Computing microRNA-gene interaction networks in pan-cancer using miRDriver

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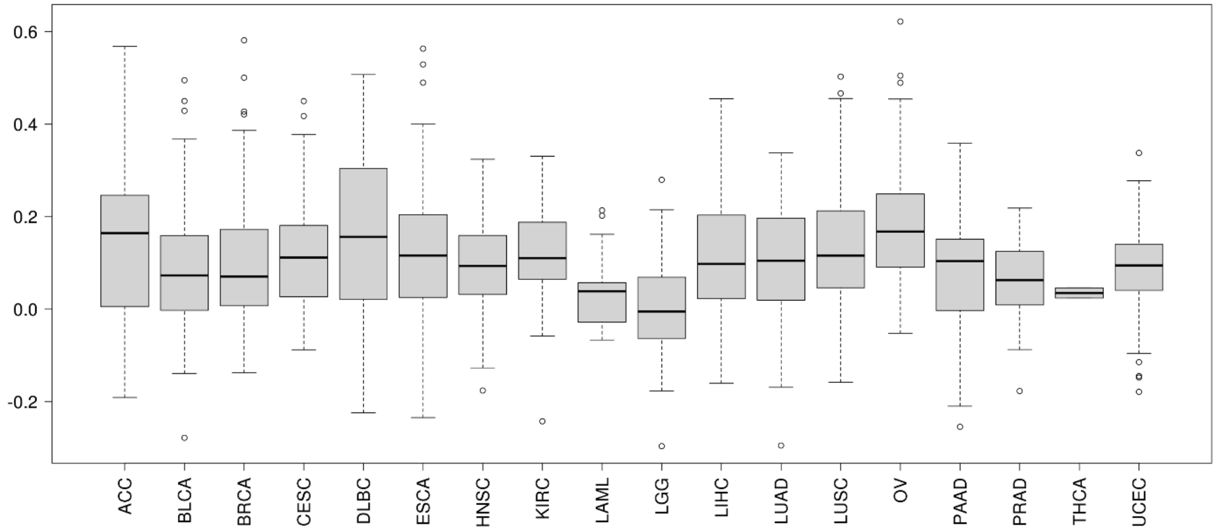

Supplemental Figure S19: Boxplots showing the Spearman correlation values between copy number and expression across all the samples of the computed miRNAs of miRDriver in eighteen different cancer types. There is a positive median distribution of correlations across all cancer types.