

Fig. S1 Transfection efficiency for RNA-seq.

(a-e) Alignments of *GNAQ* reads from RNA-sequencing focused on the region of the transfected mutation to confirm transfection efficiency. The number of reads mapped is shown in the top left corner of each replicate. Note that Q209L replicate 3 (d) has significantly fewer reads than the other replicates likely due to poor transfection.

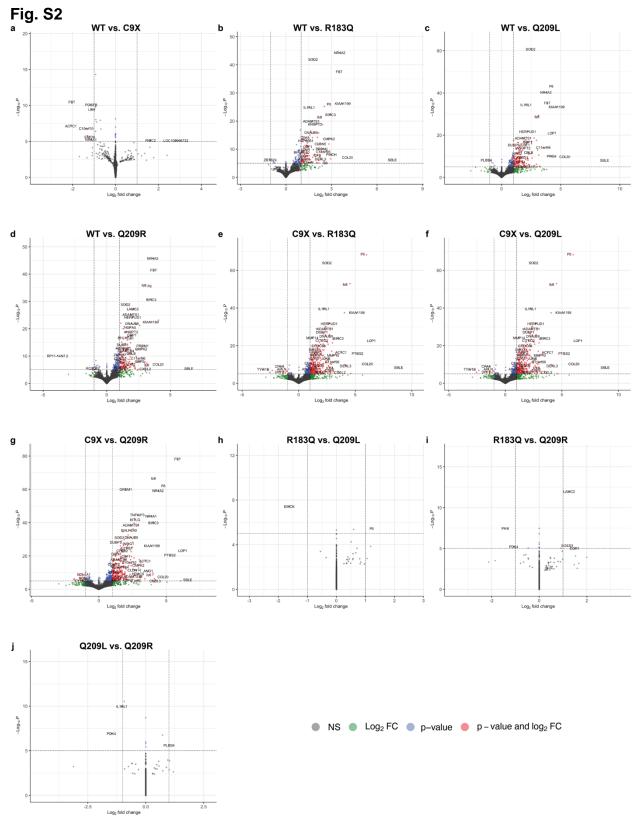


Fig. S2 Differential expression from HMEC-1 RNA-seq. (a-j) Volcano plots of differential gene expression for each pairwise comparison of *GNAQ* groups used for RNA-seq.