

Supplementary Table 2: Complete fold regulation of 84 immune-related genes of *C. vulgaris*-treated group against sham-treated control group.

Gene Symbol	Description	Fold regulation	Comment
Apcs	Serum amyloid P-component	-2.71	C
C3	Complement component 3	1.67	
C5ar1	Complement component 5a receptor 1	-1.86	
Casp1	Caspase 1	-1.31	
Ccl12	Chemokine (C-C motif) ligand 12	-1.29	
Ccl5	Chemokine (C-C motif) ligand 5	-3.83	
Ccr4	Chemokine (C-C motif) receptor 4	-1.86	
Ccr5	Chemokine (C-C motif) receptor 5	1.33	
Ccr6	Chemokine (C-C motif) receptor 6	-2.17	
Ccr8	Chemokine (C-C motif) receptor 8	-2.71	C
Cd14	CD14 antigen	1.38	A
Cd4	CD4 antigen	-1.42	
Cd40	CD40 antigen	-1.88	
Cd40lg	CD40 ligand	-1.38	
Cd80	CD80 antigen	-1.00	
Cd86	CD86 antigen	-1.16	
Cd8a	CD8 antigen, alpha chain	-1.30	A
Crp	C-reactive protein, pentraxin-related	-2.71	C
Csf2	Colony stimulating factor 2 (granulocyte-macrophage)	-3.00	
Cxcl10	Chemokine (C-X-C motif) ligand 10	-1.15	
Cxcr3	Chemokine (C-X-C motif) receptor 3	1.13	
Ddx58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	1.16	A
Fasl	Fas ligand (TNF superfamily, member 6)	1.21	
Foxp3	Forkhead box P3	-2.71	C
Gata3	GATA binding protein 3	1.07	
H2-Q10	Histocompatibility 2, Q region locus 10	-1.84	
H2-T23	Histocompatibility 2, T region locus 23	-1.64	
Icam1	Intercellular adhesion molecule 1	1.18	A
Ifna2	Interferon alpha 2	-1.33	
Ifnar1	Interferon (alpha and beta) receptor 1	-1.51	
Ifnb1	Interferon beta 1, fibroblast	-2.71	C
Ifng	Interferon gamma	1.23	
Ifngr1	Interferon gamma receptor 1	1.74	A
Il10	Interleukin 10	-2.71	C
Il13	Interleukin 13	-2.71	C
Il17a	Interleukin 17A	-2.71	C
Il18	Interleukin 18	-1.62	
Il1a	Interleukin 1 alpha	-1.23	
Il1b	Interleukin 1 beta	-1.51	A
Il1r1	Interleukin 1 receptor, type I	-1.60	
Il2	Interleukin 2	-2.71	C

Il23a	Interleukin 23, alpha subunit p19	-2.71	C
Il4	Interleukin 4	-1.84	
Il5	Interleukin 5	-2.71	C
Il6	Interleukin 6	-2.71	C
Irak1	Interleukin-1 receptor-associated kinase 1	-1.76	
Irf3	Interferon regulatory factor 3	-1.45	
Irf7	Interferon regulatory factor 7	2.03	A
Itgam	Integrin alpha M	1.28	A
Jak2	Janus kinase 2	-1.42	
Ly96	Lymphocyte antigen 96	-1.52	
Lyz2	Lysozyme 2	-1.56	
Mapk1	Mitogen-activated protein kinase 1	-1.11	
Mapk8	Mitogen-activated protein kinase 8	-1.81	A
Mbl2	Mannose-binding lectin (protein C) 2	-2.71	C
Mpo	Myeloperoxidase	2.59	
Mx1	Myxovirus (influenza virus) resistance 1	1.95	
Myd88	Myeloid differentiation primary response gene 88	-2.17	
Nfkb1	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1, p105	1.08	
Nfkbia	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	1.95	
Nlrp3	NLR family, pyrin domain containing 3	1.29	
Nod1	Nucleotide-binding oligomerization domain containing 1	1.66	A
Nod2	Nucleotide-binding oligomerization domain containing 2	-1.02	
Rag1	Recombination activating gene 1	-2.71	C
Rorc	RAR-related orphan receptor gamma	-2.96	
Slc11a1	Solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	1.38	
Stat1	Signal transducer and activator of transcription 1	2.13	
Stat3	Signal transducer and activator of transcription 3	1.92	A
Stat4	Signal transducer and activator of transcription 4	1.65	
Stat6	Signal transducer and activator of transcription 6	-1.02	
Tbx21	T-box 21	1.17	
Ticam1	Toll-like receptor adaptor molecule 1	1.73	
Tlr1	Toll-like receptor 1	-1.47	A
Tlr2	Toll-like receptor 2	-1.01	
Tlr3	Toll-like receptor 3	1.45	
Tlr4	Toll-like receptor 4	1.27	A
Tlr5	Toll-like receptor 5	1.70	
Tlr6	Toll-like receptor 6	2.05	

Tlr7	Toll-like receptor 7	4.64	A
Tlr8	Toll-like receptor 8	1.70	A
Tlr9	Toll-like receptor 9	3.04	
Tnf	Tumor necrosis factor	1.94	
Traf6	Tnf receptor-associated factor 6	1.54	
Tyk2	Tyrosine kinase 2	2.57	
Actb	Actin, beta	1.30	
B2m	Beta-2 microglobulin	-1.33	
Gapdh	Glyceraldehyde-3-phosphate dehydrogenase	-1.35	
Gusb	Glucuronidase, beta	-1.01	
Hsp90ab1	Heat shock protein 90 alpha (cytosolic), class B member 1	-1.97	

*Comments:

A: This gene's average threshold cycle is relatively high (> 30) in either the control or the test sample, and is reasonably low in the other sample (< 30). These data mean that the gene's expression is relatively low in one sample and reasonably detected in the other sample suggesting that the actual fold-change value is at least as large as the calculated and reported fold-change result.

C: This gene's average threshold cycle is either not determined or greater than the defined cut-off (default 35), in both samples meaning that its expression was undetected, making this fold-change result erroneous and un-interpretable.