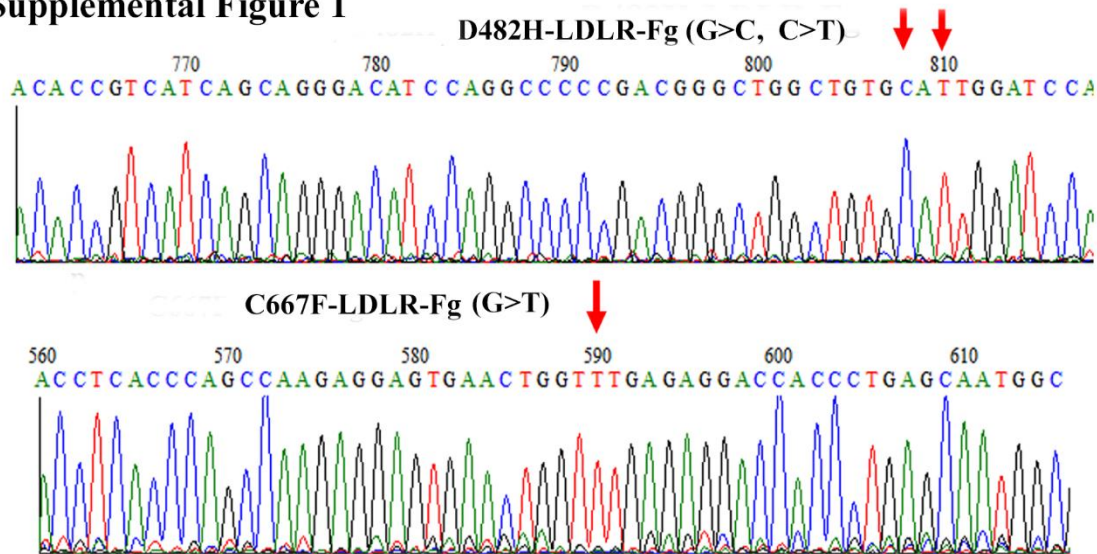


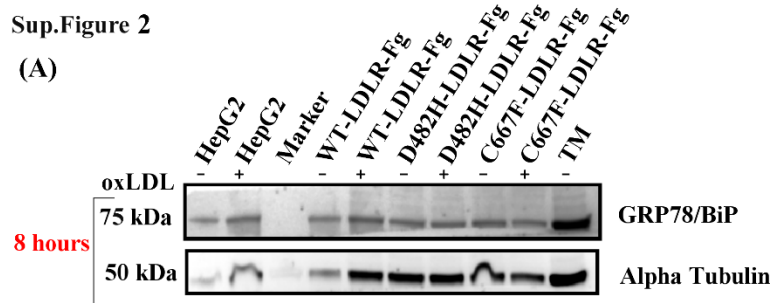
## Supplemental Figure 1



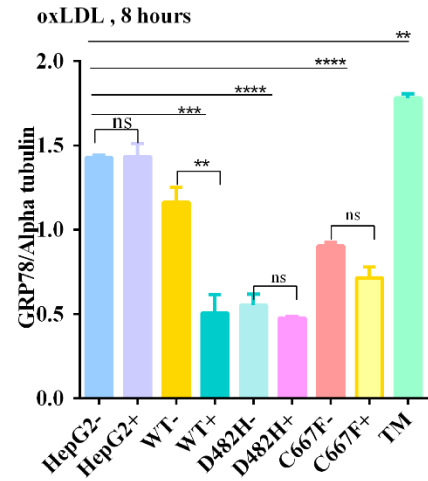
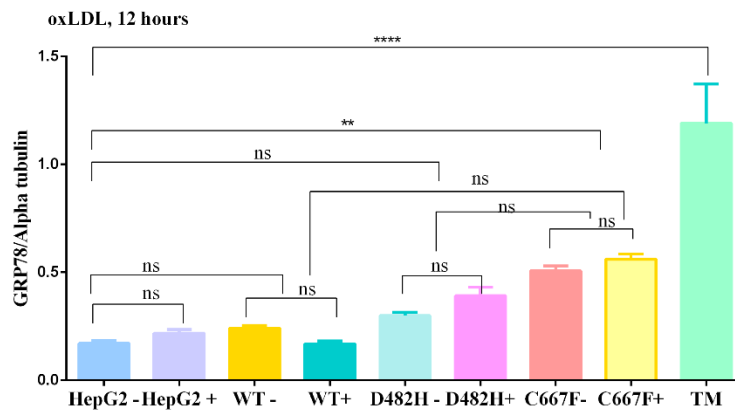
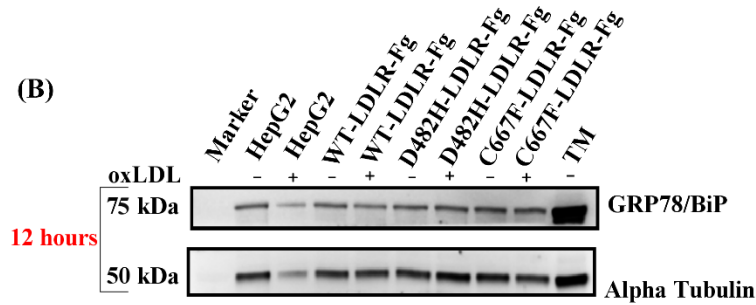
**Supplemental Figure 1- Sanger sequencing to confirm site-directed mutagenesis of FLAG-tagged WT-LDLR.** The red arrows on the chromatograms indicate the location of the nucleotides substituted to generate the open reading frames of the ER-retained, missense variants of LDLR- p.D482H-LDLR (top) and p.C667F-LDLR (bottom).

Sup.Figure 2

(A)



(B)



**Supplemental Figure 2(A-B)-BiP expression in oxLDL treated cells at early time points.** Western blots depicting GRP78/BiP expression in HepG2 cells overexpressing empty vector, WT/variants of LDLR treated with 100  $\mu$ g per ml of oxLDL at (1A) 8 hours and (1B) 12 hours. Bar diagrams denoting Alpha-tubulin normalized BiP expression at these time points are represented as mean +SD. 2-way ANOVA using Turkey's post hoc test was used to compare the corresponding treated (+) *versus* non-treated (-) conditions for each HepG2 cell type, wherein  $p < 0.05 = *$  or #,  $p < 0.01 = **$ ,  $p < 0.001 = ***$ ,  $p < 0.0001 = ****$ , is represented for the comparisons between non-transduced HepG2 control cells (HepG2-) *versus* non-treated or treated HepG2<sup>WT-LDLR</sup>, HepG2<sup>D482H-LDLR</sup>, and HepG2<sup>C667F-LDLR</sup>.  $P < 0.05 = \#$  when the treated cells were compared with the respective non-treated cell types. ns=not significant, n=3 replicates.

