Supplemental Table 1. Meglumine antimoniate induced modulation of gene expression in skin lesion biopsies and PBMCs of CL patients.

	Biopsies			***PBMCs***		
Gene	**Fold Change**	**95% CI**	***P* value**	**Fold Change**	**95% CI**	***P* value**
BCL6	0.90	(0.70, 1.11)	0.618	1.02	(0.89, 1.16)	0.613
C3	2.67	(0.40, 4.99)	***0.029***	1.20	(0.68, 1.72)	0,504
C3AR1	0.77	(0.39, 1.15)	0.438	1.20	(0.51, 1.90)	0.376
CCL11	1.84	(0.90, 2.79)	0.097	0.98	(0.48, 1.49)	0.900
CCL13	1.46	(0.38, 2.55)	0.318	1.20	(0.59, 1.81)	0.602
CCL16	1.89	(0.89, 2.89)	0.073	1.01	(0.50, 1.52	0.711
CCL17	1.78	(0.76, 2.81)	0.085	1.30	(0.61, 2.00)	0.176
CCL19	0.73	(0.04, 1.41)	0.548	0.80	(0.26, 1.36)	0.501
CCL2	0.48	(0.09, 0.88)	***0.033***	1.00	(0.57, 1.43)	0.858
CCL21	0.75	(0.30, 1.20)	0.385	1.02	(0.49, 1.55)	0.772
CCL22	0.88	(0.38, 1.38)	0.570	1.02	(0.51, 1.54)	0.735
CCL23	1.80	(1.02, 2.57)	***0.023***	1.12	(0.52, 1.72)	0.658
CCL24	2.38	(0.96, 3.80)	0.096	0.88	(0.39, 1.37)	0.688
CCL3	0.48	(0.18, 0.78)	***0.021***	0.66	(0.37, 0.96)	0.094
CCL4	0.45	(0.13, 0.77)	***0.006***	0.66	(0.29, 1.05)	0.136
CCL5	0.65	(0.19, 1.11)	0.406	0.95	(0.60, 1.31)	0.922
CCL7	0.39	(0.16, 0.63)	***0.026***	0.95	(0.44, 1.47)	0.980
CCL8	1.60	(0.66, 2.54)	0.145	0.9	(0.37, 1.43)	0.667
CCR1	0.57	(0.31, 0.82)	0.073	0.10	(0.66, 1.32)	0.952
CCR2	0.83	(0.50, 1.17)	0.391	1.02	(0.63, 1.43)	0.939
CCR3	1.50	(0.66, 2.29)	0.146	1.01	(0.08, 1.94)	0.862
CCR4	1.34	(0.73, 1.96)	0.129	1.19	(0.82, 1.57)	0.321
CCR7	0.73	(0.21, 1.26)	0.632	1.03	(0.83, 1.24)	0.774
CD14	0.51	(0.23, 0.79)	0.186	2.16	(0.56, 3.77)	0.074
CD40	0.60	(0.39, 0.83)	***0.019***	0.84	(0.48, 1.20)	0.481
CD40LG	1.38	(0.82, 1.94)	0.099	0.83	(0.60, 1.07)	0.199
CEBPB	0.68	(0.48, 0.89)	***0.024***	1.11	(0.74, 1.49)	0.386
CRP	1.60	(0.66, 2.54)	0.145	1.01	(0.50, 1.52)	0.711
CSF1	0.93	(0.60, 1.26)	0.754	0.76	(0.26, 1.27)	0.406
CXCL1	0.25	(0.04, 0.46)	0.379	1.07	(0.27, 1.89)	0.446
CXCL10	0.08	(0.03, 0.12)	***0.000***	0.58	(0.00001, 1.31)	0.397
CXCL2	0.39	(0.10, 0.67)	0.475	1.07	(0.41, 1.74)	0.564
CXCL3	0.80	(0.41, 1.20)	0.478	1.09	(0.55, 1.64)	0.603
CXCL5	0.82	(0.27, 1.37)	0.517	1.34	(0.40, 2.28)	0.450
CXCL6	1.21	(0.56, 1.87)	0.256	1.43	(0.23, 2.65)	0.462
CXCL9	0.17	(0.05, 0.29)	***0.000***	0.54	(0.04, 1.05)	0.252
CXCR1	1.35	(0.68, 2.04)	0.500	0.98	(0.51, 1.47)	0.733
CXCR2	0.71	(0.41, 1.03)	0.815	1.19	(0.43, 1.96)	0.887
CXCR4	0.74	(0.28, 1.20)	0.492	1.05	(0.75, 1.36)	0.900
FASLG	0.58	(0.26, 0.90)	0.061	0.79	(0.49, 1.09)	0.237
FOS	0.84	(0.18, 1.50)	0.384	0.84	(0.45, 1.24)	0.564
IFNG	0.28	(0.09, 0.48)	***0,000***	0.38	(0.00001, 0.83)	0.207
IL10	0.64	(0.25, 1.03)	0.292	1.15	(0.78, 1.53)	0.445
IL10RB	1.06	(0.88, 1.24)	0.397	1.08	(0.88, 1.28)	0.440
IL15	0.82	(0.49, 1.15)	0.760	0.83	(0.55, 1.12)	0.345
IL17A	1.52	(0.63, 2.42)	0.167	1.01	(0.50, 1.52)	0.711
IL18	1.08	(0.73, 1.44)	0.354	1.51	(1.04, 1.99)	0.015
IL1A	0.74	(0.23, 1.26)	0.867	0.81	(0.16, 1.48)	0.649
IL1B	0.18	(0.01, 0.35)	0.484	0.81	(0.16, 1.48)	0.563
IL1R1	1.57	(1.20, 1.95)	***0.000***	1.42	(0.66, 2.19)	0.367
IL1RAP	0.83	(0.55, 1.12)	0.537	0.91	(0.75, 1.07)	0.418
IL1RN	0.49	(0.19, 0.79)	0.701	0.83	(0.58, 1.09)	0.316
IL22	1.33	(0.62, 2.05)	0.147	0.53	(0.00001, 1.10)	0.307
IL23A	1.06	(0.64, 1.49)	0.421	0.97	(0.75, 1.20)	0.768
IL23R	1.40	(0.62, 2.18)	0.178	0.88	(0.42, 1.36)	0.718
IL5	1.67	(0.81, 2.53)	0.088	0.76	(0.24, 1.28)	0.130
IL6	0.28	(0.05, 0.53)	***0.050***	0.98	(0.00001, 1.61)	0.918
IL6R	0.79	(0.50, 1.10)	0.526	0.98	(0.65, 1.31)	0.905

CXCL8	0.21	(0.00001, 0.47)	0.533	0.89	(0.43, 1.37)	0.984
IL9	1.59	(0.66, 2.54)	0.145	0.55	(0.00001, 1.12)	0.185
ITGB2	0.73	(0.20, 1.26)	0.995	1.02	(0.68, 1.38)	0.922
KNG1	1.60	(0.66, 2.54)	0.145	1.01	(0.50, 1.52)	0.711
LTA	1.20	(0.60, 1.82)	0.229	0.70	(0.44, 0.97)	0.111
LTB	0.85	(0.28, 1.44)	0.455	0.98	(0.70, 1.26)	0.919
LY96	1.07	(0.64, 1.50)	0.571	1.07	(0.86, 1.30)	0.567
MYD88	0.7	(0.55, 0.85)	***0.004***	1.03	(0.79, 1.29)	0.805
NFKB1	0.85	(0.73, 0.99)	0.065	0.96	(0.79, 1.13)	0.574
NOS2	1.53	(0.65, 2.42)	0.142	1.00	(0.49, 1.51)	0.786
NR3C1	1.31	(1.06, 1.58)	***0.007***	1.02	(0.86, 1.19)	0.822
PTGS2	0.48	(0.15, 0.82)	0.802	0.70	(0.23, 1.18)	0.617
RIPK2	0.93	(0.63, 1.24)	0.845	0.88	(0.64, 1.13)	0.443
SELE	0.80	(0.34, 1.25)	0.455	0.96	(0.42, 1.51)	0.795
TIRAP	1.45	(1.06, 1.85)	***0.030***	1.01	(0.75, 1.29)	0.933
TLR1	0.99	(0.64, 1.36)	0.825	0.90	(0.71, 1.10)	0.283
TLR2	0.52	(0.30, 0.75)	***0.027***	0.93	(0.63, 1.24)	0.951
TLR3	0.91	(0.72, 1.10)	0.521	0.86	(0.58, 1.14)	0.531
TLR4	1.02	(0.58, 1.48)	0.587	1.22	(0.78, 1.67)	0.510
TLR5	1.60	(1.05, 2.17)	***0.023***	1.37	(0.93, 1.81)	0.176
TLR6	1.34	(0.72, 1.97)	0.112	1.08	(0.58, 1.59)	0.923
TLR7	0.98	(0.58, 1.39)	0.551	0.84	(0.51, 1.19)	0.543
TLR9	1.59	(0.66, 2.54)	0.145	1.03	(0.69, 1.37)	0.779
TNF	0.65	(0.36, 0.95)	0.270	0.66	(0.37, 0.95)	0.057
TNFSF14	1.36	(0.69, 2.03)	0.182	0.89	(0.55, 1.23)	0.631
TOLLIP	1.05	(0.76, 1.34)	0.182	1.01	(0.71, 1.32)	0.990

The p values are calculated based on a Student's t-test of the replicate 2^(- Delta CT) values for each gene in the control group and treatment groups, and p values less than 0.05 are considered significant. PCR Array Code: Inflammatory response and Autoimmunity PAHS-077Z-Qiagen.

Supplemental Table 2. Socio-demographic characteristics of participants included in the cohort for SNPs analysis.

Characteristic	Total	Cure	Treatment Failure	p
Number of patients. No. (%)	40 (100)	20 (50)	20 (50)	-
Sex , No. (%)				
Male	34 (85)	17 (85)	17 (85)	1.00*
Female	6 (15)	3 (15)	3 (15)	
Age, median (SD), years.	31 (8.9)	32.6 (8.7)	30.9 (9.2)	0.56[+]
Ethnicity, No. (%)				
Afrocolombian	28 (70)	14 (70)	14 (70)	1.00*
Other	12 (30)	6 (30)	6 (30)	
Weight, median (SD), Kg	72.4 (9.7)	71.6 (11.2)	73.2 (8.2)	0.60[+]
Time of lesion evolution, median (IR), months.	1 (1 – 2)	2 (1 – 2.5)	1 (1 – 2)	0.19[+]
Number of lesions per patient, median (IR), No.	2 (1 – 2)	2 (1 – 2-5)	1.5 (1 – 2)	0.59[+]
Prior episodes of CL, No. (%)				
Yes	2 (5)	0 (0)	2 (5)	0.48*
No	38 (95)	20 (100)	18 (95)	
Adherence to treatment, median (IR), % received/formulated ampulles	100 (100 – 100)	100 (100 – 100)	100 (100 – 100)	0.26[+]

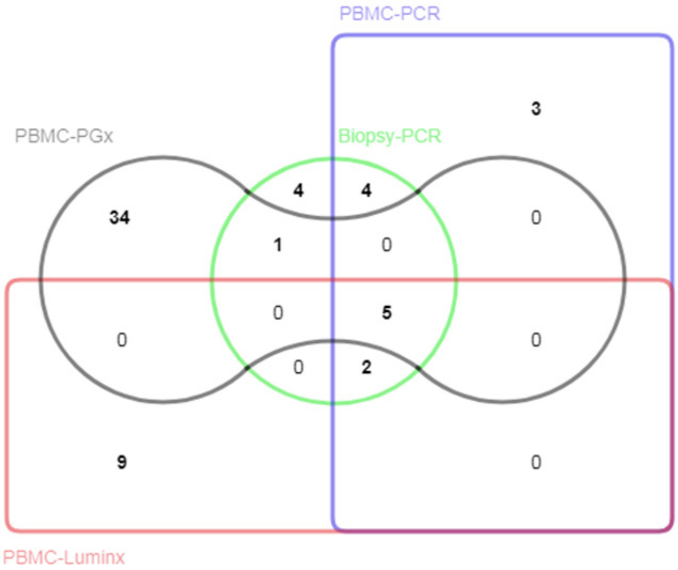
* Chi2/Fisher
[+] T-test/Wilcoxon sum rank.

Supplemental Figure 1

A

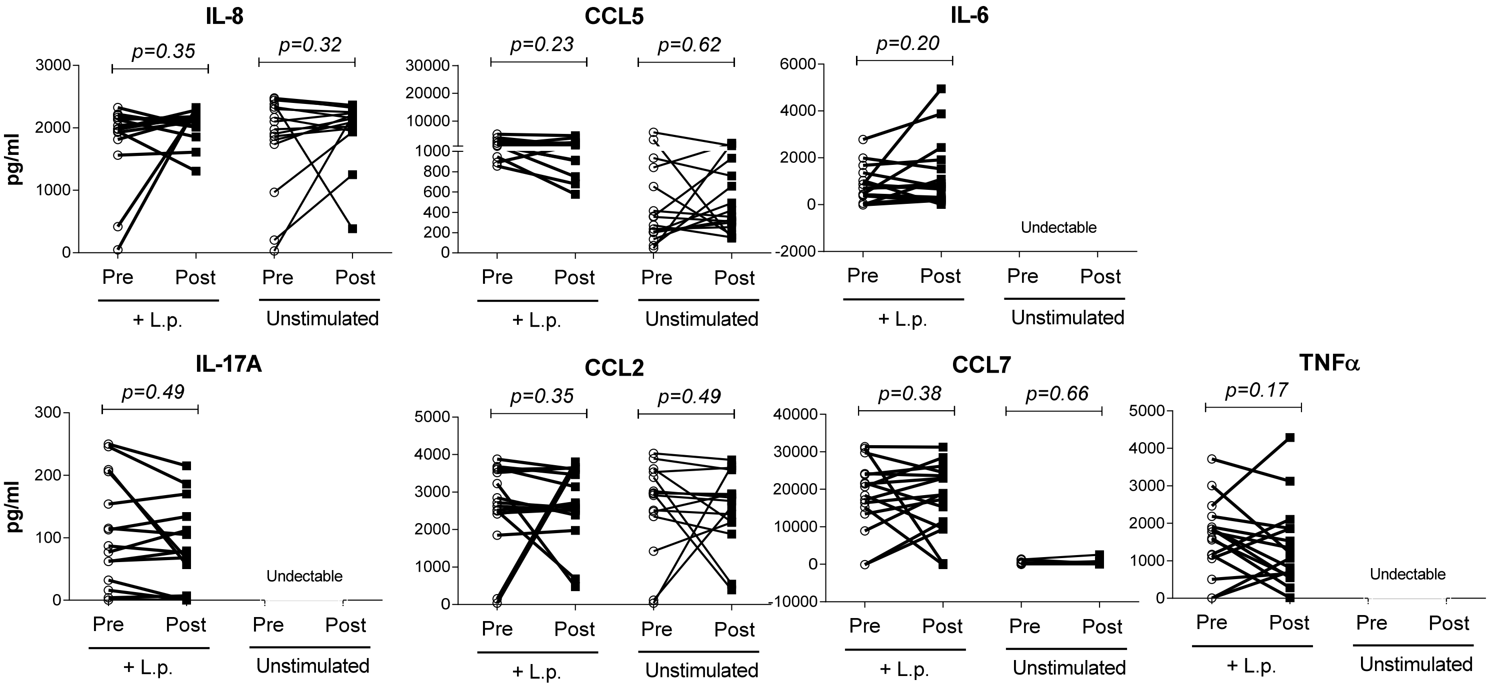
N=60	Number of participants contributing samples for each experimental approach
Paired pre and post-treatment PBMCs	**n= 23** (Gene expression PCR arrays n=14 and Luminex n=16)
Pre-treatment PBMCs	**n=40** (Pharmacogenomics - PGx)
Paired pre and post-treatment lesion biopsies	**n=16** (Gene expression PCR arrays)

B



Supplementary Figure 1. Schematic representation of total numbers of participants and samples for each experimental approach. (A) A total of 60 patients participated in this study. The sample size for each sample type and experimental procedures are shown. **(B)** The Venn diagram represents the distribution of patients contributing samples for each experimental approach. Intersections show number of patients who contributed samples for more than one experimental approach. PBMC-PCR (PBMCs used for PCR arrays); PBMC-PGx (PBMCs used for screening of CCL2 polymorphisms); PBMC-Luminx (PBMCs used for protein measurement using Luminex); Biopsy-PCR (Lesion biopsy samples used for PCR arrays).

Supplemental Figure 2



Supplementary Figure 2. Protein measurement in PBMCs obtained pre-treatment and post-treatment*.* Secreted protein levels were measured in a Luminex 200 instrument, from culture supernatants of PBMCs from CL patients (n=16) collected before and at the end of treatment, and re-exposed to *L. V panamensis* promastigotes. Median fluorescence intensity data were analyzed and data expressed in pg/mL. *P* values were calculated using a Wilcoxon matched-pair signed rank test or Paired t test depending on the distribution of the data.