

Investigating piwi-interacting RNA regulome in human neuroblastoma

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In this work, we investigated the piRNA transcriptome in IMR-32 and SH-SY-5Y neuroblastoma (NB) cell lines by employing high-throughput next-generation sequencing after confirming the expression of three associated PIWILs both at mRNAs and protein level by qRT-PCR and immunofluorescence, respectively. We identified a common pool of 525 piRNAs of 26-32 nts long expressed in both the cell lines. The possible functions of these piRNAs were charted by predicting their targeting on retrotransposon-containing 1769 mRNAs differentially expressed in 39 NB cell lines followed by network and pathway analysis. The analysis revealed that majority of the target binding sites in NB fall within retrotransposons residing within the 3'UTR of target mRNA transcripts like miRNA-targets. Further, we validated the expression of key piRNAs and their target genes enriched in cancer-related networks, pathways and biological processes which are hypothesized to play crucial roles in neoplastic events of NB. We believe that the evidence of piRNAs in human NB and their possible contribution to its pathogenesis reported in this work will open up new exciting possibilities for piRNA-mediated therapeutics for this malignancy. More in **Genes, Chromosomes and Cancer**, 57(7): 339-349 (2018); <https://doi.org/10.1002/gcc.22535>.

