



S3 Fig. The heatmap illustrates expression of genes with an absolute \log_2 fold change in fragments per kilobase of transcript per million fragments mapped > 2 in R1 (CR1, LR1, and CH1) and R2 (CR1LR1 and CR1CH1) groups compared to H3122 cell lines. Rows of each heat map correspond to genes sorted according to clustering (739 genes).