

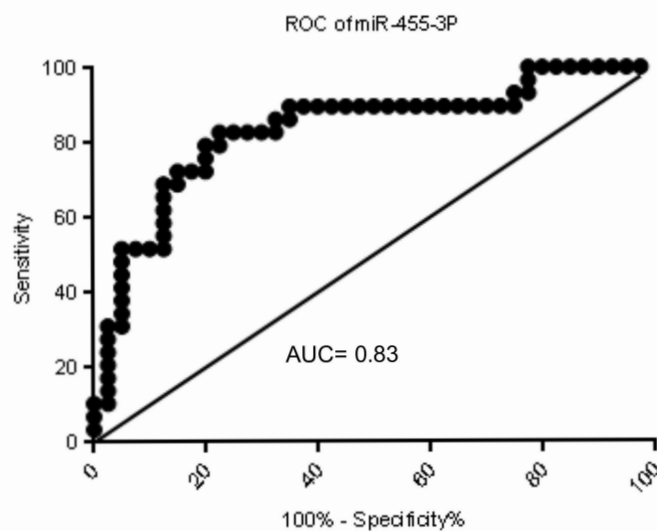
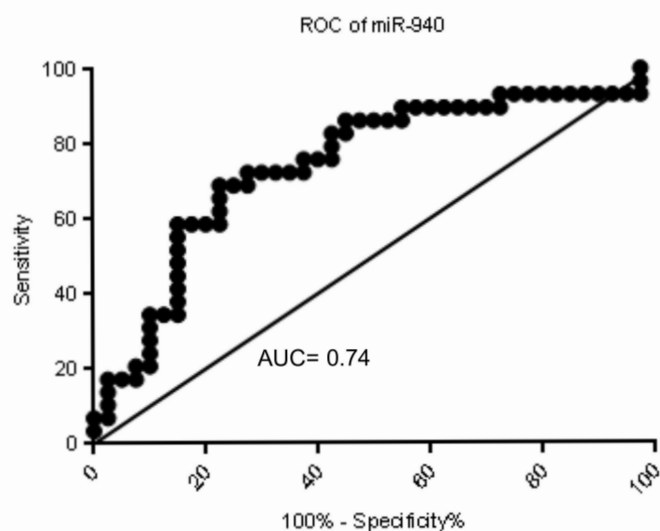
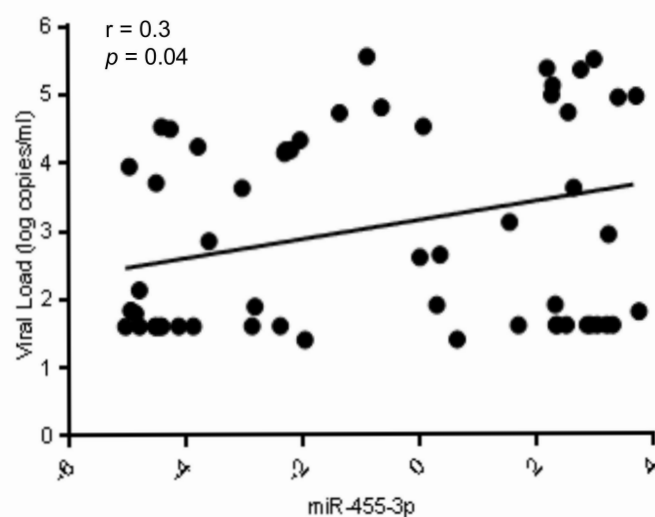
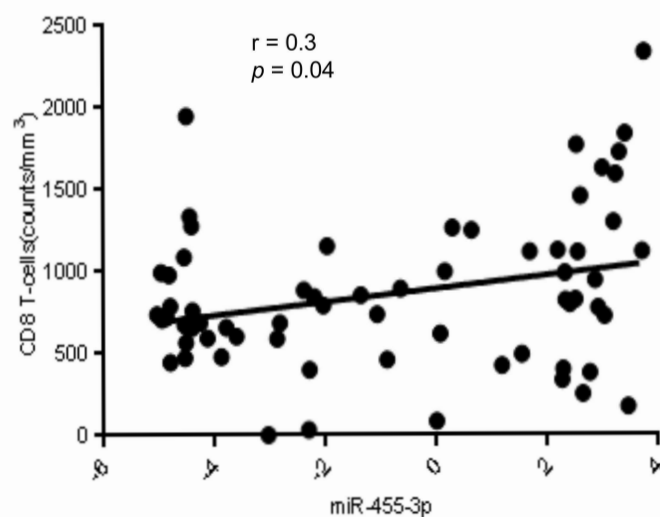
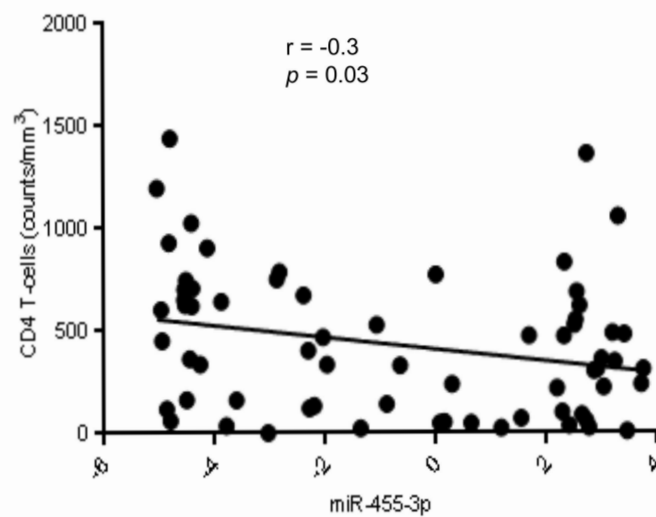
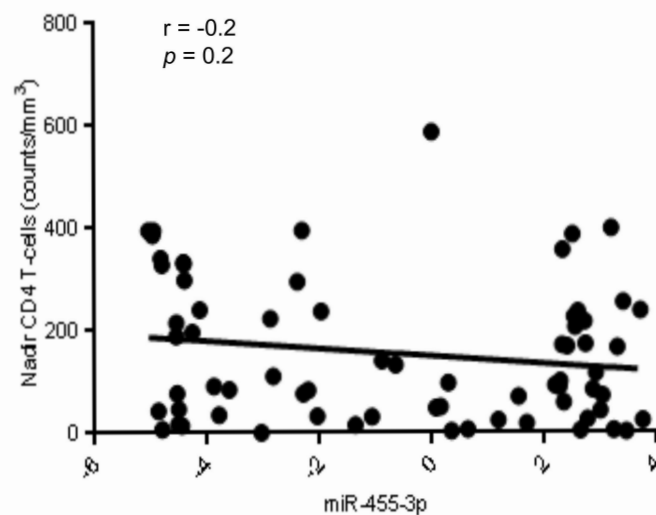
**Supplementary Fig. 1: The receiver-operating characteristic (ROC) curve and Spearman correlation analysis of array hybridization.** The expression level of miR-455-3p and miR-940 by array hybridization was used to generate ROC curves. The AUC for miR-455-3p was 0.83 (A) and for miR-940 was 0.74 (B). The Spearman correlation analyses between miR-455-3p relative fold changes and viral load (C), CD8 T-cells (D), current CD4 T-cells (E) and nadir CD4 T-cells (F).

**Supplementary Fig. 2: Vector Support Machine Analysis.** The top 10 miRNAs with highest frequency of miRNA detection based on p-value ( $p < 0.05$ ) and two sample t-test are shown.

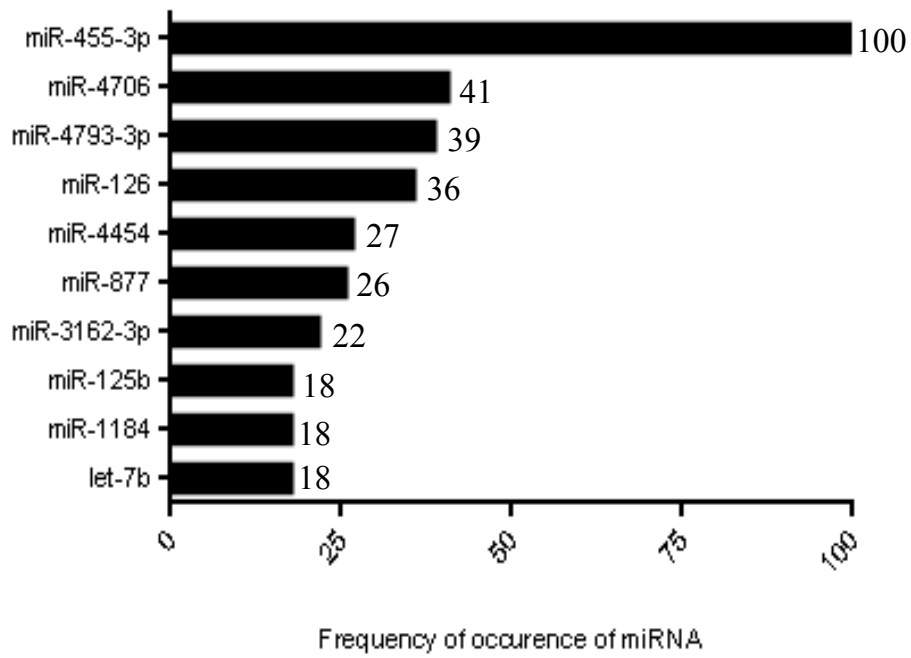
**Supplementary Fig. 3: Effects of HIV-1 Vpr on SK-N-SH.** Recombinant HIV-1 Vpr (100nM) was exposed to SK-N-SH and cell viability was assessed by staining with DAPI (A) or anti- $\beta$ -III tubulin (B). Total RNA was extracted from cells exposed to HIV-1 Vpr and mock. The RNA was used to quantify the expression level of miR-455-3p (C) and miR-940 (D). Each experiment was repeated two times and the results analyzed using One-way ANOVA (Kruskal-Wallis) test.

**Supplementary Fig. 4: NGF expression in hDRG by in-cell western and quantification of miR-455-3p expression and neurite length in transfected SK-N-SH cells.** Cultured hDRGs were transfected with miRNA-NC or miR-455-3p for 48 hrs. After transfection cells were incubated with anti-NGF antibodies and immunofluorescence was quantified by in-cell western (LI-COR Biosciences) (A). Total RNA was extracted from cells transfected with miRNA-NC and miR-455-3p. The RNA was used to quantify the expression level of miR-455-3p in transfected cells (B). For (A) and (B) each was repeated three times the results analyzed using One-way ANOVA (Kruskal-Wallis) test.

Immunofluorescence images from SK-N-SH cells transfected with miRNA-NC and miR-455-3p, and labeled with  $\beta$ -III tubulin antibody were captured by confocal microscope. The images were then uploaded into the neuromath software (<https://www.weizmann.ac.il/vet/IC/software/wis-neuromath>) to quantify the neurite length of each image. The histogram shows the mean neurite length per cell (C).

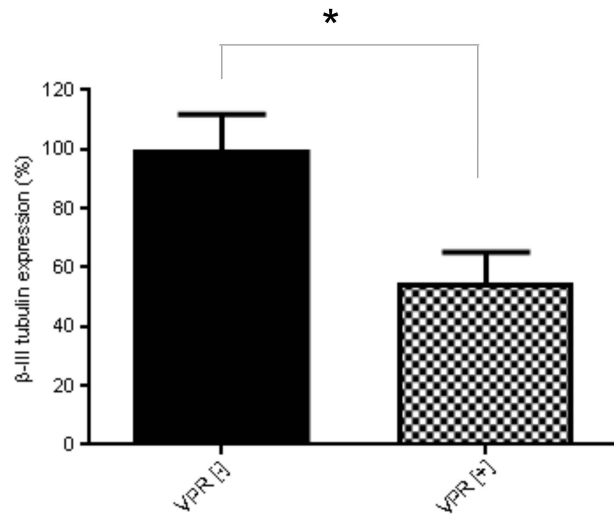
**A****B****C****D****E****F**

## Supplementary Fig. 2

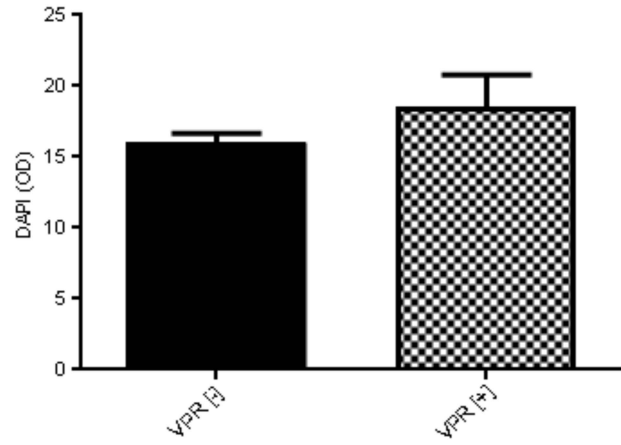


**Supplementary Fig. 3**

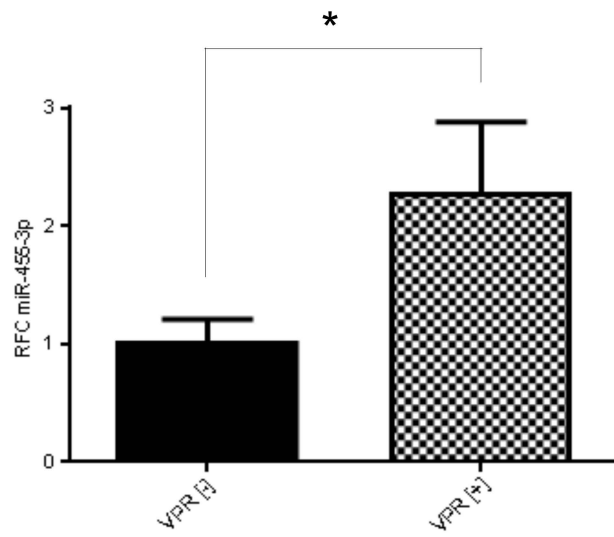
**A**



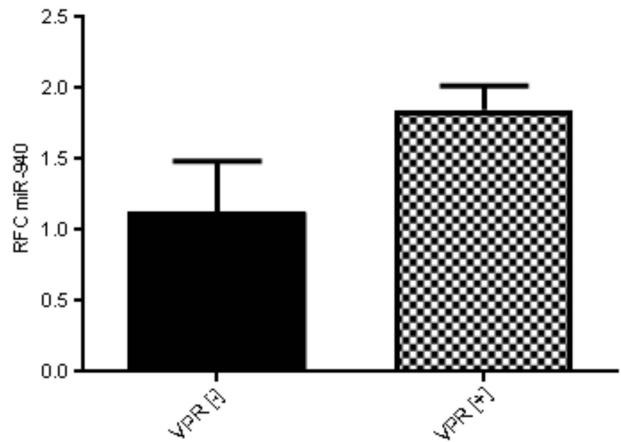
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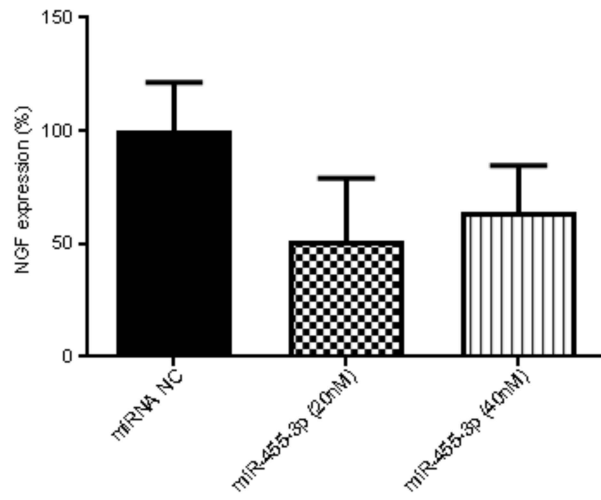
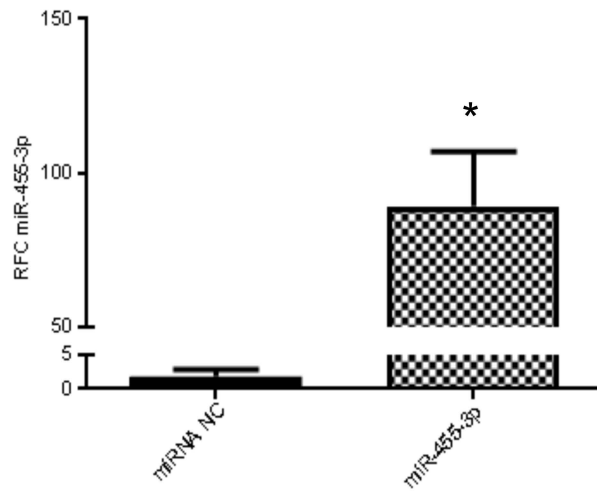


**C**



**D**



**A****B****C**