

Supplementary Table S2. Functional Enrichment Analysis of the CXCL9-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
cytokine receptor binding	9.07E-30	18	214
granulocyte chemotaxis	9.07E-30	16	105
granulocyte migration	1.08E-28	16	123
myeloid leukocyte migration	1.90E-28	17	183
leukocyte chemotaxis	3.29E-28	17	190
G protein-coupled receptor binding	6.15E-28	17	198
leukocyte migration	7.90E-28	18	281
neutrophil migration	7.98E-28	15	98
cell chemotaxis	3.04E-27	17	220
mononuclear cell migration	1.16E-20	12	88
lymphocyte migration	1.90E-20	12	92
response to interferon-gamma	8.94E-14	10	139
T cell migration	1.85E-13	8	49
lymphocyte chemotaxis	3.68E-12	7	35
response to tumor necrosis factor	1.64E-11	10	236
eosinophil migration	2.53E-11	6	20
response to interleukin-1	2.93E-11	9	159
regulation of leukocyte migration	3.93E-11	9	165
antimicrobial humoral response	4.25E-11	8	97
regulation of chemotaxis	6.83E-11	9	177

regulation of leukocyte chemotaxis	7.51E-11	8	105
CCR chemokine receptor binding	1.15E-10	6	26
regulation of ERK1 and ERK2 cascade	3.70E-10	9	216
positive regulation of leukocyte chemotaxis	5.23E-10	7	73
regulation of GTPase activity	5.23E-10	9	227
response to lipopolysaccharide	5.23E-10	8	135
cellular response to molecule of bacterial origin	5.99E-10	8	139
ERK1 and ERK2 cascade	7.51E-10	9	238
cellular response to biotic stimulus	1.85E-09	8	161
calcium ion transport	2.68E-09	9	276
regulation of lymphocyte migration	5.12E-09	6	49
positive regulation of leukocyte migration	6.21E-09	7	106
positive regulation of chemotaxis	6.21E-09	7	106
response to molecule of bacterial origin	7.53E-09	8	195
humoral immune response	7.97E-09	8	197
regulation of lymphocyte chemotaxis	1.06E-08	5	22
positive regulation of calcium ion transport	4.41E-08	6	71
positive regulation of lymphocyte migration	6.44E-08	5	31
regulation of T cell migration	1.03E-07	5	34
regulation of calcium ion transport	1.20E-07	7	165
negative regulation of sequestering of calcium ion	1.31E-07	6	86
sequestering of calcium ion	1.44E-07	6	88
regulation of sequestering of calcium ion	1.44E-07	6	88
regulation of granulocyte chemotaxis	2.80E-07	5	42
positive regulation of ion transport	3.00E-07	7	191
calcium ion transmembrane import into cytosol	3.75E-07	6	104

T cell chemotaxis	4.99E-07	4	15
calcium ion transport into cytosol	9.03E-07	6	121
regulation of cytosolic calcium ion concentration	1.6173E-06	7	246
positive regulation of mononuclear cell migration	1.66691E-06	4	20
regulation of leukocyte cell-cell adhesion	1.94537E-06	7	254
cytosolic calcium ion transport	2.20088E-06	6	142
positive regulation of cytosolic calcium ion concentration	2.77299E-06	6	148
leukocyte cell-cell adhesion	3.06297E-06	7	274
positive regulation of cell migration	3.06297E-06	7	274
regulation of monocyte chemotaxis	3.83947E-06	4	25
negative regulation of leukocyte apoptotic process	3.83947E-06	4	25
regulation of metal ion transport	4.01336E-06	7	287
monocyte chemotaxis	4.39048E-06	4	26
cellular calcium ion homeostasis	5.27527E-06	7	300
maintenance of location in cell	5.57953E-06	6	170

	6		
calcium ion transmembrane transport	6.31435E-0	6	174
	6		
negative regulation of leukocyte migration	1.43693E-0	4	35
	5		
positive regulation of calcium ion transport into cytosol	1.59167E-0	4	36
	5		
positive regulation of cation transmembrane transport	2.11994E-0	5	105
	5		
leukocyte tethering or rolling	3.50755E-0	3	10
	5		
positive regulation of ion transmembrane transport	3.54586E-0	5	117
	5		
regulation of mononuclear cell migration	4.13578E-0	4	46
	5		
dendritic cell apoptotic process	4.55906E-0	3	11
	5		
regulation of dendritic cell apoptotic process	4.55906E-0	3	11
	5		
maintenance of location	6.15505E-0	6	261
	5		
positive regulation of calcium ion transmembrane transport	6.47327E-0	4	52
	5		
regulation of leukocyte apoptotic process	7.45332E-0	4	54
	5		
regulation of release of sequestered calcium ion into cytosol	8.4254E-05	4	56

cellular extravasation	8.4254E-05	4	56
regulation of T cell chemotaxis	9.28412E-05	3	14
	5		
positive regulation of transmembrane transport	0.00012228	5	154
	7		
positive regulation of cell adhesion	0.00012502	6	299
	9		
positive regulation of T cell migration	0.00013748	3	16
	1		
leukocyte apoptotic process	0.00015441	4	66
	7		
release of sequestered calcium ion into cytosol	0.00016217	4	67
	7		
positive regulation of lymphocyte chemotaxis	0.00019307	3	18
	7		
regulation of calcium ion transport into cytosol	0.00024987	4	75
	5		
positive regulation of granulocyte chemotaxis	0.00026324	3	20
	8		
positive regulation of leukocyte cell-cell adhesion	0.00029067	5	187
	2		
dendritic cell migration	0.00033968	3	22
	9		
regulation of neutrophil chemotaxis	0.00033968	3	22
	9		
positive regulation of neutrophil migration	0.00033968	3	22

	9		
regulation of leukocyte adhesion to vascular endothelial cell	0.00038617 7	3	23
negative regulation of leukocyte cell-cell adhesion	0.00048116 8	4	90
neutrophil chemotaxis	0.00049029 7	3	25
regulation of cellular extravasation	0.00054244 9	3	26
positive regulation of cell-cell adhesion	0.00054244 9	5	216
positive regulation of lymphocyte activation	0.00059965 5	5	221
regulation of neutrophil migration	0.00082767	3	30
regulation of calcium ion transmembrane transport	0.00093688 7	4	108
regulation of endothelial cell proliferation	0.00107206 7	4	112
regulation of T cell activation	0.00109358 1	5	252
positive regulation of leukocyte activation	0.00119161 8	5	257
positive regulation of cell activation	0.00132028 9	5	263
endothelial cell proliferation	0.0014018	4	121
regulation of cation transmembrane transport	0.00152528	5	272

	8		
leukocyte adhesion to vascular endothelial cell	0.00171317	3	39
	8		
negative regulation of immune system process	0.00175296	5	281
	9		
negative regulation of cell-cell adhesion	0.00179430	4	130
	5		
negative regulation of cell migration	0.00206417	4	135
macrophage migration	0.00207020	3	42
	6		
regulation of ion transmembrane transport	0.00217399	5	296
	2		
regulation of actin filament length	0.00273722	4	146
cAMP-mediated signaling	0.00301799	4	150
	5		
positive regulation of T cell activation	0.00404874	4	162
	7		
actin polymerization or depolymerization	0.00507641	4	172
	4		
adenylate cyclase-modulating G protein-coupled receptor signaling pathway	0.00538553	4	175
	7		
cyclic-nucleotide-mediated signaling	0.00609244	4	181
	3		
establishment of lymphocyte polarity	0.00788736	2	10
	5		
dendritic cell chemotaxis	0.00788736	2	10

	5		
dendritic cell antigen processing and presentation	0.00788736	2	10
	5		
negative regulation of cell adhesion	0.00803951	4	196
G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	0.00896728	4	202
	5		
regulation of actin filament organization	0.01217350	4	219
	4		
negative regulation of cell motility	0.01295337	4	223
	5		
regulation of epithelial cell proliferation	0.01497634	4	232
	4		
response to prostaglandin	0.01515743	2	14
	2		
negative regulation of cellular component movement	0.01523958	4	234
	8		
negative regulation of blood vessel morphogenesis	0.01649923	3	88
	3		
negative regulation of vasculature development	0.01693183	3	89
	8		
regulation of actin cytoskeleton organization	0.01863280	4	248
	6		
negative regulation of locomotion	0.02089552	4	256
	0.02158925		
regulation of antigen processing and presentation		2	17
	9		
positive regulation of lymphocyte proliferation	0.02186460	3	98

	9		
chemokine-mediated signaling pathway	0.02339287	2	18
	8		
epithelial cell proliferation	0.02339287	4	266
	8		
positive regulation of glycoprotein metabolic process	0.02339287	2	18
	8		
positive regulation of mononuclear cell proliferation	0.02339287	3	101
	8		
regulation of cellular component size	0.02469359	4	271
	6		
regulation of T-helper 1 type immune response	0.02575492	2	19
	4		
positive regulation of protein polymerization	0.02770105	3	108
	5		
positive regulation of macrophage migration	0.02787250	2	20
	6		
regulation of macrophage chemotaxis	0.02787250	2	20
	6		
positive regulation of leukocyte proliferation	0.02787250	3	109
	6		
regulation of actin filament polymerization	0.03242145	3	115
	2		
regulation of supramolecular fiber organization	0.03294808	4	296
	8		
regulation of T cell proliferation	0.03536932	3	119

	3		
T-helper 1 type immune response	0.03571166	2	23
	1		
macrophage chemotaxis	0.03571166	2	23
	1		
regulation of calcium ion import	0.03867359	2	24
	6		
glycosaminoglycan binding	0.04073540	3	126
	2		
T cell proliferation	0.04336247	3	129
	2		
actin filament polymerization	0.04506840	3	131
	2		

FDR, false discovery rate.