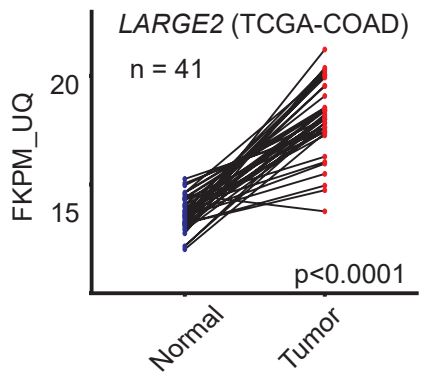
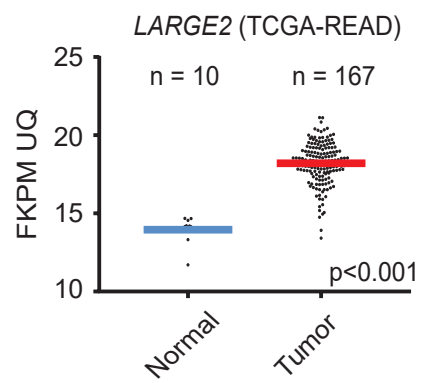
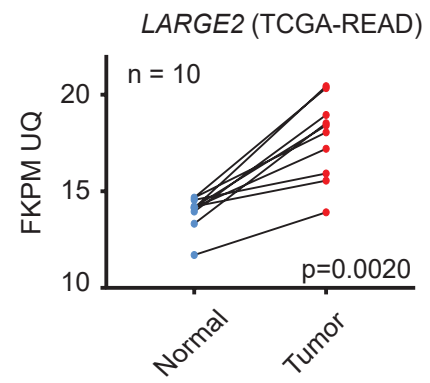
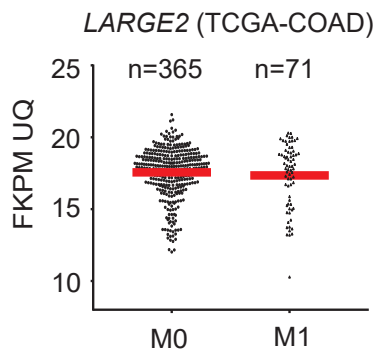
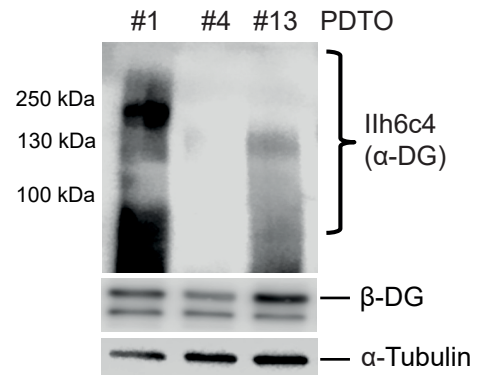
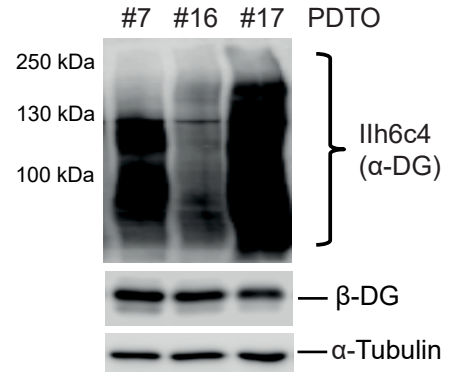
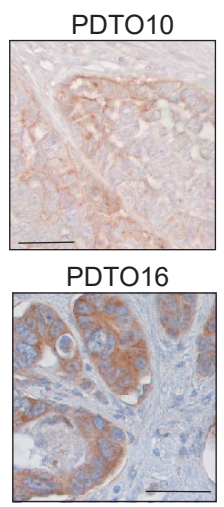
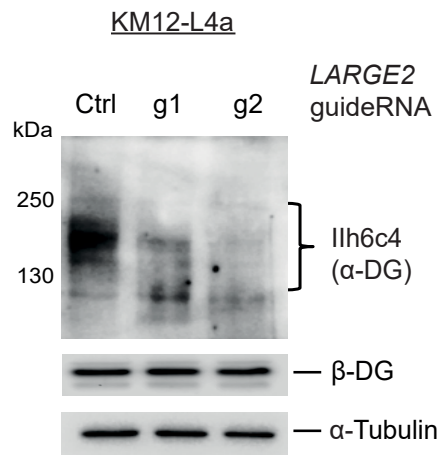
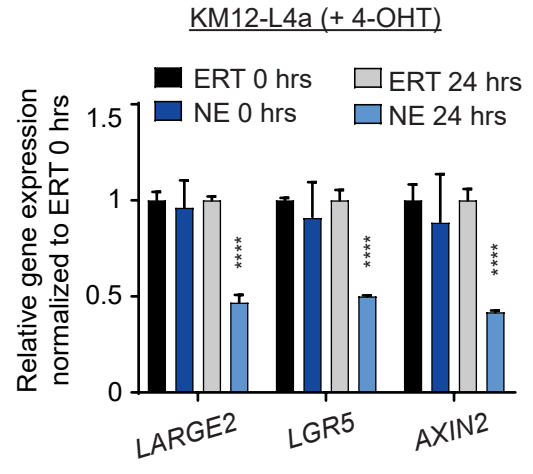
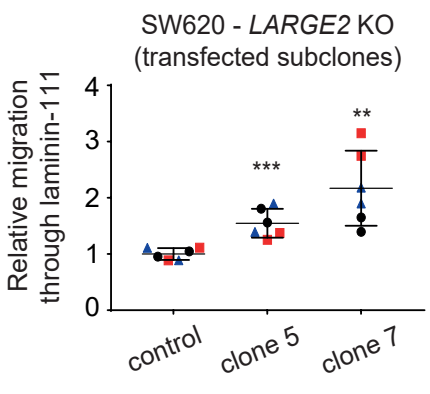


A**B****C****D****E****F****G****H****I****J**

Additional File 10: *LARGE2*/α-DG expression in primary and liver metastatic CRC

A-C) *LARGE2* expression analysis on TCGA datasets: **(A)** comparison of COAD patient-matched normal human mucosa samples and tumor tissues, **(B)** READ normal tissue and tumor tissue and **(C)** patient-matched READ tumor and normal samples.

D) *LARGE2* gene expression analysis on the TCGA-COAD dataset, comparing tissue samples M0 (not metastatic) and M1 (metastatic) CRC cases.

E,F) Immunoblot analysis of O-glycosylated α-DG in WGA-AE purified glycoprotein fractions from a panel of primary and liver metastatic CRC PDOs. WCL was used to detect β-DG and tubulin.

G) Immunohistochemistry analysis of O-glycosylated α-DG (IIh6 antibody) on formalin-fixed paraffin-embedded patient derived tissue samples (matching primary tissues to PDOs 10 and 16).

H) Immunoblot analysis of glycosylated α-DG after KO of *LARGE2* via CRISPR/Cas9 in KM12-L4a cells using two different guideRNAs. WCL was used to detect β-DG and tubulin.

I) Gene expression analysis of indicated genes via qRT-PCR from KM12-L4a-NE or -E cells after treatment with 400 nM 4-OHT for 24 hours. Expression was compared to –ERT cells, or to –NE cells without 4-OHT treatment. Mean values ± SD (n=3) are provided. **** p < 0.0001

J) Transwell migration assays of CRC cells through laminin-111 coated membranes. SW620 cell lines harboring a *LARGE2* knockout were compared to control cells. ** p < 0.01, *** p < 0.001.