

Supplementary Table S1. Functional Enrichment Analysis of the CX3CL1-Centered Interaction Network.

Function	FDR	Genes in network	Genes in genome
chemokine receptor activity	6.10E-18	9	24
G protein-coupled chemoattractant receptor activity	7.28E-18	9	26
chemokine binding	2.22E-17	9	30
regulation of cytosolic calcium ion concentration	1.44E-14	12	246
cellular calcium ion homeostasis	1.20E-13	12	300
immune receptor activity	1.20E-13	10	132
peptide receptor activity	1.20E-13	10	132
cytokine receptor activity	1.31E-13	9	80
cytokine binding	9.46E-13	9	100
G protein-coupled peptide receptor activity	1.02E-12	9	102
cell surface	5.01E-11	10	251
G protein-coupled receptor activity	5.01E-11	10	252
cell chemotaxis	5.79E-08	8	220
leukocyte migration	3.53E-07	8	281
regulation of leukocyte migration	3.53E-07	7	165
lymphocyte migration	5.55E-07	6	92
myeloid leukocyte migration	6.42E-07	7	183
leukocyte chemotaxis	7.88E-07	7	190
neutrophil migration	5.44029E-05	5	98
regulation of leukocyte chemotaxis	6.96553E-05	5	105
granulocyte chemotaxis	6.96553E-05	5	105
positive regulation of leukocyte migration	6.97334E-05	5	106
cytokine activity	0.000118292	4	45

granulocyte migration	0.000134726	5	123
T cell migration	0.000148395	4	49
regulation of lymphocyte migration	0.000148395	4	49
negative regulation of cell migration	0.000190598	5	135
cellular extravasation	0.000237717	4	56
chemokine receptor binding	0.000303882	4	60
cellular response to chemokine	0.000381695	4	64
cellular response to biotic stimulus	0.000398302	5	161
response to chemokine	0.000544577	4	71
regulation of chemotaxis	0.000580218	5	177
positive regulation of leukocyte chemotaxis	0.000580218	4	73
dendritic cell migration	0.000868093	3	22
glial cell migration	0.000868093	3	22
negative regulation of cell motility	0.001659877	5	223
negative regulation of cellular component movement	0.002045149	5	234
positive regulation of chemotaxis	0.002229905	4	106
negative regulation of locomotion	0.003010769	5	256
positive regulation of cell migration	0.004086091	5	274
macrophage migration	0.005344019	3	42
response to lipopolysaccharide	0.005344019	4	135
cellular response to molecule of bacterial origin	0.005662562	4	139
gliogenesis	0.005662562	4	139
regulation of leukocyte apoptotic process	0.010705002	3	54
leukocyte apoptotic process	0.01917077	3	66
dendritic cell chemotaxis	0.019621814	2	10
response to molecule of bacterial origin	0.019621814	4	195

G protein-coupled receptor binding	0.020007381	4	198
humoral immune response	0.020007381	4	197
positive regulation of calcium ion transport	0.021568216	3	71
dendritic cell apoptotic process	0.021587109	2	11
regulation of dendritic cell apoptotic process	0.021587109	2	11
regulation of glial cell migration	0.024252641	2	12
interleukin-1 beta production	0.024252641	3	76
cytokine receptor binding	0.024252641	4	214
regulation of ERK1 and ERK2 cascade	0.024252641	4	216
positive regulation of cell-cell adhesion	0.024252641	4	216
regulation of actin filament organization	0.025158576	4	219
negative regulation of cytokine production	0.025633471	4	221
negative regulation of neuron death	0.025797746	3	80
regulation of neuroblast proliferation	0.025797746	2	13
positive regulation of neural precursor cell proliferation	0.025797746	2	13
regulation of GTPase activity	0.02668508	4	227
regulation of interleukin-1 production	0.027094055	3	83
regulation of epithelial cell proliferation	0.028164467	4	232
ERK1 and ERK2 cascade	0.030626998	4	238
mononuclear cell migration	0.030846393	3	88
regulation of actin cytoskeleton organization	0.03437884	4	248
interleukin-1 production	0.03437884	3	92
negative regulation of cell cycle G1/S phase transition	0.034837335	3	93
regulation of neuron apoptotic process	0.03660005	3	95
regulation of apoptotic signaling pathway	0.036716127	4	255
cell junction disassembly	0.038284952	2	17

epithelial cell proliferation	0.042049155	4	266
leukocyte cell-cell adhesion	0.046226786	4	274
positive regulation of stem cell proliferation	0.046226786	2	19
calcium ion transport	0.046601743	4	276
neuron apoptotic process	0.047499442	3	107
eosinophil migration	0.049428981	2	20

FDR, false discovery rate.