

Projects- Pellegrini

- 1. Mutational profiles of Basal cell carcinoma (including merging data from 2 experiments)**
- 2. Presence of TRKAll splicing variant in melanoma samples in TGCA database**
- 3. Analysis of miRNome in glioblastoma cell lines treated with a new drug (UNIPR)**

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Mutational profiles of BCCs

- NGS sequencing

❖ 52 Basal cell carcinoma

Nodular BCC



Superficial BCC



❖ 18 NS (Normal skin)

Mutational profiles of BCCs

- NGS sequencing

- ❖ 52 Basal cell carcinoma
- ❖ 18 NS (Normal skin)

Ion torrent platform



Genetic panel (808 amplicons)

TYPE	NAME
GENE	CSMD1
GENE	DPP10
GENE	PTCH1
GENE	TP53
GENE	NOTCH1
GENE	SMO
GENE	NOTCH2
GENE	CSMD2
GENE	ITIH2
GENE	STEAP4
GENE	GLI1

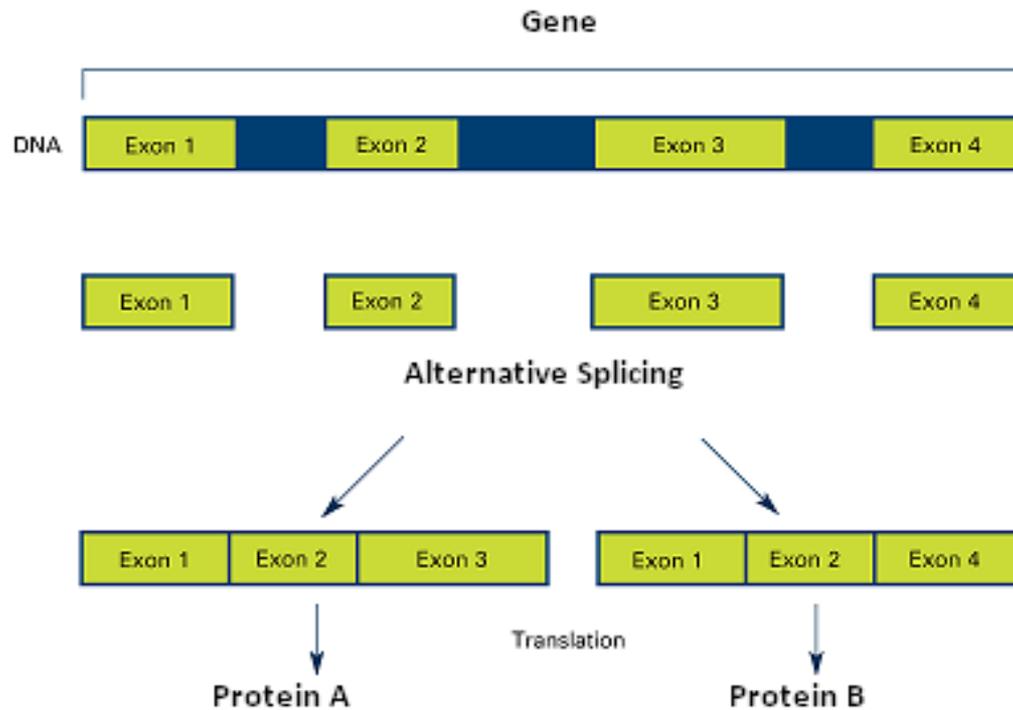
Mutational profiles of BCCs

Aim

To match NGS sequencing data of BCC tumor and Normal skin of the same patient

Presence of TRKAII splicing variant in melanoma samples in TCGA database

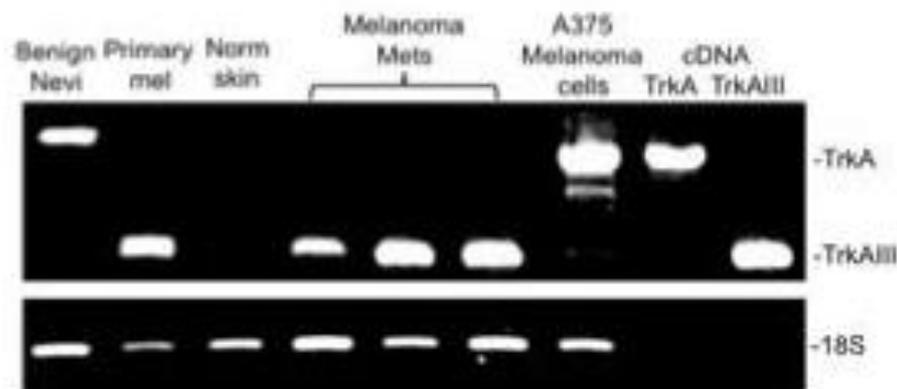
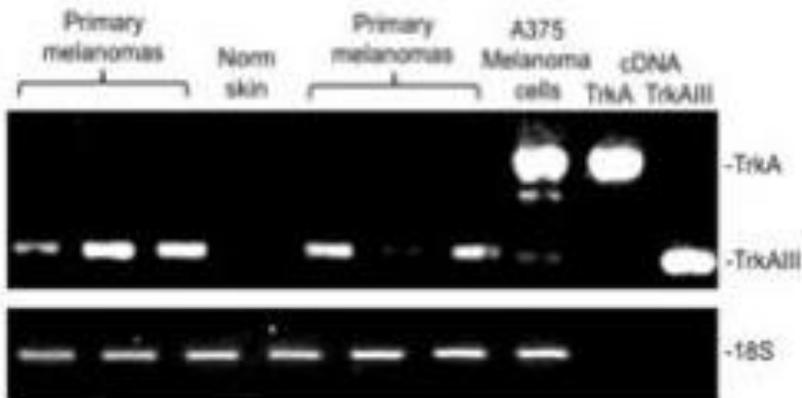
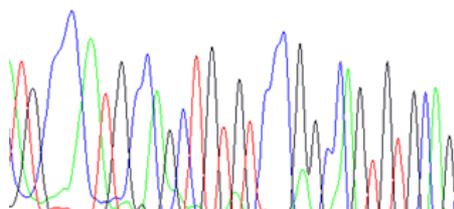
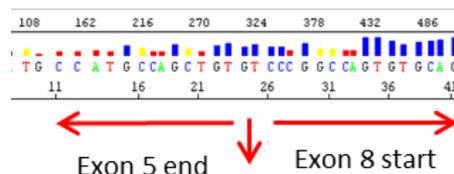
TRKA gene



Presence of TRKAIII splicing variant in melanoma samples in TCGA database

TRKA gene in melanoma

- TrkAIII splicing in 7 primary melanomas and 3 melanoma metastases
- In contrast, benign nevi express full length TrkA and normal skin samples exhibit low to undetectable TrkA expression

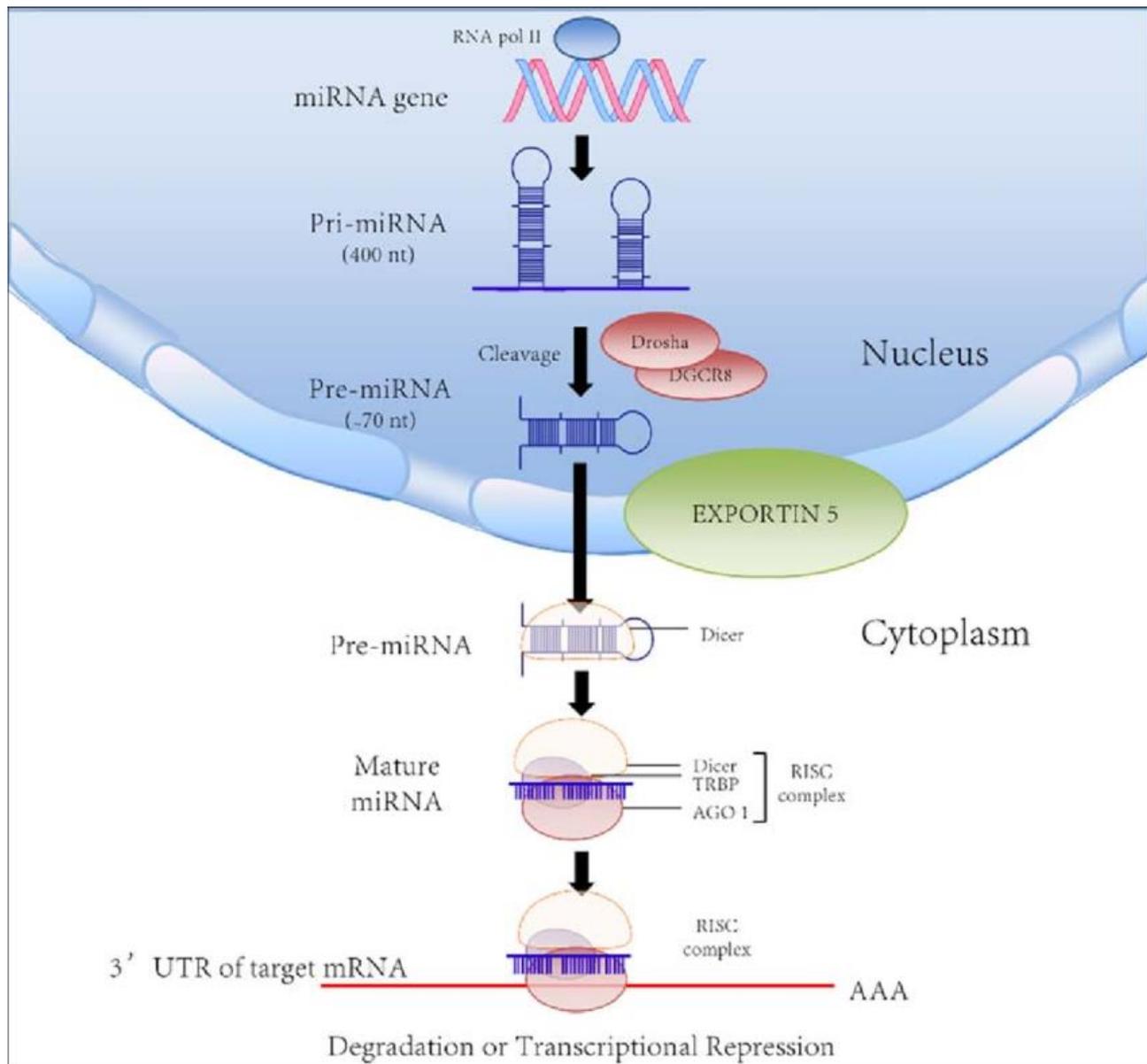


Aim

To evaluate the presence of TRKAll in melanoma sample in TGCA database, to increase the sample size of our cases

miRNome analysis

microRNA

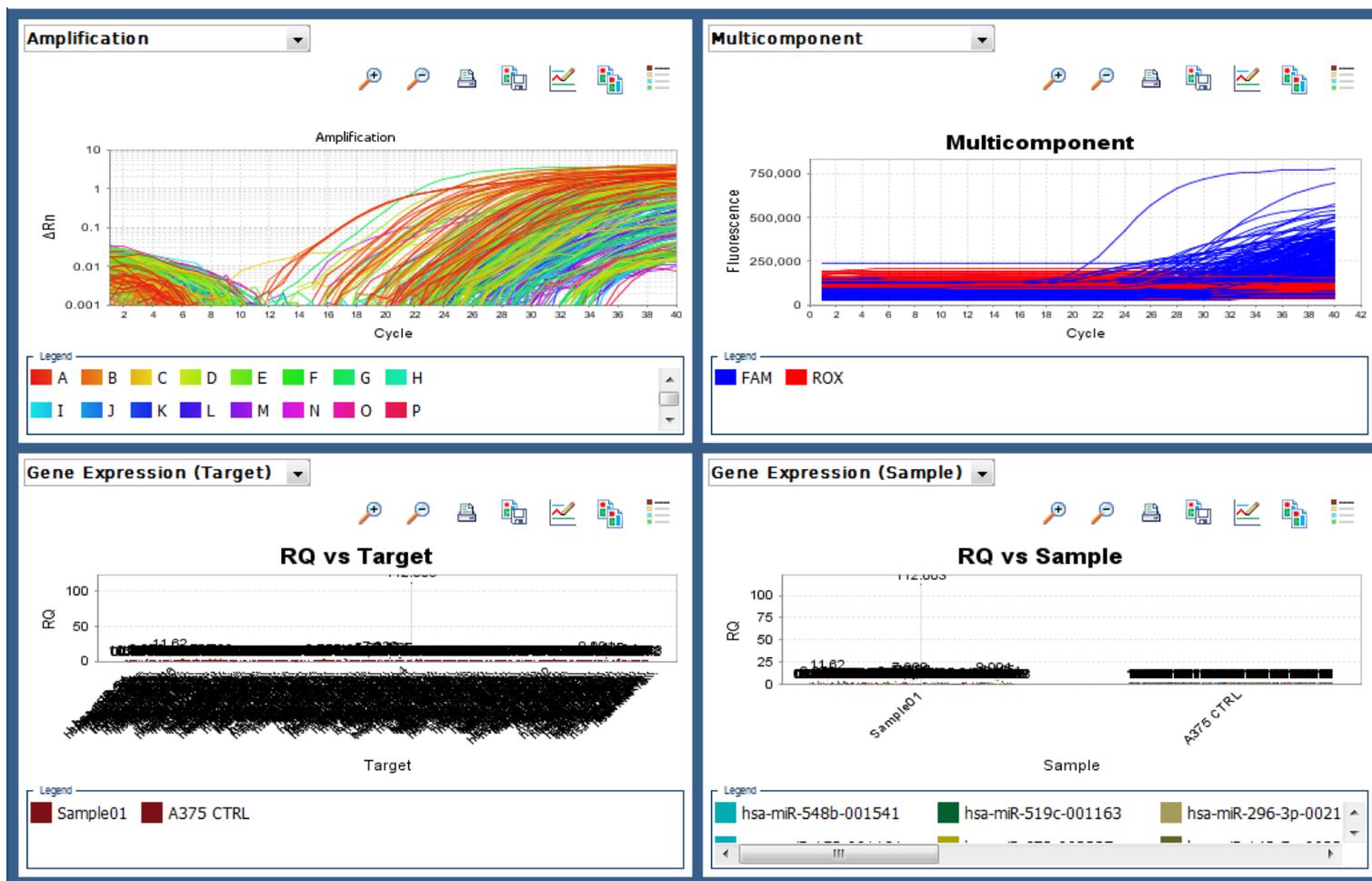


miRNome analysis

Methods: real Time PCR on 2 samples (each on duplicate, in card A and Card B)

- CTR (untreated cells)
- UNIPR (treated cells)

Example CARD A results



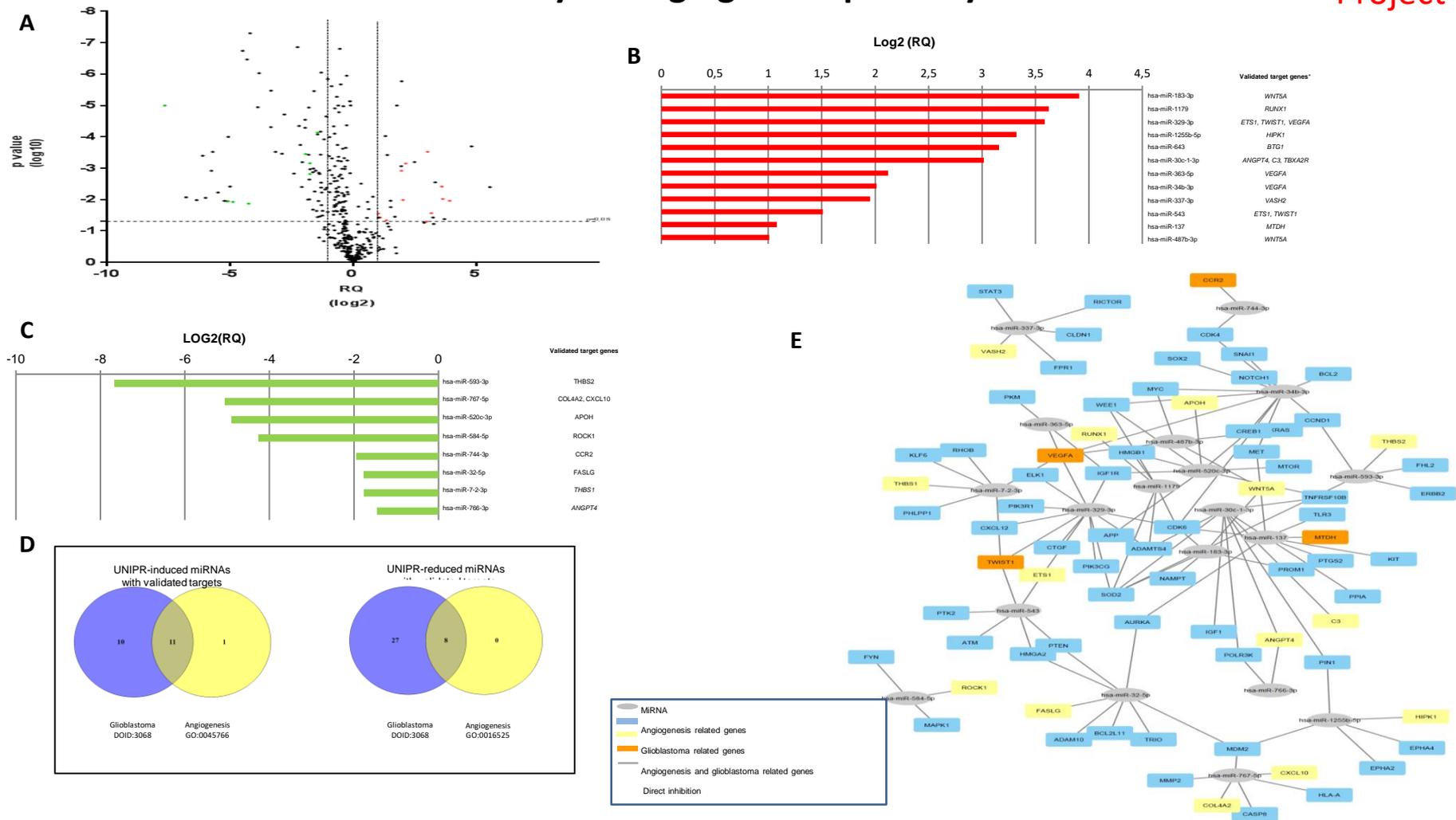


Figure 1: Identification of UNIPR-deregulated miRNAs influencing angiogenesis reduction and glioblastoma

(A) The volcano plot shows the global trend of UNIPR-deregulated miRNAs. The X axis represents the difference between miRNA mean expression level ($\log_2[RQ]$) in UNIPR-treated cells and untreated cells. The dotted vertical lines correspond to 2.0-fold up and down, respectively, and the horizontal dotted line represents a p-value of 0.05. Significant miRNAs are located above the line that indicates $\log_{10}[\text{cutoff P value}]$ considered in the statistical analysis: $p < 0.05$. Volcano Plots are useful tools for visualizing differential expression between two different conditions. It is constructed using RQ values and p-values, and thus, allow to visualize the relationship between RQ (magnitude of change) and statistical significance (which takes both magnitude of change and variability into consideration). The green points represents down-regulated miRNAs that have validated targets in GO:0016525 term; the red points represents up-regulated miRNAs that have validated targets in GO:0045766 ontology, according miRWalk analysis. (B) and (C) Relative expression levels ($\log_2[RQ]$) of UNIPR-induced and UNIPR-reduced miRNAs with experimentally proven targeted genes, respectively. (D) Venn diagram shows the numbers of UNIPR-deregulated miRNAs with validated targets influencing the angiogenesis reduction, the glioblastoma disease and their overlaps. (E) Cytoscape 3.4.0 software graphical visualization of miRNA-target interactions. The miRNA-gene network shows the relationships between nineteen UNIPR-deregulated miRNAs with validated targets in angiogenesis reduction and/or glioblastoma and signature genes they are validated to regulate. The colors of each gene node indicate the annotated function of the gene.

miRNome analysis

Aim

To evaluate the differential enrichment pathway of miRNA between treated and untreated cells.

To evaluate the enrichment of mirNA in the «differentiation» in treated and untreated cells.