Supplementary Table S1. Demographics and clinical characteristics of patients enrolled.

Demographic or Characteristic	Primary Cohort (cohort 1) (n=29)	Validation Cohort (cohort 2) (n=23)	*p*-value
Male/Female	3/26	0/23	0.322
Age, years, median (IQR)	29 (26, 36)	36 (24, 42)	0.596
Duration, years, median (IQR)	3.2 (0.6, 7.4)	2 (0.3, 10)	0.871
Skin rash, n (%)	13 (44.83)	12 (52.17)	0.598
Oral ulcers, n (%)	4 (13.79)	2 (8.68)	0.893
Alopecia, n (%)	12 (41.38)	9 (39.12)	0.870
Arthritis, n (%)	14 (48.28)	9 (39.12)	0.510
Leukopenia, n (%)	3 (10.34)	11 (47.83)	0.002
Fever, n (%)	3 (10.34)	9 (39.12)	0.014
Serositis, n (%)	1 (3.44)	2 (4.34)	0.836
Routine laboratory tests			
White blood cell, $\times 10^9$/L, median (IQR)	5.03 (4.3, 6.42)	3.09 (2.57, 4.05)	<0.001
Haemoglobin, g/L, median (IQR)	120 (112, 135)	120 (110, 128)	0.628
Platelet, ×109/L, median (IQR)	199 (144, 233)	160 (125.5, 193)	0.129
Lymphocytes, ×109/L, median (IQR)	1.11 (0.83, 1.84)	0.67 (0.52, 0.91)	0.005
24h-UPE (g/day) , median (IQR)	0.35 (0.09, 1.38)	0.42 (0.13, 1.7)	0.412
Serum creatinine, μmol/L, median (IQR)	56 (51.75, 66.25)	53 (48, 64)	0.26
Albumin, g/L, median (IQR)	39.25 (27.6,44.7)	35.4 (32, 39.5)	0.015
ESR, mm/h, median (IQR)	13 (7, 25)	28 (16.25, 52.75)	0.008
CRP, mg/L, median (IQR)	2.38 (0.57, 7.59)	3.3 (1.73, 7.42)	0.386
C3, G/L, median (IQR)	0.79 (0.68, 1.01)	0.5 (0.39, 0.61)	0.001
C4, G/L, median (IQR)	0.16 (0.1, 0.2)	0.09 (0.07, 0.15)	0.026
Antibodies, n (%)			
Anti-ANA	320 (160, 320)	320 (320, 640)	0.146
Anti-AnuA, IU/ml, median (IQR)	12.95 (4.08, 60.46)	118.58 (31.48, 170)	0.012
Anti-dsDNA, IU/ml, median (IQR)	34.80 (1.0-1783.15)	186.4 (87, 258.7)	0.002
Prednisone dose, mg/day, medain (IQR)	15 (10-30)	25 (40-50)	0.003
Use of concomitant agents, n (%)			
Hydroxychloroquine	29 (100)	23 (100)	-
Cyclophosphamide	4 (13.79)	3 (13.04)	>0.99
Azathioprine	1 (3.44)	1 (4.34)	>0.99
Cyclosporine	0 (0)	0 (0)	-
Methotrexate	1 (3.44)	0 (0)	-
Mycophenolatemofetil	9 (31.03)	7 (30.43)	0963
Leflunomide	3 (10.34)	1 (4.34)	0.778

24h-UPE: 24-hour urinary protein excretion; ESR: erythrocyte sedimentation rate; CRP: C-reactive protein; C3: complement 3; C4: complement 4.

Supplementary Table S2. Verification of predictive ability of Treg and rash on SRI-4 response in validation cohort.

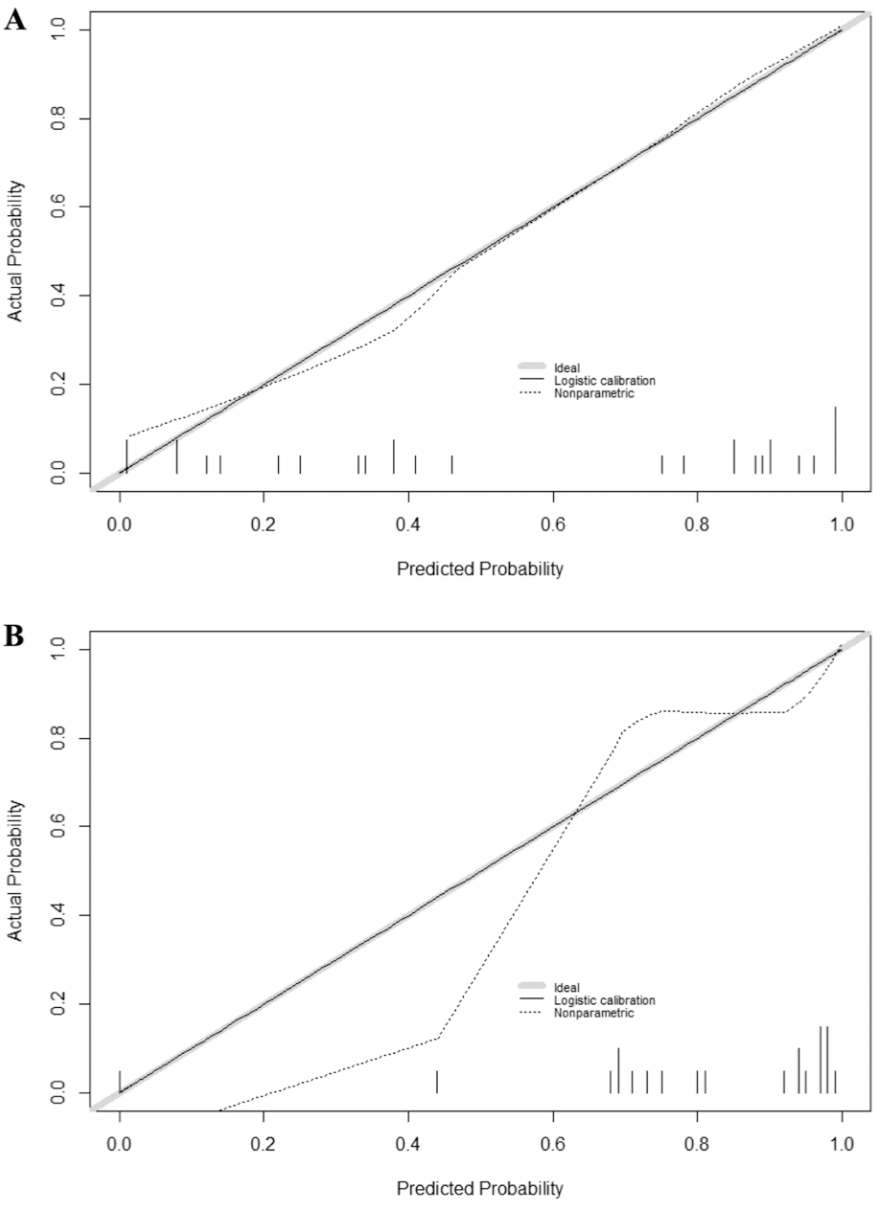
Variable	Poor responders SRI-4(-) (n=4)	Good responders SRI-4(+) (n=19)	*p*
Skin rash, n (%)	1 (25)	11 (73.33)	0.317
Treg (% in $CD4^+T$)	15.25 (13.31, 16.18)	10.6 (7.9, 12.8)	**0.088**

SRI-4, Systemic Lupus Erythematosus (SLE) Responder Index-4.

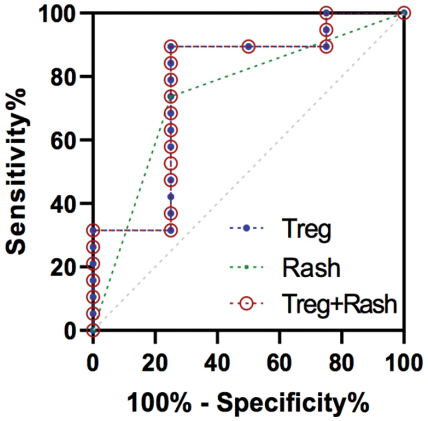
Supplementary Table S3. Difference of Treg subpopulations between good and poor responders in primary cohort.

Variable	SRI-4		*p*
	Poor responders (n=13)	Good responders (n=16)	
Non-Treg (% in $CD4^+$ T)	6.05 (5.08, 12.36)	6.74 (5.16, 9.06)	0.693
rTreg (% in $CD4^+$ T)	3.4 (3, 4.41)	2.73 (1.54, 6.09)	0.599
aTreg (% in $CD4^+$ T)	0.6 (0.47, 1.36)	0.81 (0.41, 1.03)	0.965
Non-Treg (cells/μl)	9.6 (4.59, 19.87)	10.58 (6.8, 18.18)	0.965
rTreg (cells/μl)	5.43 (2.11, 12.99)	3.18 (1.42, 14.59)	0.569
aTreg (cells/μl)	0.9 (0.5, 2.24)	1.13 (0.39, 2.34)	0.826

Data are presented as the median (IQR). Good responders were defined as patients who achieved a Systemic Lupus Erythematosus (SLE) Responder Index-4 (SRI-4), while poor responders were defined as patients who did not achieve an SRI-4. rTreg, resting Treg cells, $CD25^{++}CD45RA^+$ T cells. aTreg, activated Treg cells, $CD25^{+++}CD45RA^-$ T cells. Non-Treg, $CD25^{++}CD45RA^-$ T cells.



Supplementary Fig. S1. Calibration curves in the primary and validation cohorts. **A**: primary cohort (cohort 1). **B**: Validation cohort (cohort 2).



Supplementary Fig. S2. Receiver operator characteristic (ROC) curve of the ability of the proportion of Tregs to predict an SRI-4 response in validation cohort.