Antibody-drug conjugates targeting EGFR ligand Epiregulin inhibit colorectal tumor growth irrespective of *RAS* mutational status

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Translational Relevance

As colorectal cancer (CRC) remains a leading cause of cancer-related death, identifying novel therapeutic targets and approaches is essential to improve patient outcomes. The epidermal growth factor receptor (EGFR) ligand epiregulin (EREG) is highly expressed on the surface of *RAS* wildtype and mutant colorectal tumors with minimal expression in normal tissues, making it a favorable target for antibody-drug conjugate (ADC) development. In this work, we generated novel EREG ADCs that show high selectivity and potency in CRC cells irrespective of *RAS* mutational status. Importantly, EREG ADCs were well-tolerated, caused significant tumor growth inhibition, and increased survival in patient-derived xenograft models. While efficacy of standard of care anti-EGFR therapies, cetuximab and panitumumab, are largely limited by *RAS* mutation status, EREG ADCs may show promise for both *RAS* mutant and wildtype patients, thus improving existing treatment options.

Abstract

Purpose: The EGFR ligand, epiregulin (EREG), is highly expressed in colorectal cancers (CRCs) and a biomarker for predicting benefit in *RAS* wildtype patients receiving EGFR-targeted therapies. Here, we report the development and preclinical evaluation of EREG-targeted antibody-drug conjugates (ADCs) incorporating diverse chemical linkers and duocarmycin DM (DuoDM) payload in CRC models of different mutational status and subtypes.

Experimental Design: RNA-seq datasets from different patient cohorts were analyzed for EREG expression. EREG monoclonal antibody, H231, was characterized for specificity, affinity, internalization, and biodistribution and tumor uptake using ^{89}Zr-immunoPET. H231 was conjugated to a series of cleavable dipeptide and tripeptide linker-DuoDM payloads and cytotoxicity of EREG ADCs were assessed in a panel of CRC cell lines. Safety, antitumor efficacy, and survival was evaluated in vivo.

Results: EREG was high in both *RAS* mutant and wildtype tumors and inversely associated with microsatellite instability. ^{89}Zr-immunoPET showed significant tumor uptake of H231 with minimal uptake in normal tissues. EREG ADCs incorporating tripeptide linkers demonstrated highest potency in EREG-expressing CRC cells (IC50s = 0.01-0.50 nmol/L). EREG ADCs were safe and well-tolerated at doses tested and showed significant tumor growth inhibition with increased survival in patient-derived tumor xenograft models.

Conclusions: EREG is a promising target for the development of ADCs for treating colorectal and other tumor types that express high levels of EREG. Importantly, EREG ADCs demonstrated significant therapeutic efficacy in both *RAS* mutant and wildtype CRC cell lines and tumors, suggesting their potential as an alternative to EGFR-targeted therapy to benefit a broader patient population.

Introduction

Colorectal cancer (CRC) ranks second in cancer-related deaths in the United States and incidence and mortality has considerably increased in individuals 50 years and younger (1). Chemotherapy combinations of irinotecan or oxaliplatin with fluoropyrimidines have long been considered first-line treatment options for advanced CRC, yet are limited by systemic toxicities (2). Approved monoclonal antibodies (mAbs) that target epidermal growth factor receptor (EGFR), cetuximab and panitumumab, have greatly improved overall survival for a fraction of patients with wildtype *KRAS* and *NRAS,* though ~40-60% of patients present mutations (2). More recently, a phase 3 trial of *KRAS* G12C inhibitor, sotorasib, in combination with panitumumab showed superior progression-free survival rates versus standard of care for the 3-4% of metastatic CRC (mCRC) patients that harbor the specific mutation (3). Immune checkpoint inhibitors have shown durable response in tumors with microsatellite instability-high (MSI-H) mismatch repair deficiency, though the majority of mCRC is microsatellite stable (MSS) (2). While the development of targeted agents has improved prognosis for different CRC molecular subtypes, many patients still experience resistance and relapse, demonstrating the need for new targets and more effective therapeutic strategies.

Epiregulin (EREG), a member of the EGF family, is a surface expressed, transmembrane ligand that binds and activates EGFR and human epidermal growth factor receptor 4 (HER4/ErbB4) and can stimulate signaling of HER2/ErbB2 and HER3/ErbB3 through receptor heterodimerization (4). EREG is highly expressed in many cancer types (5-9), including CRC (10), and has been shown to drive colitis-associated CRC (11) and be predictive of colorectal liver metastasis (12). EREG correlates with left primary tumor location (PTL), MSS, wildtype *BRAF* and *RAS* status, and CpG island methylator phenotype low (CIMP-low) CRC subtypes (10). Importantly, in RAS wildtype mCRC patients, EREG predicts benefit to EGFR-targeted therapies, including right PTL disease (13-17). Overall, EREG is a promising predictive biomarker for treatment and may serve as a novel therapeutic target.

Antibody-drug conjugates (ADCs) are an emerging class of anticancer drugs, consisting of highly specific mAbs chemically linked to potent cytotoxic payloads with low nanomolar to picomolar IC50 values (18,19). These armed mAbs directly deliver payloads to target antigen-enriched tumor cells while minimizing toxicity to normal tissues (20,21). Advances in linker-payload technology have improved ADC stability and safety profiles, leading to a surge of approved ADCs within the past few years and many more entering clinical trial (22). In this study, we generated and comprehensively characterized an EREG mAb for target-specific binding, internalization, species cross-reactivity, biodistribution, and tumor uptake using ^{89}Zr-immunoPET. We then developed and evaluated a series of EREG-targeted ADCs incorporating diverse chemical linkers and the DNA minor groove alkylating payload duocarmycin DM (DuoDM). EREG ADCs were well-tolerated and demonstrated potent and selective growth inhibition in cancer cell lines and patient-derived tumor xenograft (PDX) models of CRC with or without mutant *RAS*. This preclinical data supports further development of EREG ADCs for treating EREG-high tumors irrespective of mutational status.

Methods and Materials

Plasmids and cloning

Sequences encoding human or mouse EREG (hEREG, Clone ID: 9020391 or mEREG, Clone ID: 5325124; Horizon Discovery) were subcloned and fused with the CD8 signal peptide sequence (MALPVTALLLPLALLLHAA) followed by a Myc-tag at the N-terminus in pIRESpuro3 (Clontech). Humanized EREG mAbs H231 and H206 (23) and E27 (24) were generated from patented sequences. The variable heavy and light chain (VH and VL) regions were synthesized (Epoch Life Science, Inc.), subcloned into pCEP4 containing human IgG1 heavy chain with N297A mutation for site-specific conjugation and kappa light chain constant regions. For H231, a Q57N mutation was incorporated in the VH region to prevent drug conjugation in the complementarity determining region. Similarly, CD20 mAb rituximab was

generated utilizing publicly available sequences to serve as a non-targeting isotype control (cmAb). All expression constructs were sequence verified. For hEREG CRISPR-Cas9-based knockout (KO), single guide RNA sequence (sgRNA), 5'-GACAGAAGACAATCCACGTG-3' was cloned into lentiCRISPRv2-hygro as described (25). LentiCRISPRv2-hygro was a gift from Brett Stringer (Addgene, #98291).

Commercial antibodies and recombinant proteins

Primary antibodies used in this study include anti-β-actin (#4970, 1:5000), anti-EREG (#12048, 1:1000), anti-EGFR (#4267, 1:1000), anti-phospho-EGFR Y1068 (#3777,1:1000), anti-AKT (#9272,1:1000), anti-phospho-AKT (S473) (#9271, 1:1000), anti-p44/42 MAPK (ERK 1/2, #9102, 1:1000), anti-phospho-p44/42 MAPK T202/Y204 (p-ERK 1/2, #9101, 1:1000), anti-PARP (#9532, 1:1000), and anti-LAMP1 (#9091, 1:400) from Cell Signaling Technologies and anti-Myc-Cy3 (Sigma). Recombinant hEREG (1195EP025CF) was from R&D Systems.

Antibody production

MAb production was performed by transiently expressing mAb constructs in Expi293F cells (ThermoFisher) using polyethylenimine reagent. Medium was collected 7 days post-transfection and mAbs were purified using protein A resin (Genscript) affinity chromatography and eluted in PBS (pH 7.4). MAbs were analyzed for purity and homogeneity by SDS-PAGE and reverse-phase high-performance liquid chromatography (Vanquish UHPLC) and quantified by NanoDrop (ThermoFisher).

Microbial transglutaminase (MTGase)-mediated antibody conjugation

For site-specific conjugation of Q295, H231 mAb (5.625 mL in PBS, 8.0 mg mL^{-1}, 45.0 mg) was incubated with diazide branched linker developed previously (26) (180 µL of 100 mM in H_2O, 60 equiv.) and Activa TI® (505 mg, final concentration 8%, Ajinomoto, Modernist Pantry) at RT for 20 h. The reaction was monitored using the Thermo LC-MS system consisting of a Vanquish UHPLC and Q Exactive™ Hybrid

Quadrupole-Orbitrap™ Mass Spectrometer equipped with a MabPac RP column (2.1 × 50 mm, 4 µm, Thermo Scientific). Elution conditions were as follows: mobile phase A = H_2O (0.1% formic acid); mobile phase B = acetonitrile (0.1% formic acid); gradient over 3 min from A:B = 75:25 to 45:55; flow rate = 0.25 mL min^{-1}. Conjugated mAb was purified by protein A column chromatography (MabSelect PrismA™, Cytiva) to afford a mAb-linker conjugate [42.3 mg, 94% yield determined by bicinchoninic acid (BCA) assay]. CmAb was conjugated similarly.

Strain-promoted azide-alkyne cycloaddition to attach payload

DBCO-PEG3-EGC-PABQ-DuoDM β-glucuronide (EGC-qDuoDM gluc) was synthesized (Supplementary Methods) and added (76.4 µL of 10 mM stock solution in DMSO, 1.5 equivalent per azide) to a solution of H231- or cmAb-linker conjugate in PBS (4.7 mL, 4.065 mg mL–1), and the mixture was incubated at RT for 30 min. The reaction was monitored using the Thermo LC-MS system with elution conditions stated previously. The crude products were purified by CHT-XT (Bio-Rad) after exchanging buffer to 5 mM phosphate buffer pH 6.5. Desired ADC was eluted by salt gradient and exchanged buffer to PBS. Yield was determined 79% (15.14 mg). Drug-antibody ratio (DAR) values for H231 EGC-qDuoDM gluc and cmAb EGC-qDuoDM gluc (cADC) were determined by Electrospray ionization-mass spectrometry (ESI-MS) analysis. Other ADCs incorporating BCN-PEG3–EGCit–PABC–DuoDM (EGC-cDuoDM) or DBCO-PEG4-VC-PAB-(PEG2)-DuoDM (VC-cDuoDM; Levena) were prepared in a similar manner or according to our previous reports (26).

Cell culture and transfection

DLD1, LoVo, RKO, SW48, LS180, HCT116, COLO320, HCT15, HT29, SW403, SW620, LIM1215 and HEK293T (293T) cells were purchased from ATCC. Cell lines were authenticated utilizing short tandem repeat profiling and tested for mycoplasma. 293Ts were cultured in DMEM and CRC cells in RPMI medium supplemented with 10% fetal bovine serum and penicillin/streptomycin. LIM1215 cells were additionally

supplemented with 1 µg/ml hydrocortisone, 10 µM 100X 1-Thioglycerol, 0.6 µg/ml insulin and 25 mM HEPES. Cell lines were cultured at 37°C with 95% humidity and 5% CO_2. To generate the DLD-1 EREG KO cell line, lentivirus particles were produced by co-transfecting 293Ts with lentiCRISPRv2-hygro incorporating EREG sgRNA and packaging plasmids, psPAX2 and pMD2.G, using Fugene HD (Promega). Clonal selection was performed using 50 µg/ml hygromycin.

Western blot

Protein extraction was performed using RIPA buffer supplemented with protease/phosphatase inhibitors. PDX tissues were homogenized and freeze thawed. Lysates were centrifuged 15 min, 4 °C at 13,000 x g. Protein concentrations were measured and lysates were diluted in Laemmli buffer and incubated at 37°C for 1 h prior to running SDS-PAGE. HRP-labeled secondary antibodies were utilized with the standard ECL protocol. For EREG mAb neutralization experiments, cells were seeded in a 6-well plate and cultured in 0.5% FBS in RPMI 3 h then treated with PBS, 300 ng/ml recombinant hEREG, 15 µg/ml cmAb or H231 mAb, or combination for 5 min. For PARP analysis, cells were treated with H231 EGC-qDuoDM gluc or cADC as indicated.

Cell-based binding assays

293T cells stably overexpressing hEREG, mEREG, or vector or CRC cells were seeded onto poly-D-lysine-coated black 96-well plates and incubated overnight. Serial dilutions of H231, cmAb, H231 ADCs, or cADC were added for 2 h at 4°C. Plates were washed in PBS, fixed in 4% formalin, and incubated with anti-human-Alexa-555 for 1 h at RT. Fluorescence intensity was quantified using Tecan Infinite M1000 plate reader. Each condition was tested in triplicate in 2-3 independent experiments.

Flow cytometry

Surface-expressed EREG molecules/cell were quantified by labeling H231 with phycoerythrin (PE) with the Lightning-Link PE conjugation kit (Abcam) and BD QuantiBRITE PE. Briefly, $1x10^6$ cells/sample were fixed with dropwise addition of 10% formalin for 20 min, followed by blocking with 2% BSA/PBS for 5 min and incubation with 6 µg/ml H231 or cmAb in 2% BSA/PBS at 4°C for 60 min. QuantiBRITE PE beads were run on BD FACS ARIA II SORP flow cytometer to generate the standard curve for fluorescent intensity vs. number of PE molecules/bead. Singlets were gated on the FSC-H vs. SSC plot, and the singlet bead population was analyzed using a histogram plot of FL-2 axis in linear values. Log10 for lot-specific PE/bead values vs. Log10 of geometric means for four bead peaks were plotted. Equation y=mx+c where x equals Log10 PE molecules/bead and y equals Log10 fluorescence was used to calculate slope, intercept and correlation coefficient. To determine mAbs bound per cell for different cell lines, samples were run using same settings and PE molecules/cell were calculated. Unstained cells and cmAb served as negative controls.

Immunocytochemistry

CRC cells were seeded into poly-D-lysine coated 8-well culture slides and incubated overnight. Cells were treated with H231 at 37°C for 90 mins to allow binding and internalization, then washed, fixed in 4% formalin, permeabilized in 0.1% saponin, incubated with anti-LAMP1 (lysosome marker) at RT for 45 min, followed by anti-rabbit-Alexa-488 and anti-human-Alexa-555 (Life Technologies) at RT for 1 h. Nuclei were counterstained with TO-PRO-3 (ThermoFisher). Images were acquired using confocal microscopy (Leica TCS SP5) and LAS AF Lite software.

^{89}Zr-immunoPET and biodistribution

Immuno-positron emission tomography (immunoPET) studies were carried out in accordance with IACUC at UTHealth Houston (AWC-20-0144 and AWC-23-0106). 2.5 x 10^6 DLD-1 cells in 50 % Matrigel were subcutaneously implanted into the lower right flank of female 6-8-week-old nu/nu mice. Desferrioxamine

(DFO) immunoconjugates were prepared via lysine conjugation as previously described (27). DFO-H231 or DFO-cmAb (200µg) were radiolabeled with zirconium-89 (^{89}Zr; Washington University, St. Louis, MO). Once tumors reached ~4-6 mm diameter, ^{89}Zr-H231 or^{89}Zr-cmAb were injected with 139-215 µCi per mouse. Imaging was performed 5 days post-injection (dpi) using an Albira small animal PET/CT scanner (Bruker) and tumor-to-muscle ratios where determined. Mice were euthanized and organs were resected, weighted, and analyzed using a Cobra II auto-γ counter (Packard) to determine tracer biodistribution. Standard aliquots of known activity were used to calculate the percentage of the injected dose per gram of tissue (%ID/g).

In vitro viability

CRC cells were plated at ~1,000 cells/well in 96 half-well plates. Serial dilutions of unconjugated H231, cmAb, H231 ADCs or cADC were added and incubated at 37 °C for 4 or 5 days. Cell viability was measured using CellTiter-Glo (Promega) according to the manufacturer's protocol. Luminescence was measured using Tecan Infinite M1000 plate reader.

Tolerability Study

Female 6-8-week-old C57BL/6 mice (n= 4/group, The Jackson Laboratory) received a single dose H231 VC-DuoDM (5 or 10 mg/kg), H231 EGC-cDuoDM ADC (5 or 10 mg/kg), or PBS vehicle via tail vein. Body weight was monitored every 2-3 days for 2 weeks. Humane endpoints were defined as >20% weight loss or severe signs of distress. However, no mice met these criteria throughout the study. Fourteen dpi, mice were terminally anesthetized and whole blood was drawn by heart puncture for blood chemistry analysis in the Department Veterinary Medicine & Surgery at MD Anderson Cancer Center.

In vivo efficacy studies

Animal studies were carried out in accordance with IACUC (AWC-20-0144, AWC-21-0142, and AWC-23-0106). For efficacy studies, nu/nu (Charles River Laboratories or The Jackson Laboratory) and NSG (The Jackson Laboratory) mice were used for CRC cell xenografts and PDX models, respectively. PDX CRC-001 was from Jackson Laboratory (#TM00849) and XST-GI-010 was established in our laboratory at UTHealth with patient consent and appropriate approvals (HSC-MS-20-0327, HSC-MS-21-0074). Female 6-8-week-old mice were implanted subcutaneously with 3-4 x 10^6 LoVo or DLD-1 CRC cells or 2-3 mm PDX fragments into the right flank. When tumors reached ~100–200 mm^3, mice were randomized based on equivalent average tumor volume for each treatment group. Animals without palpable tumors were excluded. No blinding to group allocation was performed and sample sizes were determined based on prior experience with the models to reach statistical significance. Mice were intravenously or interperitoneally dosed weekly with PBS vehicle, H231, cADC or H231 ADCs as indicated. Mice were routinely monitored for morbidity and mortality. Tumor volumes were measured bi-weekly and estimated by the formula: tumor volume = (length × $width^2$)/2. Mice were euthanized when tumor diameter reached 15 mm. Percentage of tumor growth inhibition (% TGI) was calculated using the formula [1 – (change of tumor volume in treatment group/change of tumor volume in vehicle group)] × 100 (%).

Statistical Analysis

All data were analyzed using GraphPad Prism software. Data are presented as mean ± SEM or ± SD, as indicated. In vitro binding and viability data were analyzed using the logistic nonlinear regression model. Each condition was tested in triplicate in 3 independent experiments. The Cancer Genome Atlas (TCGA) data from matched normal and tumor samples or *KRAS* status were compared and analyzed using paired Student's t test. EREG in tumor vs. normal tissues and distribution in MSI/MSS was compared using one-way analysis of variance (ANOVA) and Tukey's multiple comparison test. Kaplan-Meier analysis was performed to determine significance of EREG on disease-free and overall survival. Statistical significance of in vitro experiments was analyzed with ANOVA and Tukey's multiple comparison test. Differences

between groups for biodistribution studies were analyzed by Student's t test. Statistical analysis of tumor volume was assessed by one-way ANOVA and Dunnett's multiple comparison test or Student's t test for two groups. P value less than < 0.05 was considered significant.

Data Availability

The data generated in this study are available within the article and supplementary files. Materials and reagents will be made available through collaboration in agreement with UTHealth Houston and the corresponding author.

Results

EREG is highly expressed in MSS colorectal tumors with minimal expression in normal tissues

We analyzed *EREG* expression in TCGA RNA-seq data to identify CRC patients that may benefit from EREG-targeted ADCs (28). Though *EREG* has minimal expression in normal tissues, mRNA can be detected in skin, esophagus, vagina, lung, and colon as confirmed the Genotype-Tissue Expression (GTEx) project (Fig. 1A and Supplementary Fig. S1). Importantly, *EREG* is significantly higher in tumors from the colorectal adenocarcinoma (COADREAD) cohort compared to normal colon/rectum, lung, esophagus (average fold differences ≈ 3.7, 7.1, and 9.6, respectively; Fig. 1A) and other tissues. Matched tumor and adjacent normal samples from 32 patients showed *EREG* is upregulated >2-fold in ~60% of patients (average fold difference in EREG-high patients ≈ 16.8; Fig. 1B). *EREG* expression is significantly upregulated in MSI-L and MSS tumors compared with MSI-H tumors (Fig. 1C), consistent with previous reports from other CRC cohorts (10,17). Furthermore, *EREG* levels are highly expressed in subsets of both *KRAS* wildtype and mutant (G12/G13) patients, however there is significant association with wildtype status (Fig. 1D). Partitioning of data from the COADREAD cohort showed no significant correlation between *EREG* expression and survival (Figs. 1E-F), though EREG-high patients trended toward poorer survival at later time-points (disease-free, median value = high, 63.37 vs. low, 78.65 months; overall survival, median value

= 65.80 vs. 92.67 months). Notably, EREG-high status confers an overall survival advantage at earlier time-points (Fig. 1F), which has been shown to be significant for KRAS wildtype patients who received anti-EGFR therapy (17,29). Analysis of a recent study of 18 matched primary tumors, synchronous liver metastases, and normal colonic epithelium (17 MSS and 1 MSI-H) showed *EREG* was significantly elevated in both primary tumors and their metastases (30). Western blot analysis of EREG in MSS, *RAS* mutant CRC PDX models showed high EREG expression in 4/5 samples (Fig. 1H). Furthermore, RNA-seq data from the Cancer Cell Line Encyclopedia (CCLE) revealed *EREG* is amply expressed in a majority of CRC cell lines with or without mutant *RAS* and was consistent with protein levels (Fig. 1I-J) (31). These results show EREG correlates with MSI-L/MSS, which accounts for the majority of mCRC patients, and is highly expressed in both *RAS* wild-type and mutant subtypes, suggesting EREG ADCs may be a promising treatment option for a sizeable patient population.

H231 binding and internalization in CRC cell lines

To develop a novel EREG-targeted ADC, we first set out to identify an optimal EREG mAb with high affinity and specificity. We cloned and purified three individual EREG mAbs that bind both surface-expressed, uncleaved pro-EREG and mature, cleaved EREG: H206, H231, and E27 (23,24). To determine mAb target specificity, we utilized 293T cells that do not express endogenous EREG and established lines overexpressing myc-tagged hEREG, mEREG, or vector. Expression was confirmed using anti-myc-tag antibody (Supplementary Fig. S2A). Adherent cell-based binding assays show all EREG mAbs bind hEREG-293T cells (Kd values = H231, 0.01 µg/ml or 0.1 nmol/L; H206, 0.06 µg/ml or 0.4 nmol/L; E27, 0.08 µg/ml or 5.6 nmol/L; Fig. 2A and Supplementary Fig. S2B). H206 (Kd = 0.10 µg/ml or 0.7 nmol/L) and H231 (Kd = 0.18 µg/ml or 1.2 nmol/L), but not E27, bind mEREG-293T cells (Fig. 2A and Supplementary Fig. S2C). Non-targeting cmAb shows no binding and H231 failed to bind vector cells, verifying specificity (Fig. 2A and Supplementary Fig. S2C). H231 was selected as lead mAb for further characterization and ADC development due to its high affinity and maximum binding, species cross-reactivity, and high production

yield. We showed H231 has high affinity binding to endogenous EREG on DLD-1 (Kd= 0.36 µg/ml or 2.4 nmol/L; Fig. 2B) and LoVo (Kd= 0.15 µg/ml or 1.0 nmol/L; Fig. 2C) cells. No binding was detected for cmAb. We next quantified surface pro-EREG ligands/cell. CRC cells were incubated with H231 or cmAb conjugated with PE or left unstained and flow cytometric analysis was performed. DLD-1 EREG-KO cell line was established using CRISPR-Cas9 to further verify H231 specificity for endogenous EREG. KO was confirmed by western blot (Fig. 2D). Pro-EREG ranged between 367-24,998 ligands/cell in EREG-high cells (HCT116 and DLD-1) and were much lower in CRC cells with moderate (SW48) to low (SW620) EREG expression and DLD-1 EREG-KO cells (Fig. 2E and Supplementary Table S1). Mean pro-EREG/cell for HCT116 and DLD-1 cells were 2,644 and 4507, respectively, consistent with the acceptable number of targets/cell for clinically approved ADCs (Fig. 2E and Supplementary Table S1) (32,33).

Along with cell surface availability, an ideal target for ADC development should rapidly internalize and traffic to the lysosome for payload release. Immunocytochemistry (ICC) data shows H231 binds EREG-expressing LoVo, HCT116, and DLD-1 cells, internalizes, and co-localizes with the lysosome marker, LAMP1, after 1 h at 37 °C (Fig. 2F). As anticipated, H231 does not bind DLD-1 EREG KO cells and cmAb does not bind any CRC cell lines (Fig. 2F and Supplementary Fig. S2D). Next, to determine if EREG internalization is dependent on the presence of its receptors, we overexpressed hEREG in SW620 cells that do not express endogenous EREG, EGFR, or HER4/ERBB4 (Fig. 1I and Supplementary Fig. S2E). As shown in Fig. 2G, the H231-EREG complex effectively co-internalized to lysosomes, suggesting H231-mediated EREG internalization is independent of EGFR and HER4.

H231 Neutralization Activity

Mature, cleaved EREG binds to EGFR to potentiate signaling through PI3K/Akt or MAPK pathways (4). Thus, we tested the ability for H231 to neutralize EREG signaling. *KRAS* mutant DLD-1 and wildtype LIM1215 cells were treated with recombinant hEREG in the presence and absence of H231 or cmAb.

Treatment with hEREG for 5 min increased phosphorylation of EGFR and ERK1/2 in both cell lines and p-AKT only in LIM1215 cells, as DLD-1 cells also harbor a *PIK3CA* mutation (Fig. 2H). However, addition of H231, and not cmAb, inhibited downstream signaling mediated by hEREG, demonstrating H231-mediated neutralization (Fig. 2H).

ImmunoPET and biodistribution of ^{89}Zr-labeled H231

ImmunoPET imaging using ^{89}Zr-labeled mAbs provides a means to measure whole-body biodistribution and verify optimal tumor delivery of therapeutic mAbs to predict safety and efficacy (20,27). First, H231-DFO and cmAb-DFO immunoconjugates were generated and HPLC showed minimal variance in retention time and peak profiles, with no effect on H231 affinity (Fig. 3A and Supplementary Figs. S3A-B). Upon radiolabeling, ^{89}Zr-H231 showed high radiochemical yield >70% and purity >99% (Supplementary Fig. S3C), comparable to ^{89}Zr-cmAb. ImmunoPET of EREG-high DLD-1 cell xenografts demonstrated a marked increase in tumor uptake of ^{89}Zr-H231 compared to ^{89}Zr-cmAb, which showed minimal tracer accumulation at 5 dpi (Fig. 3B). Quantification of tumor-to-muscle ratios for ^{89}Zr-H231 (12.6 ± 6.3) were significantly higher than those for ^{89}Zr-cmAb (2.7 ± 0.4; Fig. 3C). Ex vivo biodistribution of tumor and normal tissues showed significant and 3.75-fold higher tumor uptake for ^{89}Zr-H231 and both tracers were predominantly cleared through the liver with increased renal clearance for ^{89}Zr-H231 (Fig. 3D). No notable EREG-specific uptake was observed in other organs.

Generation and validation of EREG ADCs using diverse linker-duocarmycin payloads

For development of an optimal EREG ADC, we generated three candidates with diverse linkers incorporating highly cytotoxic duocarmycins, which we previously showed to be an effective payload in CRC (34). H231-based ADCs were produced via a site-specific chemo-enzymatic approach using MTGase as previously described (Fig. 4A) (35). Briefly, a branched bis-azido linker was conjugated to H231 via the Q295 sites of the Fc region, followed by strain-promoted alkyne-azide cycloaddition to attach a series of

linker-duocarmycin DM (DuoDM) payloads incorporating clinically approved dipeptide (valine-citrulline; VC) or novel tripeptide (glutamic acid-glycine-citrulline; EGC) cleavable linkers shown to enhance ADC hydrophilicity and stability (Fig. 4A and Supplementary Fig. S4A-C) (26). Successful production and purification of EGC-cDuoDM was previously shown (26) and novel EGC-qDuoDM gluc linker-payload showed product purity >95% (Supplementary Fig. S5). Importantly, β-glucuronidation of qDuoDM-gluc allows it to function more as a prodrug that is more hydrophilic compared to cDuoDM (36). ESI-MS analysis confirmed homogeneity of each ADC with a uniform DAR= 4 (Fig. 4B) and Coomassie SDS-PAGE and size-exclusion chromatography (SEC) revealed high purity with no significant aggregation or dissociation (Supplementary Figs. S6 and S7A). Non-targeting cADC was generated with EGC-qDuoDM gluc and validated similarly (Supplementary Fig. S7B). Linker-payload conjugation did not affect H231 binding to LoVo and DLD-1 cells and cADC showed no binding (Supplementary Fig. S7C-D).

EREG ADCs demonstrate high selectivity and potency in a panel of CRC cells

Prior to evaluating therapeutic efficacy, we measured binding of all three EREG ADCs in parallel in DLD-1 cells. All ADCs demonstrated comparable binding affinities (Kd≈ 2.0 nmol/L; Fig. 5A). We showed EREG ADCs had subnanomolar potency in EREG-high DLD-1 and LoVo cells, whereas unconjugated H231, cmAb, and cADC had no activity (Figs. 5B-C and Supplementary Table S2). CRC cell-killing, rather than senescence, was demonstrated by increased PARP cleavage in DLD-1 and LoVo cells after 48 h treatment with H231 EGC-qDuoDM-gluc ADC (Supplementary Figs. S7E-F). Minimal PARP effects were observed with cADC (Supplementary Fig. S7F). Next, we evaluated activity of individual EREG ADCs in CRC cell lines expressing different levels of endogenous EREG and different *KRAS* mutational statuses. Overall, ADC potency for EREG-expressing CRC cell lines was: H231 EGC-qDuoDM-gluc > H231 EGC-cDuoDM > H231 VC-cDuoDM (Figs. 5D-F and Supplementary Table S2). For EREG-high *KRAS* mutant DLD-1, LoVo, and HCT116 cells IC50 values for EREG ADCs were: H231 EGC-qDuoDM-gluc (IC50s = 0.01-0.014 nmol/L), H231 EGC-cDuoDM (IC50s = 0.06-0.38 nmol/L), and H231 VC-cDuoDM (IC50s = 0.12-0.52 nmol/L). For EREG-high *KRAS*

wildtype SW48 cells, IC50 values ranged from 0.31-0.50 nmol/L. Furthermore, EREG ADCs had minimal in EREG-null SW620 or DLD-1 EREG KO cells, demonstrating efficacy is target-dependent (Figs 5D-F). These results show EREG ADCs mediate potent cell-killing efficacy in EREG-expressing CRC cells independent of *KRAS* mutational status.

EREG ADCs are well-tolerated and show significant antitumor efficacy in preclinical models of CRC

As H231 binds both hEREG and mEREG, we performed a single-dose escalation study to test for ADC on/off-target effects in immunocompetent C57BL/6 mice. Mice were administered vehicle (PBS) or 5 mg/kg or 10 mg/kg EREG ADCs and monitored for weight loss or other signs of overt toxicity. After 2 weeks, mice showed no significant changes in weight, white blood cell counts, liver enzymes (alanine and aspartate aminotransferases; ALT or AST), or kidney creatinine (CRE) (Fig. 6A-E). These findings suggest EREG ADCs are well-tolerated with no observable on- or off-target effects.

Antitumor efficacy was then evaluated in EREG-high *KRAS* mutant MSI-H xenograft models of LoVo and DLD-1 CRC cells (Fig. 6F-I). Mice were administered 5 mg/kg of EREG ADCs weekly for 3 doses, as it was determined safe and most FDA-approved ADCs are dosed ≤ 5 mg/kg (37). For LoVo xenografts, H231 VC-cDuoDM, H231 EGC-cDuoDM, and H231 EGC-qDuoDM gluc resulted in 64%, 70%, and 70% TGI, respectively, at day 19 when the vehicle cohort reached maximum tumor burden (Fig. 6F). As the tripeptide EGC linkers showed greatest efficacy and increased survival (Fig. 6G), we proceeded with evaluating these 2 ADCs in additional models. In the DLD-1 model, treatment with H231 EGC-cDuoDM and H231 EGC-qDuoDM gluc resulted in 29% and 68% TGI, respectively, at day 18 (Fig. 6H). Importantly, H231 EGC-qDuoDM gluc showed greatest increase in survival in DLD-1 xenograft models (Fig. 6I). We next evaluated EREG ADCs in two EREG-high MSS PDX models of CRC (Fig. 1H): *KRAS* mutant XST-GI-010 and *NRAS* mutant CRC-001. In the XST-GI-010 model, H231 EGC-cDuoDM and H231 EGC-qDuoDM gluc treatment resulted in 88% and 86% TGI at day 23 with similar impact on survival (Figs. 6J-K and

Supplementary Fig. 8A). Though unconjugated H231 showed no in vitro activity, treatment in vivo resulted in 50% TGI. As H231 EGC-qDuoDM gluc showed highest efficacy in all models, it was tested in the CRC-001 and showed 38% TGI and moderate increase in survival (Figs. 6L-M and Supplementary Fig. 8B). Treatment with cADC had no significant impact on tumor growth or survival in CRC cell xenografts, yet had 32% TGI in the XST-GI-010 model (Figs. 6F-J). No significant effects in bodyweight or overt toxicity were observed during treatment in nu/nu or NSG mice (Supplementary Figs. S8C-D). These findings demonstrate EREG ADCs have significant efficacy in EREG-expressing CRC tumor models irrespective MSI-H/MSS subtype or RAS mutations.

Discussion

Many clinical reports, including a recent large cohort study of mCRCs, have validated the prognostic role of EREG expression in *RAS* wildtype patients receiving EGFR-targeted therapies, cetuximab and panitumumab (13-17). While EGFR mAbs only benefit patients with wildtype *RAS*, EREG is highly expressed in both wildtype and mutant *RAS* tumors. Thus, EREG may not only serve as a prognostic marker, but a viable target for the development of novel therapies that benefit patients irrespective of *RAS* or other mutations. Importantly, EREG has considerably low expression in normal human and rodent tissues (4) and *Ereg* KO mice are viable and show no major developmental phenotype (38), suggesting minimal toxicity of EREG-targeted therapies. EREG expression is highest in MSS subtype that typically has worse prognosis and accounts for the majority of CRC. Furthermore, EREG is overexpressed in many other cancers with defined roles in tumor progression including lung, bladder, pancreatic, and breast (5-9). Thus, EREG-targeted therapies could hold benefit to several different tumor types.

In this study, we generated highly-specific EREG mAbs for the development of rationally-designed ADCs for improved CRC treatment. H231 was selected as the lead candidate based on high affinity, species cross-reactivity, and its ability to internalize into cancer cells and traffic to lysosomes, which is critical for

payload release (20,21). ImmunoPET and biodistribution studies showed ^{89}Zr-labeled H231 was sufficiently taken up by EREG-expressing tumors with minimal uptake in normal tissues (Fig. 3). H231 clearance was largely through the liver, as expected for therapeutic mAbs, though increased renal clearance was observed compared to cmAb. However, EREG ADC safety studies showed no adverse effects or changes in liver or kidney enzymes, suggesting they are well-tolerated. Previously, an EREG mAb was shown to have significant efficacy in a metastatic model of CRC based on antibody-dependent cell cytotoxicity (ADCC), not growth inhibitory activity (39). Similarly, we found H231 mAb to have no effect on CRC cell survival in vitro, yet moderate antitumor activity in NSG mice. Although NSG mice lack natural killer cells to mediate ADCC, other immune cells (e.g. macrophages and neutrophils) could be involved, though further investigation is needed.

For development of EREG ADCs with enhanced efficacy compared to unconjugated EREG mAb, selection of ADC payload and linker were carefully considered. Typical payloads being used in ADC development consist of microtubule inhibitors (e.g. MMAE and maytansines), topoisomerase inhibitors (e.g. camptothecins), and DNA-damaging agents (e.g. duocarmycins and pyrrolobenzodiazepines) (40,41). However, we and others have found colorectal tumors to be relatively resistant to microtubule inhibitors, yet respond to duocarmycins (34,42). Importantly, trastuzumab duocarmazine (SYD985), an ADC incorporating a duocarmycin payload, demonstrated progression-free and overall survival benefits and is anticipated to be clinically approved for the treatment of HER2^{+} metastatic breast cancers (43). Linkers can control efficacy and stability in systemic circulation and are broadly characterized as cleavable or non-cleavable by which payload release is dependent on lysosomal enzyme cleavage or proteolytic degradation, respectively (44,45). Cleavable linkers have the advantage of bystander effect, meaning released payloads can diffuse and kill neighboring cancer cells to better target tumor heterogeneity. We screened different cleavable linkers: one commercial and clinically validated dipeptide (VC) linker and two

tripeptide (EGC) linkers. Consistent with our previous report (26), ADCs incorporating the EGC linker showed enhanced potency in CRC cells in vitro and increased antitumor efficacy and survival in vivo. While ADCs with VC linkers have demonstrated increased risk of adverse effects and low tolerability attributed to premature payload release (46,47), EGC linkers have improved stability against multiple degradation events and potentially broader therapeutic windows (26). The increased TGI and survival of H231 EGC qDuoDM- compared to H231 EGC-cDuoDM-treated DLD-1 xenografts may then be attributed to its enhanced stability and tumor targeting capacity. Whereas cDuoDM contains an exposed tertiary amine that may foster non-specific binding, qDuoDM-gluc has a covalent bond between PAB and DuoDM that is more cleavage-resistant during circulation and minimizes non-specific binding, as observed in cell-killing at high concentration range in EREG-negative SW620 cells (Fig. 5E-F). Additionally, β-glucuronidation of qDuoDM-gluc increases ADC hydrophilicity and permits an extra layer of prodrug-based selectivity to avoid prelease of active payload (36,48). It is postulated that only after linker is cleaved by cathepsins in the lysosomes followed by β-glucuronidase conversion of seco-DuoDM to active form that payload can kill tumor cells and elicit bystander effect. Future work will involve testing additional tumor models and elucidating the precise mechanism for increased potency of H321 EGC-qDuoDM gluc. While tumor models were treated at 5 mg/kg, different dosing concentrations and frequencies should be conducted to determine if EREG ADCs can ultimately eliminate tumors and prevent relapse.

EREG expression positively correlates with expression of another EGFR ligand, amphiregulin (AREG). Similar to EREG, AREG levels predict superior response of mCRC patients to EGFR-targeted therapy (13,15,17). Notably, combined EREG/AREG expression was shown to be associated with progression-free and overall survival among *RAS* wildtype patients treated with anti-EGFR therapy (13,15,17). Another group recently reported the development of an AREG-targeted ADC that showed efficacy in a breast cancer xenograft model (49). AREG ADCs were generated using a mAb that selectively recognizes a neo-

epitope of the transmembrane stalk of cleaved AREG. Unlike our EREG ADCs that bind pro-EREG at the tumor cell surface, the AREG ADC did not recognize pro-AREG. Thus, it would be of interest to evaluate how post-translational processing effects these EGFR ligand-targeted ADCs and if co-targeting EREG and AREG provides an improved therapeutic strategy.

Our data show EREG is a promising target for the development of ADCs with broad utility for treating colorectal and other EREG-high tumor types. Importantly, EREG ADCs demonstrated therapeutic efficacy in both *KRAS* mutant and wildtype CRC cell lines and tumors, suggesting their potential to benefit a broader patient population than current EGFR-targeted therapies. As EREG is highly expressed on tumors with minimal surface expression on normal tissues, it will likely have a promising safety profile. However, future evaluation in non-human primates and clinical trials are warranted. Recent and exciting progress in validation of EREG as a well-defined biomarker for predicting patient response to EGFR mAbs could be employed to discriminate patients that would respond to EREG ADC therapies, irrespective of tumor mutational status.

Authors' Contributions

Conceptualization and Design: K.S.C; Methodology: K.S.C., J.J., Y.A., K.T., A.A.; Investigation: K.S.C., J.J., Y.A., P.H., Z.L., S.S., S.C.G., S.A., C.G., Q.J.L., J.R., A.A., K.T.; Data curation: K.S.C., J.J., Y.A., P.H., Z.L., S.S., S.C.G., S.A., C.G., H.T.; Formal Analysis: K.S.C., J. J., Y.A.; Writing original draft: K.S.C. and J.J.; Review and Editing: K.S.C, J.J., P.H., C.G., H.T.; Resources: K.S.C., Q.J.L., J.H.R., A.A., K.T.; Funding acquisition: K.S.C.. Q.J.L.; Supervision: K.S.C.

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Figure Legends

Figure 1. EREG is highly expressed in colorectal tumors and cancer cell lines. A, *EREG* RNA-Seq expression data from patient tumors of the colorectal adenocarcinoma (COADREAD) TCGA cohort. Values are Log2 RNA-Seq by expectation–maximization (Log2 RSEM). **B,** *EREG* RNA-Seq RSEM values for matched tumor and adjacent normal from the COADREAD cohort (N=32). Distribution of **C,** MSI-H (N=23), MSI-L (N=30), and MSS (N=129) subtypes and **D**, *KRAS* WT (N=109) and MUT (N=56) status based on *EREG* expression. Values are read per kilobase of transcript per million (RPKM). Kaplan-Meier analyses of **E,** disease-free survival (*EREG*-High, N=86; *EREG*-Low, N=245) and **F,** overall survival (*EREG*-High, N=92; *EREG*-Low, N=279) in patients from the COADREAD cohort. P values were obtained by the log-rank test. **G**, *EREG* RNA-seq values from cohort of 18 matched normal colonic epithelium, primary adenocarcinoma, and synchronous liver metastases (NCBI GSE50760). **H**, Western blot endogenous EREG protein expression in patient-derived xenograft (PDX) models. *indicates mutant *NRAS*. **I,** *EREG* RNA-seq values for select CRC cell lines used in this study from Cancer Cell Line Encyclopedia (CCLE). **J**, Western blot of endogenous EREG protein expression across CRC cell lines. Quantitative data presented as mean ± SEM and statistical analysis performed using one-way analysis of variance (ANOVA) and Tukey's multiple comparison test or paired Student's t test for two groups. ** $P < 0.01$, *** $P < 0.001$.

Figure 2. Characterization of H231 mAb binding, neutralization, and internalization. A, Cell-based binding assays show H321 mAb binds recombinant hEREG- and mEREG-overexpressing 293T cells and not vector cells. H231 and not cmAb binds endogenous EREG in B, DLD-1 and C, LoVo cells. Data presented as mean ± SD. D, Western blot of DLD-1 cells with high EREG expression stably transduced with CRISPR-Cas9 vector containing sgRNA to generate EREG knockout (KO) line. E, H231 and cmAb conjugated to phycoerythrin (PE) were utilized for the flow cytometric analysis to quantify surface pro-EREG ligands/cell using QuantBRITE PE kit. F, Confocal images shows H231 binds to EREG and co-localizes with lysosome

marker, LAMP1, after 90 mins at 37 °C in EREG-expressing LoVo, HCT116, and DLD-1 cells and not DLD-1 EREG KO cells. Yellow indicates colocalization. G, Overexpressed (O.E.) EREG co-localizes with lysosomes in EGFR-negative SW620 CRC cells after H231 treatment. H, Western blot of DLD-1 and LIM1215 cells treated in the presence of 15 µg/ml cmAb or H231 for 5 min with or without 300 ng/ml EREG.

Figure 3. ImmunoPET imaging and biodistribution of H231 in EREG-high colorectal tumors. A, Cell-based binding assay shows equivalent binding for unconjugated H231 mAb and lysine-conjugated H231-DFO on DLD-1 cells. **B,** Representative PET/CT images acquired 5 days post-injection of ^{89}Zr-radiolabeled EREG-targeting H231 mAb or non-targeting cmAb in DLD-1 tumor xenografts. **C,** Quantification of PET images tumor/muscle ratio (%ID/cc) of ^{89}Zr-H231 (N=4) and ^{89}Zr-cmAb (N=3). **D,** Biodistribution data (ID/g%) measured ex vivo in tumor and normal tissues (^{89}Zr-H231, N=5; ^{89}Zr-cmAb (N=4). Statistical analysis using Student's t-test. Quantitative data presented as mean ± SD. *P< 0.05, **P< 0.01, *** P< 0.001.

Figure 4. Generation of EREG-targeting antibody-drug conjugates. A, Schematic depiction of microbial transglutaminase (mTGase)-mediated conjugation of a branched linker to Q295 of the Fc region of H231 mAb followed by strain promoted alkyne-azide cycloaddition of duocarmycin DM (DuoDM) payload attached to either a cleavable dipeptide valine-citrulline (VC) or tripeptide glutamic acid-glycine-citrulline (EGC) linker to generate H321 ADCs (DAR = 4). **B**, Deconvoluted ESI-mass spectra. First panel, H231 mAb; second panel, H231-branched linker conjugate, third panel, H231-VC-cDuoDM ADC; fourth panel, H231-EGC-cDuoDM ADC; fifth panel, H231-EGC-qDMDM gluc ADC. All homogeneous ADCs have a DAR of 4. *Fragment ions detected in ESI-MS analysis.

Figure 5. Therapeutic potency and selectivity of EREG ADCs in CRC cell lines. A, Binding of H231 ADCs and non-targeting control ADC (cADC, DAR=4) with same linker-payload. **B,** Efficacy of H231 ADCs modified with different linkers, H231, cmAb, and cADC in DLD-1 cells. **C**, Dose-dependent cytotoxicity of H231 EGC-qDuoDM gluc ADC in LoVo cells. H231, cmAb, and cADC have minimal effects. Efficacy of **D**,

H231 VC-cDuoDM, **E,** H231 EGC-cDuoDM, and **F,** H231 EGC-qDuoDM glu in a panel of CRC cell lines with different levels of EREG expression. Quantitative data presented as mean ± SD.

Figure 6. EREG ADC safety assessment and antitumor efficacy in CRC cell line and patient-derived xenograft models. Immunocompetent C57BL/6 mice were treated with single-dose EREG ADCs consisting of VC or EGC cleavable linkers as indicated, or PBS vehicle. **A,** Bodyweight measurements of C57BL/6 mice (n=4/group). **B,** White blood cell (WBC) counts on day 14. **C,** Alanine aminotransferase (ALT) and **D**, aspartate aminotransferase (AST) liver enzyme analysis and **E**, kidney creatinine in serum collected from mice on day 14. **F**, Antitumor efficacy of EREG ADCs in LoVo nu/nu xenografts (n=9, vehicle; n=5 for all other groups). **G**, Kaplan-Meier survival plot and log-rank test for LoVo xenografts. Vehicle and cADC showed similar survival. **H**, Antitumor efficacy of EREG ADCs as indicated in DLD-1 nu/nu xenografts (n=6, vehicle and H231 EGC-qDuoDM; n=5, cADC and H231 EGC-qDuoDM gluc) **I,** Kaplan–Meier survival plot and log-rank test for DLD-1 xenografts. (**J-M**) Antitumor efficacy in patient-derived tumor xenograft (PDX) models. **J,** XST-GI-010 individual animals (n=13, vehicle; n=5, cADC and H231 EGC-cDuoDM; n=7, H231 EGC-qDuoDM) and **K,** average tumor volume at day 23. **L**, CRC-001 individual animals (n=5, vehicle; n=6, H231 EGC-qDuoDM) and **M**, average tumor volume at Day 27. Statistical analysis performed using Student's unpaired two-tailed t test for two groups or one-way analysis of variance (ANOVA) and Dunnett's multiple comparison test. Quantitative data presented as mean ± SD. *P< 0.05, **P< 0.01, ***P< 0.001.

Figure 1

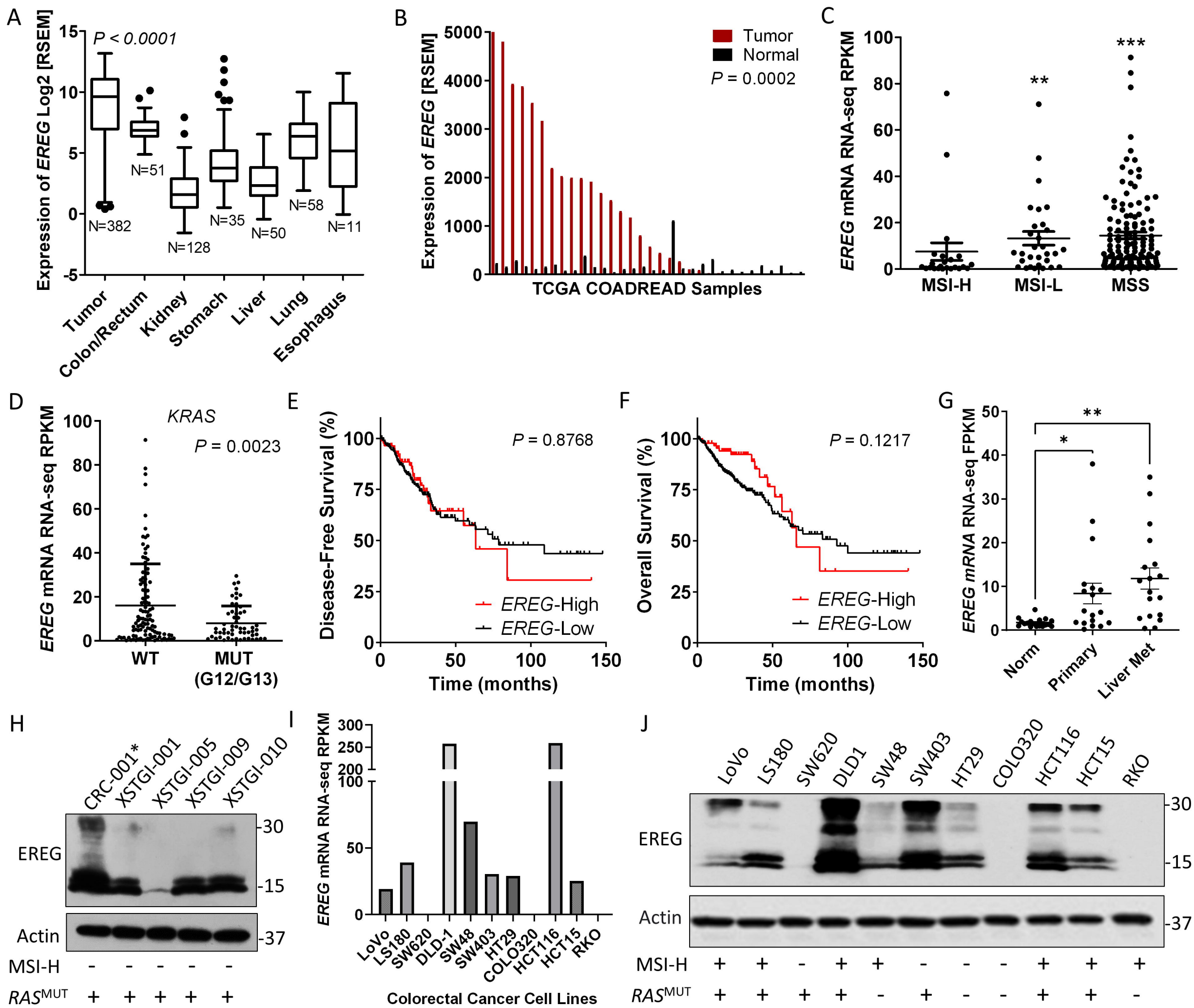

A
Expression of EREG Log2 [RSEM]
P < 0.0001
N=382
N=51
N=128
N=35
N=50
N=58
N=11
Tumor
Colon/Rectum
Kidney
Stomach
Liver
Lung
Esophagus
B
Expression of EREG [RSEM]
Tumor
Normal
P = 0.0002
TCGA COADREAD Samples
C
EREG mRNA RNA-seq RPKM
MSI-H
MSI-L
MSS
D
EREG mRNA RNA-seq RPKM
KRAS
P = 0.0023
WT
MUT (G12/G13)
E
Disease-Free Survival (%)
P = 0.8768
EREG-High
EREG-Low
Time (months)
F
Overall Survival (%)
P = 0.1217
EREG-High
EREG-Low
Time (months)
G
EREG mRNA RNA-seq FPKM
Norm
Primary
Liver Met
H
CRC-001*
XSTGI-001
XSTGI-005
XSTGI-009
XSTGI-010
EREG
Actin
MSI-H
RASMUT
I
EREG mRNA RNA-seq RPKM
LoVo
LS180
SW620
DLD-1
SW48
SW403
HT29
COLO320
HCT116
HCT15
RKO
Colorectal Cancer Cell Lines
J
LoVo
LS180
SW620
DLD1
SW48
SW403
HT29
COLO320
HCT116
HCT15
RKO
EREG
Actin
MSI-H
RASMUT

Figure 2

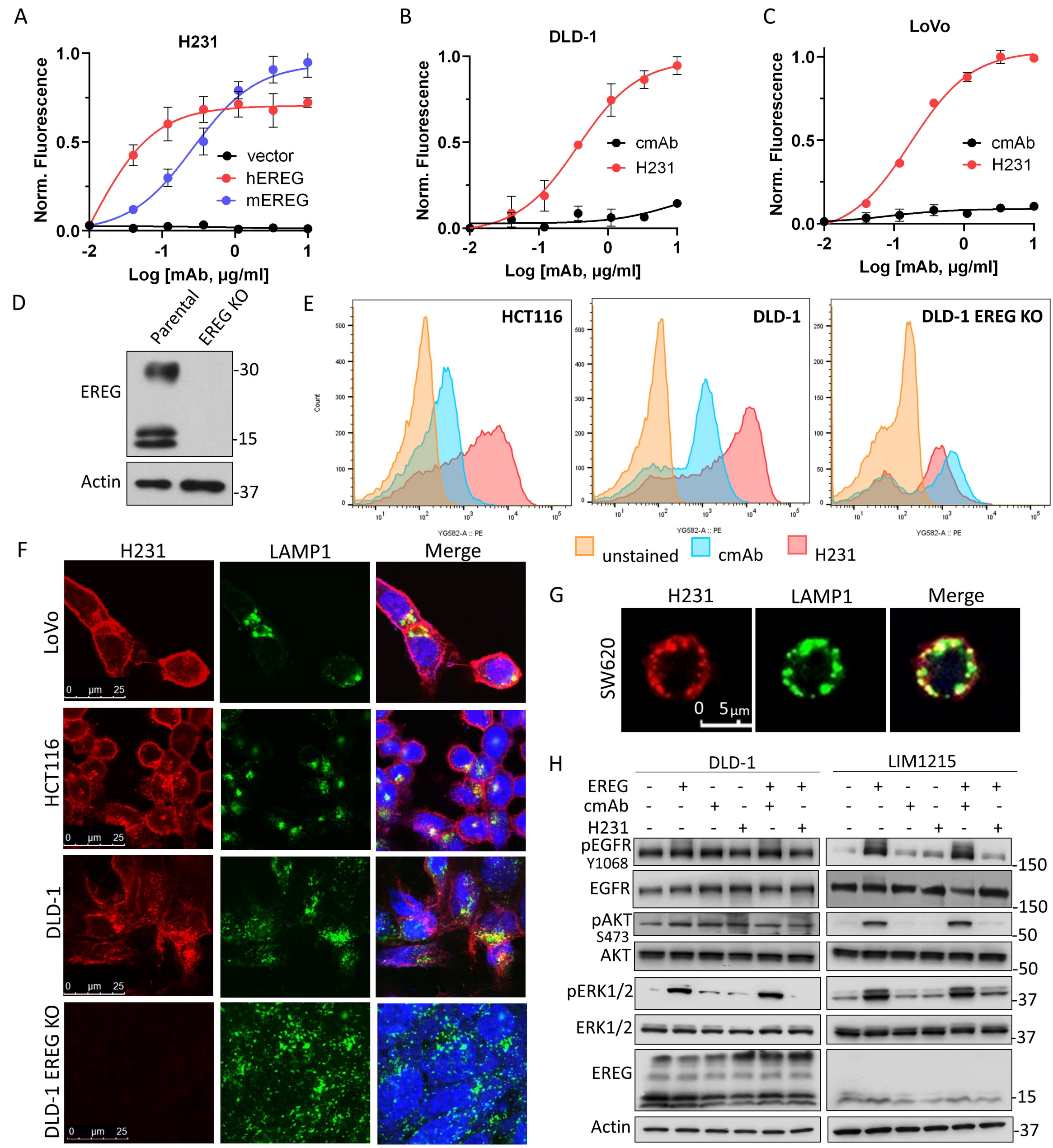

A
H231
Norm. Fluorescence
Log [mAb, µg/ml]
vector
hEREG
mEREG
B
DLD-1
cmAb
H231
C
LoVo
D
Parental
EREG KO
EREG
Actin
-30
-15
-37
E
HCT116
DLD-1
DLD-1 EREG KO
Count
YG582-A :: PE
unstained
cmAb
H231
F
H231
LAMP1
Merge
LoVo
HCT116
DLD-1
DLD-1 EREG KO
0 µm 25
G
H231
LAMP1
Merge
SW620
0 5µm
H
DLD-1
LIM1215
EREG
cmAb
H231
pEGFR Y1068
EGFR
pAKT S473
AKT
pERK1/2
ERK1/2
EREG
Actin
150
150
50
50
37
37
15
37

Figure 3

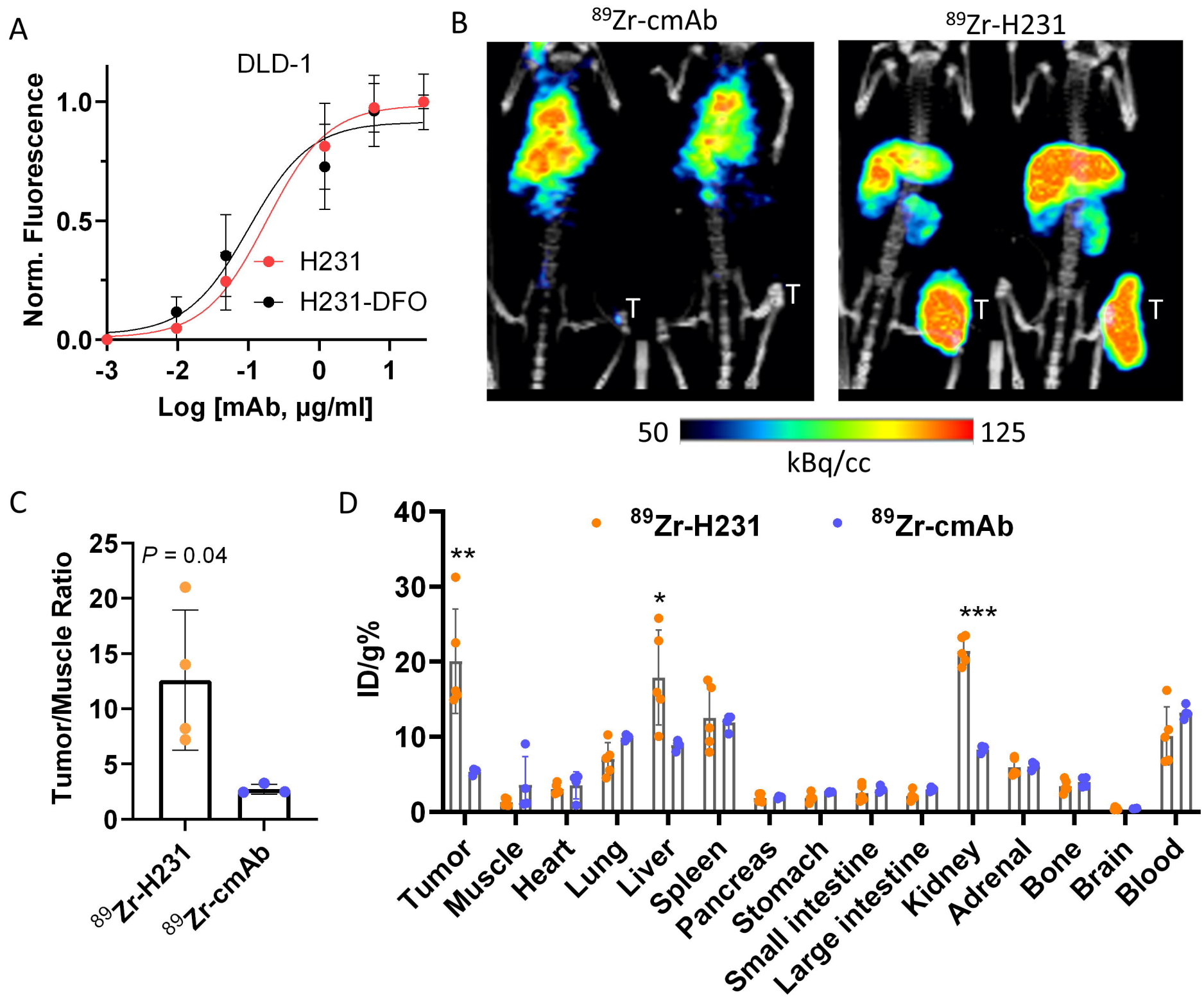
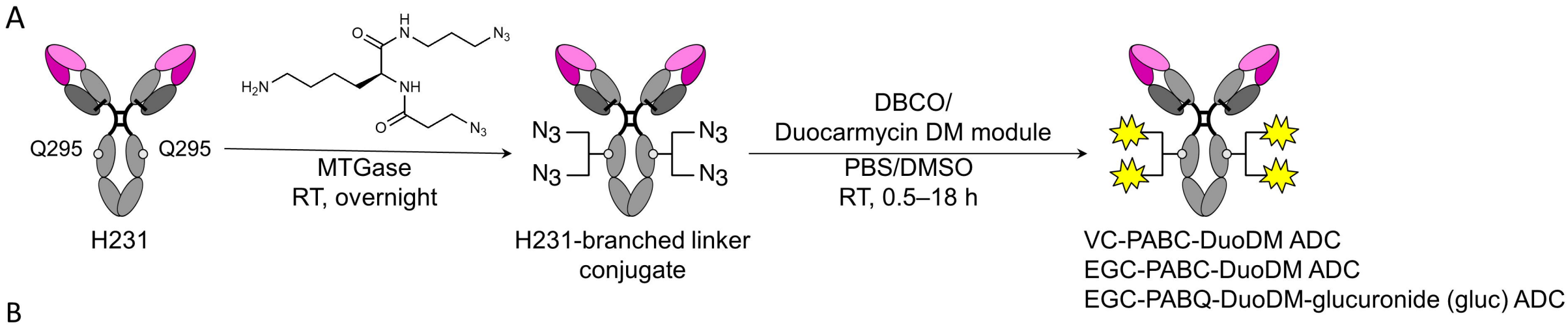

A
DLD-1
Norm. Fluorescence
1.0
0.5
0.0
-3
-2
-1
0
1
Log [mAb, µg/ml]
H231
H231-DFO
B
89Zr-cmAb
89Zr-H231
T
T
T
T
50
125
kBq/cc
C
Tumor/Muscle Ratio
P = 0.04
25
20
15
10
5
0
89Zr-H231
89Zr-cmAb
D
ID/g%
40
30
20
10
0
89Zr-H231
89Zr-cmAb
**
*
***
Tumor
Muscle
Heart
Lung
Liver
Spleen
Pancreas
Stomach
Small intestine
Large intestine
Kidney
Adrenal
Bone
Brain
Blood

Figure 4

A


Q295
Q295
MTGase
RT, overnight
N3
N3
N3
N3
DBCO/
Duocarmycin DM module
PBS/DMSO
RT, 0.5–18 h
H231
H231-branched linker conjugate
VC-PABC-DuoDM ADC
EGC-PABC-DuoDM ADC
EGC-PABQ-DuoDM-glucuronide (gluc) ADC

B

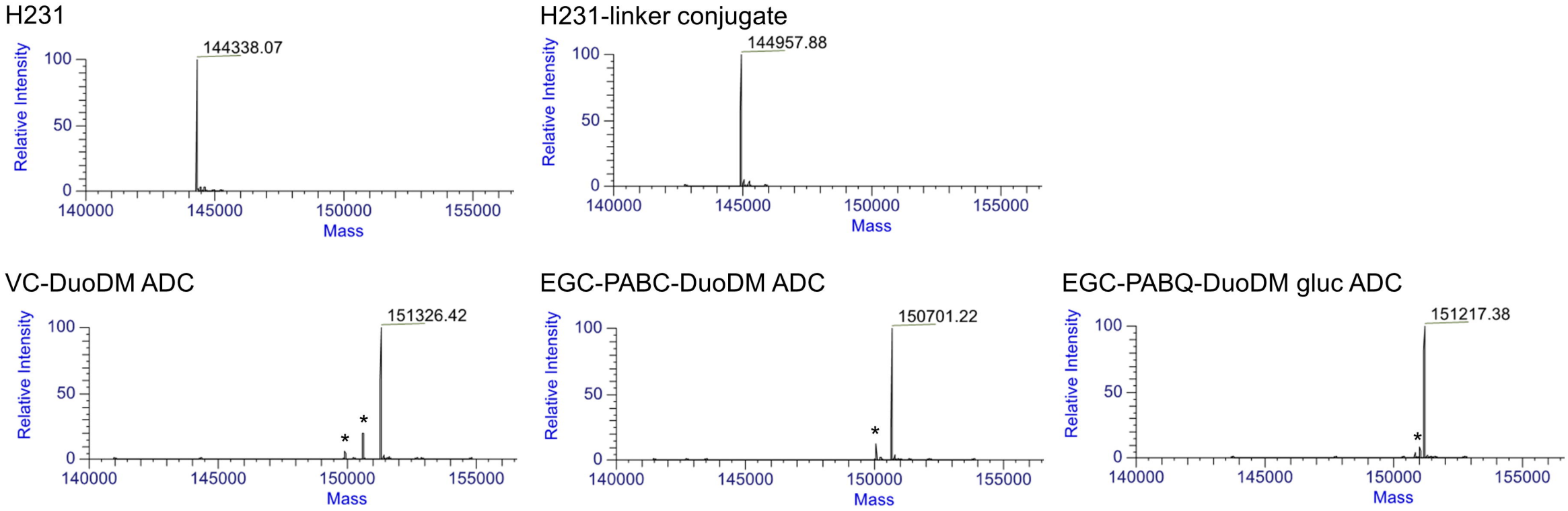

H231
144338.07
H231-linker conjugate
144957.88
VC-DuoDM ADC
151326.42
EGC-PABC-DuoDM ADC
150701.22
EGC-PABQ-DuoDM gluc ADC
151217.38
Relative Intensity
Mass
140000
145000
150000
155000
0
50
100

Figure 5

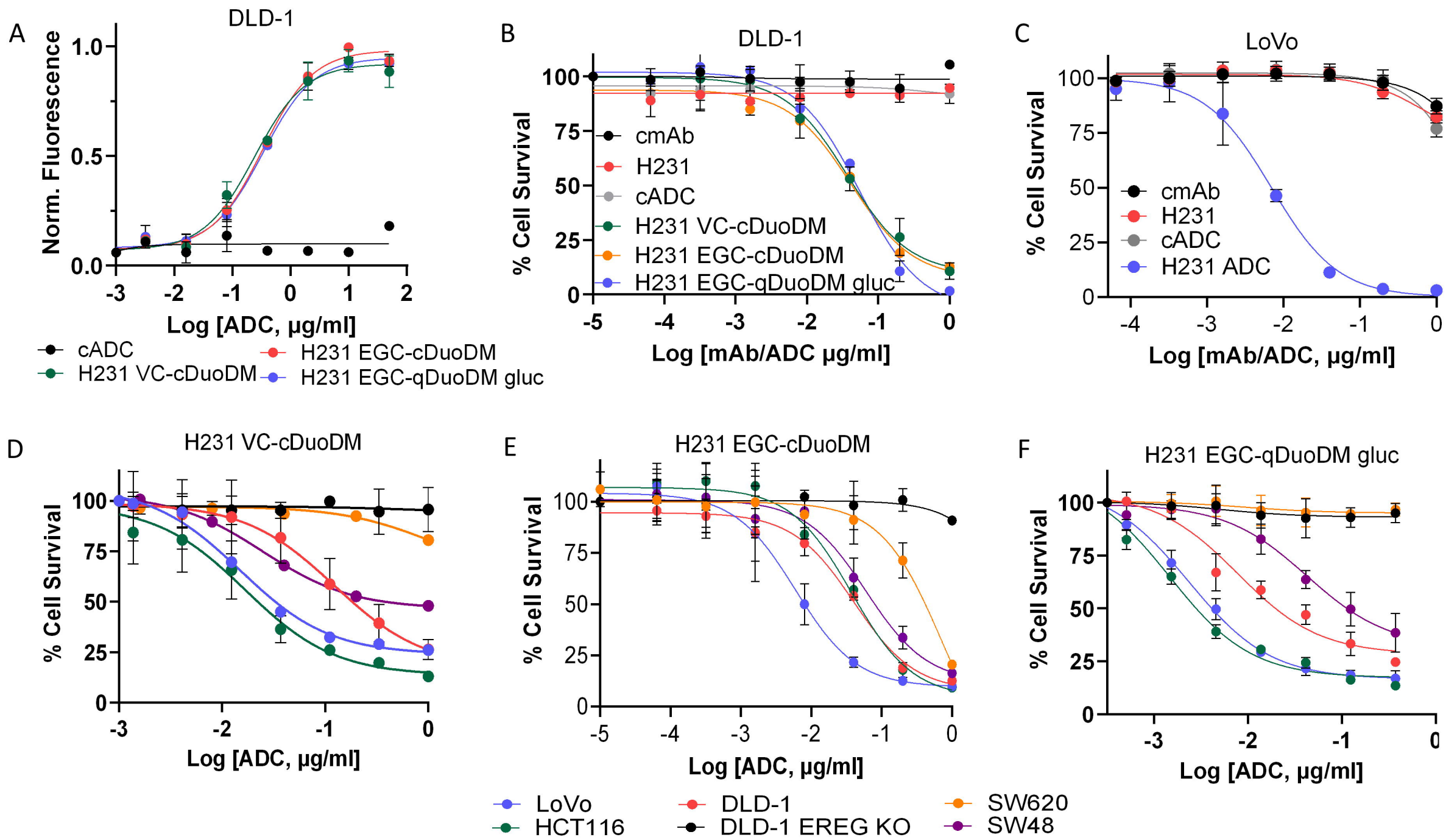
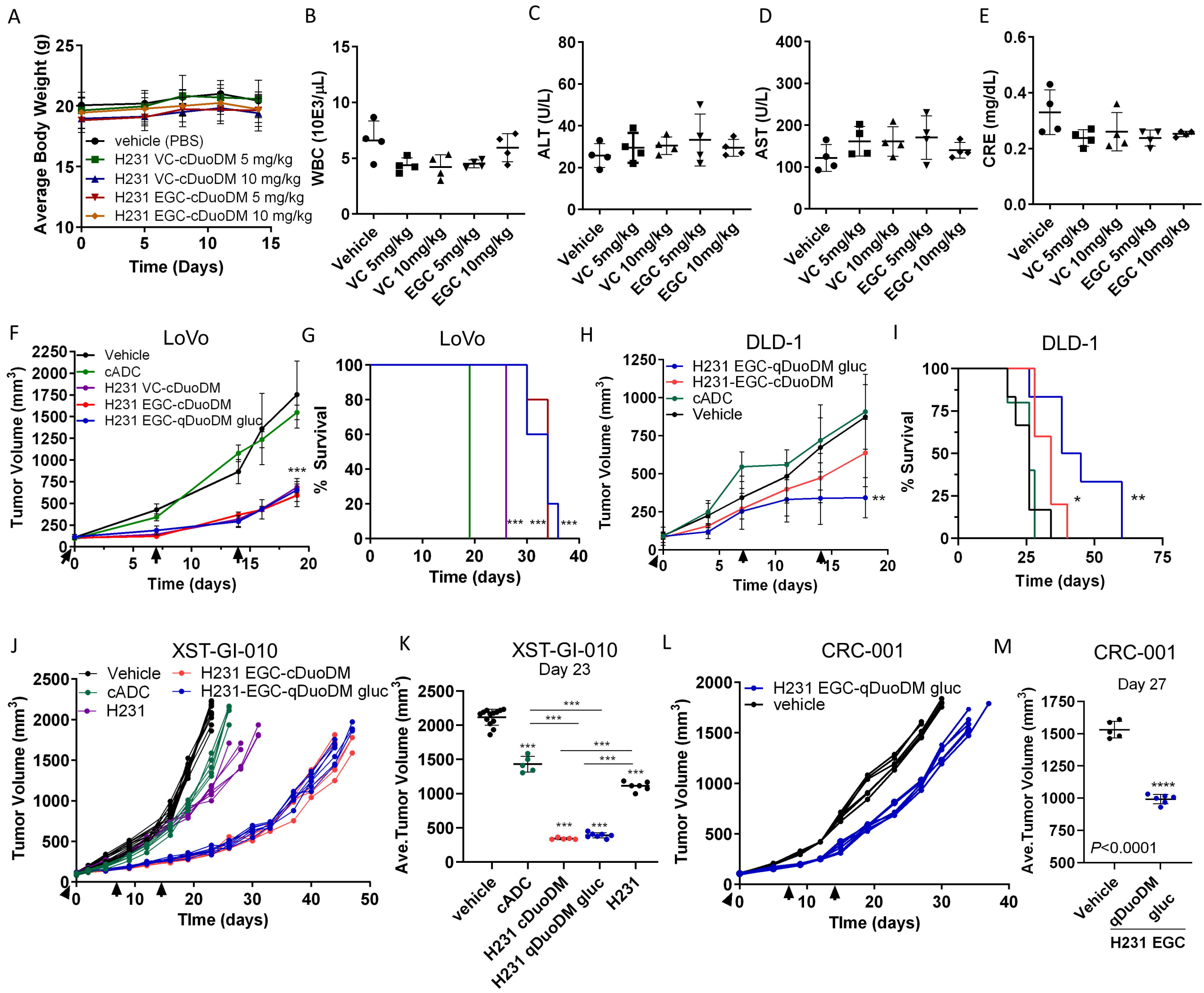

A
DLD-1
Norm. Fluorescence
Log [ADC, µg/ml]
cADC
H231 VC-cDuoDM
H231 EGC-cDuoDM
H231 EGC-qDuoDM gluc
B
DLD-1
% Cell Survival
Log [mAb/ADC µg/ml]
cmAb
H231
cADC
H231 VC-cDuoDM
H231 EGC-cDuoDM
H231 EGC-qDuoDM gluc
C
LoVo
% Cell Survival
Log [mAb/ADC, µg/ml]
cmAb
H231
cADC
H231 ADC
D
H231 VC-cDuoDM
% Cell Survival
Log [ADC, µg/ml]
E
H231 EGC-cDuoDM
% Cell Survival
Log [ADC, µg/ml]
F
H231 EGC-qDuoDM gluc
% Cell Survival
Log [ADC, µg/ml]
LoVo
HCT116
DLD-1
DLD-1 EREG KO
SW620
SW48

Figure 6


A
Average Body Weight (g)
Time (Days)
vehicle (PBS)
H231 VC-cDuoDM 5 mg/kg
H231 VC-cDuoDM 10 mg/kg
H231 EGC-cDuoDM 5 mg/kg
H231 EGC-cDuoDM 10 mg/kg
B
WBC (10E3/μL)
C
ALT (U/L)
D
AST (U/L)
E
CRE (mg/dL)
Vehicle
VC 5mg/kg
VC 10mg/kg
EGC 5mg/kg
EGC 10mg/kg
F
LoVo
Tumor Volume (mm3)
Time (days)
Vehicle
cADC
H231 VC-cDuoDM
H231 EGC-cDuoDM
H231 EGC-qDuoDM gluc
G
LoVo
% Survival
Time (days)
H
DLD-1
Tumor Volume (mm3)
Time (days)
H231 EGC-qDuoDM gluc
H231-EGC-cDuoDM
cADC
Vehicle
I
DLD-1
% Survival
Time (days)
J
XST-GI-010
Tumor Volume (mm3)
TIme (days)
Vehicle
cADC
H231
H231 EGC-cDuoDM
H231-EGC-qDuoDM gluc
K
XST-GI-010
Day 23
Ave.Tumor Volume (mm3)
vehicle
cADC
H231 cDuoDM
H231 qDuoDM gluc
H231
L
CRC-001
Tumor Volume (mm3)
TIme (days)
H231 EGC-qDuoDM gluc
vehicle
M
CRC-001
Day 27
Ave.Tumor Volume (mm3)
P<0.0001
Vehicle
qDuoDM
gluc
H231 EGC