

Supplementary Table S1. List of miRNAs primers. All miRNA primers used in this study were pre-designed and validated by Qiagen and their corresponding GeneGlobe IDs were obtained from the Qiagen GeneGlobe database (Qiagen, Hilden, Germany).

miRNA	Gene Globe ID	miRNA	Gene Globe ID	miRNA	Gene Globe ID
hsa-miR-130a-3p	YP00204658	hsa-miR-144-3p	YP00204754	hsa-miR-148b-3p	YP00204047
hsa-miR-29c-3p	YP00204729	hsa-miR-320d	YP00205667	hsa-miR-181a-3p	YP00204110
hsa-miR-29b-3p	YP00204679	hsa-miR-4454	YP02114119	hsa-let-7d-3p	YP00205627
hsa-miR-107	YP00204468	hsa-miR-4281	YP02119448	hsa-miR-186-5p	YP00206053
hsa-miR-148a-3p	YP00205867	hsa-miR-374b-5p	YP00204608	hsa-miR-130b-5p	YP00204456
hsa-miR-21-5p	YP00204230	hsa-miR-574-3p	YP00206011	hsa-miR-4285	YP02104979
hsa-miR-20a-5p	YP00204292	hsa-miR-16a-5p	YP00205702	hsa-miR-320e	YP02103235
hsa-miR-222-5p	YP00204314	hsa-miR-30e-3p	YP00204410	hsa-miR-146a-3p	YP00204401
hsa-miR-27a-5p	YP00206021	hsa-miR-21-3p	YP00204302	hsa-let-7d-5p	YP00204124

Supplementary Table S2. Demographic, clinical characteristics and *MEFV* genotype of FMF patients. VSU: variant of uncertain significance.

A.			
Participants	FMF patients	Healthy subjects	<i>p</i> -value
n (total number)	34	25	
Gender, n (%)	Male: 11 (32.4%) Female: 23 (67.6%)	Male: 12 (48%) Female: 13 (52%)	>0.9999
Age (mean $\pm$ SD)	35.35 $\pm$ 13.96	30.72 $\pm$ 12.55	0.2227
Age at diagnosis (mean $\pm$ SD)	12.77 $\pm$ 9.965	-	
Clinical manifestations, n (%)			
Abdominal pain	32 (94.1%)		
Fever	31 (91.2%)		
Joint pain	28 (82.3%)		
Thoracic pain	18 (52.9%)		
Sensitivity to cold	15 (44.1%)		
Constipation	15 (44.1%)	-	
Diarrhoea	12 (37.3%)		
Arthritis	11 (32.3%)		
Vomiting	10 (29.4%)		
Rash	4 (11.8%)		
Amyloidosis	3 (8.8%)		
Colchicine intake	30 (88.2%)	-	
B.			
Category	<i>MEFV</i> Genotype	N (%)	
Homozygous	M694V/M694V	9 (26.5%)	
	V726A/V726A	5 (14.7%)	
	M680I/M680I	2 (5.9%)	
	R761H/R761H	1 (3%)	
Compound heterozygous	M694V/V726A	2 (5.9%)	
	M694V/M694I	2 (5.9%)	
	M680I/V726A	2 (5.9%)	
	M694I/V726A	2 (5.9%)	
	M694V/R761H	1 (3%)	
	V726A/I692del/E148Q	1 (3%)	
Heterozygous	M694V/-	2 (5.9%)	
	M694I/-	2 (5.9%)	
	V726A/-	1 (3%)	
Other	VUS	2 (6%)	