

Supplementary Table 1. List of suggested biomarkers for MF and SS.

Category	Biomarkers
Serum biomarkers	LDH [1] Beta2 microglobulin [2] Soluble IL-2 receptor [3] IL-13 [4], IL-31 [5], IL-12 [3] CCR4 [6] TNFR1/2 [3] HSP60/75/A5 [7]
Cell population changes	Elevated WBC, ALC, eosinophil count [8-10] CD4/CD8 ratio [11] Large cell transformation [12]
Cell surface markers	CD26 [13], CD3 ^{dim} [14], CD27 [15], CD52 [16], CTLA-4 [17], CD45R0 [18] KIR3DL2 [19, 20] NKp46 [21] PD-1 [22]
Gene and epigenetic markers	Gene expression; TOX [23], T-plastin [24-26], JUNB [25], GATA3 [25], SATB1 [27], STAT4 [25, 28], Twist [26, 29], Fas [30] Non-coding RNAs; miRNAs; miR-21, miR-155, miR-214, miR-486, miR-42-5p, miT-146a [31-34] Long non-coding RNAs [35] Chromosomal changes; Altered 17p11.2-q25.3, 8q24.1-8q24.3, and 10p12.1-q26.3 [36-38] Gains of <i>TCRB</i> , <i>TCRC</i> , <i>TNFR2</i> , and <i>cMYC</i> [38-40] Loss of <i>BCL2</i> , cMYC antagonists [38, 41] Genetic mutations; NFKB2 truncations, TNFAIP3, PLCC1, PRKCQ and TNFAIP3 [42, 43] ZEB1 [44] PDGFR, ERK, JAK/STAT, and MAPK [43, 45] DNMT3A, ASLX3, TET1-3 [46] RAD51C, BRCA2, POLD1 [43] TP53 [44, 46]

Supplementary Table 1 References

1. Scarisbrick JJ, Whittaker S, Evans AV, et al. Prognostic significance of tumor burden in the blood of patients with erythrodermic primary cutaneous T-cell lymphoma. *Blood* 2001;97:624-30.
2. Marti RM, Pujol RM, Servitje O, et al. Sézary syndrome and related variants of classic cutaneous T-cell lymphoma. A descriptive and prognostic clinicopathologic study of 29 cases. *Leuk Lymphoma* 2003;44:59-69.
3. Geskin LJ, Akilov OE, Lin Y, Lokshin AE. Distinct age-matched serum biomarker profiles in patients with cutaneous T-cell lymphoma. *Exp Dermatol* 2014;23:598-600.
4. Geskin LJ, Viragova S, Stolz DB, Fuschiotti P. Interleukin-13 is overexpressed in cutaneous T-cell lymphoma cells and regulates their proliferation. *Blood* 2015;125:2798-805.
5. Cedeno-Laurent F, Singer EM, Wysocka M, et al. Improved pruritus correlates with lower levels of IL-31 in CTCL patients under different therapeutic modalities. *Clin Immunol* 2015;158:1-7.
6. Kakinuma T, Sugaya M, Nakamura K, et al. Thymus and activation-regulated chemokine (TARC/CCL17) in mycosis fungoides: serum TARC levels reflect the disease activity of mycosis fungoides. *J Am Acad Dermatol* 2003;48:23-30.
7. Forger M, Gellrich S, Sharav T, Sterry W, Walden P. Proteome-based analysis of serologically defined tumor-associated antigens in cutaneous lymphoma. *PLoS One* 2009;4:e8376.
8. Scarisbrick JJ, Prince HM, Vermeer MH, et al. Cutaneous lymphoma international consortium study of outcome in advanced stages of mycosis fungoides and Sézary syndrome: effect of specific prognostic markers on survival and development of a prognostic model. *J Clin Oncol* 2015;33:3766-73.
9. Tancrede-Bohin E, Ionescu MA, de La Salmonière P, et al. Prognostic value of blood eosinophilia in primary cutaneous T-cell lymphomas. *Arch Dermatol* 2004;140:1057-61.
10. Abeni D, Frontani M, Sampogna F, et al. Circulating CD8+ lymphocytes, white blood cells, and survival in patients with mycosis fungoides. *Br J Dermatol* 2005;153:324-30.
11. Vermeer MH, van Doorn R, Dukers D, Bekkenk MW, Meijer CJ, Willemze R. CD8+ T cells in cutaneous T-cell lymphoma: expression of cytotoxic proteins, Fas Ligand, and killing inhibitory receptors and their relationship with clinical behavior. *J Clin Oncol* 2001;19:4322-9.
12. Diamandidou E, Colome-Grimmer M, Fayad L, Duvic M, Kurzrock R. Transformation of mycosis fungoides/Sézary syndrome: clinical characteristics and prognosis. *Blood* 1998;92:1150-9.
13. Bernengo MG, Novelli M, Quaglino P, et al. The relevance of the CD4+ CD26- subset in the identification of circulating Sézary cells. *Br J Dermatol* 2001;144:125-35.
14. Klemke CD, Brade J, Weckesser S, et al. The diagnosis of Sézary syndrome on peripheral blood by flow cytometry requires the use of multiple markers. *Br J Dermatol* 2008;159:871-80.
15. Fierro MT, Novelli M, Quaglino P, et al. Heterogeneity of circulating CD4+ memory T-cell subsets in erythrodermic patients: CD27 analysis can help to distinguish cutaneous T-cell lymphomas from inflammatory erythroderma. *Dermatology* 2008;216:213-21.
16. Jiang L, Yuan CM, Hubacheck J, et al. Variable CD52 expression in mature T cell and NK cell malignancies: implications for alemtuzumab therapy. *Br J Haematol* 2009;145:173-9.
17. Kamarashev J, Burg G, Kempf W, Hess Schmid M, Dummer R. Comparative analysis of histological and immunohistological features in mycosis fungoides and Sézary syndrome. *J Cutan Pathol* 1998;25:407-12.
18. Scala E, Russo G, Cadoni S, et al. Skewed expression of activation, differentiation and homing-related antigens in circulating cells from patients with cutaneous T cell lymphoma associated with CD7- T helper lymphocytes expansion. *J Invest Dermatol* 1999;113:622-7.
19. Poszepczynska-Guigné E, Schiavon V, D'Incan M, et al. CD158k/KIR3DL2 is a new phenotypic marker of Sezary cells: relevance for the diagnosis and follow-up of Sezary syndrome. *J Invest Dermatol* 2004;122:820-3.
20. Bouaziz JD, Remtoula N, Bensussan A, Marie-Cardine A, Bagot M. Absolute CD3+ CD158k+ lymphocyte count is reliable and more sensitive than cytomorphology to evaluate blood tumour burden in Sézary syndrome. *Br J Dermatol* 2010;162:123-8.
21. Bensussan A, Remtoula N, Sivori S, Bagot M, Moretta A, Marie-Cardine A. Expression and function of the natural cytotoxicity receptor NKp46 on circulating malignant CD4+ T lymphocytes of Sézary syndrome patients. *J Invest Dermatol* 2011;131:969-76.
22. Cetinözman F, Jansen PM, Vermeer MH, Willemze R. Differential expression of programmed death-1 (PD-1) in Sézary syndrome and mycosis fungoides. *Arch Dermatol* 2012;148:1379-85.
23. Zhang Y, Wang Y, Yu R, et al. Molecular markers of early-stage mycosis fungoides. *J Invest Dermatol* 2012;132:1698-706.
24. Booken N, Gratchev A, Utikal J, et al. Sézary syndrome is a unique cutaneous T-cell lymphoma as identified by an expanded gene signature including diagnostic marker molecules CDO1 and DNMT3. *Leukemia* 2008;22:393-9.
25. Nebozhyn M, Loboda A, Kari L, et al. Quantitative PCR on 5 genes reliably identifies CTCL patients with 5% to 99% circulating tumor cells with 90% accuracy. *Blood* 2006;107:3189-96.
26. Michel L, Jean-Louis F, Begue E, Bensussan A, Bagot M. Use of PLS3, Twist, CD158k/KIR3DL2, and NKp46 gene expression combination for reliable Sézary syndrome diagnosis. *Blood* 2013;121:1477-8.
27. Wang Y, Su M, Zhou LL, et al. Deficiency of SATB1 expression in Sezary cells causes apoptosis resistance by regulating FasL/CD95L transcription. *Blood* 2011;117:3826-35.
28. Litvinov IV, Cordeiro B, Fredholm S, et al. Analysis of STAT4 expression in cutaneous T-cell lymphoma (CTCL) patients and patient-derived

- cell lines. *Cell Cycle* 2014;13:2975-82.
29. van Doorn R, Dijkman R, Vermeer MH, et al. Aberrant expression of the tyrosine kinase receptor EphA4 and the transcription factor twist in Sézary syndrome identified by gene expression analysis. *Cancer Res* 2004;64:5578-86.
 30. Zoi-Toli O, Vermeer MH, De Vries E, Van Beek P, Meijer CJ, Willemze R. Expression of Fas and Fas-ligand in primary cutaneous T-cell lymphoma (CTCL): association between lack of Fas expression and aggressive types of CTCL. *Br J Dermatol* 2000;143:313-9.
 31. Narducci MG, Arcelli D, Picchio MC, et al. MicroRNA profiling reveals that miR-21, miR486 and miR-214 are upregulated and involved in cell survival in Sézary syndrome. *Cell Death Dis* 2011;2:e151.
 32. Ralfkiaer U, Hagedorn PH, Bangsgaard N, et al. Diagnostic microRNA profiling in cutaneous T-cell lymphoma (CTCL). *Blood* 2011;118:5891-900.
 33. Benner MF, Ballabio E, van Kester MS, et al. Primary cutaneous anaplastic large cell lymphoma shows a distinct miRNA expression profile and reveals differences from tumor-stage mycosis fungoides. *Exp Dermatol* 2012;21:632-4.
 34. Marosvári D, Téglási V, Csala I, et al. Altered microRNA expression in folliculotropic and transformed mycosis fungoides. *Pathol Oncol Res* 2015;21:821-5.
 35. Lee CS, Ungewickell A, Bhaduri A, et al. Transcriptome sequencing in Sezary syndrome identifies Sezary cell and mycosis fungoides-associated lncRNAs and novel transcripts. *Blood* 2012;120:3288-97.
 36. Barba G, Matteucci C, Girolomoni G, et al. Comparative genomic hybridization identifies 17q11.2 approximately q12 duplication as an early event in cutaneous T-cell lymphomas. *Cancer Genet Cytogenet* 2008;184:48-51.
 37. Caprini E, Cristofolletti C, Arcelli D, et al. Identification of key regions and genes important in the pathogenesis of Sezary syndrome by combining genomic and expression microarrays. *Cancer Res* 2009;69:8438-46.
 38. Vermeer MH, van Doorn R, Dijkman R, et al. Novel and highly recurrent chromosomal alterations in Sézary syndrome. *Cancer Res* 2008;68:2689-98.
 39. Salgado R, Gallardo F, Servitje O, et al. Absence of TCR loci chromosomal translocations in cutaneous T-cell lymphomas. *Cancer Genet* 2011;204:405-9.
 40. Ungewickell A, Bhaduri A, Rios E, et al. Genomic analysis of mycosis fungoides and Sézary syndrome identifies recurrent alterations in TNFR2. *Nat Genet* 2015;47:1056-60.
 41. Mao X, Orchard G, Lillington DM, et al. BCL2 and JUNB abnormalities in primary cutaneous lymphomas. *Br J Dermatol* 2004;151:546-56.
 42. Choi J, Goh G, Walradt T, et al. Genomic landscape of cutaneous T cell lymphoma. *Nat Genet* 2015;47:1011-9.
 43. Woollard WJ, Pullabhatla V, Lorenc A, et al. Candidate driver genes involved in genome maintenance and DNA repair in Sézary syndrome. *Blood* 2016;127:3387-97.
 44. McGirt LY, Jia P, Baerenwald DA, et al. Whole-genome sequencing reveals oncogenic mutations in mycosis fungoides. *Blood* 2015;126:508-19.
 45. Kiel MJ, Sahasrabudhe AA, Rolland DCM, et al. Genomic analyses reveal recurrent mutations in epigenetic modifiers and the JAK-STAT pathway in Sézary syndrome. *Nat Commun* 2015;6:8470.
 46. da Silva Almeida AC, Abate F, Khiabani H, et al. The mutational landscape of cutaneous T cell lymphoma and Sézary syndrome. *Nat Genet* 2015;47:1465-70.

Supplementary Table 2. Response criteria for MF and SS (modified from Olsen EA *et al.* Blood. 2022;140:419-37).

		Response in specific tissues	
Sites	Response	Definition	
Skin	CR*	100% clearance of skin lesions ^{b)}	
	PR	50 to < 100% clearance of skin disease ^{b)} from baseline without advancement in stage. May designate subset of Very Good PR based on 90 to < 100% clearing of total body involvement. Without new tumors (T3) in MF/SS patients with T1, T2, or T4 only skin disease	
	SD	< 25% increase or < 50% clearance in skin disease from baseline ^{b)} Without new tumors (T3) in MF/SS patients with T1, T2, or T4 only skin disease	
	PD ^{a)}	1. $\geq 25\%$ increase in skin disease from baseline ^{b)} OR 2. Loss of response: in those with CR or PR, increase of skin score of greater than the sum of nadir plus 50% baseline score. New tumors (T3) in MF/SS patients with T1, T2, or T4 only skin disease Additional suggestions for confirming PD in T1 MF and T1 non-MF/non-SS PCLs may be considered depending on the aims of the study ^{c)}	
Lymph nodes**	CR	Complete metabolic response. Score 1, 2, or 3 ^{d)} with or without a residual mass on 5PS.	Target LNs ^{e)} /nodal masses must regress to ≤ 1.5 cm LDi All target LNs or nodal masses that previously were > 1.5 cm are now ≤ 1.5 cm LDi by method used to assess size of LNs at baseline/screening or biopsy negative for lymphoma
	PR	Partial metabolic response. Score of 4 or 5 ^{d)} with reduced uptake compared with baseline.	$\geq 50\%$ decrease in SPD of up to 6 target measurable LNs. No clear increase in nonmeasured LNs or new LN 1.5 cm LDi. Cumulative reduction > 50% of the SPD of up to 6 target LNs and no new LN > 1.5 cm LDi unless proven pathologically negative for lymphoma
	SD	No metabolic response. Score of 4 or 5 ^{d)} with no significant change in FDG uptake from baseline.	< 50% decrease from screening/baseline in SPD of up to 6 target measurable LNs. Criteria for PD not met. Fails to meet criteria for CR, PR or PD
	PD	Progressive metabolic disease. Score of 4 or 5 ^{d)} with an increase in intensity of uptake.	1. Any LN of LDi 1.5 cm which has increased by $\geq 50\%$ from PPD nadir 2. New LN 1.5 cm any axis 3. New or clear progression of preexisting nonmeasured LNs 1. Any LN > 1.5 cm LDi which has increased by $\geq 50\%$ from PPD nadir 2. Any prior LN < 1.5 cm LDi, which has increased by > 50% from PPD nadir to > 1.5 cm LDi
Viscera**	CR	Complete metabolic response. Score of 1, 2, or 3 ^{d)} with or without a residual mass on 5PS. No evidence of FDG-avid disease.	No extralymphatic sites of disease. Any abnormal size of organ at screening/baseline has returned to normal size. BM normal by morphology.
	PR	Partial metabolic response. Score of 4 or 5 ^{d)} with reduced uptake compared with baseline and residual mass(es) of any size. Residual uptake in BM higher than normal but less than baseline.	1. $\geq 50\%$ decrease in SPD from baseline of any measurable extranodal site 2. Spleen 50% regression in length beyond normal (≤ 13 cm) 3. No new lesions 4. No increase in nonmeasured lesions
	SD	No metabolic response. Score of 4 or 5 ^{d)} with no significant change in FDG uptake from baseline. BM no change from BL.	Fails to attain criteria CR, PR, or PD. No clear progression or improvement.
	PD	1. Progressive metabolic disease 2. New FDG-avid foci consistent with lymphoma	1. New extranodal site > 1 cm any axis or if < 1 cm, must be attributable to lymphoma 2. An increase in LDi or SDi from nadir of 0.5 cm for lesions ≤ 2 cm or 1 cm for lesions > 2 cm 3. Regrowth of previously resolved lesions 4. In the setting of splenomegaly at BL, an increase in splenic length by > 50% from BL or if no splenomegaly at BL, new increase length > 2 cm from BL 5. New or clear progression of preexisting nonmeasured lesions
Blood	CR	B0 ^{f)} , ***	
	PR	> 50% decrease in quantitative measurements of blood tumor burden from baseline in those with B2 classification ^{f),g)} , ***	
	SD	Fails to attain criteria for CR, PR, or PD	
	PD ^{h)}	B0 to B2 ^{f)} , *** OR > 50% increase from baseline and $\geq 5,000$ neoplastic cells/ μL ⁱ⁾ OR Loss of response in those with PR who were originally B2 at baseline, > 50% increase from nadir and $\geq 5,000$ neoplastic cells/ μL ⁱ⁾	

Supplementary Table 2. Continued.

Global score [§]	Definition	Global response score ¹			
		Skin	Lymph nodes	Viscera	Blood
CR	Complete disappearance of all clinical evidence of disease	CR	All categories have CR/NI.		
PR	Regression of measurable disease	CR PR	All categories do not have a CR/NI and no category has a PD. No category has a PD and if any category involved at baseline, at least one has a CR or PR.		
SD	Failure to attain CR, PR, or PD representative of all disease	PR	No category has a PD and if any category involved at baseline, no CR or PR in any.		
PD	Progressive disease	SD	R/NI, PR, SD in any category and no category has a PD.		
Relapse	Recurrence of disease in prior CR	PD in any category. Relapse in any category.			

^aWhichever criterion occurs first. ^bOne form of assessment of skin disease should be used throughout a given clinical trial. For a global response score and a designation of Very Good PR, a comparison of total body skin assessment based on mSWAT assessment or sum of the product of perpendicular tumor measurements (SLAT score is one example) at baseline is necessary. Regional or lesional skin scoring may also have CR, PR, SD and PD response but may not be representative of the response of skin disease on the entire body skin surface and cannot be used to assess global response. ^cFor patients with limited T1 stage disease, there is a potential for a $\geq 25\%$ increase in patch/plaque skin score to lead to a PD despite an insignificant change in total skin lymphoma. This is of particular concern in studies where global response is the primary endpoint and skin the primary determinant of that response. In these cases, study design may elect to add additional requirements for PD in patients with T1 disease at BL, including a T1 to T2 change in skin classification in addition to the $\geq 25\%$ increase in skin score. ^d5PS: 1=no FDG uptake > background; 2=FDG uptake \leq mediastinum; 3=FDG uptake > mediastinum but \leq liver; 4=FDG uptake moderately > liver; 5=FDG uptake markedly > liver and/or new lesions. ^eTarget LNs are those > 1.5 cm with representative abnormal node positive pathologically for lymphoma. In MF/SS, this is currently the LN classification of N3. ^fThe absolute number of CD4+CD26- and/or CD4+CD7- lymphocytes may be used to assess blood involvement in clinical trials. In the case where more than one aberrant population of lymphocytes is recorded, the population with the highest absolute number at baseline should determine the B classification and the highest absolute number at each assessment should be used to determine the number of aberrant lymphocytes for response purposes. ^gThere is no PR in those with B1 disease at baseline as the difference within the range of neoplastic cells that define B1 is not considered significant and should not affect determination of global objective response. ^hWhichever occurs first. ⁱThe determination of what constitutes a significantly high count of neoplastic cells above 1,000 neoplastic cells/ μ L and what should be used here to help define PD in MF/SS blood involvement is at present arbitrary and based on expert opinion. We cede modification of this number to published data showing prognostic value for a different number of neoplastic cells per microliter than what is published here.

*A biopsy of normal appearing skin is unnecessary to assign a CR. However, a skin biopsy should be performed of a representative area of the skin if there is any question of residual disease (persistent erythema or pigmentary change) where otherwise a CR would exist. If histologic changes are suspicious or suggestive of PCL, the response should be considered a PR only.

**Based on Cheson *et al.* J Clin Oncol. 2014;32:3059-68.

***As determined by absolute numbers of neoplastic cells/mL by flow cytometry.

¹Modified from Olsen *et al.* J Clin Oncol. 2011;29:2598-607 and Kempf *et al.* Blood. 2011;118:4024-35. This table assumes that (1) all patients at baseline have measurable skin disease and (2) in patients with PCL and no extracutaneous disease at baseline, any new nodal or visceral involvement constitutes PD in those compartments.

[§]This assumes that the response (CR, PR, SD, PD, or relapse) has been maintained for at least 4 weeks in any involved category.

Abbreviations: 5PS, 5-point scale; FDG, fluorodeoxyglucose; LDi, longest diameter; LN, lymph node; NI, noninvolved; PD, progressive disease; SD, stable disease; SDi, short axis (longest perpendicular diameter to the LDi); SPD, sum of the products of the perpendicular diameters for multiple lesions.