



Figure S16: Pipeline followed for NGS data analysis. This diagram illustrates detailed protocol followed for NGS Data (RNA-seq, sRNA-seq and CLIP-seq) in analysis for expression of pre-miRNA, mature miRNA, RBP, and potential RBP:miRNA interaction sites. RNA-seq data was filtered using filter and trimomatic. RNA-seq reads were mapped across human genome (hg38) using Seqmap. rSeq was used for quantification of gene expression. For expression analysis of pre-miRNAs, RNA-seq reads were mapped across known pre-miRNA sequences. mirDeep2 was used for expression analysis of mature miRNAs. sRNA-seq reads were mapped across known mature miRNAs, using mapper.pl script. Quantifier.pl script was executed for quantification of mature miRNAs expression. For processing of CLIP-seq data FastX was used. Those reads were kept which had at least 75% of bases with a quality score of 25 or more and unique reads were selected. The unique CLIP-seq reads were mapped across pri-miRNA and pre-miRNA regions using Bowtie considering a maximum of two mismatch. Potential binding sites of RBPs on different miRNAs were considered on those regions where at least five reads mapped and these reads existed at least in two independent samples.