

Supplementary Table S3. Functional Enrichment Analysis of the CXCL10-Centered Interaction Network.

Function	FDR	Genes in network	Genes in genome
cytokine activity	4.56E-39	17	45
chemokine receptor binding	7.98E-37	17	60
cellular response to chemokine	2.63E-33	16	64
response to chemokine	1.29E-32	16	71
granulocyte chemotaxis	1.00E-29	16	105
granulocyte migration	1.26E-28	16	123
myeloid leukocyte migration	2.17E-28	17	183
leukocyte chemotaxis	3.70E-28	17	190
G protein-coupled receptor binding	6.83E-28	17	198
leukocyte migration	8.68E-28	18	281
neutrophil migration	8.71E-28	15	98
cytokine receptor binding	2.02E-27	17	214
cell chemotaxis	3.04E-27	17	220
lymphocyte migration	5.92E-18	11	92
mononuclear cell migration	8.29E-16	10	88
antimicrobial humoral response	2.16E-15	10	97
T cell migration	1.85E-13	8	49
humoral immune response	2.78E-12	10	197
lymphocyte chemotaxis	3.49E-12	7	35
response to lipopolysaccharide	6.86E-12	9	135
cellular response to molecule of bacterial origin	8.55E-12	9	139
eosinophil migration	2.30E-11	6	20
cellular response to biotic stimulus	3.00E-11	9	161
response to molecule of bacterial origin	1.65E-10	9	195

positive regulation of lymphocyte migration	3.82E-10	6	31
positive regulation of leukocyte chemotaxis	6.03E-10	7	73
regulation of T cell migration	6.44E-10	6	34
response to interferon-gamma	6.63E-10	8	139
T cell chemotaxis	1.67E-09	5	15
regulation of leukocyte migration	2.48E-09	8	165
regulation of chemotaxis	4.24E-09	8	177
regulation of lymphocyte migration	5.59E-09	6	49
regulation of leukocyte chemotaxis	6.51E-09	7	105
positive regulation of leukocyte migration	6.56E-09	7	106
positive regulation of chemotaxis	6.56E-09	7	106
regulation of lymphocyte chemotaxis	1.17E-08	5	22
regulation of GTPase activity	2.61E-08	8	227
CCR chemokine receptor binding	2.77E-08	5	26
response to interleukin-1	1.04E-07	7	159
regulation of T cell chemotaxis	4.67E-07	4	14
positive regulation of T cell migration	8.27E-07	4	16
regulation of ERK1 and ERK2 cascade	8.27E-07	7	216
positive regulation of lymphocyte chemotaxis	1.32393E-06	4	18
response to tumor necrosis factor	1.46075E-06	7	236
ERK1 and ERK2 cascade	1.51446E-06	7	238
regulation of cytosolic calcium ion concentration	1.86341E-06	7	246
positive regulation of mononuclear cell migration	1.91517E-06	4	20
positive regulation of cell migration	3.7649E-06	7	274
calcium ion transport	3.878E-06	7	276
positive regulation of calcium ion transport	4.03673E-06	5	71

regulation of monocyte chemotaxis	4.59231E-06	4	25
monocyte chemotaxis	5.31923E-06	4	26
regulation of calcium ion transport	5.72378E-06	6	165
cellular calcium ion homeostasis	6.25217E-06	7	300
negative regulation of sequestering of calcium ion	9.71667E-06	5	86
sequestering of calcium ion	1.05324E-05	5	88
regulation of sequestering of calcium ion	1.05324E-05	5	88
positive regulation of ion transport	1.25286E-05	6	191
positive regulation of calcium ion transport into cytosol	1.83447E-05	4	36
calcium ion transmembrane import into cytosol	2.32342E-05	5	104
regulation of granulocyte chemotaxis	3.35758E-05	4	42
leukocyte tethering or rolling	3.96013E-05	3	10
regulation of mononuclear cell migration	4.65454E-05	4	46
calcium ion transport into cytosol	4.65454E-05	5	121
positive regulation of calcium ion transmembrane transport	7.56875E-05	4	52
regulation of release of sequestered calcium ion into cytosol	9.93443E-05	4	56
cytosolic calcium ion transport	9.93443E-05	5	142
regulation of metal ion transport	0.000117848	6	287
positive regulation of cytosolic calcium ion concentration	0.000117848	5	148
leukocyte apoptotic process	0.0001853	4	66
release of sequestered calcium ion into cytosol	0.000194155	4	67
maintenance of location in cell	0.000224468	5	170
calcium ion transmembrane transport	0.00024836	5	174
regulation of calcium ion transport into cytosol	0.000293772	4	75
regulation of leukocyte adhesion to vascular endothelial cell	0.000478859	3	23
negative regulation of leukocyte cell-cell adhesion	0.000595129	4	90

negative regulation of leukocyte apoptotic process	0.000604912	3	25
regulation of cellular extravasation	0.000674584	3	26
positive regulation of cation transmembrane transport	0.001060031	4	105
regulation of cell adhesion mediated by integrin	0.001133205	3	31
regulation of calcium ion transmembrane transport	0.001156651	4	108
regulation of leukocyte cell-cell adhesion	0.001413673	5	254
positive regulation of ion transmembrane transport	0.00155185	4	117
maintenance of location	0.001556578	5	261
negative regulation of leukocyte migration	0.001556578	3	35
leukocyte cell-cell adhesion	0.00194802	5	274
glycosaminoglycan binding	0.001986396	4	126
leukocyte adhesion to vascular endothelial cell	0.002083069	3	39
negative regulation of cell-cell adhesion	0.00219752	4	130
negative regulation of cell migration	0.002522874	4	135
positive regulation of cell adhesion	0.002809262	5	299
cell adhesion mediated by integrin	0.003081032	3	45
regulation of actin filament length	0.00332587	4	146
cAMP-mediated signaling	0.003660122	4	150
positive regulation of transmembrane transport	0.004016741	4	154
regulation of leukocyte apoptotic process	0.00512948	3	54
cellular extravasation	0.005665642	3	56
sulfur compound binding	0.005948121	4	172
actin polymerization or depolymerization	0.005948121	4	172
adenylate cyclase-modulating G protein-coupled receptor signaling pathway	0.006301078	4	175
positive regulation of protein-containing complex assembly	0.006522344	4	177
cyclic-nucleotide-mediated signaling	0.00704812	4	181

cell-cell adhesion mediated by integrin	0.009265739	2	10
negative regulation of cell adhesion	0.009430963	4	196
G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	0.010504533	4	202
dendritic cell apoptotic process	0.010894429	2	11
regulation of dendritic cell apoptotic process	0.010894429	2	11
interaction with symbiont	0.013127576	3	77
positive regulation of cell-cell adhesion	0.013127576	4	216
regulation of actin filament organization	0.013722859	4	219
negative regulation of cell motility	0.014587134	4	223
negative regulation of cellular component movement	0.017416672	4	234
regulation of actin cytoskeleton organization	0.021600864	4	248
negative regulation of locomotion	0.024194813	4	256
chemokine-mediated signaling pathway	0.028071454	2	18
regulation of cellular component size	0.02958974	4	271
regulation of cation transmembrane transport	0.029754075	4	272
positive regulation of protein polymerization	0.032817602	3	108
positive regulation of granulocyte chemotaxis	0.032817602	2	20
positive regulation of macrophage migration	0.032817602	2	20
regulation of macrophage chemotaxis	0.032817602	2	20
negative regulation of immune system process	0.032817602	4	281
regulation of ion transmembrane transport	0.037980169	4	296
regulation of supramolecular fiber organization	0.037980169	4	296
dendritic cell migration	0.037980169	2	22
regulation of actin filament polymerization	0.037980169	3	115
regulation of neutrophil chemotaxis	0.037980169	2	22

positive regulation of neutrophil migration	0.037980169	2	22
macrophage chemotaxis	0.041248353	2	23
neutrophil chemotaxis	0.048472518	2	25

FDR, false discovery rate.