

Supplemental Table 1. Patient demographics (N=95).

	Cohort A N=29	Cohort B N=66
Age, median (Range)	63 (34-81)	63 (19-84)
Sex		
Men	24	44
Women	5	22
Ethnic Origin		
White	27	62
Black or African-American	1	2
Other	1	2

Supplemental Table 2. Pathway analyses based on Enrichr assessment and KEGG 2106.

CRP upregulated pathways	P-value	Adjusted P-value (q value)	Z-score	Combined Score	Genes
Cytokine-cytokine receptor interaction_hsa04060	2.316e-8	0.00001551	-1.88	33.00	CCL22, CSF2, CXCL8, IL1B, CCL1, INHBA
Legionellosis_Homo sapiens_hsa05134	0.00008747	0.0002930	-1.88	21.87	C3, CXCL8, IL1B
Leishmaniasis_Homo sapiens_hsa05140	0.00002057	0.0003737	-1.81	19.54	C3, IL1B, PTGS2
Pertussis_hsa05133	0.00002231	0.0003737	-1.64	16.58	C3, CXCL8, IL1B
Rheumatoid arthritis_Homo sapiens_hsa05323	0.00003856	0.0004071	-1.63	10.01	CSF2, CXCL8, IL1B
Amoebiasis_Homo sapiens_hsa05146	0.00005283	0.0004421	-1.68	16.52	CSF2, CXCL8, IL1B

CRP downregulated pathways	P-value	Adjusted P-value (q value)	Z-score	Combined Score	Genes
Osteoclast differentiation_Homo sapiens_hsa04380	1.508e-7	0.000009648	-1.86	29.28	LILRA6, SIRPA, ACP5, TREM2, FCGR1A, LILRB4, LILRB5
Phagosome_Homo sapiens_hsa04145	0.00007401	0.0002368	-1.68	19.88	MARCO, CLEC7A, CD209, CD14, CD36, FCGR1A
Staphylococcus aureus infection_Homo sapiens_hsa05150	0.00002554	0.0005449	-1.75	18.50	FPR1, FCGR1A, C1QC, C2
Complement and coagulation cascades_Homo sapiens_hsa04610	0.00009917	0.001269	-1.69	15.61	SERPINA1, SEPPING1, C1QC, C2
Pertussis_Homo sapiens_hsa05133	0.00008096	0.001269	-1.64	15.46	SERPINA1, CD14, C1QC, C2
Hematopoietic cell lineage_Homo sapiens_hsa04640	0.0001508	0.001608	-1.64	14.44	CSF3R, CD14, CD36, FCGR1A