

Legends for supplemental files
(In same order)

Figure S1: Novel miRNA (a) and fibrosis related miRNA(b) differentially expressed between classical and pigmentary phenotypes of pseudoexfoliation with heat map of specific miRNA predicted KEGG pathway using mirPath (C).

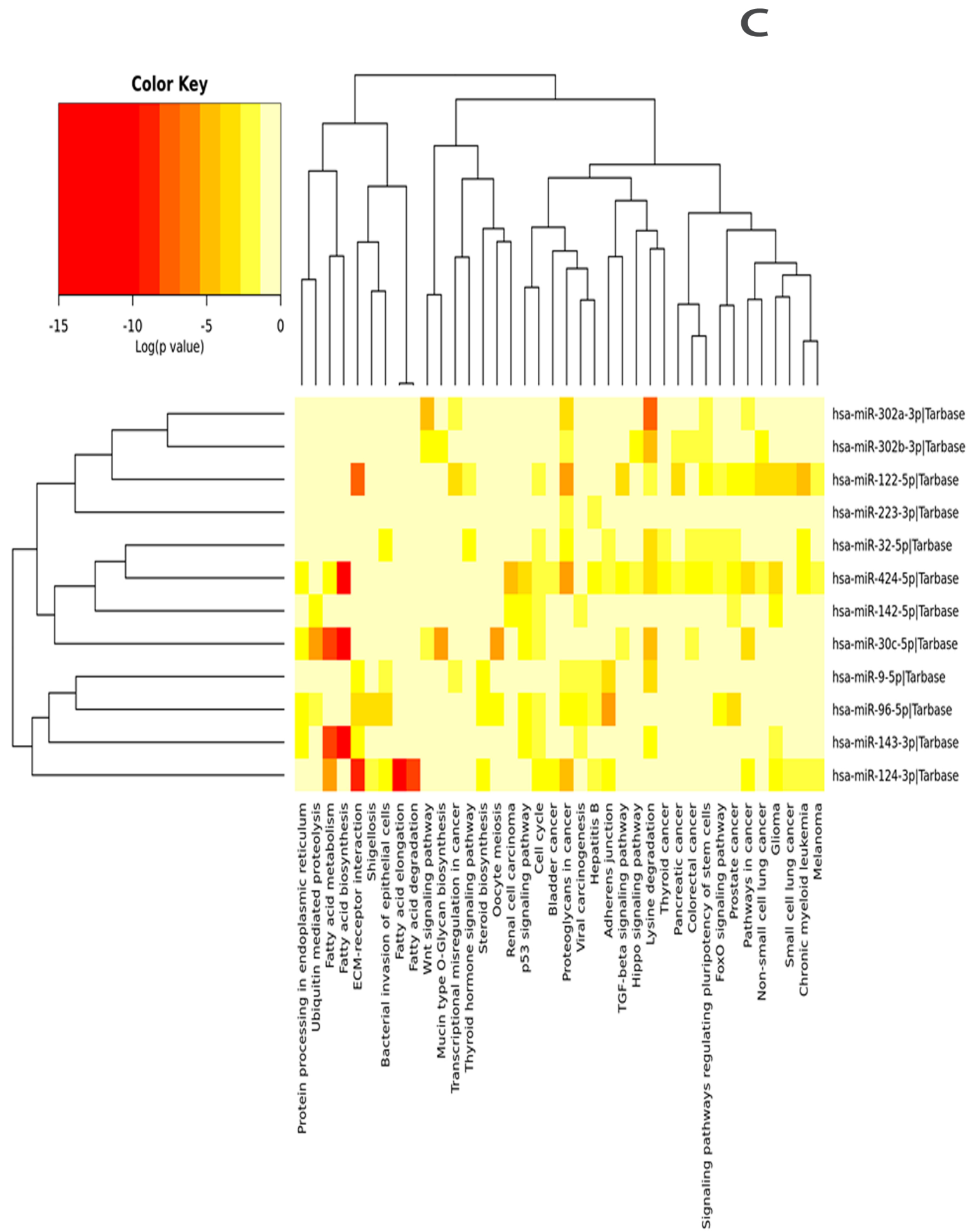
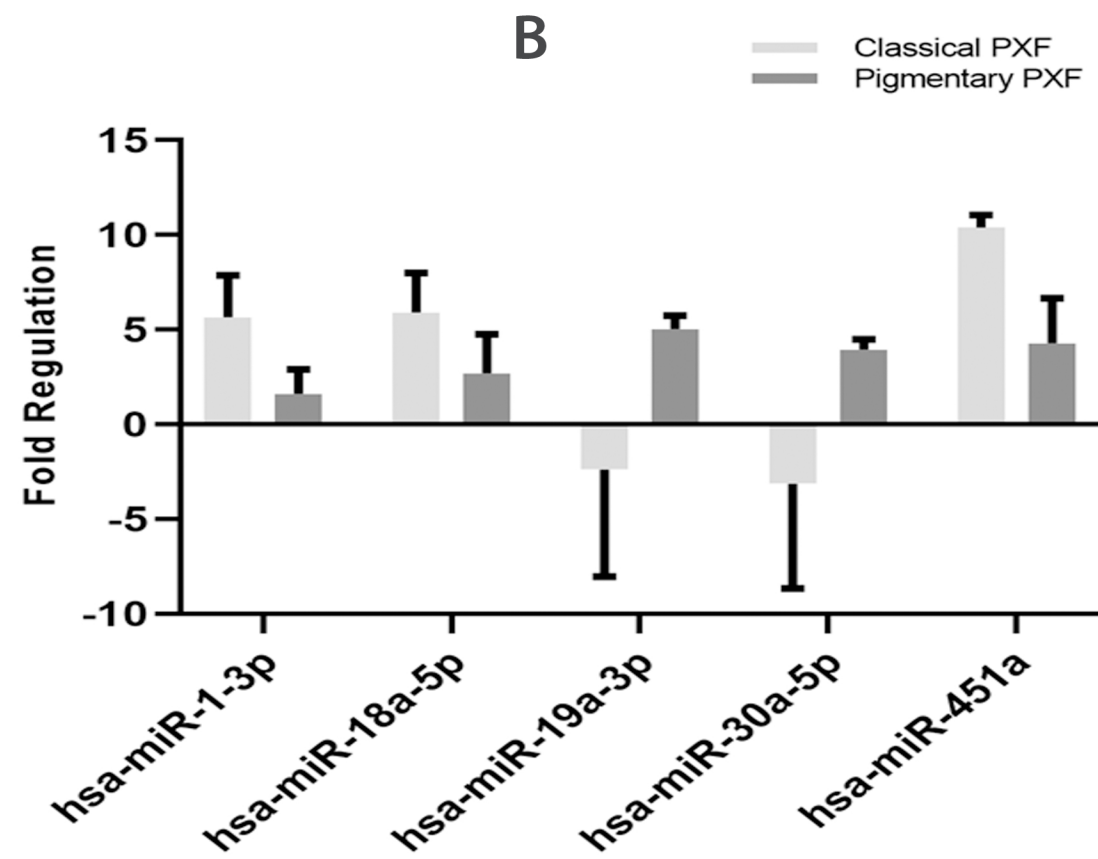
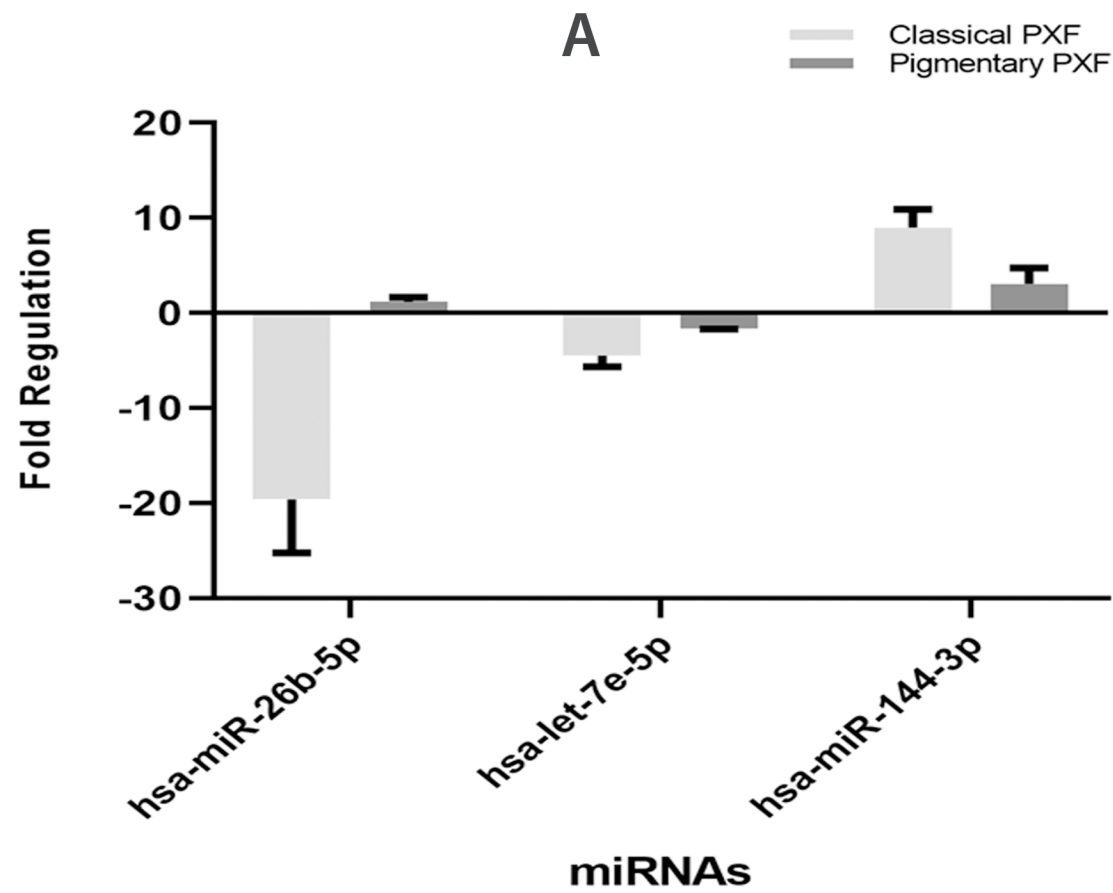
Figure S2: Downstream targets of SMADs (a) and TGF beta pathway related effectors (b, c) differentially expressed between classical and pigmentary phenotypes of pseudoexfoliation.

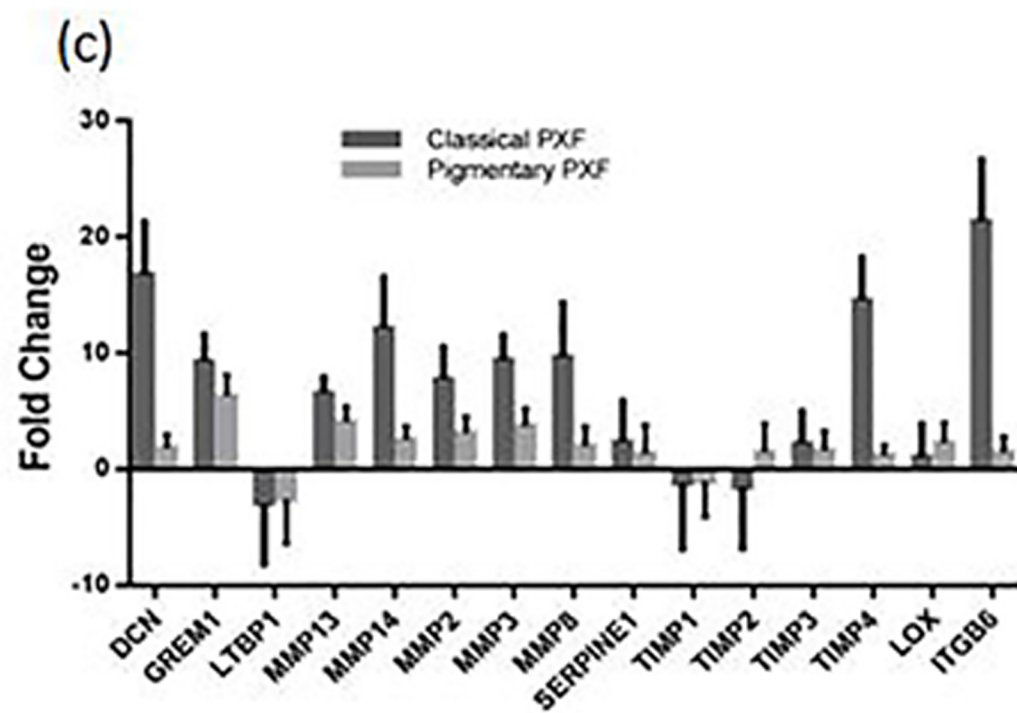
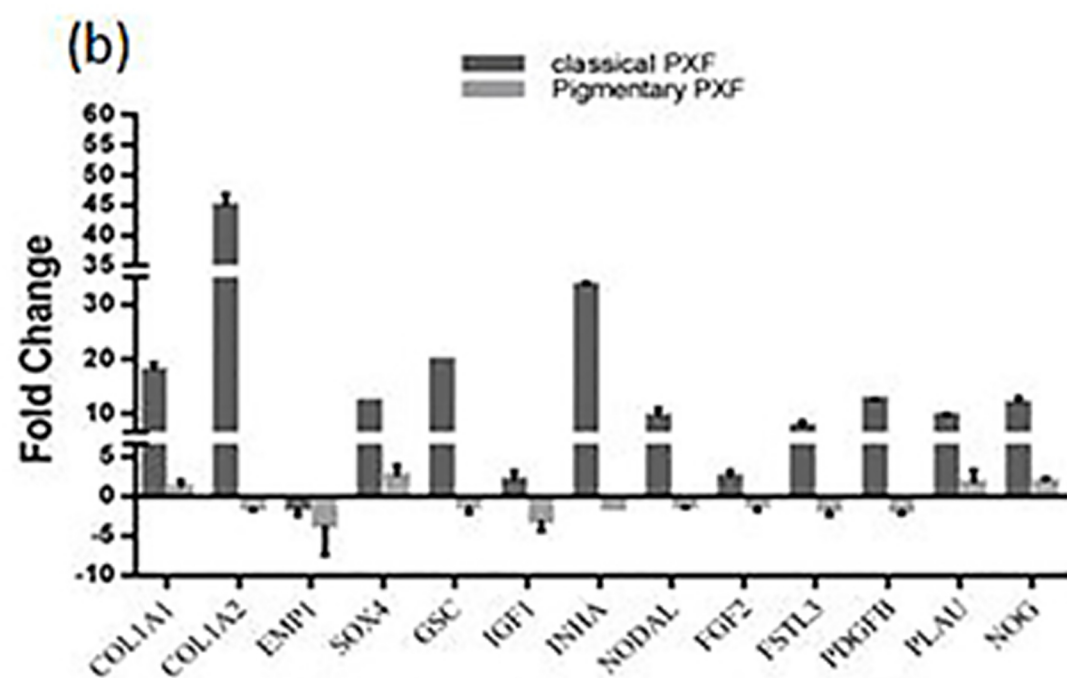
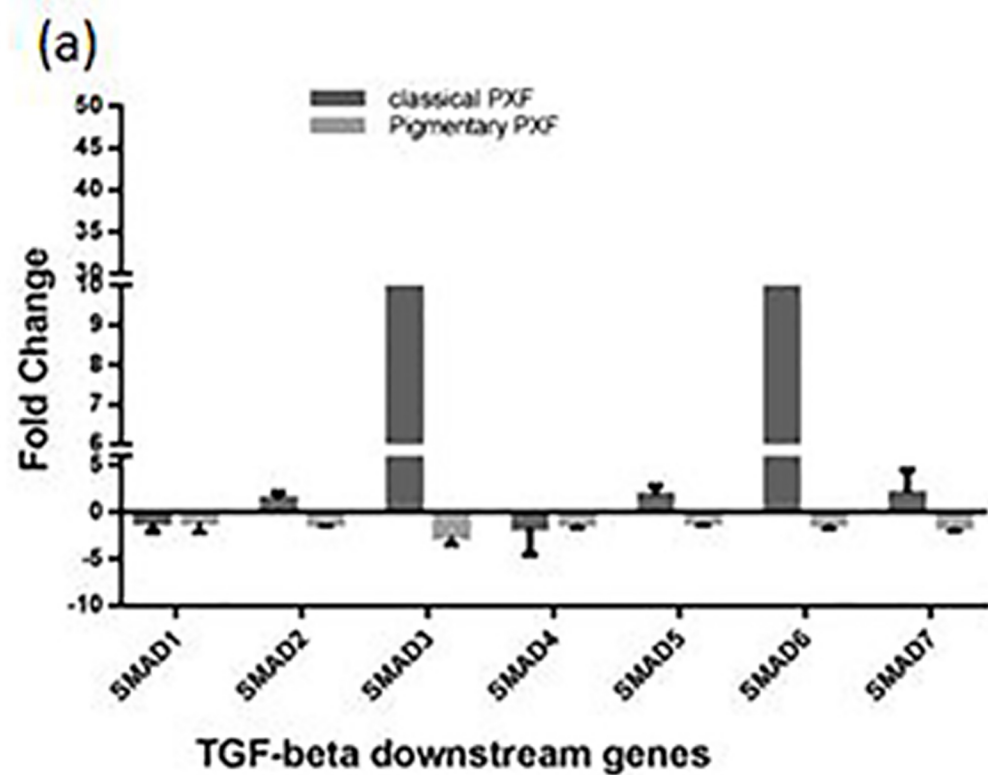
Figure S3: Gel pictures of housekeeping genes in miRNA obtained from serum and PBMC samples from patients with pseudoexfoliation.

Table S1: Novel miRNA related to TGF pathway with targeted functions patients with pseudoexfoliation phenotypes.

Table S2: Fibrosis miRNA related to protein processing with targeted functions of patients with pseudoexfoliation phenotypes.

Supplemental data: Workflow of patients included into different phases of the study





M

PBMC SNORD 68

Serum SNORD 68

PBMC 122-5p

Serum 122-5p

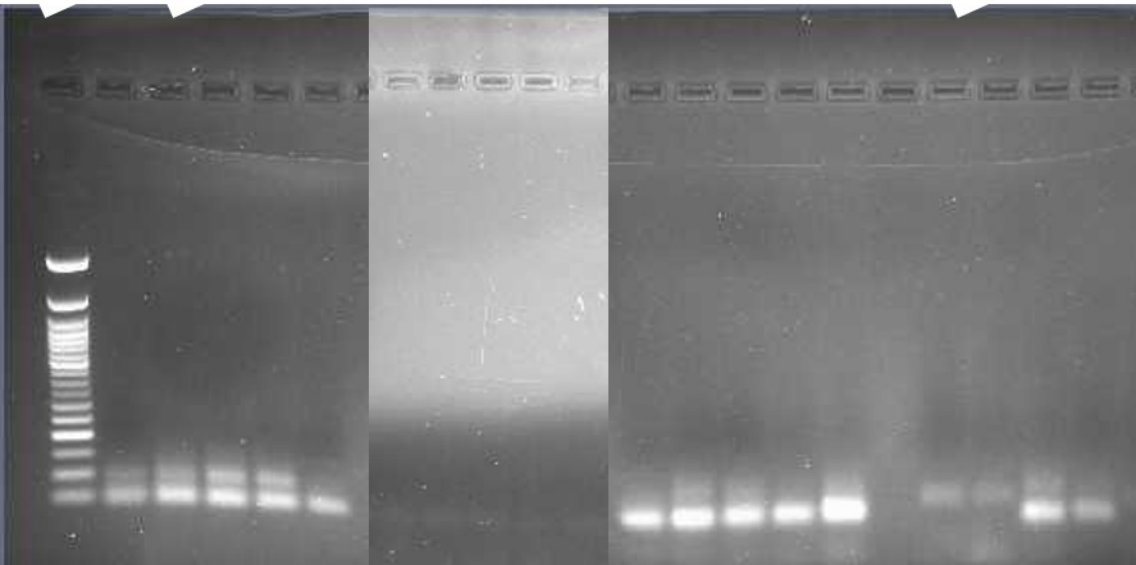


Table S1: Predicted targeted functions of novel miRNA related to TGF pathway in patients with pseudoexfoliation phenotypes.

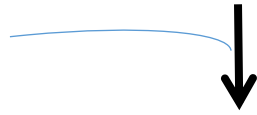
Id of miRNA (mifinder) phenotypes	TGF pathway (n=32 genes)	Accession numbers	Function
hsa-miR-26b-5p	21	MIMAT000083	Positive regulation of tau-protein kinase activity and apoptotic pathway
hsa-let-7e-5p	19	MIMAT000066	Posttranslational gene silencing, extracellular space homeostasis
hsa-miR-144-3p	1	MIMAT0000436	regulation of cholesterol efflux

Table S2: Targeted functions of fibrosis miRNA related to protein processing in patients with pseudoexfoliation phenotypes.

Id of miRNA mifibrosis phenotypes	Proteoglycan pathway (n=69 genes)	Protein processing in ER/RNA transport (n=36)	Accession numbers	Function
hsa-miR-30a-5p	39	36	MIMAT0000087	Negative regulation of apoptosis and posttranscriptional gene silencing
hsa-miR-1-3p	44	0	MIMAT0000416	Regulation of sequestered calcium release by sarcoplasmic reticulum
hsa-miR-19a-3p	44		MIMAT0000073	Negative regulation of TLL-like receptor signaling pathway, gene silencing
hsa-miR-18a-5p	-	-	MIMAT0000072	Negative regulation of sprouting angiogenesis and positive regulation of vascular smooth muscle cell differentiation
hsa-miR-451a	-	-	MI0001729	Domain for CXCL16

Screening n=94

Excluded 44



Out of 50 included-Samples used for standardisations to offset variability from
Mirna extr: SNORD 68 : miRNA 122 reproducibility of SNORD68 and miRNA 122-5

PXF	5	6	4	2
PXG	5	6	4	3
			Total=n=35	



Discovery stage-mFINDER array

controls	3
Classical PXF	3
Pigmentary PXF	3
Ocular hypertension	3
PXG	3



Validation Stage-miRNA and TGF downstream targets

controls	3
Classical PXF	3
Pigmentary PXF	3
Ocular hypertension	3
PXG	3
	Serum TGF ELISA
Classical PXF	5
Ocular hypertension	5
PXG	5
controls	5

Total n=50