Table SI. *Expression profile of miRNAs in dermatomyositis (DM) skin as measured with the PCR array*

Fold-change	Normal	DM
Up-regulated miRNAs in DM skin		
miR-142-3p	0.152	1.591
miR-206	0.917	16.912
miR-302c	<0.001	0.001
miR-370	0.005	0.039
miR-503	0.006	0.060
Down-regulated miRNAs in DM skin		
let-7d	0.055	ND
let-7e	0.455	ND
let-7f	0.012	0.001
let-7i	0.572	0.006
miR-7	0.037	ND
miR-10a	0.498	ND
miR-17	0.459	ND
miR-18a	0.044	0.001
miR-20a	0.681	ND
miR-20b	0.043	ND
miR-22	0.874	ND
miR-33a	0.060	ND
miR-96	0.086	ND
miR-103	0.862	<0.001
miR-134	0.041	ND
miR-137	0.002	<0.001
miR-141	0.345	ND
miR-142-5p	0.006	<0.001
miR-146a	0.815	<0.001
miR-146b-5p	0.530	ND
miR-192	0.067	ND
miR-194	0.068	ND
miR-208	0.003	<0.001
miR-222	0.300	ND
miR-223	0.898	ND
miR-378	0.911	ND
miR-424	0.191	ND

miRNA expression profile *in vivo* was evaluated using PCR array: equal amount of cDNAs reverse-transcribed from miRNAs from 3 normal skin or 3 DM skin were pooled and used in a single experiment. The raw threshold cycle (Ct) was normalized using the mean values of small RNA housekeeping genes (SNORD47 and 48). The fold-change was calculated as 1/2(Ct of each miRNA – Ct of house keeping genes). ND: not detected (no amplification by 40 cycles of PCR).