

Table SI. Differentially expressed miRNAs in psoriatic skin (PSO, $n = 82$, fold-change >2 , $p < 0.05$) and early-stage mycosis fungoides (MF) lesions ($n = 109$, FC >2 , $p < 0.05$) compared with healthy controls (HC) [AQ9]

	PSO vs HC	MF vs HC		PSO vs HC	MF vs HC
miR-31-3p	*	*	miR-9-3p	*	*
miR-31-5p	*	*	miR-149-5p	*	*
miR-21-3p	*	*	miR-10b-5p	*	*
miR-7-5p	*	*	miR-30a-3p	*	*
miR-663a	*	*	miR-338-3p	*	*
miR-509-3p	*	*	miR-99a-5p	*	*
miR-142-5p	*	*	miR-375	*	*
miR-188-5p	*	*	miR-204-5p	*	*
miR-130b-3p	*	*	miR-10a-5p	*	*
miR-18b-5p	*	*	miR-224-5p	*	
miR-18a-5p	*	*	miR-211-5p	*	
miR-155-5p	*	*	miR-33a-5p	*	
miR-154-3p	*	*	miR-96-5p	*	
miR-16-1-3p	*	*	miR-602	*	
miR-18a-3p	*	*	miR-493-3p	*	
miR-187-3p	*	*	miR-106a-5p	*	
miR-381-3p	*	*	miR-432-5p	*	
miR-127-5p	*	*	miR-218-5p	*	
miR-135b-5p	*	*	miR-125b-5p	*	
miR-30b-3p	*	*	miR-125b-2-3p	*	
miR-22-5p	*	*	miR-100-5p	*	
miR-370-3p	*	*	miR-142-3p		*
miR-329-3p	*	*	miR-150-5p		*
miR-337-5p	*	*	miR-146b-5p		*
miR-21-5p	*	*	miR-483-3p		*
miR-146a-5p	*	*	miR-940		*
miR-33b-5p	*	*	miR-766-3p		*
miR-495-3p	*	*	miR-29a-3p		*
miR-671-5p	*	*	miR-342-3p		*
miR-1248	*	*	miR-128-3p		*
miR-487b-3p	*	*	miR-484		*
miR-423-5p	*	*	miR-32-5p		*
miR-376b-3p	*	*	miR-425-5p		*
miR-340-5p	*	*	miR-424-5p		*
miR-34b-3p	*	*	miR-433-3p		*
miR-584-5p	*	*	miR-625-3p		*
miR-212-3p	*	*	miR-181c-5p		*
miR-501-5p	*	*	miR-29b-3p		*
miR-34a-5p	*	*	miR-138-5p		*
miR-361-3p	*	*	miR-26a-2-3p		*
miR-193a-3p	*	*	miR-877-5p		*
miR-330-3p	*	*	miR-517a-3p		*
miR-326	*	*	miR-542-5p		*
miR-223-3p	*	*	miR-874-3p		*
miR-345-5p	*	*	miR-539-5p		*
miR-431-5p	*	*	miR-34c-5p		*
miR-598-3p	*	*	miR-29c-3p		*
miR-362-5p	*	*	miR-185-5p		*
let-7i-5p	*	*	miR-425-3p		*
miR-377-3p	*	*	miR-215-5p		*
miR-22-3p	*	*	miR-503-5p		*
miR-373-3p	*	*	miR-652-3p		*
miR-301a-3p	*	*	miR-449a		*
miR-654-5p	*	*	miR-181d-5p		*
miR-589-5p	*	*	miR-627-5p		*
miR-15a-5p	*	*	miR-135a-5p		*
miR-93-5p	*	*	miR-642a-5p		*
miR-346	*	*	miR-454-3p		*
miR-181a-3p	*	*	miR-30a-5p		*
miR-424-3p	*	*	miR-196a-5p		*
miR-629-5p	*	*			

*Differentially expressed

Table SII. Characteristics and main findings of studies on epigenetic changes in cutaneous T-cell lymphoma (CTCL) referred to in the current study

Author, year	Study period, study population, comparators	Sample quality, analysis, validation	Main findings
Lindahl et al. (18) 2018	1981–2013 Study population: MF, <i>n</i> = 82, stage < IIB Controls: HC, <i>n</i> = 20 Validation cohort: MF, <i>n</i> = 72, stage < IIB	Sample quality FFPE Main analysis qRT-PCR Validation qRT-PCR	MF vs HC 123 differentially expressed miRNAs (Student's <i>t</i> -test <0.05) ↓ 72 miRNAs including miR-106b-5p ↓ 51 miRNAs including miR-148a-3p and miR-338-3p Prognostic classifier for prediction of progression-free survival 3 miRNAs (miR-106b-5p, miR-148a-3p, and miR-338-3p) All 3 miRNAs also differentially expressed in the validation cohort
Lindahl et al. (16) 2016	Study period not stated Study population: CTCL patients, <i>n</i> = 47 MF, stage I–IIA, <i>n</i> = 21 MF, stage IIB–IVB, <i>n</i> = 21 SS, <i>n</i> = 5 Controls HC, <i>n</i> = 21	Sample quality Liquid nitrogen Main analysis qRT-PCR No validation	CTCL vs HC miR-21 was 9-fold 1- regulated in MF and 6.3-fold in SS Inhibition of JAK3/ STAT3/STAT5 pathway Down-regulation of miR-21 and miR-155 miR-21 expression in situ hybridization analyses Staining in malignant T-cell, reactive lymphocytes and stromal cells IL-2 culture in SS cells Increased miR-21 expression IL-2 starvation <i>ex vivo</i> in SS cells Decreased miR-21 expression Depletion of JAK3, STAT3 and STAT5 Decreased miR-21 expression
Sandoval et al. (31) 2015	Study period not stated Study population: CTCL patients, <i>n</i> = 32 MF, tumour stage, <i>n</i> = 21 CD30+ CALCL, <i>n</i> = 11 Controls: ID, <i>n</i> = 5 SCLE, <i>n</i> = 3 PP, <i>n</i> = 2 Validation cohort: CTCL, <i>n</i> = 10 SCLE, <i>n</i> = 6 PP, <i>n</i> = 7	Sample quality FFPE Main analysis Microarray Validation qRT-PCR	MF vs ID 40 miRNAs differentially expressed (<i>p</i> -value <0.05, FC >1.2) ↓ 13 miRNAs including miR-146a, miR-142-3p/5p, miR-21, miR-181a/b, and miR-155 ↓ 27 miRNAs including miR-200ab/429 cluster, miR-10b, miR-193b, miR-141/200c, and miR-23b/27b. CD30+ CALCL vs ID 39 miRNAs differentially expressed (<i>p</i> -value <0.05, FC >1.2) ↓ 13 miRNAs including miR-155, miR-21, and miR-142-3p/5p ↓ 26 miRNAs including miR-141/200c, miR-23b/miR-27b, miR203, miR-205, and miR-125b Promoter miRNA methylation analysis 36% of the differentially expressed miRNAs showed DNA methylation differences between MF and the CD30+ CALCL group MF and CD30+ CALCL showed 2 different miRNA methylation signatures
Sibbesen et al. (17) 2015	Study period not stated Number of CTCL patients not stated	Sample quality Cultured cell lines Main analysis Oligonucleotide pulldown assay Western blotting qRT-PCR No validation	Malignant vs non-malignant T-cells Decreased expression of a miR-22 STAT5 binds the promoter of the miR-22 host gene Inhibition of Jak3, STAT3, and STAT5 Increased expression of pri-miR-22 and miR-22
Ralfkiaer et al. (24) 2014	1985–2010 Study population: CTCL patients, <i>n</i> = 55 MF stage 1, <i>n</i> = 13 MF stage 2, <i>n</i> = 23 MF stage 3, <i>n</i> = 2 MF stage 4, <i>n</i> = 3 PTL, NOS, <i>n</i> = 14 Controls: AD, <i>n</i> = 20	Sample quality FFPE Main analysis qRT-PCR No validation	MF stage 1 vs AD 38 differentially expressed miRNAs (FC ≥ 2) ↓ 21 miRNAs including miR-155, miR-146a, 146b-5p, miR-342-3p, and let-7i ↓ 17 miRNAs including miR-203 and miR-205 MF stage 1 vs MF stage 2–4 and PTL, NOS 36 differentially expressed miRNAs (<i>p</i> -value <0.05, FC ≥ 2) ↓ 30 miRNAs including miRNAs part of the miR-17/92, 106b/25, and 106a/363 clusters Progressive vs stable disease 72 differentially expressed miRNAs (<i>p</i> -value <0.05, FC ≥ 2) ↓ 70 miRNAs including miR-155, miR-21, let-7i, miR-16, miR-142-3p, miR-146b-5p, miR-92a, miR-93, and miR-106a.
Ralfkiaer et al. (19) 2011	1979–2004 Study population: CTCL patients, <i>n</i> = 63 MF, <i>n</i> = 39 SS, <i>n</i> = 7 CALCL, <i>n</i> = 8 PTL, NOS, <i>n</i> = 9 Controls: Benign skin diseases, <i>n</i> = 85 AD, <i>n</i> = 20 ND, <i>n</i> = 4 PP, <i>n</i> = 42 PN, <i>n</i> = 17 HC, <i>n</i> = 2	Sample quality FFPE Main analysis Microarray Validation qRT-PCR	CTCL vs benign skin disease 27 miRNAs differentially expressed (<i>p</i> -value <0.001, FC >1.5) ↓ 18 miRNA including miR-326, miR-663b, miR-711 ↓ 9 miRNA including miR-203, miR-205 miR-326, miR-663b, miR-203, and miR-205 also differentially expressed in the validation cohort
Van Kester et al. (20) 2011	Study period not stated Study population: MF, <i>n</i> = 19 Tumour stage Controls: Benign skin diseases, <i>n</i> = 12 EZ, <i>n</i> = 5 LP, <i>n</i> = 7	Sample quality FFPE Main analysis Microarray Validation qPCR	MF vs benign skin disease 49 miRNAs differentially expressed (<i>p</i> -value <0.05) of which 23 miRNAs had a FC >2 ↓ 30 miRNA (16 with FC >2) including miR-93, miR-155, miR-30b, miR-16, miR-30c, miR-92a ↓ 19 miRNA (7 with FC > 2) including miR-383 All 7 miRNAs also differentially expressed in the validation cohort
Ballabio et al. (21) 2010	Study period not stated Study population: SS, <i>n</i> = 21 Controls: HC, <i>n</i> = 6 Validation cohort: SS, <i>n</i> = 15 MF, <i>n</i> = 11 HC, <i>n</i> = 12	Sample quality Peripheral blood Main analysis Microarray Validation qRT-PCR	SS vs HC 114 miRNAs differentially expressed (<i>p</i> -value <0.05, FC >1.2) ↓ 10 miRNAs ↓ 104 miRNAs SS vs Controls (i.e. MF and healthy controls), validation of 6 miRNAs miR-223 correctly discriminated between SS and controls in 34 of 38 cases. miR-342 subanalysis: Downregulation is mediated by miR-199a* miR-199a* targets the miR-342-encoding gene EVL miR-17-92 (and homologous) clusters subanalysis: Down-regulated Increased apoptosis in SS Decreased cell proliferation in SS.

AD: atopic dermatitis; CALCL: cutaneous anaplastic large cell lymphoma; CD: cluster of differentiation; DNA: deoxyribonucleic acid; EZ: eczema; FC: fold-change; FFPE: formalin-fixed paraffin-embedded; HC: healthy controls; ID: inflammatory dermatoses; JAK: janus kinase; let: lethal; LP: lichen planus; MF: mycosis fungoides; miR/ miRNA: micro ribonucleic acid; ND: unspecified dermatitis; PN: psoriasis, nonlesional skin; PP: psoriasis patients; PTL, NOS: peripheral T-cell lymphoma, not otherwise specified; qPCR: quantitative polymerase chain reaction; qRT-PCR: quantitative real-time polymerase chain reaction; SCLE: subacute cutaneous lupus erythematosus; SS: Sézary syndrome; STAT: signal transducer and activator of transcription proteins.