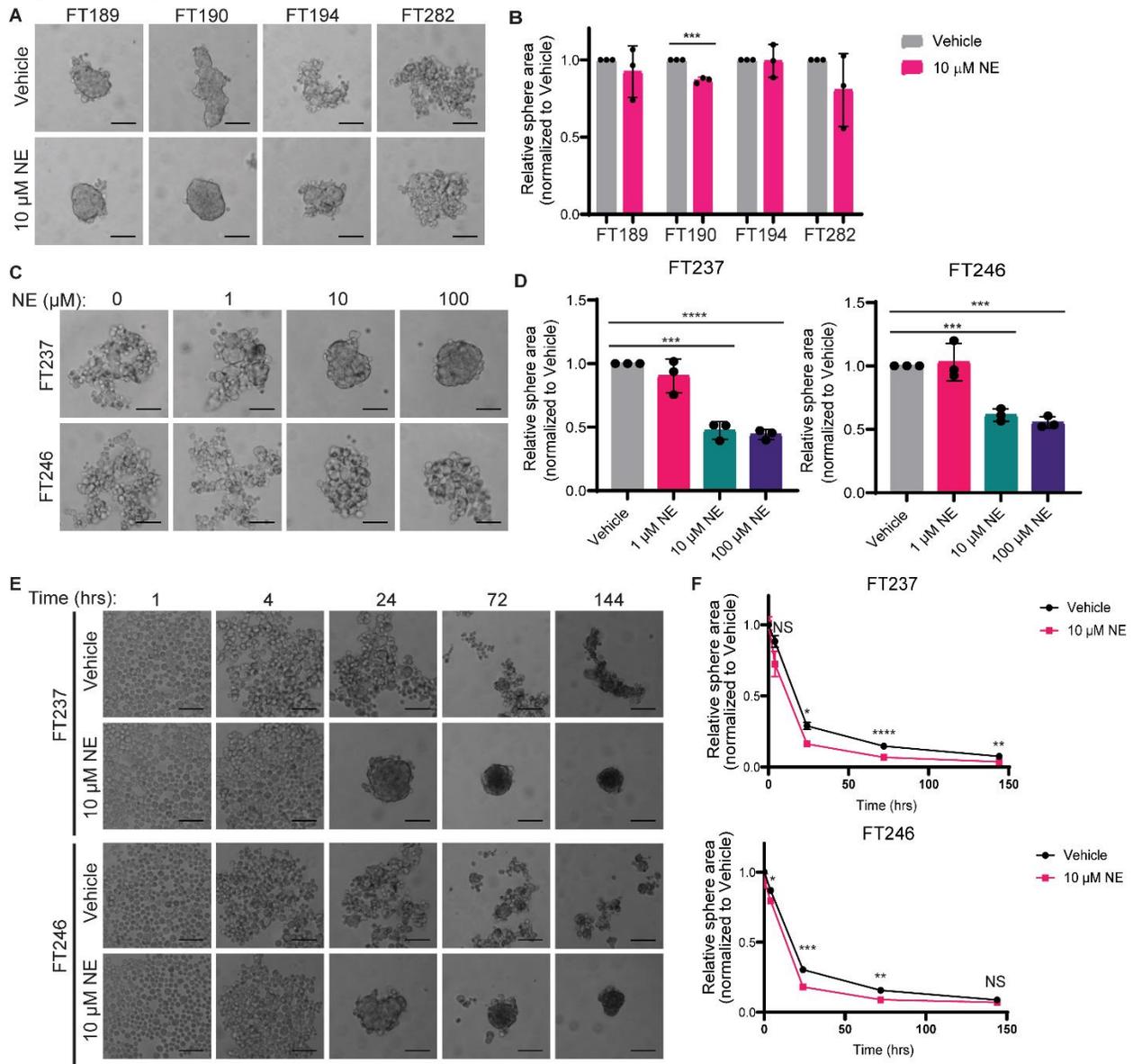
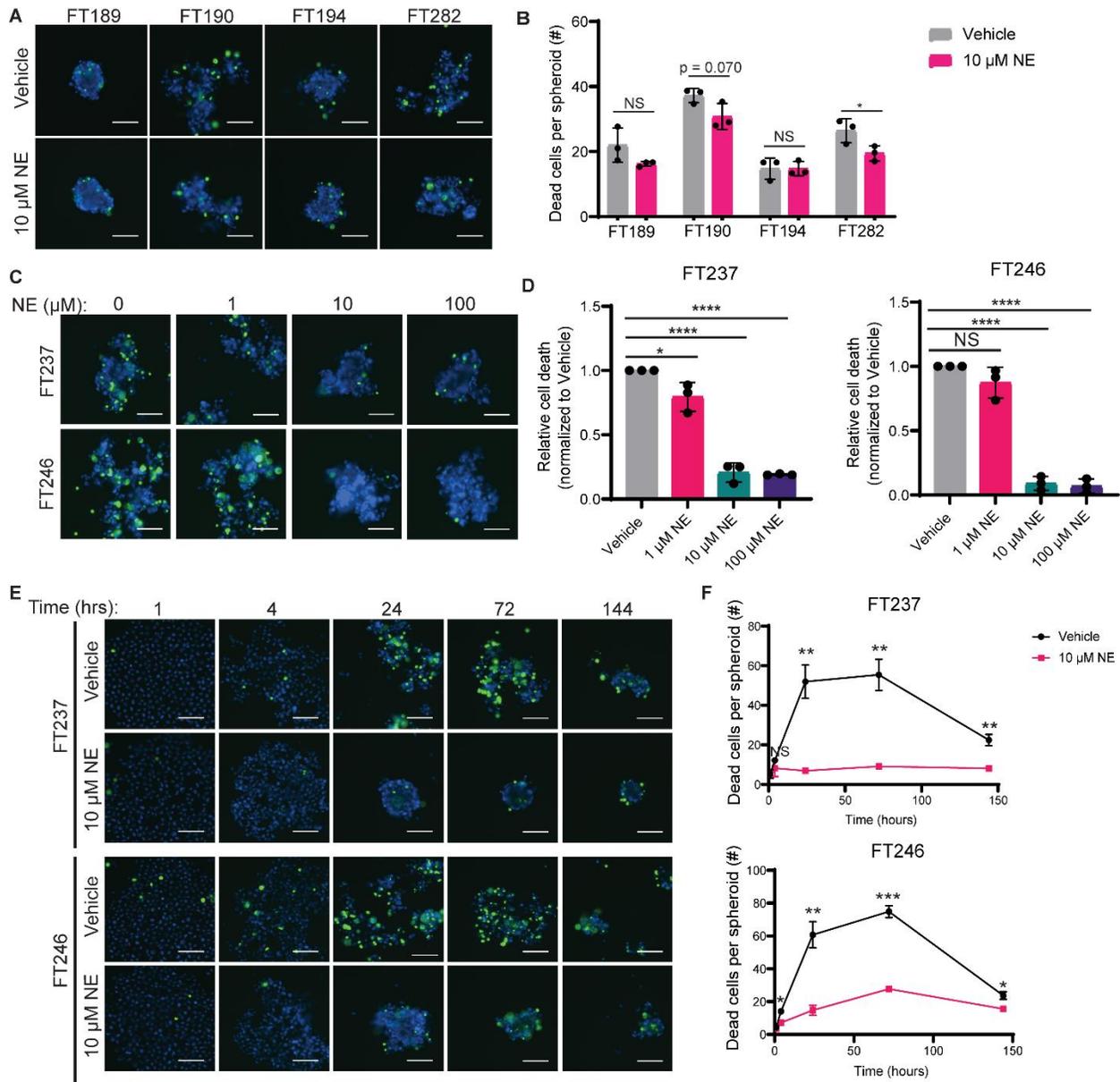


Supplemental Figure 1



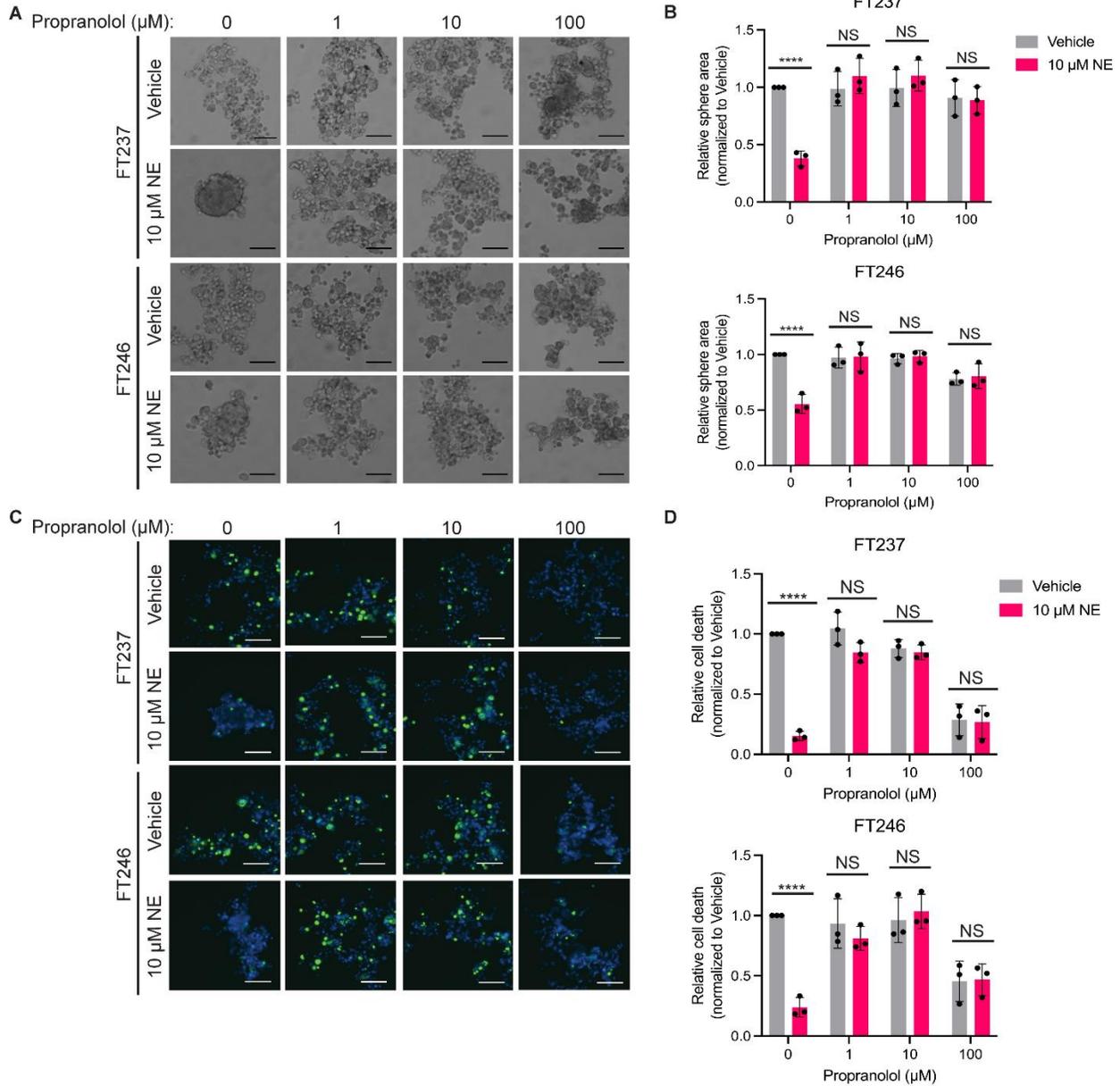
Supplemental Figure 1: Brightfield images and quantification of ultra-low attachment (ULA) spheroid areas for (A,B) 4 additional immortalized FTE cell lines (FT189, FT190, FT240, FT282) grown for 24 hrs \pm 10 μ M NE, (C,D) FT237 and FT246 cells grown for 24 hrs in various concentrations of NE, (E,F) FT237 and FT246 cells grown \pm 10 μ M NE at various timepoints. Statistical analyses were conducted via: (B,F) Student's t-tests, or (D) one-way ANOVA with Dunnett's correction for multiple comparisons. Data are represented as mean \pm standard deviation.

Supplemental Figure 2



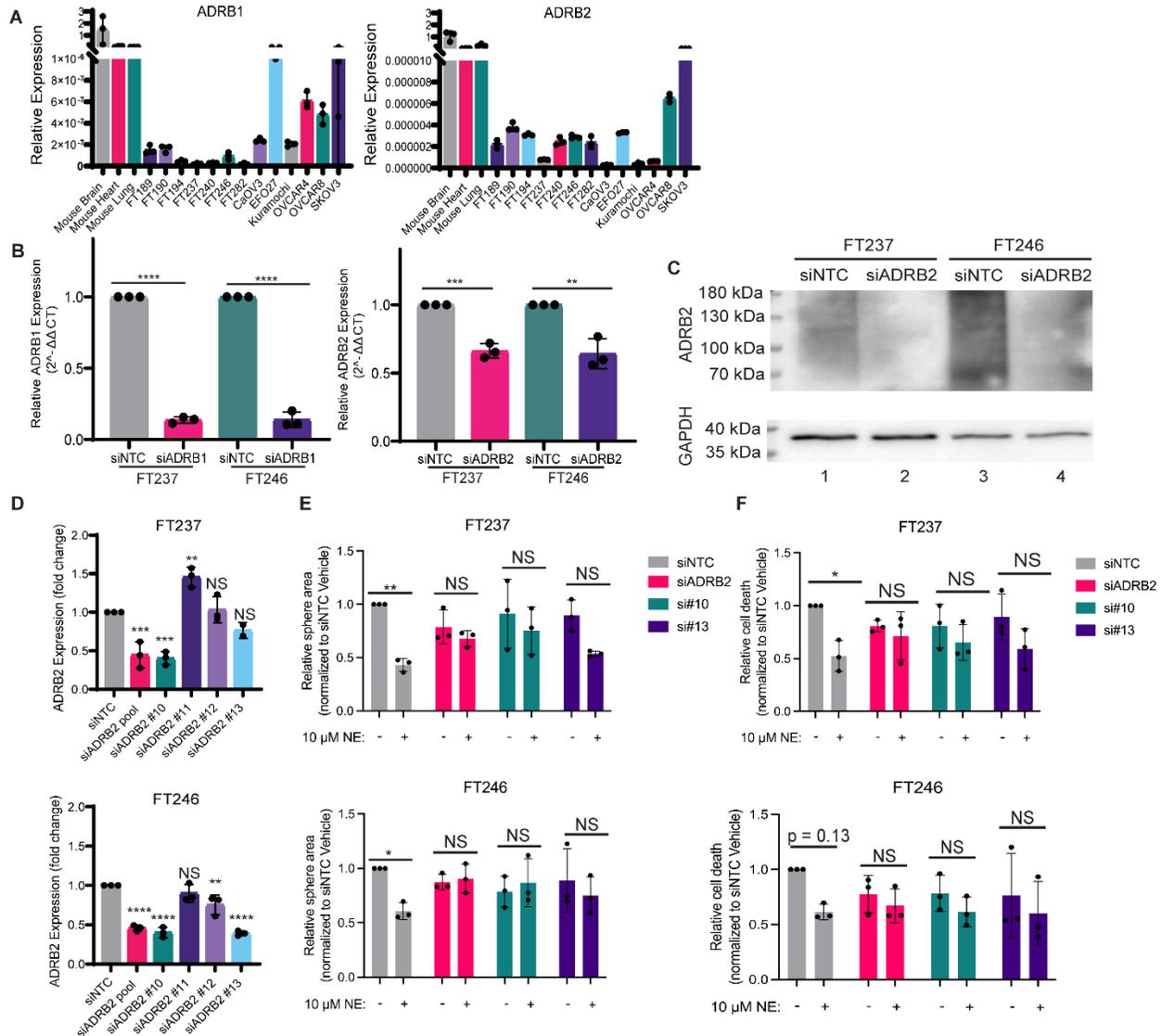
Supplemental Figure 2: Fluorescent images and quantification of dead cells (green) in spheroids (blue) cultured under ULA conditions. **(A,B)** 4 additional immortalized FTE cell lines (FT189, FT190, FT240, FT282) grown for 24 hrs +/- 10 μ M NE, **(C,D)** FT237 and FT246 cells grown for 24 hrs in various concentrations of NE, **(E,F)** FT237 and FT246 cells grown +/- 10 μ M NE at various timepoints. Statistical analyses were conducted via: **(B,F)** Student's t-tests, or **(D)** one-way ANOVA with Dunnett's correction for multiple comparisons. Data are represented as mean \pm standard deviation.

Supplemental Figure 3



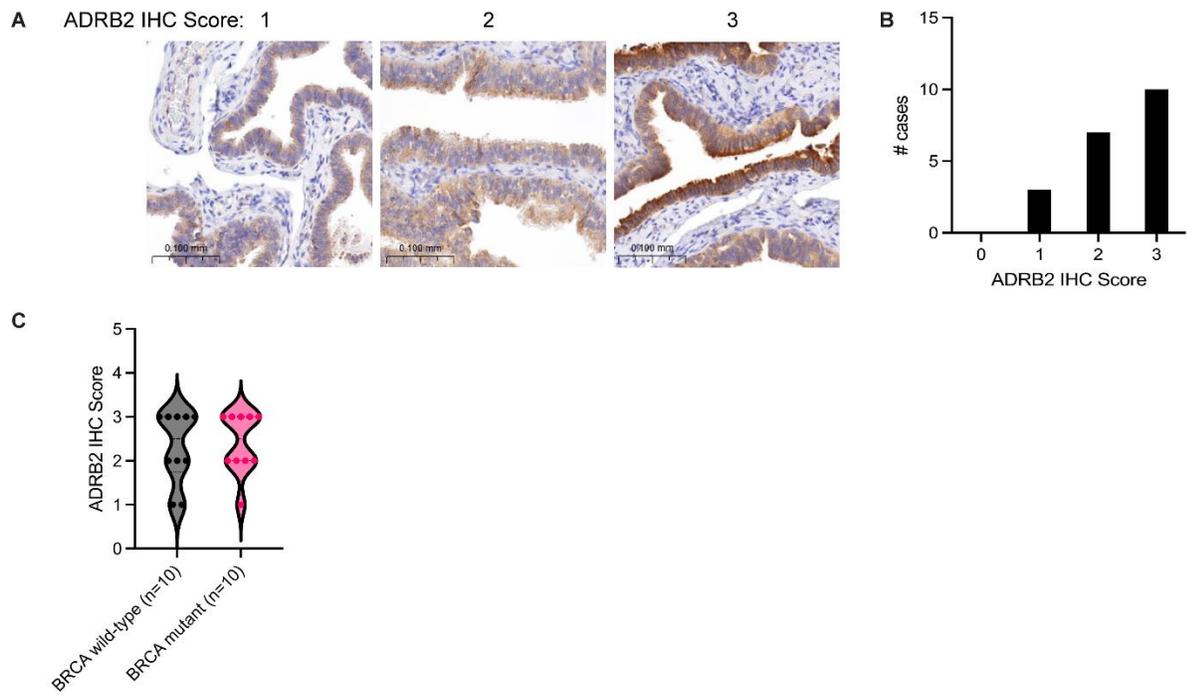
Supplemental Figure 3: (A,B) Brightfield images and quantification of spheroid areas for FT237 and FT246 cells cultured under ULA conditions for 24 hrs in various concentrations of propranolol. **(C,D)** Fluorescent images and quantification of dead cells (green) in spheroids (blue) as cultured in **(A)**. All statistical analyses for this figure were conducted via two-way ANOVA with Sidak's correction for multiple comparisons. Data are represented as mean \pm standard deviation.

Supplemental Figure 4



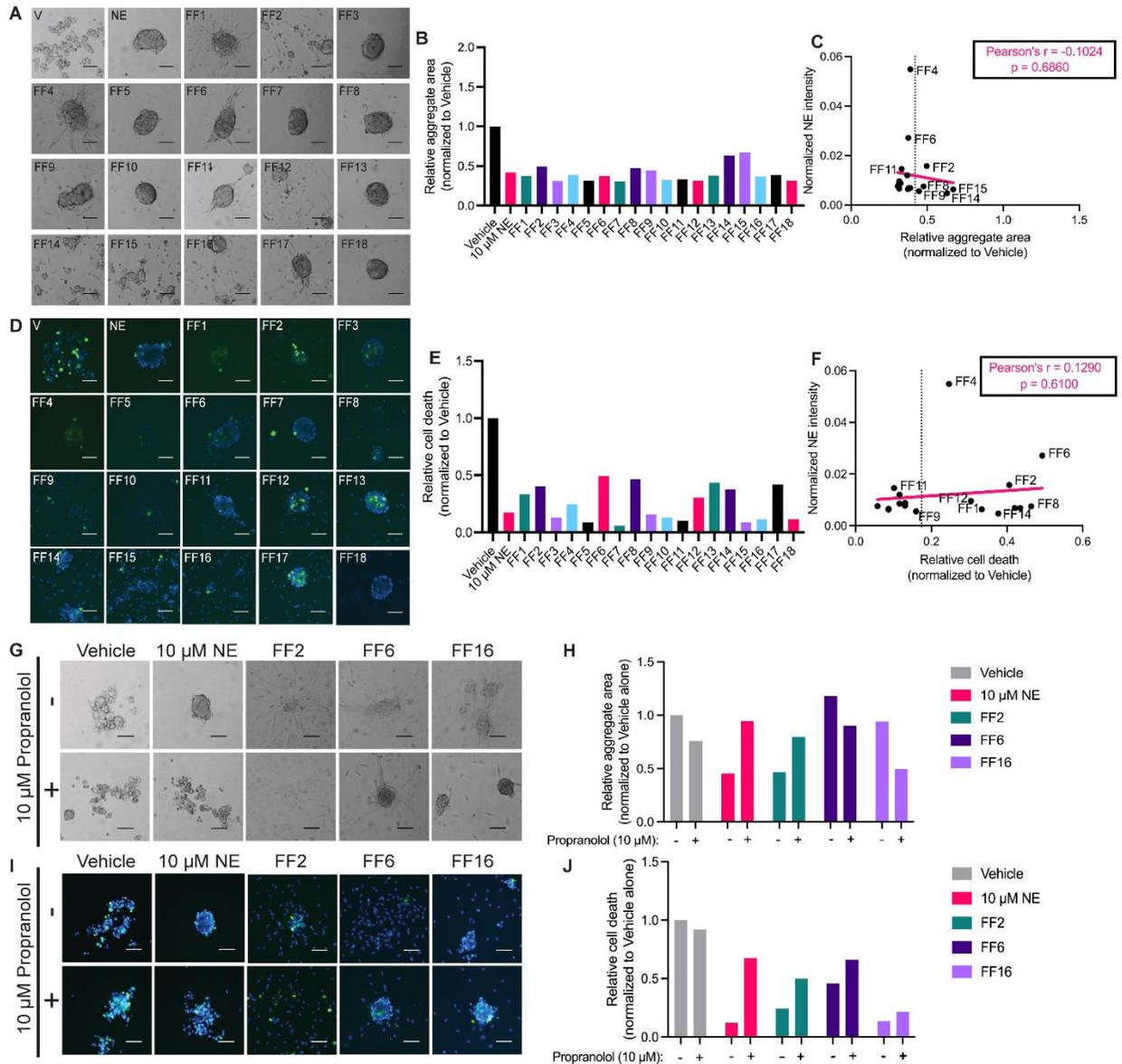
Supplemental Figure 4: (A) Relative RNA expression levels of ADRB1 and ADRB2 in control tissues and immortalized FTE and HGSC cell lines. (B) RTqPCR validation of knockdown for pooled siRNAs targeting ADRB1 and ADRB2 in FT237 and FT246. (C) Western blot validation of ADRB2 knockdown. (D) RTqPCR deconvolution of individual siRNAs within the siADRB2 pool in FT237 and FT246. (E) Quantification of relative changes in sphere areas upon knockdown of ADRB2 with pooled or individual siRNAs. (F) Quantification of relative changes in cell death for spheres described in (E). Statistical analyses were conducted via: (B) Student's t-tests, (D) one-way ANOVA with Dunnett's correction for multiple comparisons, and (E,F) two-way ANOVA with Sidak's correction for multiple comparisons. Data are represented as mean \pm standard deviation.

Supplemental Figure 5



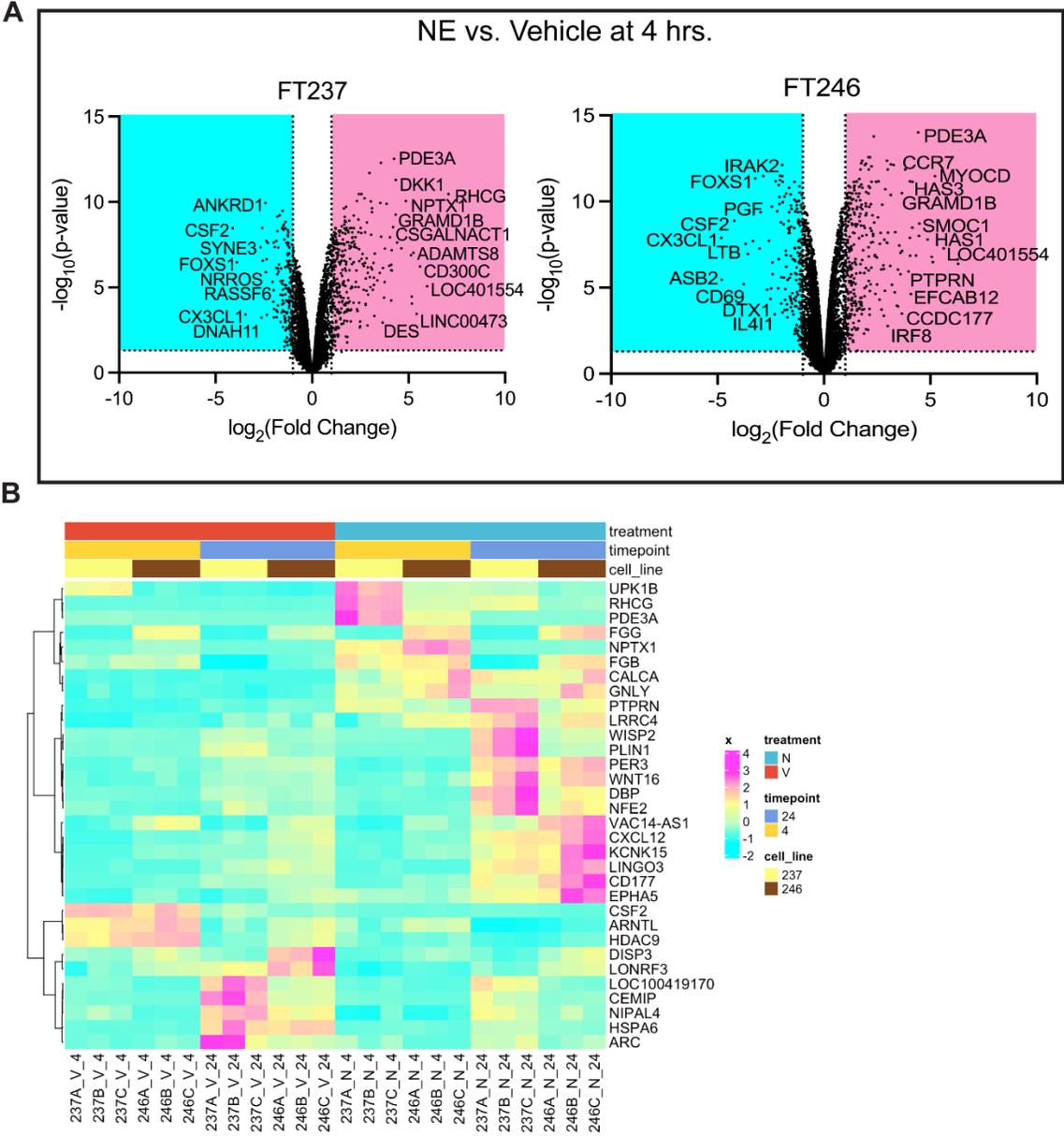
Supplemental Figure 5: (A) Representative images of H&E stained human fallopian tube epithelial tissue with low (1), medium (2) and high (3) ADRB2 staining (brown). (B) Distribution of ADRB2 staining intensity for the immunohistochemistry of samples in (A) (n=20). (C) Violin plots depicting ADRB2 staining levels according to BRCA status.

Supplemental Figure 6



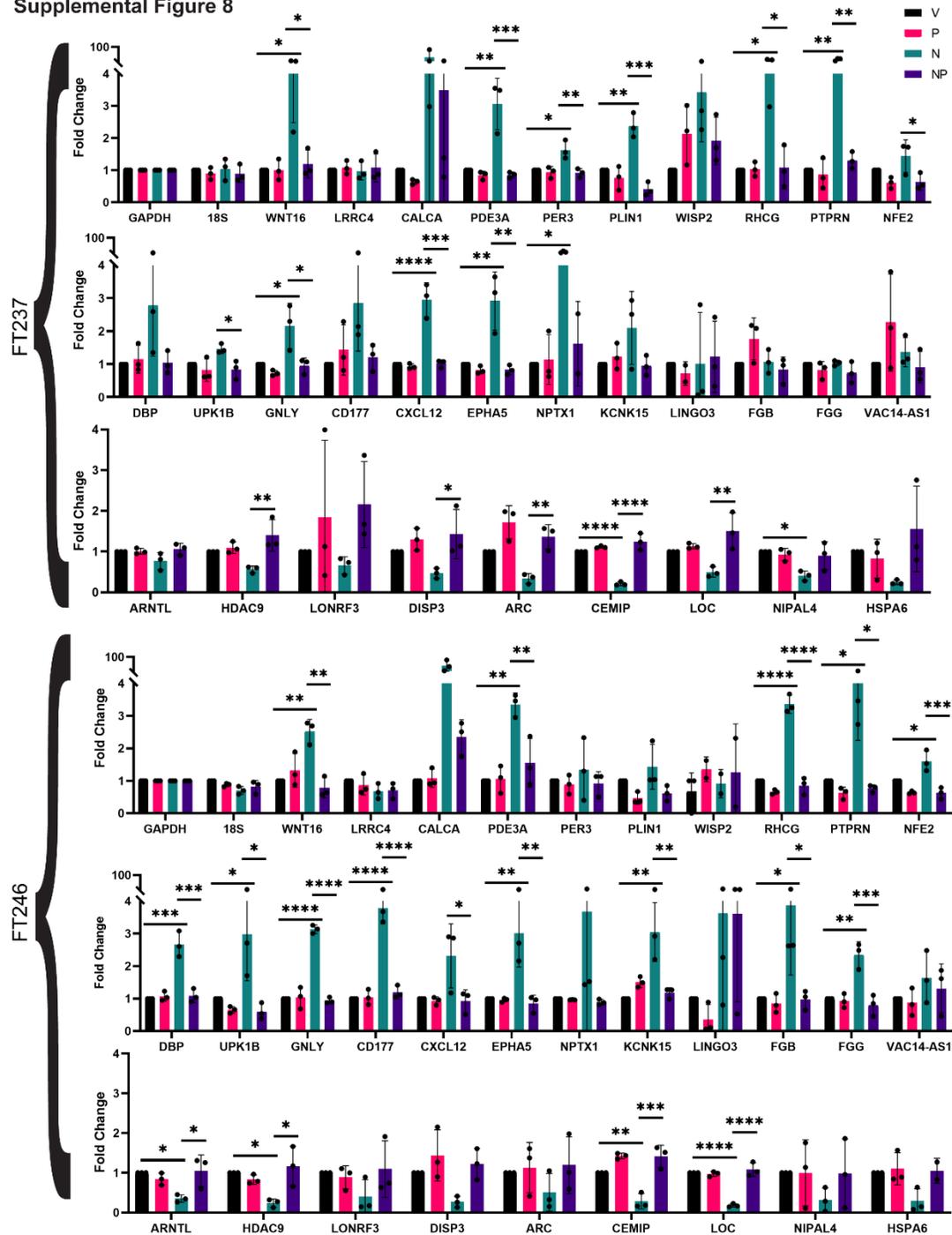
Supplemental Figure 6: (A,B) Brightfield images and area measurements for FT237 cells treated for 24 hrs in ULA with 18 different follicular fluid samples collected from 17 different patients (10% volume). (C) Linear regression for correlation between FT237 aggregate area and relative NE concentration quantified via mass spectrometry analysis. (D,E) Fluorescent images of total cells (blue) and dead cells (green) in each FT237 cell aggregate, cultured as in A. (F) Linear regression for correlation between the number of dead cells in FT237 aggregates and relative NE concentration per sample. (G,H) Brightfield images and area measurements for FT237 cells treated with vehicle, NE, FF2, FF6, or FF16 in the presence or absence of 10μM propranolol. (I,J) Fluorescent images and dead cell quantification for cells as cultured in (G). Each experiment was conducted in technical triplicate.

Supplemental Figure 7



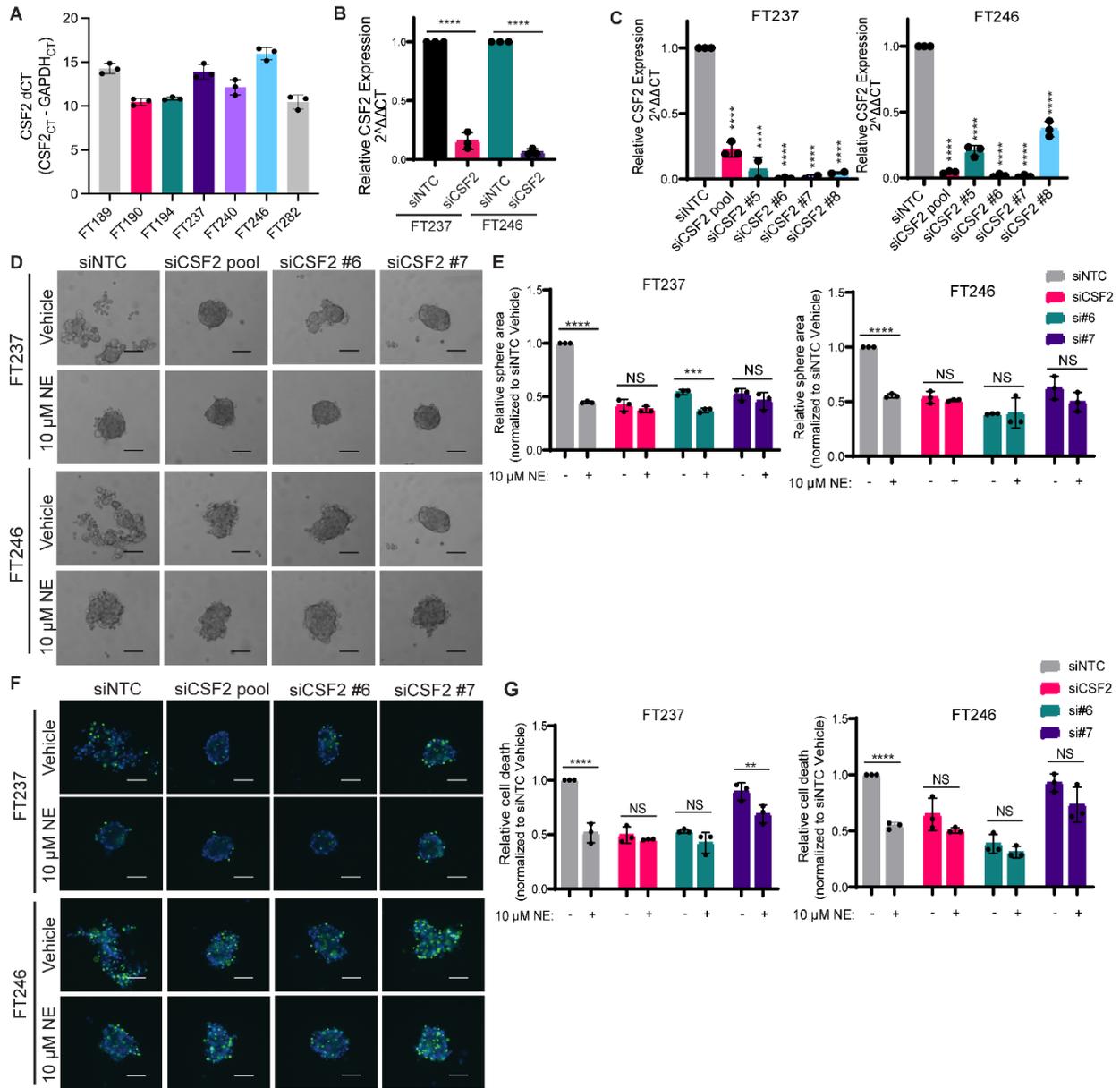
Supplemental Figure 7: (A) Volcano plots for differentially expressed transcripts in ULA-cultured FT237 and FT246 that are upregulated (magenta) and downregulated (cyan) after 4 hrs of 10 μ M NE treatment relative to vehicle. **(B)** Temporal heatmap for top differentially expressed transcripts common to both cell lines at early (4hr) and late (24hr) timepoints, relative to the baseline cell profiles prior to ULA culture.

Supplemental Figure 8



Supplemental Figure 8: RTqPCR validation of RNAsequencing hits common to both FT237 and FT246. All statistical analyses for this figure were conducted using one-way ANOVA with Tukey's correction for multiple comparisons. Data are represented as mean \pm standard deviation.

Supplemental Figure 9



Supplemental Figure 9: (A) RTqPCR panel of CSF2 mRNA expression across FTE cell lines. (B) RTqPCR validation of knockdown for pooled siRNA targeting *CSF2* in FT237 and FT246. (C) RTqPCR deconvolution of individual siRNAs within the siCSF2 pool in FT237 and FT246. (D,E) Representative brightfield images and quantification of sphere areas for FTE cell lines transfected with two of the most efficient siRNAs (#6 and #7) when cultured under ULA conditions for 24 hrs in the presence or absence of 10 μM NE. (F,G) Representative fluorescent images of total cells (blue) and dead cells (green) and quantification of relative cell death in each condition as cultured in (D). Statistical analyses were conducted via: (B) Student's t-tests, (C) one-way ANOVA with Dunnett's correction for multiple comparisons, or (E, G) two-way ANOVA with Sidak's correction for multiple comparisons. Data are represented as mean ± standard deviation.

Supplemental Table 1. List of primers used for RTqPCR experiments

Primer	Sequence (5' ---> 3')	Primer	Sequence (5' ---> 3')
<i>GAPDH_F</i>	GAGTCAACGGATTTGGTCGT	<i>PER3_F</i>	GCAGAGGAAATTGGCGGACA
<i>GAPDH_R</i>	TTGATTTTGGAGGGATCTCG	<i>PER3_R</i>	GGTTTATTGCGTCTCTCCGAG
<i>ADRB1_F</i>	CGAGACCCTGTGTGTCATTG	<i>CXCL12_F</i>	ATTCTCAACACTCCAAACTGTGC
<i>ADRB1_R</i>	ACGACTTGGGGTCGTTGTAG	<i>CXCL12_R</i>	ACTTTAGCTTCGGGTCAATGC
<i>ADRB2_F</i>	GAGCACAAGCCCTCAAGAC	<i>LRRC4_F</i>	CTCCCGTTTCGTCTACCTCAC
<i>ADRB2_R</i>	TGGAAGGCAATCCTGAAATC	<i>LRRC4_R</i>	GGTGTTCGAGGGAATACCCTG
<i>18S_F</i>	GGAAAGCAGACATTGACCTCAC	<i>FGG_F</i>	TTATTGTCCAACACTACCTGTGGC
<i>18S_R</i>	CCATCCTTTACATCCTTCTGTCTGT	<i>FGG_R</i>	GACTTCAAAGTAGCAGCGTCTAT
<i>CALCA_F</i>	TGCAGATGAAGGCCAGTGAG	<i>FGB_F</i>	AGTGATTCAGAACCCTCAAGAC
<i>CALCA_R</i>	TACTCAGATTACCGCACCCGC	<i>FGB_R</i>	CATCCTGGTAAGCTGGCTAATTT
<i>RHCG_F</i>	GGTTCCAATTCTTACAAGACCG	<i>LINGO3_F</i>	TGCCTCAATCTGTCCGACAA
<i>RHCG_R</i>	GGGCTGACTTTACCCAGAACT	<i>LINGO3_R</i>	CAGCGTCTTAGCGTGTTC
<i>UPK1B_F</i>	CCAAAGACAACACTCAACTGTTTCGT	<i>PLIN1_F</i>	CCATGTCCCTATCAGATGCC
<i>UPK1B_R</i>	AATGCCGCAACAACCAATAATC	<i>PLIN1_R</i>	CTGGTGGGTTGTGATGTC
<i>GNLY_F</i>	CCTGTCTGACGATAGTCCAAAAA	<i>VAC14AS1_F</i>	TACGAGGGTGTCCCAAAAGC
<i>GNLY_R</i>	GACCTCCCCGTCCTACACA	<i>VAC14AS1_R</i>	TTCTGGATGCGGGAGACTA
<i>CD177_F</i>	ATGAGCGCGGTATTACTGCTG	<i>HSPA6_F</i>	CGTGCCCGCCTATTTCAATG
<i>CD177_R</i>	GGTCGGACACCTTCCACAC	<i>HSPA6_R</i>	AAAATGAGCACGTTGCGCT
<i>PDE3A_F</i>	CCACGGCCTCATTACCGAC	<i>CSF2_F</i>	TCCTGAACCTGAGTAGAGACAC
<i>PDE3A_R</i>	TTGCTCACGGCTCTCAAGG	<i>CSF2_R</i>	TGCTGCTTGTAGTGGCTGG
<i>NFE2_F</i>	GCAGGAACAGGGTGATACAGC	<i>CEMIP_F</i>	GCTCTTGAGTTGCATGGACA
<i>NFE2_R</i>	GCAGCTCGGTGATGGACAT	<i>CEMIP_R</i>	ACCGCGTTCAAATACTGGAC
<i>WNT16_F</i>	TTCAGACACGAGAGATGGAAC	<i>LOC100419170_F</i>	GGAAGCCTGAAGCTCCCTAT
<i>WNT16_R</i>	CCAGCCTTCACTTGCTGAG	<i>LOC100419170_R</i>	CCTCGTGTCTGGGAAACAAT
<i>KCNK15_F</i>	GCTCTCCGGAGGAAGTTCG	<i>DISP3_F</i>	CACAGCCTGCAGAACAACAT
<i>KCNK15_R</i>	TGATGACGGTGATGGCGAAG	<i>DISP3_R</i>	AGGCGCTCTATACACCTGGA
<i>PTPRN_F</i>	CGGGACACATGATTCTGGCAT	<i>HDAC9_F</i>	AGTAGAGAGGCATCGCAGAGA
<i>PTPRN_R</i>	CTGCTTGGTAGGCACAGAGG	<i>HDAC9_R</i>	GGAGTGTCTTTCGTTGCTGAT
<i>NPTX1_F</i>	CACCGAGGAGAGGGTCAAGAT	<i>ARNTL_F</i>	AAGGGAAGCTCACAGTCAGAT
<i>NPTX1_R</i>	CAGGGCGGTTGTCTTTCTGA	<i>ARNTL_R</i>	GGACATTGCGTTGCATGTTGG
<i>WISP2_F</i>	CCTCCTCTCAAAGGTGCGTA	<i>NIPAL4_F</i>	CCAACCTTTGGAGCCTACGCAT
<i>WISP2_R</i>	CTGTGCTCCTCTGCCAAGA	<i>NIPAL4_R</i>	TCCATGATGGTAGTGACCTTCT
<i>DBP_F</i>	CTGATCTTGCCCTATCAAGCATT	<i>LONRF3_F</i>	ATGGAGTCAGTACGGATCGAA
<i>DBP_R</i>	CGATGTCTTCGAGGGTCAAAG	<i>LONRF3_R</i>	GTCCCCGGAGACTGCTCTT
<i>EPHA5_F</i>	TAGGACCTCTAAGCAAAAAGGGA	<i>ARC_F</i>	AGCGGGACCTGTACCAGAC
<i>EPHA5_R</i>	GAGCCTGACACTTCGAGCAA	<i>ARC_R</i>	GCAGGAAACGCTTGAGCTTG