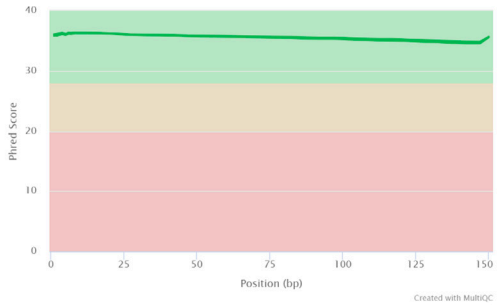
ON 0G

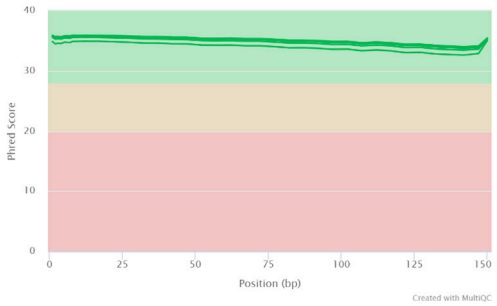
R1

FastQC: Mean Quality Scores



R2

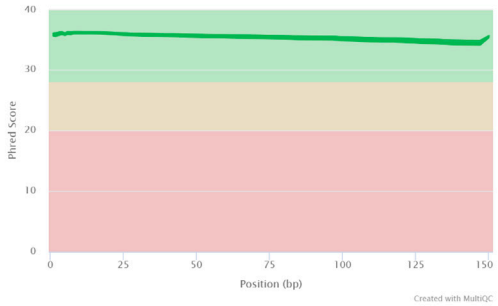
FastQC: Mean Quality Scores



ON 0.33G

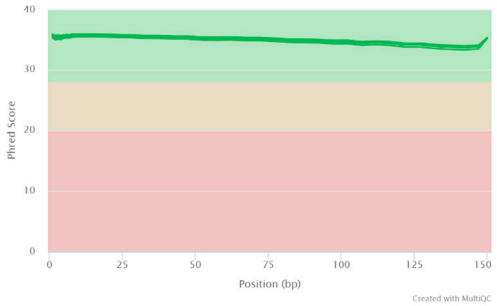
R1

FastQC: Mean Quality Scores



R2

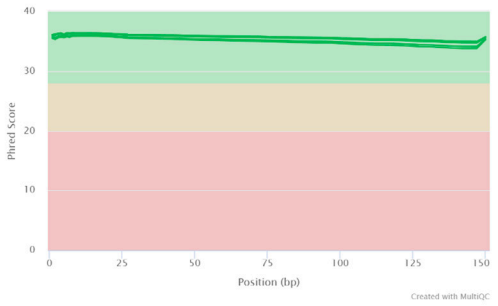
FastQC: Mean Quality Scores



ON 0.67G

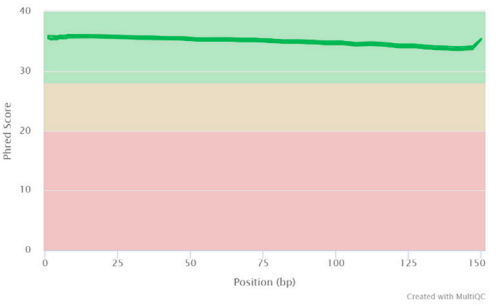
R1

FastQC: Mean Quality Scores



R2

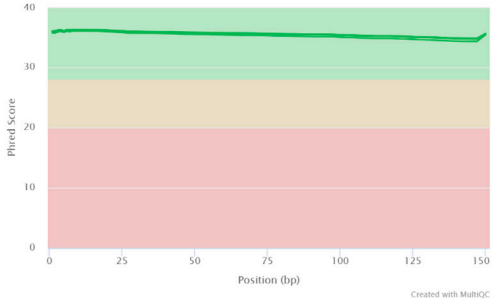
FastQC: Mean Quality Scores



ON 1G

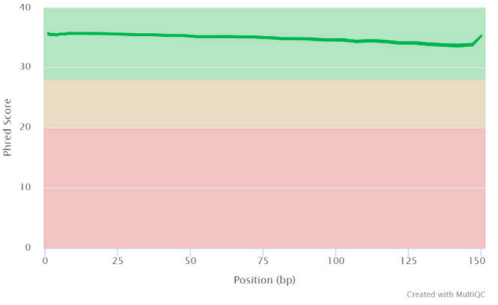
R1

FastQC: Mean Quality Scores

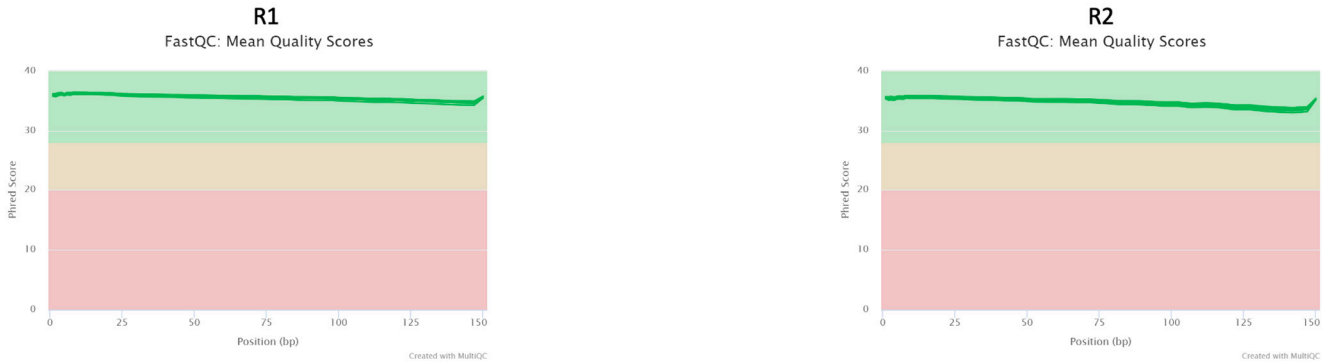


R2

FastQC: Mean Quality Scores

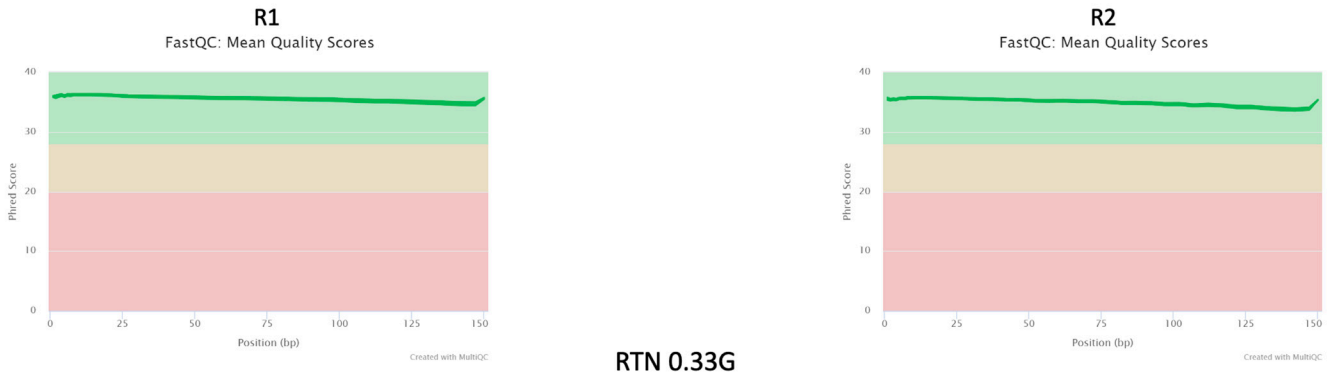


ON HGC

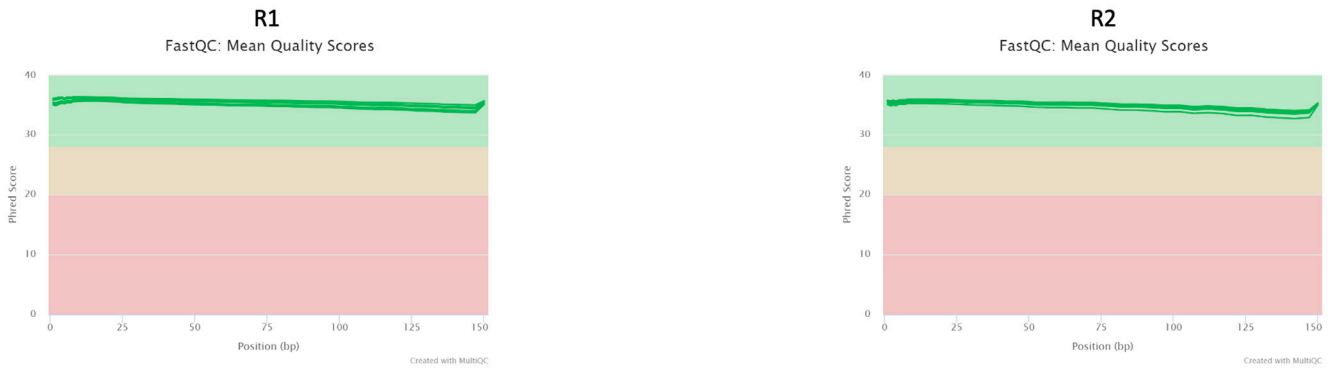


(a) MultiQC Analysis ON

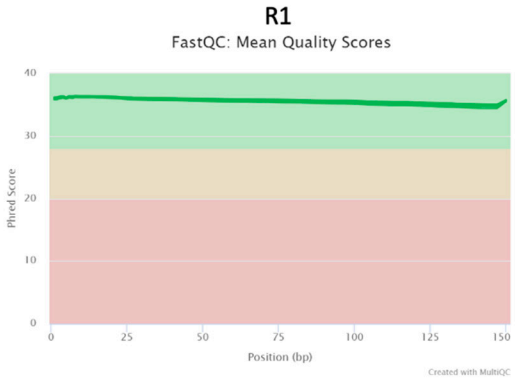
RTN 0G

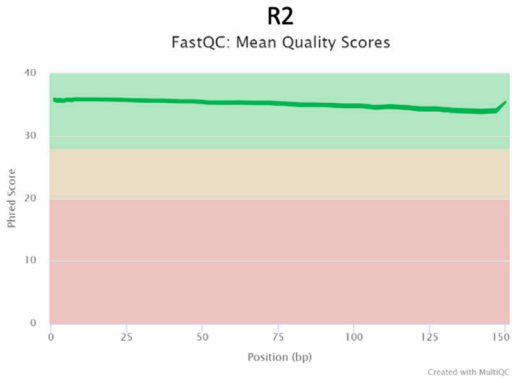


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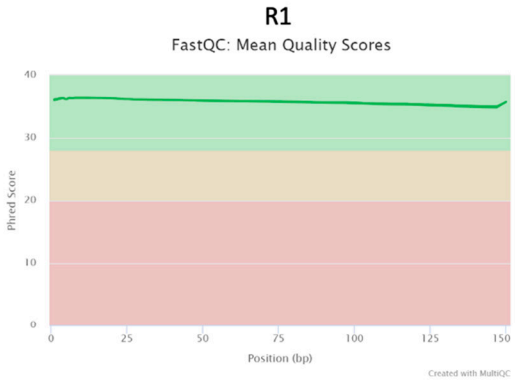


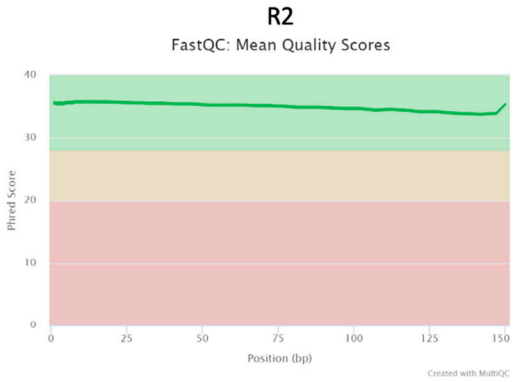
RTN 0.67G



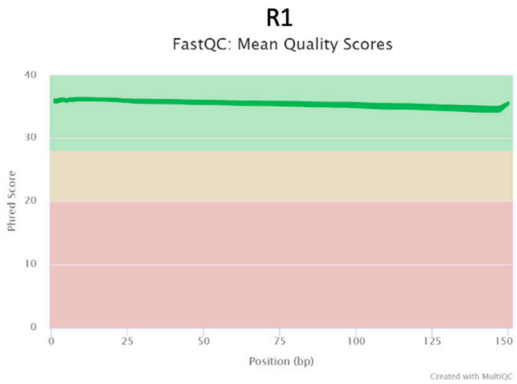


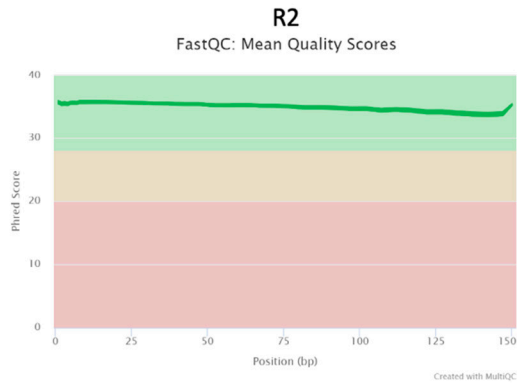
RTN 1G



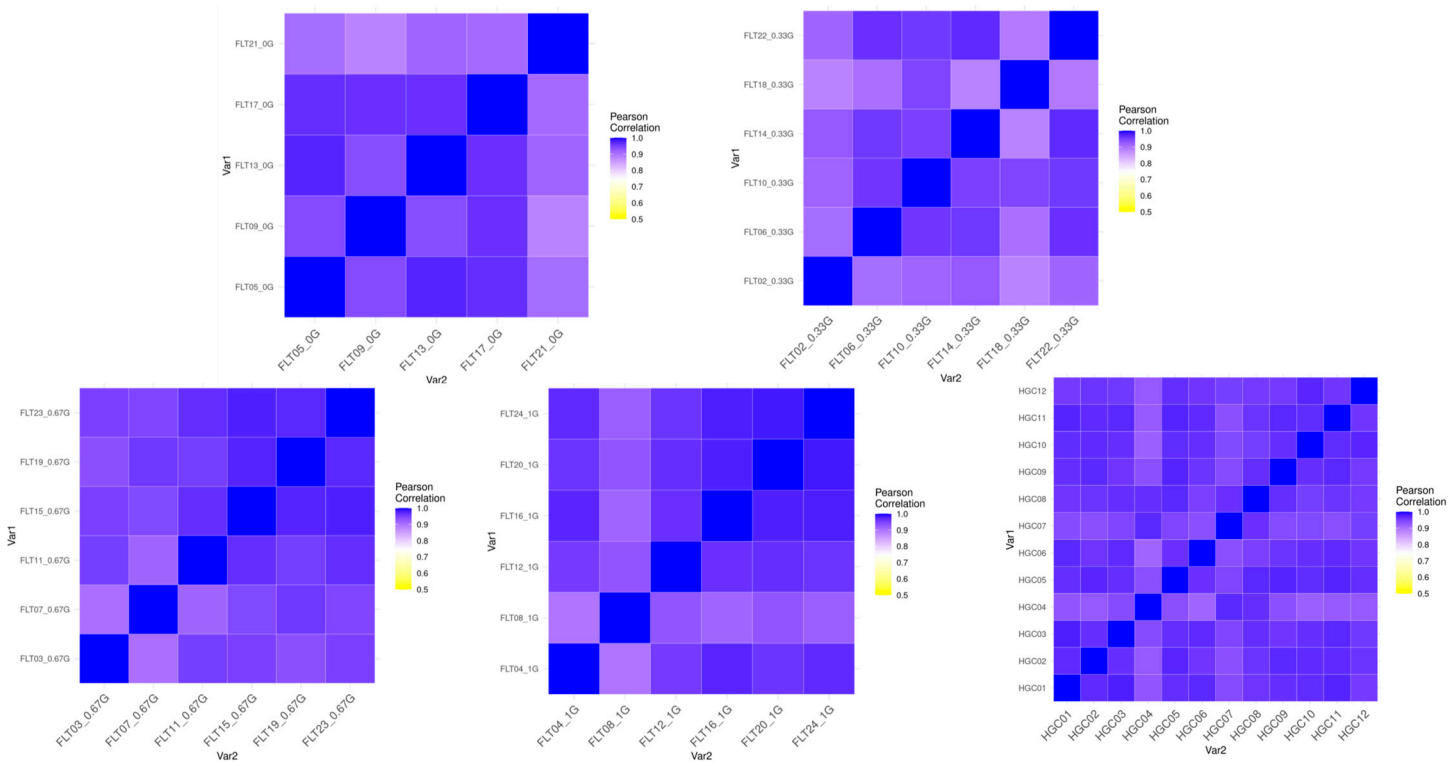


RTN HGC

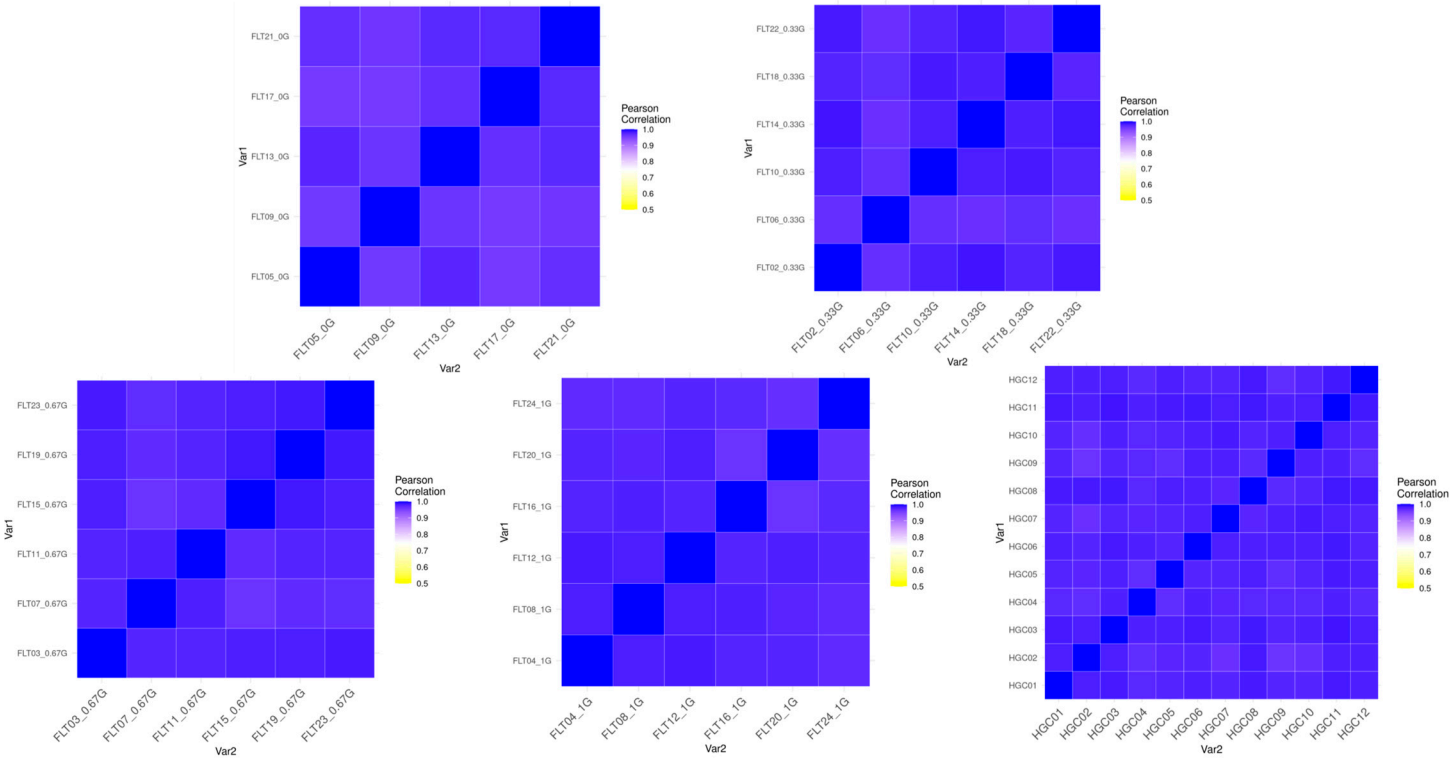




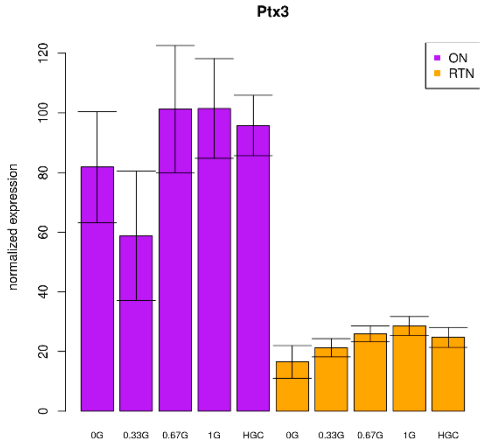
(b) MultiQC Analysis RTN



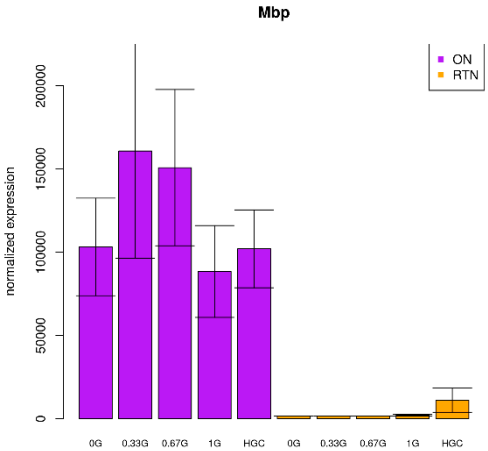
(c) Replicate correlations ON



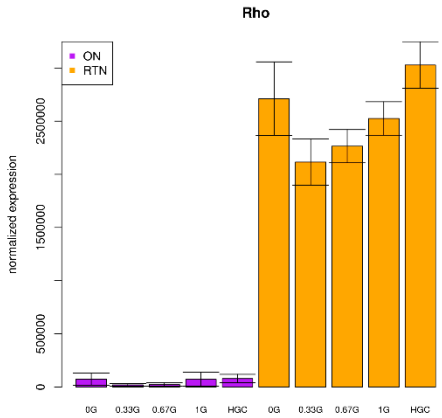
(d) Replicate correlations RTN



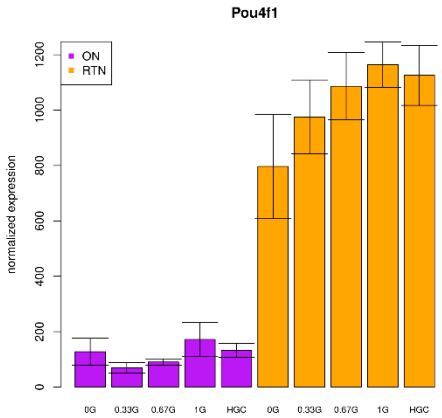
(e)



(f)

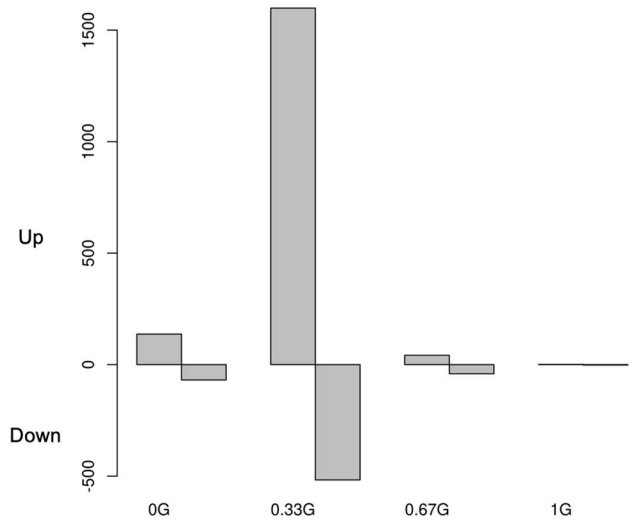


(g)

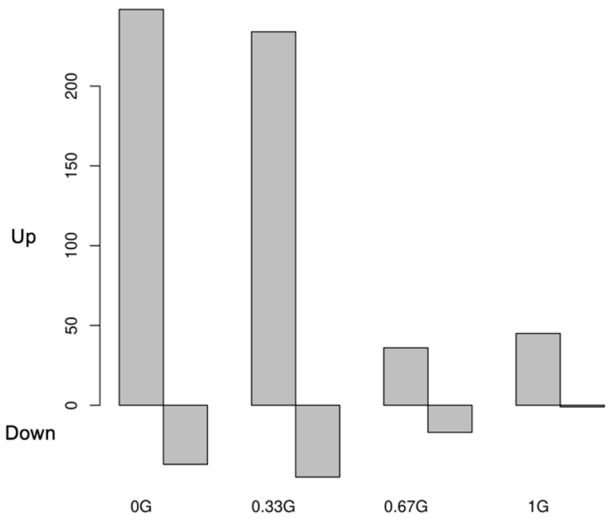


(h)

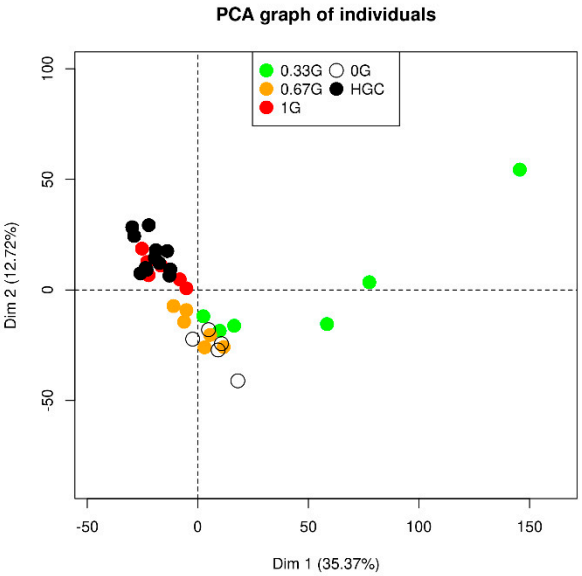
Figure S1. RNA-seq quality control. (a),(b) Per-base mean quality scores of all replicates of the indicated treatment group and sample type from MultiQC using FastQC. For each group, separate plots of mate1 (R1) and mate 2 (R2) reads are shown. **(c),(d)** Heatmaps visualizing Pearson's correlation coefficient between the natural logarithm of 1 + normalized expression of replicates of the indicated treatment group and sample type. **(e)–(h)** Barplots indicating the mean ± S.E.M. of the normalized gene expression of the indicated gene across replicates of the indicated treatment group and sample type.



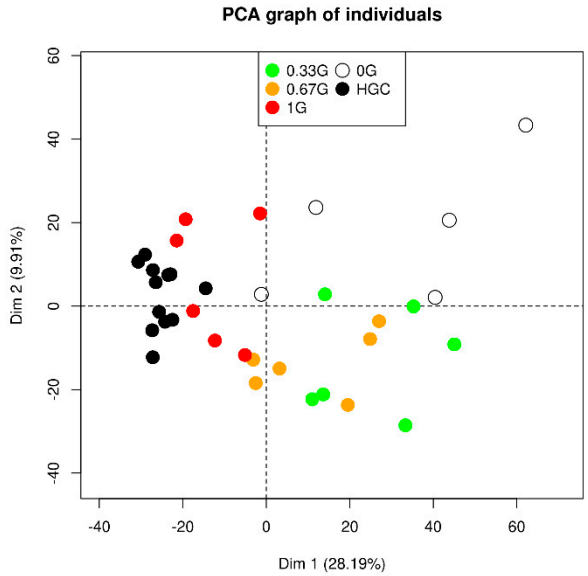
(a) ON



(b) RTN



(c) ON



(d) RTN

Figure S2. Related to Figure 3. (a),(b) Barplots showing the number of differentially expressed genes in the indicated treatment groups compared to HGC. **(c),(d)** Principal Components Analysis (PCA) plots showing individual replicates of the indicated treatment group and sample type.

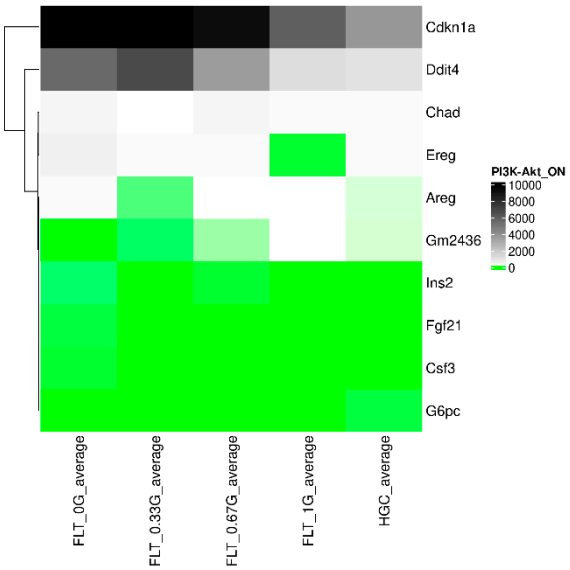


Figure S3. Related to Figure 4. Heatmap of normalized gene expression, averaged over replicates of the indicated treatment groups, of the genes with the top ten magnitude of log2 FC in ON 0G vs. HGC from the PI3k-Akt signaling pathway. Gene symbols are shown to the right of each heatmap. Genes are sorted by hierarchical clustering.