Table S1

Variable	CD169 N	CD169 r	CD169 p value	CD64 N	CD64 r	CD64 p value
ESSDAI score	28	0.28	n.s.	18	0.03	n.s.
Laboratory parameters						
Rf (IE/ml)	26	0.19	n.s.	18	0.39	n.s.
C3 (g/l)[a]	33	0.13	n.s.	20	0.14	n.s.
C4 (g/l)	33	0.07	n.s.	20	-0.161	n.s.
IgG (g/l)[a]	34	0.40	0.02	20	0.18	n.s.
IgA (g/l)	33	0.10	n.s.	20	0.37	n.s.
IgM (g/l)	33	0.36	0.04	20	0.18	n.s.
CRP (mg/l)	31	0.14	n.s.	19	0.16	n.s.
Hb (mmol/l)	34	-0.29	n.s.	20	-0.04	n.s.
Thrombocytes (*10E9/l)[a]	33	-0.01	n.s.	19	-0.31	n.s.
Lymphocytes (*10E9/l)[a]	31	0.00	n.s.	19	0.23	n.s.
Neutrophiles (*10E9/l)	31	-0.24	n.s.	19	-0.11	n.s.

Variable	CD169 N (%)	CD169 Z	CD169 p value	CD64 N (%)	CD64 Z	CD64 p value
Auto-antibodies						
Anti-SSA	29/34 (85)	-2.16	0.03	16/20 (80)	-0.95	n.s.
Anti-Ro52	21/27 (78)	-0.99	n.s.	15/19 (79)	-1.20	n.s.
Anti-Ro60	19/27 (70)	-1.97	0.05	14/19 (74)	-1.94	n.s.
Anti-SSB	22/34 (65)	-2.05	0.04	13/20 (65)	-0.83	n.s.
Medical therapy						
Pilocarpine	9/34 (26)	-2.25	0.03	6/20 (30)	-0.17	n.s.
Plaquenil	25/34 (74)	-1.93	n.s.	13/20 (65)	-0.20	n.s.
Corticosteroids	3/34 (9)	-1.12	n.s.	2/20 (10)	-0.25	n.s.

Data are presented as Spearman's rho (r) or according to κ2 test (Z), unless otherwise mentioned

[a]Data normally distributed are presented as Pearson's rho (r)

Rf, Rheumatoid factor; CRP, C-reactive protein; Hb, Hemoglobin

SUPPLEMENTAL FIGURES LEGENDS

Figure S1. MxA Enzyme immunoassay (EIA)

MxA-EIA was executed as previously described with new monoclonal antibodies and recombinant MxA as standard, subsequent to validation for corresponding results[19]. Mouse MAbs AFI-7B3 and AFI-10G10 (Institute of Clinical Medicine, University of Eastern Finland) were used as capture and biotinylated detector-antibody, respectively. MAbs were used as IgG, purified from cell culture supernatants by using FPLC with CIM protein G monolithic column (BIA separations, Ljubljana, Slovenia). Detector antibody was biotinylated with NHS-PEO_4-Biotin reagent (Pierce, Rockford, IL) according to manufacturer's instructions. Recombinant MxA, produced with baculovirus expression system, was kindly provided by Ilkka Julkunen and Krister Melen (National Institute of Health and Welfare, Helsinki, Finland)[26]. The heparinized whole blood samples (25µl) were lysed by diluting 1:20 in hypotonic buffer containing 1.5% bovine serum albumin (BSA), 1% ascorbic acid, 0.5% $NaHCO_3$ and 0.05% NaN3 and stored at -70°C until assayed. Standard dilutions for the assay were prepared in hypotonic buffer. Microtitre strip wells were coated by overnight incubation with 0.4 µg per well of AFI-7B3 IgG in 0.1 M carbonate, pH 9.6. The strips were washed twice with 5 mm Tris, 0.15 M NaCl, 0.05% Tween 20, pH 7.75 and saturated for 1 h with the assay buffer containing 0.5% BSA, 0.05% Tween 20 and 0.1 mM merthiolate in PBS. Strips were washed four times, and 50 µl each of the sample and 0.8 µg/ml biotinylated AFI-10G10 IgG, in the assay buffer, were added into the duplicate wells. After overnight incubation with shaking at 8°C, the strips were washed six times, and 100 µl of streptavidin–peroxidise-HRP (Pierce, #21127) diluted 1:15.000 in assay buffer was added into the wells. Strips were shaken for 75±15 min, washed eight times and incubated with 100 µl of tetramethylbenzidine (TMB) peroxidise substrate solution (Ani Labsystems, Vantaa, Finland) for 10–30 min in the dark. Color development was stopped by adding 100µl of 0.5 N H_2SO_4 and absorbance values were measured at 450 nM using Victor^3 multilabel counter (PerkinElmer, Turku, Finland). MxA concentrations (µg/l) of the specimens were read from a master curve (50-800µg/l) plotted with the standard values using Mutlicalc software with spline smoothed fitting algorithm. Hypotonic buffer was used as the negative control. The limit of detection of the MxA EIA

assay was 10µg/l, which was determined as three times the standard deviations (SD) of eight negative control replicates. One negative and one positive control sample were also included in each assay.

Figure S2. Flow cytometric analysis was performed on $CD14^+$ cells isolated from HC and pSS patients (stratified in IFNneg and IFNpos). **(A)** Representative dot plots show CD14 and consecutive CD64, CD169 and BAFF protein expression (top to bottom) on monocytes from study subjects. Appropriate isotype-matched controls were used to confirm antibody-specificity. **(B)** CD64 **(C)** CD169 and **(D)** BAFF protein expression for IFNneg (left) and IFNpos (right) pSS patients are shown. Representative histograms are depicted; Shaded histogram represents the isotype control, dotted line represents the HC and the solid line the pSS patients.

Figure S3. For relative BAFF mRNA gene expression **(A)** a correlation plot shown with IFNscores for all study subjects and **(B)** BAFF mRNA gene expression levels stratified in HC (n=27), IFNneg (n=14) and IFNpos (n=21) pSS patients. Each symbol represents an individual sample; horizontal lines represent the mean. The correlation coefficient (r) and *P* values are shown. For BAFF a Pearson correlation was used and to compare means the independent T-test was used.

Figure S4. In a small cohort of systemic lupus erythemathosis (SLE) patients **(A)** a correlation plot is shown between IFNscores (for all age and gender matched study subjects) and intracellular MxA (µg/l) levels, as assessed by the MxA-EIA. **(B)** IFNscores shown for HC (n=12) and SLE patients (n=12), stratified in IFNneg and IFNpos by red dotted line at 10; Red dots represent IFNpositivity (IFNscore≥10). **(C)** MxA-EIA (µg/l) levels shown for HC (n=12) and SLE patients (n=12). Each symbol represents an individual sample; horizontal lines represent the median. The correlation coefficients (r) and *P* values are shown. For correlations Spearman's rho correlation test was used and to compare medians the Mann-Whitney U test was used.