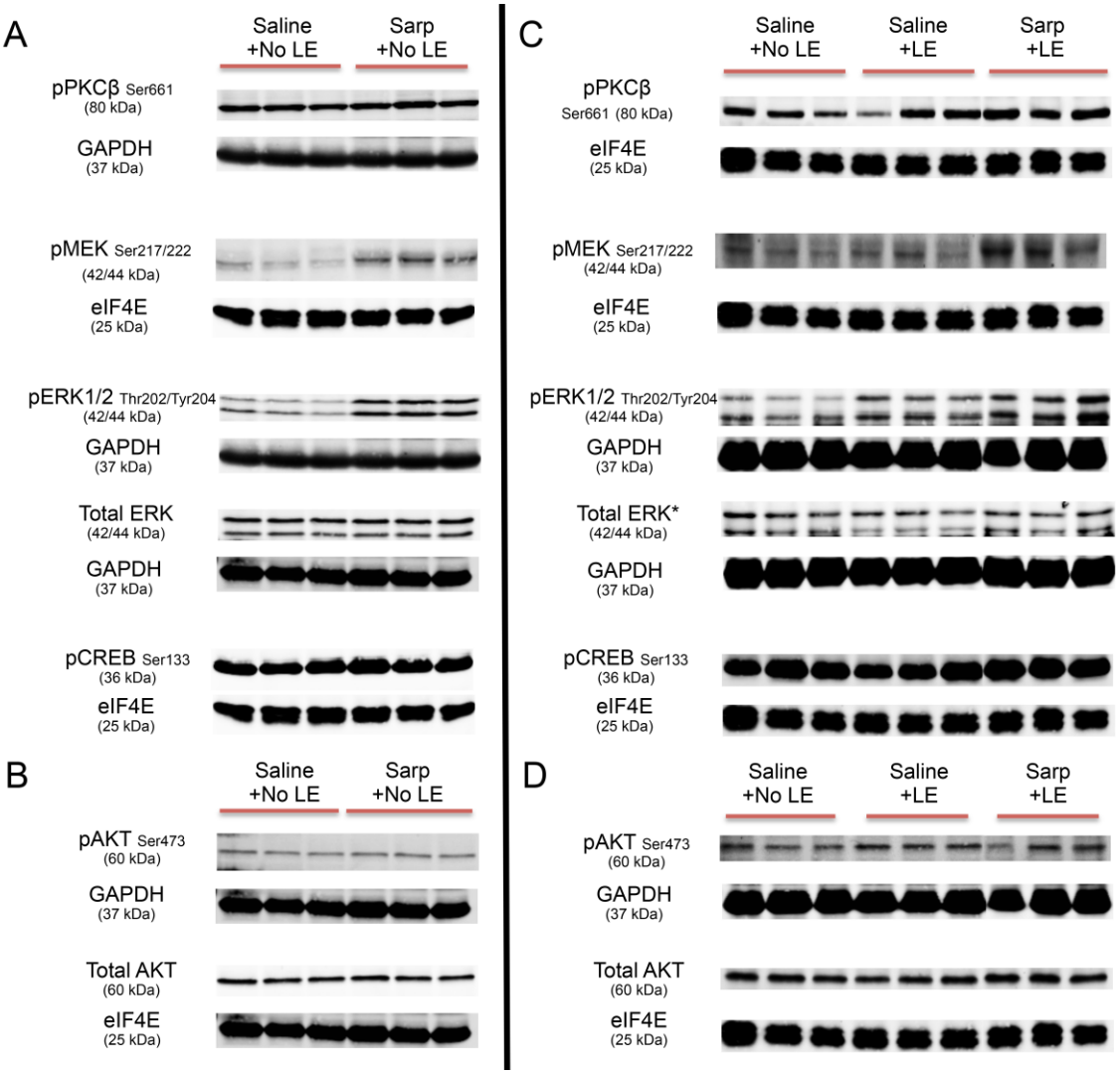
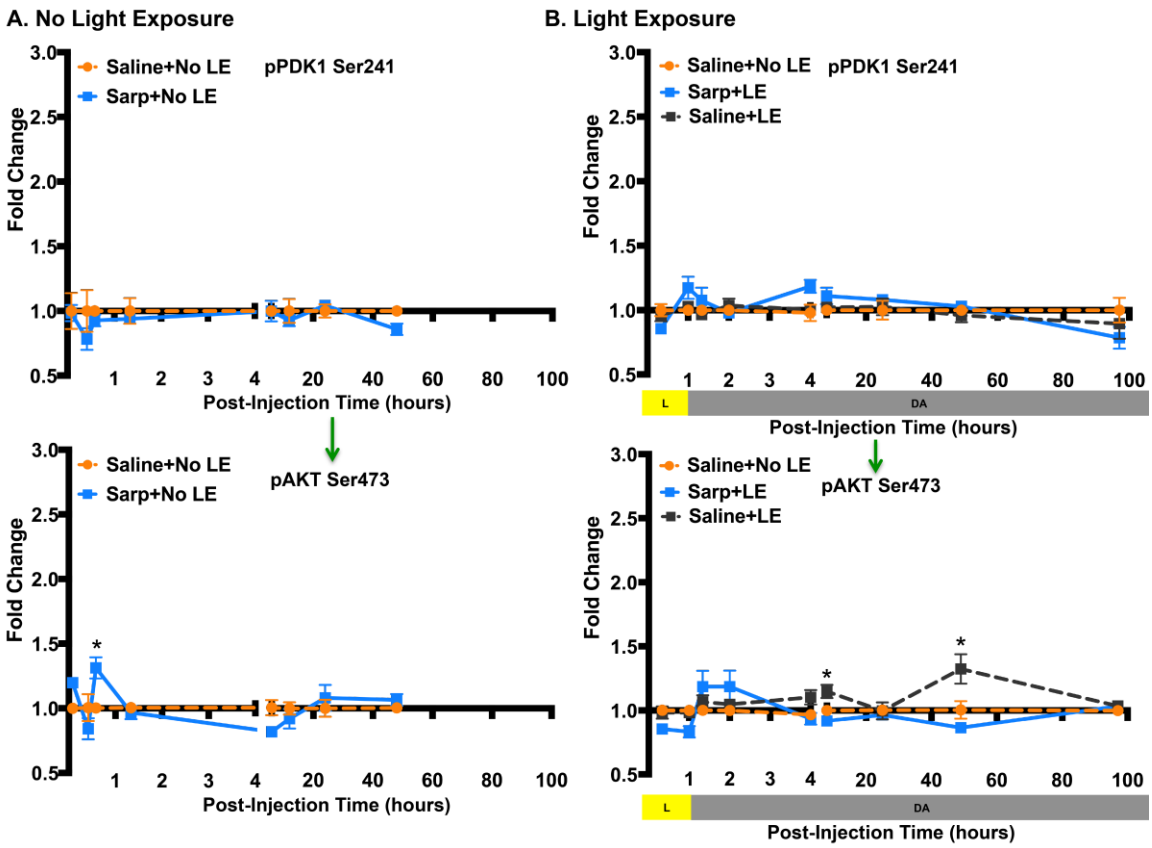


Supplemental Figure 1. Raw Western blot data. Western blots of retinal proteins in the MAPK/ERK pathway (A) and PI3K/PDK/AKT pathway (B) at 1 hour and 20 min after 25 mg/kg sarpogrelate injection. Western blots of retinal proteins in the MAPK/ERK pathway (C) and PI3K/PDK/AKT pathway (D) at 3 hours post-light exposure. *Total ERK western blot is from 24 hour post-light exposure time point. GAPDH and eIF4E were used as internal controls. LE, light exposure; Sarp, 25 mg/kg sarpogrelate; p, phosphorylated; PKC, protein kinase C; GAPDH, glyceraldehyde 3-phosphate dehydrogenase; MEK, mitogen-activated protein kinase kinase; eIF4E, eukaryotic translation initiation factor 4E; ERK1/2, extracellular signal-related kinase 1/2; CREB, cAMP response element binding protein; Akt, protein kinase B.



Supplemental Figure 2. Akt activation associated with sarpogrelate treatment. Line graphs showing average fold change in phosphorylation of key proteins in the PI3K/PDK/AKT pathway at multiple times post-injection (A) and post-light exposure (B). Data points are presented as mean ± standard error. A two-way ANOVA multiple comparisons test was used to compare fold changes between Sarp+No LE and Saline+No LE groups in panel A and also used to compare fold change difference between Sarp+LE and Saline+LE in panel B. *Indicates $P \leq 0.05$. n=3-5 animals per group. LE, light exposure; Sarp, 25 mg/kg sarpogrelate; p, phosphorylated; PDK1, phosphoinositide-dependent kinase 1; Akt, protein kinase B.

TABLE LEGENDS

Supplemental Table 1. Changes in phosphorylated proteins associated with light exposure alone, and sarpogrelate treatment post-light exposure. Table showing the changes in phosphorylation at multiple phosphorylation sites essential to the activation and de-activation of cell signaling proteins in common signaling pathways. Phosphorylation changes were calculated as a ratio between phosphorylated and total protein. Changes in phosphorylation as an effect from light exposure were expressed as a ratio from the group saline with light

exposure compared to saline without light exposure ((Saline+LE)/(Saline+No LE)). Changes in phosphorylation from sarpogrelate treatment were expressed as a ratio from the group sarpogrelate with light exposure compared to saline with light exposure ((Sarp+LE)/(Saline+LE)). Data was averaged from n=3 animals per group, and averaged between two independent experiments. Data was expressed as this mean ± standard error of the mean. Data was also color coded with shades of green indicating decreases in ratio change, shades of red indicating increases in ratio change, and white as ratio change near or at 1.00.

Supplementary Table 2. Gene expression changes associated with sarpogrelate treatment, MEKi treatment and light exposure. Gene expression changes were assessed using a customized RT^2 Profiler™ PCR Array examining genes involved in oxidative stress, iron metabolism, apoptosis, autophagy and necrosis at 48 hours-post light exposure. Gene expression was calculated in the QIAGEN GeneGlobe data analysis center (www.SAbiosciences.com/pcrarraydataanalysis.php), and verified through manual ΔΔCT calculations. Color coded values represent genes that showed significant changes with $P \leq 0.05$ and greater than 2-fold change, n=3 animals per group with two independent experiments. Red numbers indicate increased fold differences in the experimental group as compared to control, green numbers indicate decreased fold differences. Fold changes for sarpogrelate were calculated as a ratio between sarpogrelate with LE as compared to saline with LE. Fold changes for MEKi were calculated as a ratio between mice given MEKi pre-treatment prior to sarpogrelate and LE, as compared to saline pre-treatment prior to sarpogrelate and LE. Fold changes for light exposure were calculated as a ratio between mice receiving saline and LE, as compared to saline without LE. Fold change values were transformed to obtain fold regulation values, as calculated through the QIAGEN analysis software.