

SUPPLEMENTARY TABLE S3. FC FILTERED TOP GENES IN CGD COHORT (CGD/HEALTHY CONTROL)

<i>Fold change</i>	<i>Adj. p-value</i>	<i>Symbol</i>	<i>Category</i>	<i>Gene</i>
28.9	9.0E-4	<i>IFI27</i>	IRG	Interferon, alpha-inducible protein 27 (IFI27), transcript variant 2
8.9	2.3E-3	<i>IFI44L</i>	IRG	Interferon-induced protein 44-like (IFI44L)
5.5	1.1E-2	<i>OTOF</i>	Misc.	Otoferlin (OTOF), transcript variant 4
4.7	1.6E-3	<i>ISG15</i>	IRG	ISG15 ubiquitin-like modifier (ISG15)
4.6	6.3E-4	<i>LY6E</i>	IRG	Lymphocyte antigen 6 complex, locus E (LY6E)
3.8	5.6E-3	<i>EPSTI1</i>	IRG	Epithelial stromal interaction 1 (breast) (EPSTI1), transcript variant 2
3.7	1.7E-2	<i>IFI6</i>	IRG	Interferon, alpha-inducible protein 6 (IFI6), transcript variant 2
3.3	9.7E-3	<i>IFI44</i>	IRG	Interferon-induced protein 44 (IFI44)
3.3	6.0E-3	<i>OAS1</i>	IRG	2',5'-oligoadenylate synthetase 1, 40/46 kDa (OAS1), transcript variant 3
3.2	4.6E-3	<i>OAS1</i>	IRG	2',5'-oligoadenylate synthetase 1, 40/46 kDa (OAS1), transcript variant 3
3.2	3.6E-2	<i>SERPING1</i>	IRG	Serpin peptidase inhibitor, clade G (C1 inhibitor), member 1 (SERPING1), transcript 2
3.2	6.3E-4	<i>LOC652694</i>	LC	PREDICTED: similar to Ig kappa chain V-I region HK102 precursor (LOC652694)
3.2	2.3E-2	<i>RSAD2</i>	IRG	Radical S-adenosyl methionine domain containing 2 (RSAD2)
3.2	9.9E-3	<i>MX1</i>	IRG	Myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) (MX1)
3.1	5.6E-3	<i>IFI6</i>	IRG	Interferon, alpha-inducible protein 6 (IFI6), transcript variant 3
3.1	7.4E-4	<i>VPREB3</i>	LC	Pre-B lymphocyte gene 3 (VPREB3)
3.0	3.9E-2	<i>OAS3</i>	IRG	2'-5'-oligoadenylate synthetase 3, 100 kDa (OAS3)
2.9	1.5E-2	<i>TCL1A</i>	LC	T-cell leukemia/lymphoma 1A (TCL1A), transcript variant 2
2.8	1.7E-3	<i>XAF1</i>	IRG	XIAP-associated factor 1 (XAF1), transcript variant 2
2.8	6.3E-4	<i>OAS2</i>	IRG	2'-5'-oligoadenylate synthetase 2, 69/71 kDa (OAS2), transcript variant 1
2.8	4.8E-2	<i>HERC5</i>	IRG	Hect domain and RLD 5 (HERC5)
2.6	2.7E-2	<i>OASL</i>	IRG	2'-5'-oligoadenylate synthetase-like (OASL), transcript variant 2
2.5	4.6E-3	<i>CD79A</i>	LC	CD79a molecule, immunoglobulin-associated alpha (CD79A), transcript variant 1
2.4	4.6E-3	<i>CD79A</i>	LC	CD79a molecule, immunoglobulin-associated alpha (CD79A), transcript variant 2
2.4	1.7E-2	<i>MAFA</i>	Misc.	v-maf musculoaponeurotic fibrosarcoma oncogene homolog A (avian) (MAFA)
2.4	5.6E-3	<i>LGALS3BP</i>	IRG	Lectin, galactoside-binding, soluble, 3 binding protein (LGALS3BP)
2.4	6.3E-3	<i>IFI35</i>	IRG	Interferon-induced protein 35 (IFI35)
2.3	1.2E-3	<i>CD19</i>	LC	CD19 molecule (CD19)
2.3	1.3E-2	<i>LOC651751</i>	Misc.	PREDICTED: similar to Ig kappa chain V-II region RPMI 6410 precursor (LOC651751)
2.3	2.2E-2	<i>IRF7</i>	IRG	Interferon regulatory factor 7 (IRF7), transcript variant b
2.2	1.6E-3	<i>CD79B</i>	LC	CD79b molecule, immunoglobulin-associated beta (CD79B), transcript variant 3
2.2	1.0E-2	<i>CD79B</i>	LC	CD79B antigen (immunoglobulin-associated beta) (CD79B), transcript variant 1
2.2	1.6E-3	<i>CD79B</i>	LC	CD79B antigen (immunoglobulin-associated beta) (CD79B), transcript variant 2
2.1	7.5E-3	<i>CD38</i>	IRG	CD38 molecule (CD38)
2.1	2.7E-2	<i>IRF7</i>	IRG	Interferon regulatory factor 7 (IRF7), transcript variant b
2.1	1.6E-3	<i>7050201</i>	Misc.	602145539F1 NIH_MGC_48 cDNA clone IMAGE:4309424 5, mRNA sequence
2.1	1.6E-3	<i>CD72</i>	LC	CD72 molecule (CD72)
2.1	1.3E-2	<i>MT1A</i>	IRG	Metallothionein 1A (MT1A)
2.0	4.8E-3	<i>PRICKLE1</i>	Misc.	Prickle homolog 1 (Drosophila) (PRICKLE1)
2.0	1.6E-2	<i>SAMD9L</i>	IRG	Sterile alpha motif domain containing 9-like (SAMD9L)
2.0	6.9E-3	<i>EIF2AK2</i>	IRG	Eukaryotic translation initiation factor 2-alpha kinase 2 (EIF2AK2)

CGD, chronic granulomatous disease; FC, fold change; IRG, interferon regulated gene.