

# MINCR is not a MYC-induced lncRNA

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We would like to offer two critical comments on the PNAS paper by Doose et al. entitled “MINCR is a MYC-induced lncRNA able to modulate MYC’s transcriptional network in Burkitt lymphoma cells” (1).

Doose et al.’s (1) paper claims that MINCR is a MYC-induced long noncoding (lnc) RNA. The authors base this claim upon three pieces of evidence, correlation of expression in P493-6 cells, in hT-RPE-MycER cells, and in Burkitt lymphoma cells versus germinal center B-cell lymphoma cells. However, an examination of publicly available data (some of which were also used by the authors) shows that this correlation between MINCR and MYC is not universal, nor is it reproducible using independent Burkitt lymphoma data. An analysis of the normal tissue data (2) from which figure S3C in ref. 1 is derived reveals no correlation between MYC and MINCR expression in the various tissue types, as demonstrated in Fig. 1, Left.

Additionally, independent RNAseq data on Burkitt lymphoma cell lines obtained from the Cancer Cell Line Encyclopedia also fail to show such a correlation (3). Here, both MYC and MINCR levels vary substantially, but do not correlate with each other, as shown in Fig. 1, Right. Although such a correlation is seen in the particular dataset presented by Doose et al. (1), this dataset appears not to be broadly representative of the transcriptional regulation of MINCR. Because the expression of MYC and MINCR do not generally correlate, nor do they correlate in Burkitt lymphoma, we consider the term “MINCR” as “MYC-induced noncoding RNA” a misnomer.

Doose et al. (1) claim that they are the first to analyze the MYC-regulated noncoding transcriptome with RNAseq. As a matter of fact, at least three publications that use RNAseq for the analysis of MYC-regulated lncRNAs preceded their publication (4–6), in addition to numerous studies using microarray and quantitative PCR. This would be a minor breach of scientific etiquette, except for the fact that the paper by Doose et al. (1) relies extensively on the lncRNA expression data from two of these previously published studies (5, 6). In the first section of the *Results* and in figure 1 of ref. 1, Doose et al. use RNAseq data from the lymphoblastic cell line P493-6 as one of the selection criteria for MYC-regulated lncRNAs, and cite two early papers that merely document the origin of P493-6 cells, but do not deal with lncRNAs. The ordinary reader would then assume that the P496-3 lncRNA data are generated by Doose et al. Only in the *SI Materials and Methods* of ref. 1 is it revealed that the data are taken from a published study, but no appropriate attribution is given. We consider the listing of Gene Expression Omnibus identifiers here as not adequate. It is not in accordance with currently accepted norms of data reuse and data reanalysis and is particularly problematic in conjunction with claims of priority.

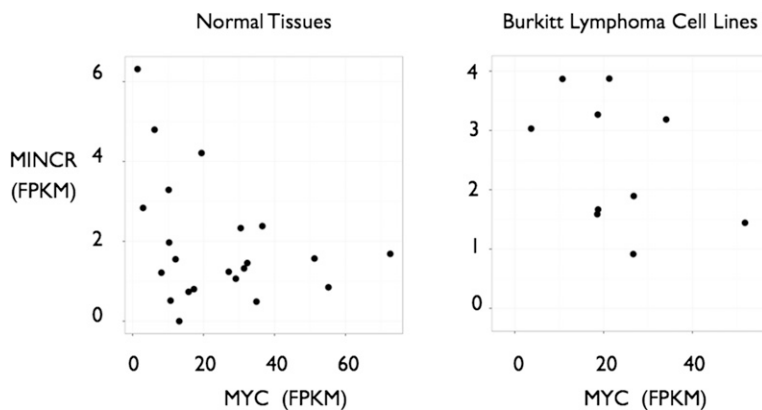


Fig. 1. Expression levels of MINCR plotted against levels of MYC taken from normal tissues and cell lines (Left, data from ref. 2) and Burkitt lymphoma cell lines (Right, data from ref. 3) show a lack of significant positive correlation between MYC and MINCR. FPKM, fragments per kilobase of transcript per million mapped reads.

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