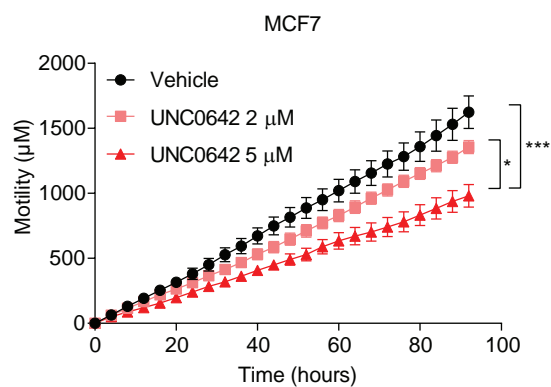
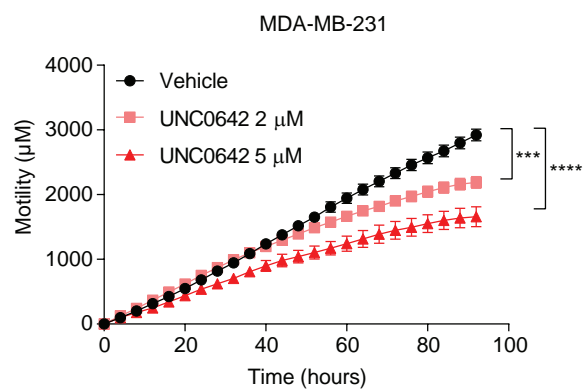
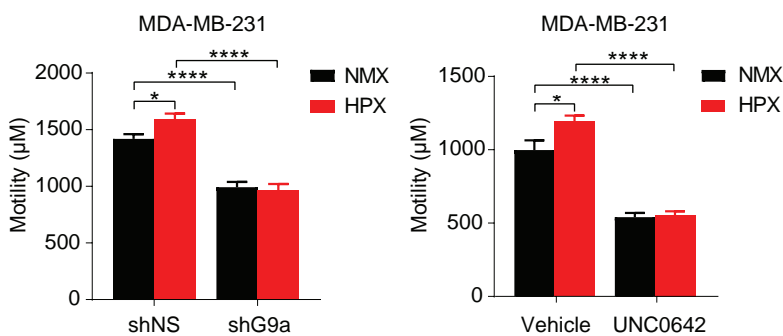
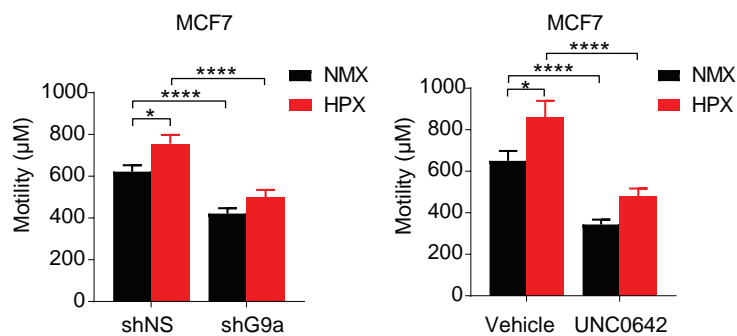
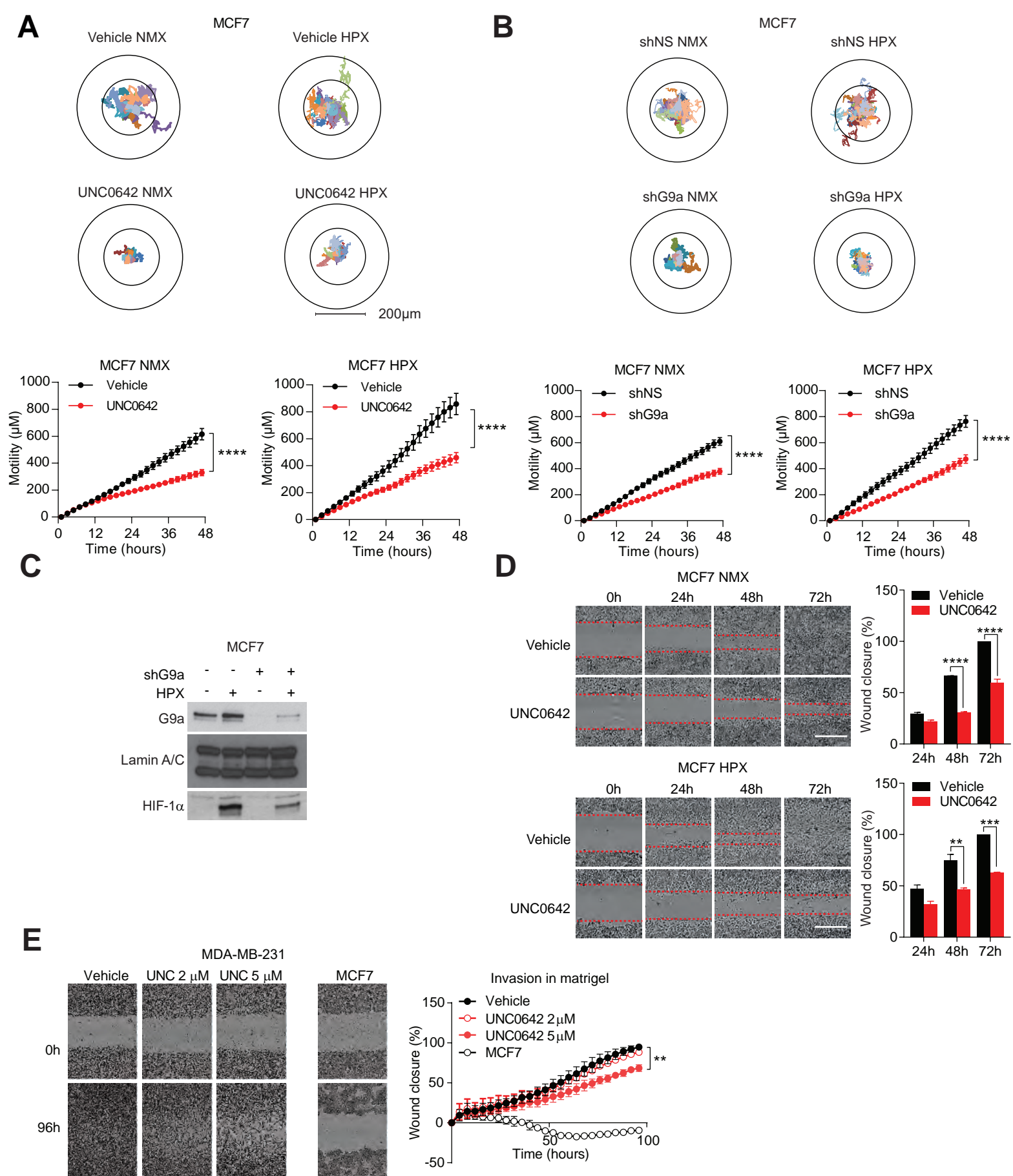


A**B****C****Figure S1**

(A) Holomonitor analysis of cellular motility in MCF7 and MDA-MB-231 cell lines following treatment with UNC0642 (2 or 5 μM) for 96 hours. (B) Bar graph representing the total distance covered by MDA-MB-231 and (C) MCF7 tracked through holographic microscopy for 48 hours under normoxic (21% O_2) or hypoxic (1% O_2) conditions, following G9a knock down or UNC0642 treatment (5 μM). Data are represented as mean \pm SEM (One-way ANOVA, * $p < 0.05$, *** $p < 0.0005$, **** $p < 0.0001$).



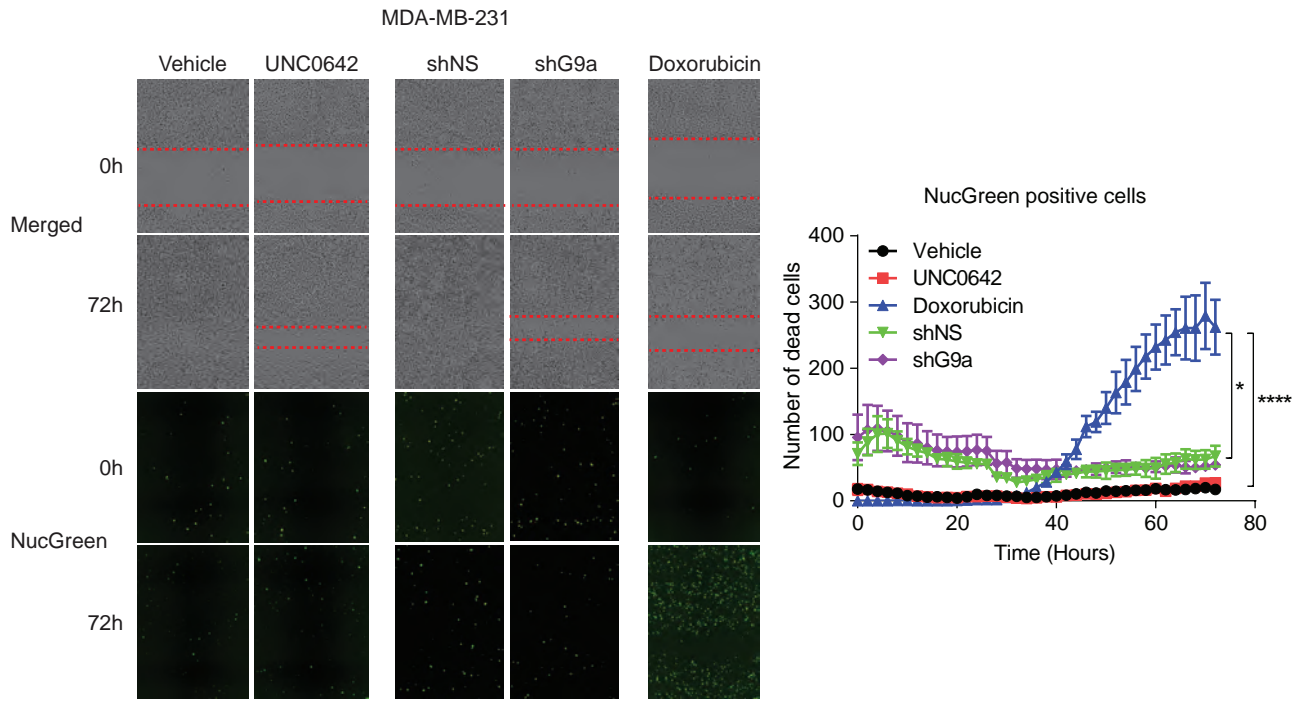


Figure S3
 Scratch wound healing assay in MDA-MB-231 cells treated with UNC0642 (5 μ M) or following G9a KD in the presence of NucGreen dead cells stain. Top phase-contrast images are merged with Green channel. Bottom images show only the relative green signal. Graph represents NucGreen quantification over time. Doxorubicin (1 μ M) was used as positive control. Data are represented as mean \pm SEM (non-parametric, Student's t-test), * $p < 0.05$, **** $p < 0.0001$).

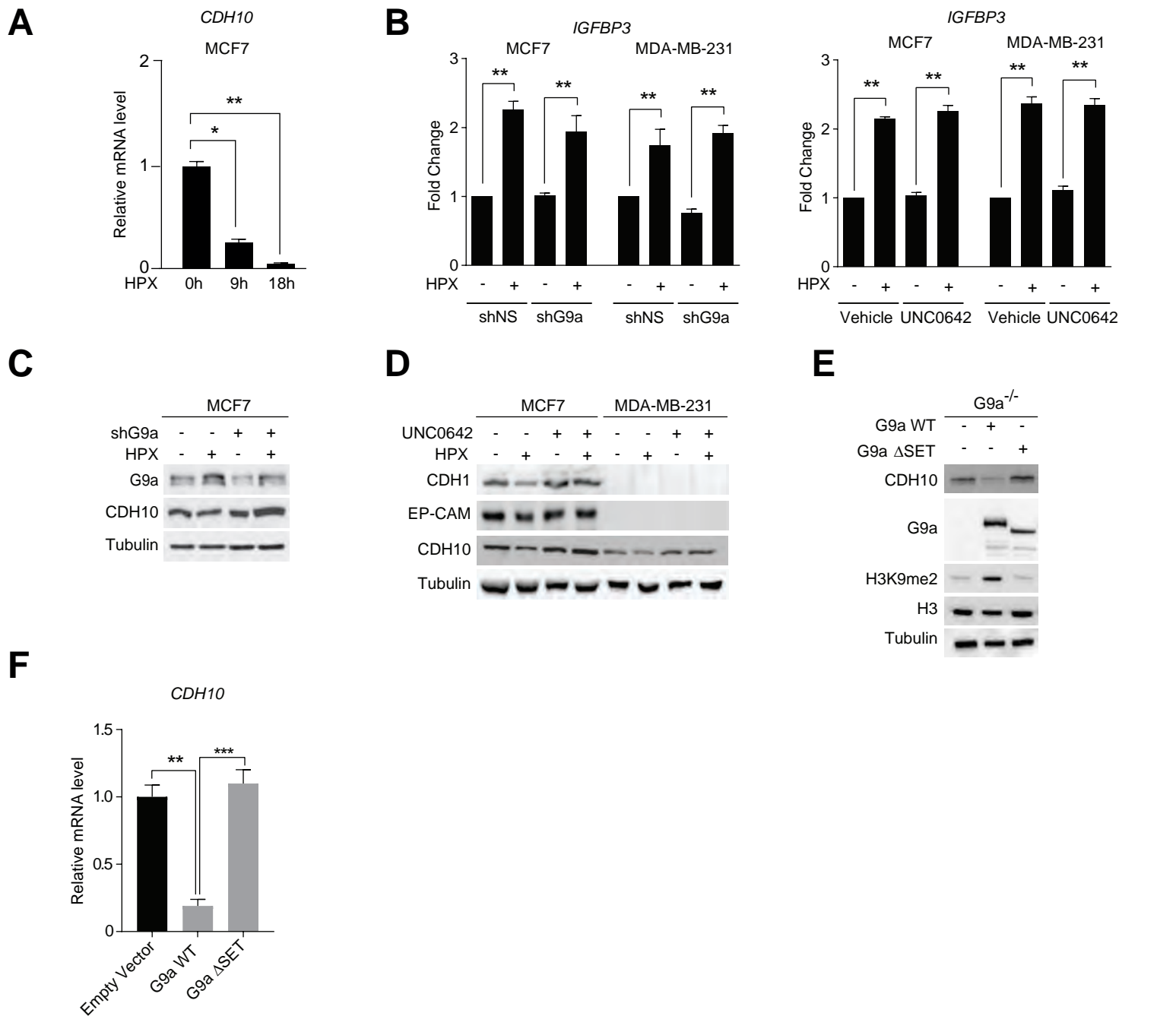


Figure S4. (A) *CDH10* expression in MCF7 cells cultured under hypoxic conditions for the indicated times. (B) *IGFBP3* expression evaluated in MDA-MB-231 and MCF7 cells as positive control for the hypoxic environment. (C) Western Immunoblotting analysis of *CDH10* in MCF7 cells transfected with shG9a and exposed to normoxia or hypoxia for 24 hours. (D) Western Immunoblotting analysis of *CDH1*, *EpCAM* and *CDH10* in MCF7 and MDA-MB-231 following exposure to normoxia or hypoxia for 24 hours in the presence or in the absence of UNC0642 (5 μ M). (E) Western immunoblotting analysis of *CDH10* and H3K9me2 in *G9a*^{-/-} MEFs transfected with WT *G9a* or *G9a* Δ SET. (F) *CDH10* mRNA levels in *G9a*^{-/-} MEFs transfected as described. Data are represented as mean \pm SEM (non-parametric, Student's t-test), * $p < 0.05$, ** $p < 0.005$, *** $p < 0.005$.

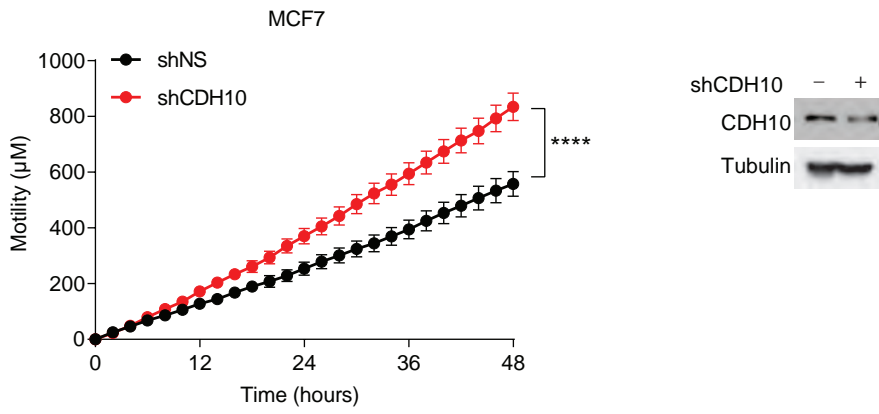


Figure S5. Evaluation of the migratory distance covered in 48 hours by MCF7 following CDH10 KD using the HoloMonitor M4. Data are represented as mean \pm SEM (non-parametric, Student's t-test), **** $p < 0.0001$.

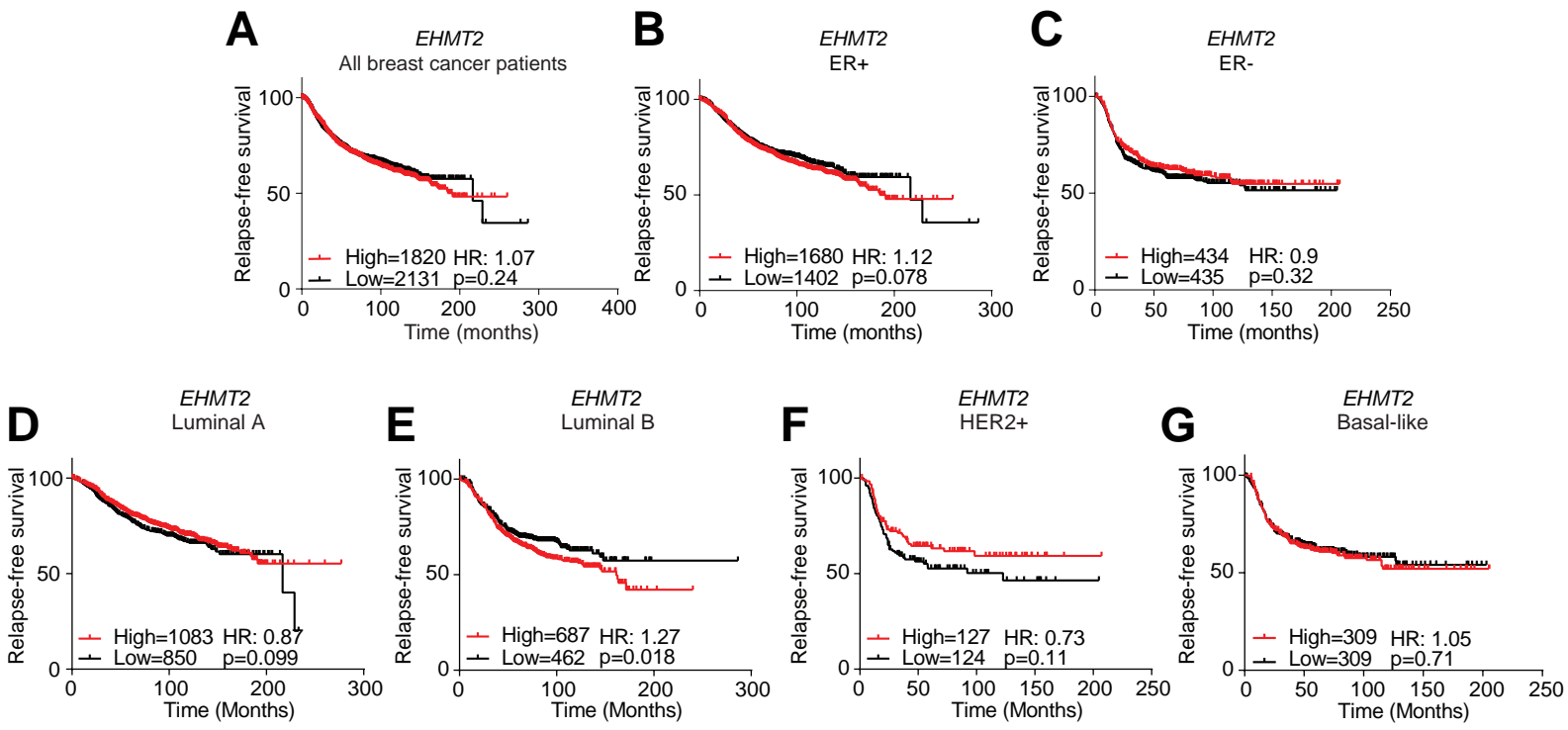
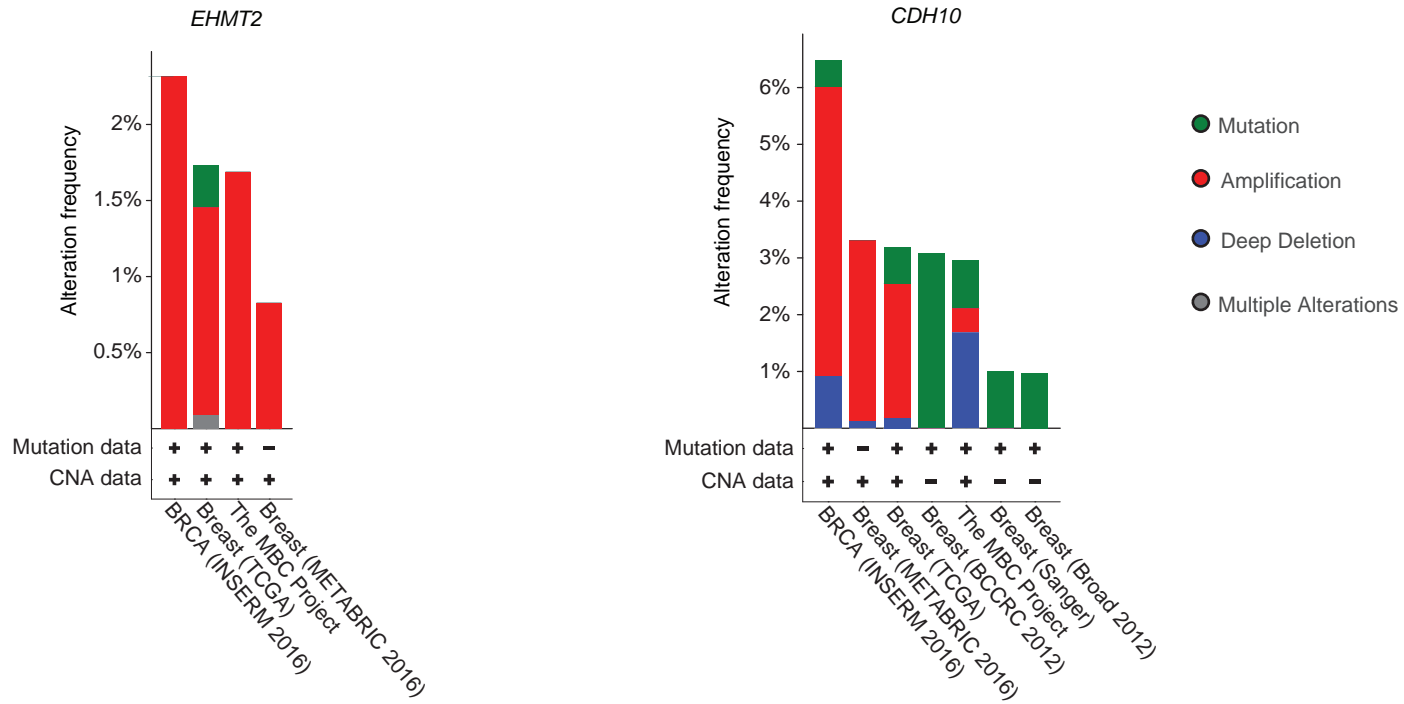


Figure S6. Kaplan-Meier relapse-free survival analysis of *EHM2* expression in (A) all breast cancer patients, (B) ER+, (C) ER-, (D) luminal A, (E) luminal B, (F) HER2+ and (G) basal-like.

A



B

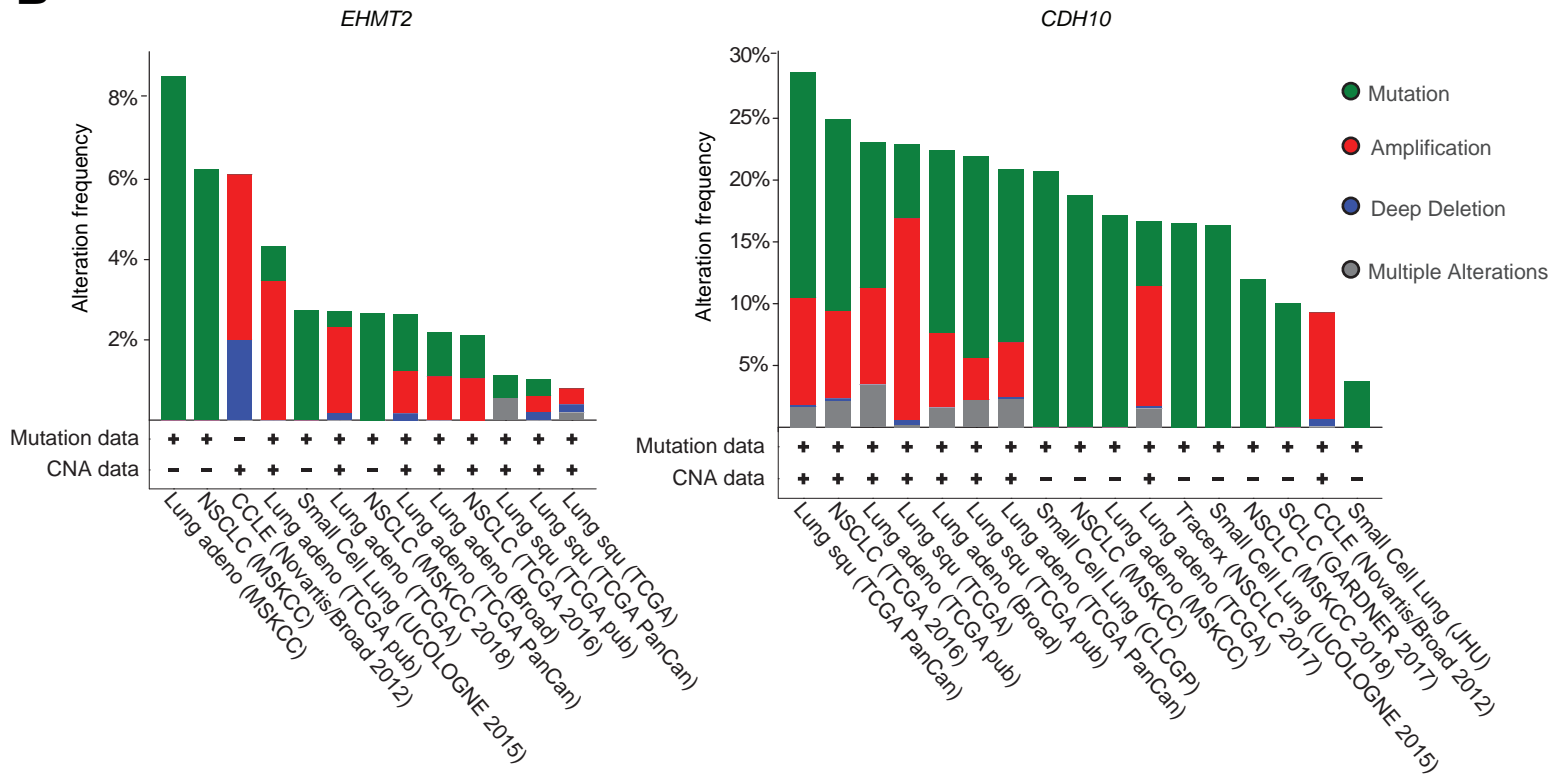


Figure S7. (A) Percentage and type of alterations in the *EHMT2* and *CDH10* genes in breast cancer patients and (B) lung cancer patients, subdivided by cancer study.

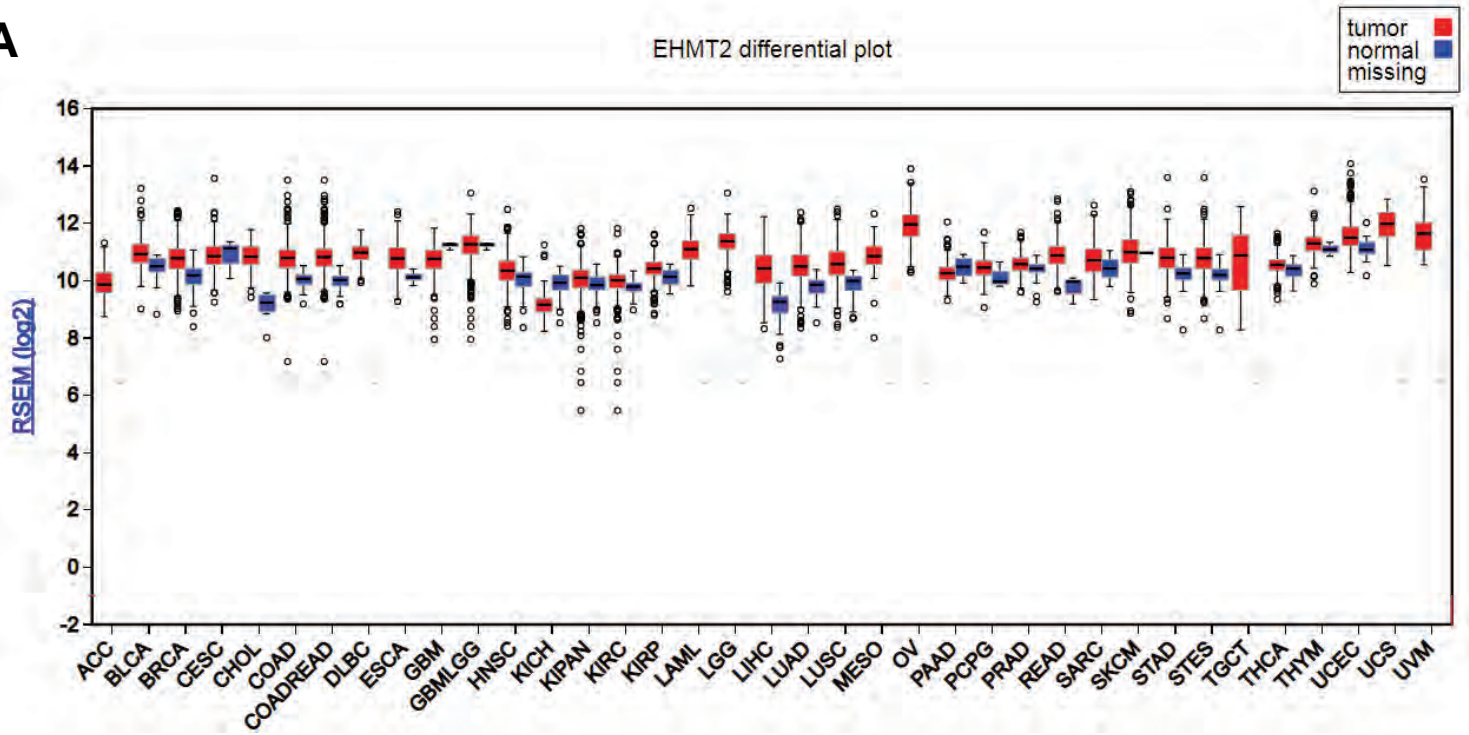
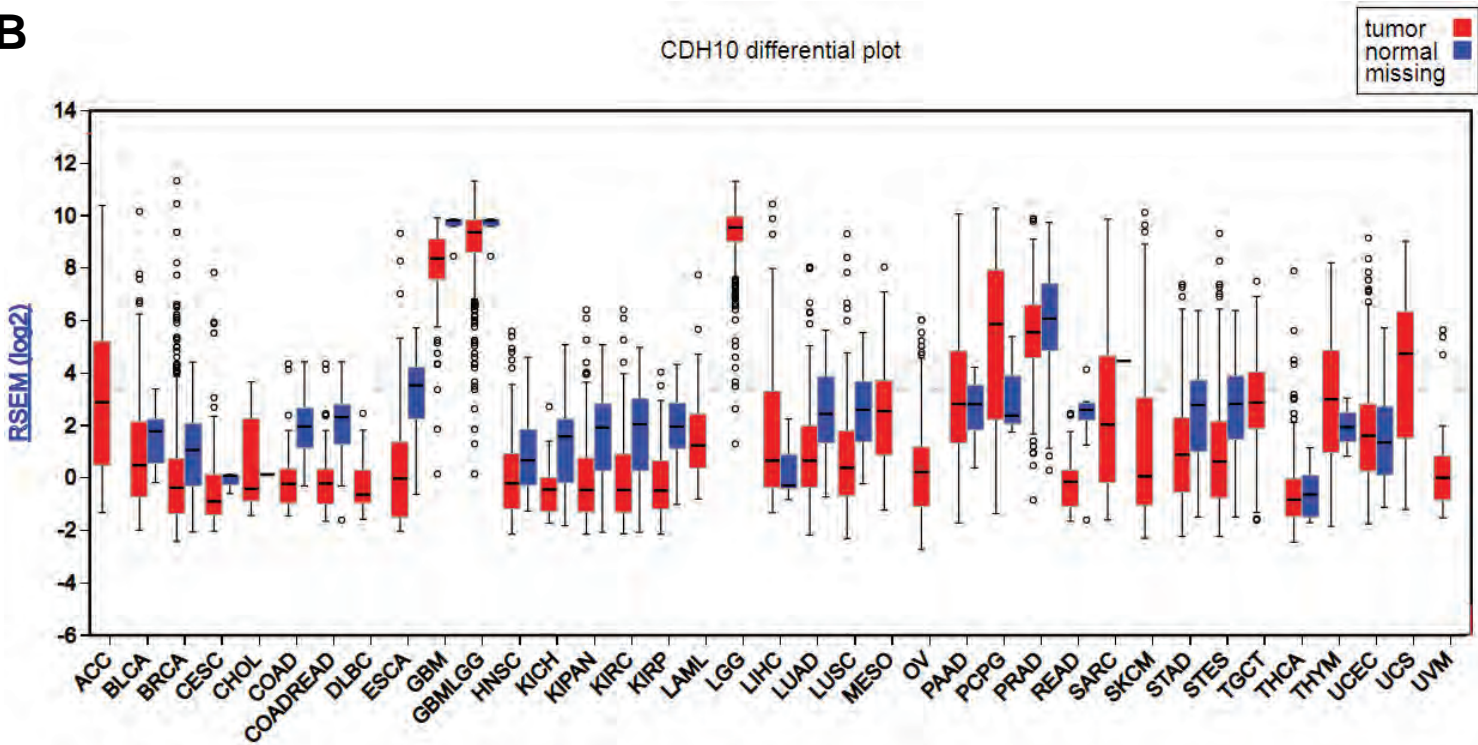
A**B**

Figure S8. (A) TCGA Pan-cancer data comparing the expression levels of *EHMT2* in tumor and normal tissue samples. (B) TCGA Pan-cancer data comparing the expression levels of *CDH10* in tumor and normal tissue samples.

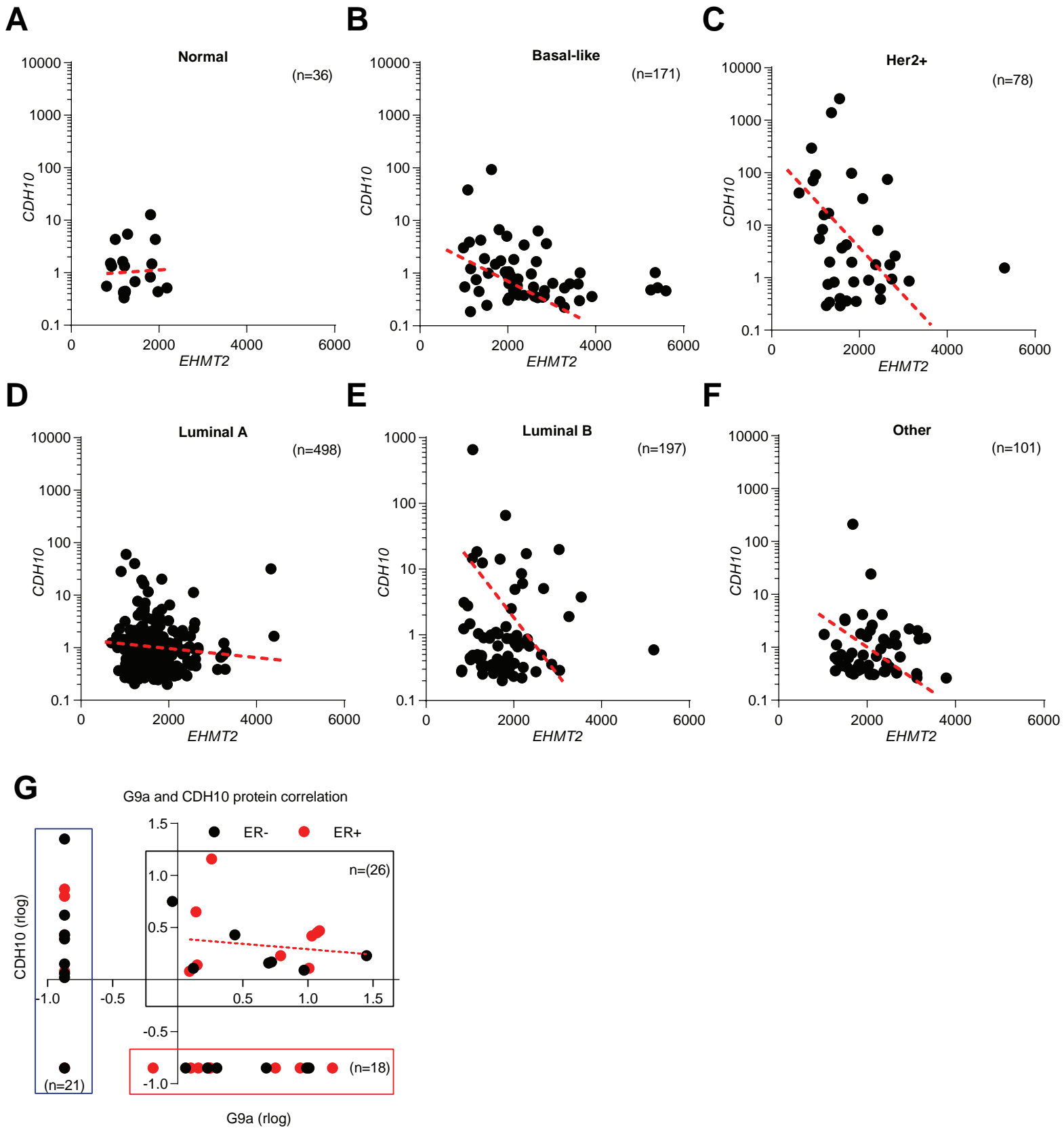


Figure S9. Correlation between *CDH10* and *EHMT2* (*G9a*) mRNA levels in (A) normal, (B) basal-like, (C) Her2+, (D) Luminal A, (E) Luminal B and (F) others in patient samples. (G) Correlation between *G9a* and *CDH10* protein levels in breast cancer patients using publicly available databases. Blue square identifies patients with no detectable *G9a*. In the red square are patients with no detectable *CDH10*. In the black square are patients for which both proteins were detectable.

Table S1. Table S1: RT-PCR and ChIP primers

RT-PCR primers		
<i>SIGLEC14</i>	FWD	AGGATTTATTCTCCCATCTCGCT
	REV	GATGCTGATGGCGAGGTTCTG
<i>IGSF5</i>	FWD	CGGCGATGGCATCCTTCCTT
	REV	GACTCCGACATCTCCTCTTCAGGTAA
<i>CDH10</i>	FWD	GCAGTCCTGTTCTGAGATTG
	REV	GCTGGCTTCTGCGAGCACACAGCG
<i>CDH11</i>	FWD	CCCGCCCCCCCCGCCCCGCAC
	REV	CCCGGCCCCAGTCCCGGTCC
<i>HPRT</i>	FWD	TGACACTGGCAAACAATGCA
	REV	GGTCCTTTTCACCAGCAAGCT
<i>VEGF</i>	FWD	CAGGTCAGAAACCAGCCAG
	REV	CGTGATGATTCAAACCTACC
<i>IGFBP3</i>	FWD	AGAGCACAGATACCCAGAACT
	REV	TGAGGAACTTCAGGTGATTCAGT
<i>CEACAM7</i>	FWD	TCAGCCTGTCCATACAGAGTG
	REV	TTGAACGGCACGACATCAATA
ChIP primers		
<i>CDH10</i>	FWD	GCAGTCCTGTTCTGAGATTG
	REV	GCTGGCTTCTGCGAGCACACAGCG

Table S2. Pan-cancer analysis of CDH10 and EHMT2.

Abbreviation	Tumor type	N of samples			
		CDH10		EHMT2	
		Normal	Tumor	Normal	Tumor
READ	Rectum adenocarcinoma	10	40	10	167
COADREAD	Colorectal adenocarcinoma	50	134	51	626
COAD	Colon adenocarcinoma	40	94	41	459
LUAD	Lung adenocarcinoma	52	354	59	517
LUSC	Lung squamous cell carcinoma	49	321	51	501
BRCA	Breast invasive carcinoma	89	469	112	1100
STES	Stomach and Esophageal carcinoma	39	329	46	600
UCEC	Uterine Corpus Endometrial Carcinoma	29	359	35	546
KIRP	Kidney renal papillary cell carcinoma	28	79	32	291
KIRC	Kidney renal clear cell carcinoma	59	252	72	534
HNSC	Head and Neck squamous cell carcinoma	32	180	44	522
PRAD	Prostate adenocarcinoma	51	495	52	498
THYM	Thymoma	2	100	2	120
GBMLGG	Glioma	5	695	5	696
CESC	Cervical squamous cell carcinoma and endocervical adenocarcinoma	3	67	3	306
GBM	Glioblastoma multiforme	5	166	5	166
KICH	Kidney Chromophobe	20	24	25	66