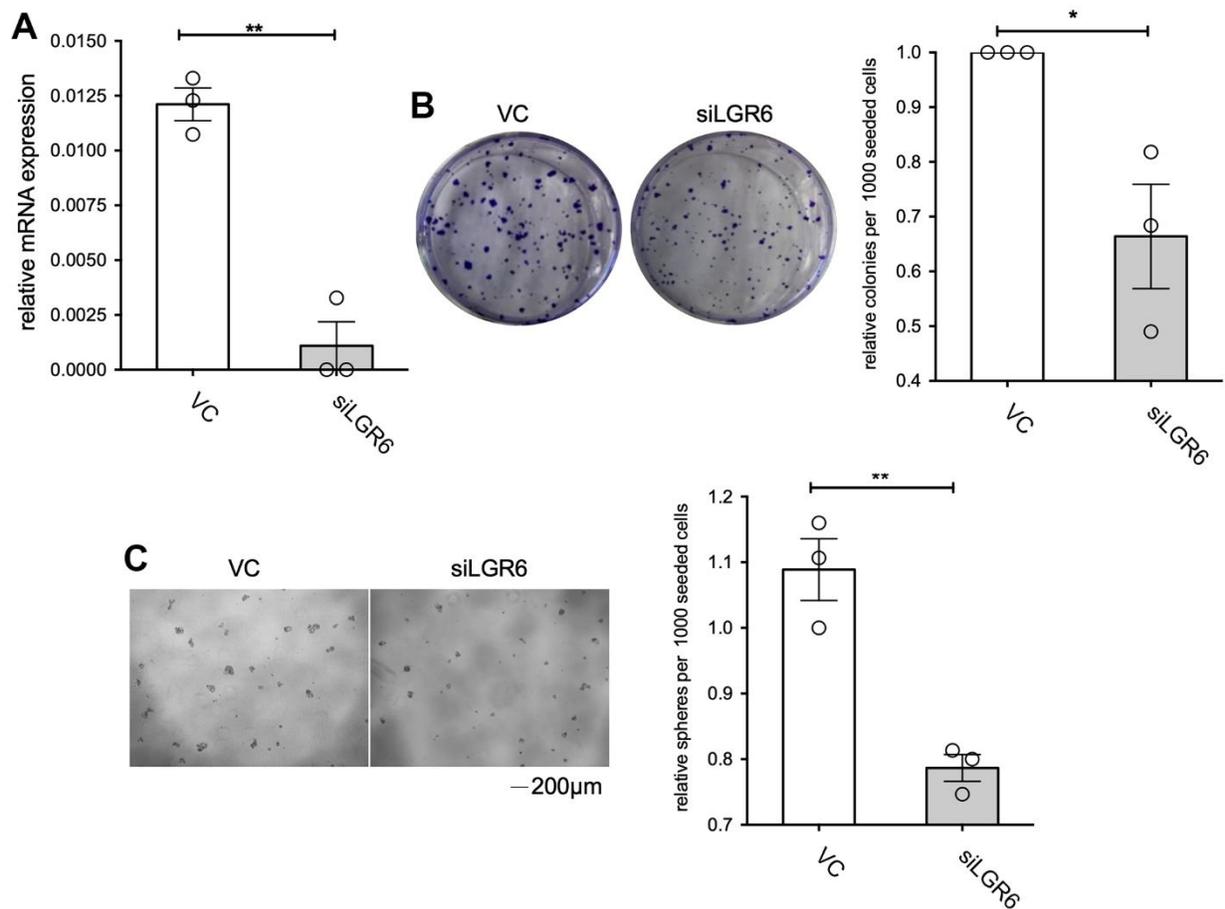
**Supplementary Figure 4. LGR6 knock-down reduces features of cancer stemness in PDAC.** (**A**) Knock-down (KD) efficiency was tested by PCR for LGR6 mRNA levels; vector control (VC) vs. siLGR6 revealed significant KD. (**B**) colony-formation units and (**C**) sphere-formation ability after VC or siLGR6 treatment was carried out and resulted in decreased and smaller colony or sphere numbers.