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# Integrated whole transcriptome and small RNA analysis revealed multiple regulatory networks in colorectal cancer

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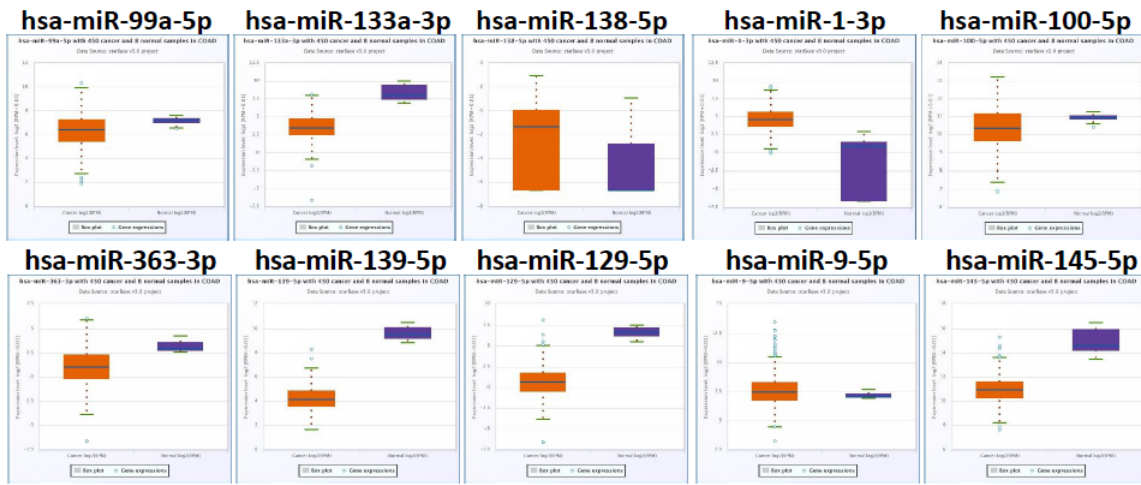
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Upregulated



Downregulated



**Supplementary figure 3. Expression of top 10 upregulated and top 10 downregulated miRNAs in the TCGA COAD database.** Expression of the indicated gene in COAD (n=471) compared to normal tissue (n=41) is shown as box plot. Data were retrieved from the starBase V3.0 database.