Supplementary Material

Table 1a. Clinical characteristics of Control, Sarcoidosis subjects of Koth(17) and Crouser Cohort(18).

	Koth et al				Crouser et al			
	Control n=20	Sarcoidosis n=38	Sarcoidosis n=38		Control n=6	Sarcoidosis n=6	Control n=11	Sarcoidosis n=11
			Low lung function n=18	Normal lung function n=20				
Age (yr)	51±12	50.8±11.2	50.3±12.2	51.2±10.7	51±10	41±9	62±8	47±7
Gender (M/F)	5/15	17/21	11/7	6/14	3/3	2/4	6/5	4/7
Race (W/AA/other)	16/2/2	31/1/6	15/2/1	16/2/2	4/2/0	4/2/0	8/3/0	6/5/0
Smoking status (CS/FS/NS/unknown)	0/0/20/0	2/0/36/0	2/0/16/0	0/0/20/0	5/0/1/0	3/0/2/1	7/0/3/1	5/0/4/2
FEV1,L	NA	2.56±0.8	2.15±0.7	2.93±0.6	NA	NA	NA	NA
FEV1, % predicted	NA	82.2±23.3	61.6±13	100.7±12.2	NA	NA	NA	NA
FVC,L	NA	3.6±0.8	3.42±0.9	3.75±0.7	NA	NA	NA	NA
FVC, % predicted	NA	90.3±16.7	77.3±9.1	102±12.6	NA	85±13	NA	83±14
TLC, L	NA	5.47±1.0	5.31±1.1	5.61±1.0	NA	NA	NA	NA
TLC, % predicted	NA	94.3±14.9	84.6±9	103±13.7	NA	84±11	NA	89±12
DLco	NA	21.1±6.0	21.1±6.0	22.5±5.5	NA	NA	NA	NA
DLco, % predicted	NA	75.1±20.6	63.7±17.2	85.3±18.1	NA	71±16	NA	73±20
Inhaled corticosteroids	NA	9(24%)	7(39%)	2(11%)	NA	NA	NA	NA
systemic therapy	NA	12-17 (32%-45%)	8-13 (45%-72%)	4 (22%)	NA	NA	NA	NA

Table 1b. Genes upregulated in CBD-stimulated PBMCs compared with BeS -stimulated PBMCs

Symbol	Name	Fold change	Parametric p-value
CCL3	chemokine (C-C motif) ligand 3	2.63	0.00152
GEM	GTP binding protein overexpressed in skeletal muscle	2.33	0.00157
SLC15A3	solute carrier family 15 (oligopeptide transporter), member 3	2.27	0.00116
LILRB4	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4	2.22	0.00119
IER3	immediate early response 3	2.04	0.00082
MSR1	macrophage scavenger receptor 1	1.96	0.00134
CSRNP1	cysteine-serine-rich nuclear protein 1	1.89	0.00028
LILRB2	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	1.89	0.00184
C2	complement component 2	1.85	0.00137
PPP1R15A	protein phosphatase 1, regulatory subunit 15A	1.85	0.00129
DTHD1	death domain containing 1	1.82	0.00150
ETS2	v-ets avian erythroblastosis virus E26 oncogene homolog 2	1.82	0.00240
UNC93B1	unc-93 homolog B1 (C. elegans)	1.82	0.00080
FNIP2	folliculin interacting protein 2	1.79	0.00097
GADD45G	growth arrest and DNA-damage-inducible, gamma	1.79	0.00045
JUNB	jun B proto-oncogene	1.75	0.00017
KLF10	Kruppel-like factor 10	1.72	0.00233
PRKD2	protein kinase D2	1.72	0.00152
RNF19B	ring finger protein 19B	1.72	0.00094
GRN	granulin	1.67	0.00234
HLA-DPB1	major histocompatibility complex, class II, DP beta 1	1.64	0.00055
CD81	CD81 molecule	1.61	0.00001
CD97	CD97 molecule	1.61	0.00223
CTSD	cathepsin D	1.61	0.00238
NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	1.61	0.00141
TRIB1	tribbles pseudokinase 1	1.59	0.00020
BCKDK	branched chain ketoacid dehydrogenase kinase	1.56	0.00000
PLK3	polo-like kinase 3	1.56	0.00019
RBCK1	RanBP-type and C3HC4-type zinc finger containing 1	1.56	0.00157
BAK1	BCL2-antagonist/killer 1	1.54	0.00165
DUSP4	dual specificity phosphatase 4	1.54	0.00130
LILRA6	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6	1.54	0.00014
PLOD3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	1.54	0.00000
RHBDF2	rhomboid 5 homolog 2 (Drosophila)	1.54	0.00013

SLC25A25	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25	1.54	0.00038
FERMT3	fermitin family member 3	1.52	0.00002
MYO1G	myosin IG	1.52	0.00020
NEU1	sialidase 1 (lysosomal sialidase)	1.52	0.00098
P2RX4	purinergic receptor P2X, ligand-gated ion channel, 4	1.52	0.00006
SERTAD3	SERTA domain containing 3	1.52	0.00022
SNORD4A	small nucleolar RNA, C/D box 4A	1.52	0.00117
UBTD2	ubiquitin domain containing 2	1.52	0.00004

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Tabel 1c. Genes downregualted in CBD-stimulated PBMCs compared with BeS-stimulated PBMCs.

Symbol	**Name**	**Fold-change**	**Parametric p-value**
MIR181C	microRNA 181c	0.57	0.00038
RNASE3	ribonuclease, RNase A family, 3	0.58	0.00174
MIR134	microRNA 134	0.65	0.00018
EIF3E	eukaryotic translation initiation factor 3, subunit E	0.65	0.00133
SNORD116-15	small nucleolar RNA, C/D box 116-15	0.66	0.00086

Table 2a. Top 50 genes upregulated in CBD-stimulated PBMCs compared with Con -stimulated PBMCs.

Symbol	Name	Fold-change	Parametric p-value
CXCL9	chemokine (C-X-C motif) ligand 9	7.33	0.00166
HCAR3	hydroxycarboxylic acid receptor 3	5.85	0.00111
HCAR2	hydroxycarboxylic acid receptor 2	5.65	0.00038
CD274	CD274 molecule	5.48	0.00065
CLEC6A	C-type lectin domain family 6, member A	4.14	0.00234
EGR2	early growth response 2	3.45	0.00039
IL3RA	interleukin 3 receptor, alpha (low affinity)	3.29	0.00010
SECTM1	secreted and transmembrane 1	3.25	0.00023
ICAM1	intercellular adhesion molecule 1	2.97	0.00036
HBEGF	heparin-binding EGF-like growth factor	2.92	0.00196
P2RX7	purinergic receptor P2X, ligand-gated ion channel, 7	2.81	0.00128
ATF3	activating transcription factor 3	2.74	0.00020
STX11	syntaxin 11	2.72	0.00017
SLC15A3	solute carrier family 15 (oligopeptide transporter), member 3	2.72	0.00013
SOCS3	suppressor of cytokine signaling 3	2.68	0.00023
FAM26F	family with sequence similarity 26, member F	2.65	0.00084
ARRDC4	arrestin domain containing 4	2.65	0.00045
GEM	GTP binding protein overexpressed in skeletal muscle	2.6	0.00050
LILRB4	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4	2.56	0.00074
CCR1	chemokine (C-C motif) receptor 1	2.55	0.00246
SDC4	syndecan 4	2.44	0.00088
IRF1	interferon regulatory factor 1	2.44	0.00026
PSME2	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	2.35	0.00103
CISH	cytokine inducible SH2-containing protein	2.32	0.00010
SOCS1	suppressor of cytokine signaling 1	2.3	0.00045
CCRL2	chemokine (C-C motif) receptor-like 2	2.24	0.00066
TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	2.23	0.00103
ARHGAP31	Rho GTPase activating protein 31	2.23	0.00020
CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	2.19	0.00033
STEAP4	STEAP family member 4	2.13	0.00037
KLF10	Kruppel-like factor 10	2.11	0.00043
TRIM25	tripartite motif containing 25	2.1	0.00168
RASGEF1B	RasGEF domain family, member 1B	2.1	0.00113
NUP62	nucleoporin 62kDa	2.09	0.00229
NEK6	NIMA-related kinase 6	2.04	0.00019

IGSF6	immunoglobulin superfamily, member 6	2	0.00108
DOCK4	dedicator of cytokinesis 4	2	0.00130
PRKD2	protein kinase D2	1.99	0.00026
PPIF	peptidylprolyl isomerase F	1.99	0.00040
ITGAX	integrin, alpha X (complement component 3 receptor 4 subunit)	1.99	0.00219
CSF2RB	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	1.98	0.00026
CSRNP1	cysteine-serine-rich nuclear protein 1	1.96	0.00152
PIM1	Pim-1 proto-oncogene, serine/threonine kinase	1.95	0.00002
FGL2	fibrinogen-like 2	1.95	0.00183
C2	complement component 2	1.95	0.00108
GADD45G	growth arrest and DNA-damage-inducible, gamma	1.92	0.00021
TYMP	thymidine phosphorylase	1.91	0.00011
HLA-DPB1	major histocompatibility complex, class II, DP beta 1	1.91	0.00003
SLC31A2	solute carrier family 31 (copper transporter), member 2	1.9	0.00203
DUSP5	dual specificity phosphatase 5	1.89	0.00164

Table 2b. Genes downregulated in CBD-stimulated PBMCs compared with Controls -stimulated PBMCs.

Symbol	Name	Fold-change	Parametric p-value
SNORD116-6	small nucleolar RNA, C/D box 116-6	0.5	0.00027
VPS29	vacuolar protein sorting 29 homolog (S. cerevisiae)	0.58	0.00070
EIF3E	eukaryotic translation initiation factor 3, subunit E	0.6	0.00060
MAP2K6	mitogen-activated protein kinase kinase 6	0.63	0.00071

Tabel 3 a. Genes up-regulated in CBD compared with BeS.

Symbol	Name	Fold change	Parametric p-value
CYHR1	cysteine/histidine-rich 1	1.56	0.00014
GPR162	G protein-coupled receptor 162	1.54	0.00108
IER3	immediate early response 3	1.52	0.00089

Tabel 3 b. Genes down-regulated in CBD compared with BeS.

Symbol	Name	Fold-change	Parametric p-value
SNORD94	small nucleolar RNA, C/D box 94	0.52	0.00040
SNORD116-24	small nucleolar RNA, C/D box 116-24	0.55	0.00003
SNORD116-15	small nucleolar RNA, C/D box 116-15	0.59	0.00011
SNORD116-1	small nucleolar RNA, C/D box 116-1	0.63	0.00043
ZNF737	zinc finger protein 737	0.66	0.00133
SNORD116-8	small nucleolar RNA, C/D box 116-8	0.67	0.00100

Tabel 4 a. Genes up-regulated in CBD compared with con.

Symbol	Name	Fold change	Parametric p-value
FUCA1	fucosidase, alpha-L- 1, tissue	2.17	0.02971
CD9	CD9 molecule	2	0.02137
CYP27A1	cytochrome P450, family 27, subfamily A, polypeptide 1	1.79	0.02583
ACP5	acid phosphatase 5, tartrate resistant	1.71	0.00778
ST14	suppression of tumorigenicity 14 (colon carcinoma)	1.7	0.00349
ANPEP	alanyl (membrane) aminopeptidase	1.67	0.00260
DSC2	desmocollin 2	1.67	0.00568
LY86	lymphocyte antigen 86	1.66	0.01340
OLFML2B	olfactomedin-like 2B	1.64	0.02168
PLIN2	perilipin 2	1.64	0.03484
SLCO2B1	solute carrier organic anion transporter family, member 2B1	1.63	0.02741
MS4A1	membrane-spanning 4-domains, subfamily A, member 1	1.61	0.02032
FCRLA	Fc receptor-like A	1.58	0.00599
TPCN1	two pore segment channel 1	1.57	0.01567
DHRS9	dehydrogenase/reductase (SDR family) member 9	1.56	0.04433
LRP1	low density lipoprotein receptor-related protein 1	1.54	0.03392
PDGFC	platelet derived growth factor C	1.54	0.01085

ALOX5	arachidonate 5-lipoxygenase	1.52	0.00423
FCGRT	Fc fragment of IgG, receptor, transporter, alpha	1.52	0.00504
IL1R1	interleukin 1 receptor, type I	1.52	0.00886
SLC37A2	solute carrier family 37 (glucose-6-phosphate transporter), member 2	1.51	0.01003
TLR5	toll-like receptor 5	1.51	0.00974
ABHD6	abhydrolase domain containing 6	1.5	0.00093
CTSD	cathepsin D	1.5	0.00689
DAGLB	diacylglycerol lipase, beta	1.5	0.00400
MPP1	membrane protein, palmitoylated 1, 55kDa	1.5	0.03872
THUMPD3-AS1	THUMPD3 antisense RNA 1	1.5	0.01140

Tabel 4 b. Genes down-regulated in CBD compared with con.

Symbol	Name	Fold change	Parametric p-value
SNORD115-20	small nucleolar RNA, C/D box 115-20	0.40	0.03214
MIR382	microRNA 382	0.47	0.02974
KRTAP4-6	keratin associated protein 4-6	0.53	0.01259
SNORD115-25	small nucleolar RNA, C/D box 115-25	0.55	0.04714
SNORD116-6	small nucleolar RNA, C/D box 116-6	0.55	0.02461
TMEM51-AS1	TMEM51 antisense RNA 1	0.55	0.03077
LOC388692	uncharacterized LOC388692	0.57	0.03039
KRTAP4-11	keratin associated protein 4-11	0.59	0.01491
LOC441233	uncharacterized LOC441233	0.59	0.01782
OR8B8	olfactory receptor, family 8, subfamily B, member 8	0.60	0.00141
KRTAP4-9	keratin associated protein 4-9	0.61	0.01542
KRTAP5-6	keratin associated protein 5-6	0.61	0.00961
FFAR2	free fatty acid receptor 2	0.63	0.03334
KRTAP5-10	keratin associated protein 5-10	0.63	0.03733
KRTAP5-7	keratin associated protein 5-7	0.63	0.03269
KRTAP5-9	keratin associated protein 5-9	0.63	0.04512
KRTAP9-2	keratin associated protein 9-2	0.63	0.00670
KRTAP9-8	keratin associated protein 9-8	0.63	0.01127
FLJ38773	uncharacterized protein FLJ38773	0.64	0.02792
KRTAP4-4	keratin associated protein 4-4	0.64	0.03689
OR10G2	olfactory receptor, family 10, subfamily G, member 2	0.64	0.00211
KRTAP4-7	keratin associated protein 4-7	0.65	0.03223
KRTAP9-4	keratin associated protein 9-4	0.65	0.01480
MRGPRX4	MAS-related GPR, member X4	0.65	0.00806
SNORD115-31	small nucleolar RNA, C/D box 115-31	0.65	0.03071
CFB	complement factor B	0.66	0.03070
KRTAP10-4	keratin associated protein 10-4	0.66	0.01179

SNORD115-41	small nucleolar RNA, C/D box 115-41	0.66	0.03977

Table 5a. upregulated genes shared between CBD and sarcoidosis peripheral blood gene expression from Koth et al (GDS4587)(17)

Symbol	Name	Parametric p-value
NFKBIE	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	0.00004
ICAM1	intercellular adhesion molecule 1	0.00005
LILRB4	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4	0.00006
NEK6	NIMA (never in mitosis gene a)-related kinase 6	0.00007
STX11	syntaxin 11	0.00007
SOCS1	suppressor of cytokine signaling 1	0.00010
P2RX7	purinergic receptor P2X, ligand-gated ion channel, 7	0.00010
BAK1	BCL2-antagonist/killer 1	0.00011
FLVCR2	feline leukemia virus subgroup C cellular receptor family, member 2	0.00011
CD274	CD274 molecule	0.00012
IRF1	interferon regulatory factor 1	0.00013
ATF3	activating transcription factor 3	0.00014
WDFY1	WD repeat and FYVE domain containing 1	0.00015
LRP10	low density lipoprotein receptor-related protein 10	0.00015
CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	0.00015
KIAA0040	KIAA0040	0.00016
RHBDF2	rhomboid 5 homolog 2 (Drosophila)	0.00016
CD97	CD97 molecule	0.00017
RNF19B	ring finger protein 19B	0.00017
CTSC	cathepsin C	0.00020
TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	0.00025
PLEK	pleckstrin	0.00026
IDO1	indoleamine 2,3-dioxygenase 1	0.00026
GBP5	guanylate binding protein 5	0.00027
SOCS3	suppressor of cytokine signaling 3	0.00031
JUNB	jun B proto-oncogene	0.00031
MMP14	matrix metallopeptidase 14 (membrane-inserted)	0.00032
ARSB	arylsulfatase B	0.00032
PDCD1LG2	programmed cell death 1 ligand 2	0.00034
CASP4	caspase 4, apoptosis-related cysteine peptidase	0.00034
SQRDL	sulfide quinone reductase-like (yeast)	0.00035
RAB20	RAB20, member RAS oncogene family	0.00035
RIPK2	receptor-interacting serine-threonine kinase 2	0.00036
CXCL9	chemokine (C-X-C motif) ligand 9	0.00036
TYMP	thymidine phosphorylase	0.00037

TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	0.00038
NRP2	neuropilin 2	0.00041
MSR1	macrophage scavenger receptor 1	0.00044
LMNB1	lamin B1	0.00044
DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides	0.00045
NLRC5	NLR family, CARD domain containing 5	0.00046
SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	0.00049
ADAM19	ADAM metallopeptidase domain 19	0.00057
CCRL2	chemokine (C-C motif) receptor-like 2	0.00058
SNX10	sorting nexin 10	0.00061
SLC25A28	solute carrier family 25, member 28	0.00062
CLEC4E	C-type lectin domain family 4, member E	0.00064
ASPHD2	aspartate beta-hydroxylase domain containing 2	0.00064
ANKFY1	ankyrin repeat and FYVE domain containing 1	0.00065
PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	0.00068
PRKD2	protein kinase D2	0.00068
SLC31A2	solute carrier family 31 (copper transporters), member 2	0.00068
GBP2	guanylate binding protein 2, interferon-inducible	0.00072
IGSF6	immunoglobulin superfamily, member 6	0.00073
TRIM25	tripartite motif-containing 25	0.00074
FAM26F	family with sequence similarity 26, member F	0.00074
PSMB10	proteasome (prosome, macropain) subunit, beta type, 10	0.00077
ABCD1	ATP-binding cassette, sub-family D (ALD), member 1	0.00078
AKIRIN2	akirin 2	0.00078
SCPEP1	serine carboxypeptidase 1	0.00080
CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	0.00081
EGR2	early growth response 2	0.00081
PSME2	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	0.00082
SECTM1	secreted and transmembrane 1	0.00084
LIMK1	LIM domain kinase 1	0.00085
APOL1	apolipoprotein L, 1	0.00089
ADPGK	ADP-dependent glucokinase	0.00089
TMEM140	transmembrane protein 140	0.00089
TRIM21	tripartite motif-containing 21	0.00091
MVP	major vault protein	0.00093
MYOF	myoferlin	0.00096
ZNFX1	zinc finger, NFX1-type containing 1	0.00098
DRAM1	DNA-damage regulated autophagy modulator 1	0.00100
KLF10	Kruppel-like factor 10	0.00101
WARS	tryptophanyl-tRNA synthetase	0.00103
CTSZ	cathepsin Z	0.00107
B4GALT5	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5	0.00107

TMEM150B	transmembrane protein 150B	0.00108
CXCL11	chemokine (C-X-C motif) ligand 11	0.00108
KCNJ2	potassium inwardly-rectifying channel, subfamily J, member 2	0.00108
FGD2	FYVE, RhoGEF and PH domain containing 2	0.00114
TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b	0.00115
OGFR	opioid growth factor receptor	0.00115
BLVRA	biliverdin reductase A	0.00119
CLCN7	chloride channel 7	0.00124
PLAUR	plasminogen activator, urokinase receptor	0.00125
GBP4	guanylate binding protein 4	0.00127
SEMA7A	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)	0.00129
KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	0.00129
CD40	CD40 molecule, TNF receptor superfamily member 5	0.00130
LILRB3	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	0.00131
HBEGF	heparin-binding EGF-like growth factor	0.00133
NBN	nibrin	0.00136
MTF1	metal-regulatory transcription factor 1	0.00137
TRAFD1	TRAF-type zinc finger domain containing 1	0.00138
NAPA	N-ethylmaleimide-sensitive factor attachment protein, alpha	0.00140
TRIB1	tribbles homolog 1 (Drosophila)	0.00142
PML	promyelocytic leukemia	0.00144
PARP3	poly (ADP-ribose) polymerase family, member 3	0.00144
ACP2	acid phosphatase 2, lysosomal	0.00146
DOT1L	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	0.00147
SIRT7	sirtuin 7	0.00149
RBCK1	RanBP-type and C3HC4-type zinc finger containing 1	0.00153
SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	0.00154
ACOT9	acyl-CoA thioesterase 9	0.00157
LY6E	lymphocyte antigen 6 complex, locus E	0.00160
SLAMF8	SLAM family member 8	0.00160
SERPING1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	0.00163
RSAD2	radical S-adenosyl methionine domain containing 2	0.00164
INHBA	inhibin, beta A	0.00166
NRP1	neuropilin 1	0.00173
RNF213	ring finger protein 213	0.00174
CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	0.00177
OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	0.00179
APOL2	apolipoprotein L, 2	0.00181
STAT2	signal transducer and activator of transcription 2, 113kDa	0.00193
MT2A	metallothionein 2A	0.00196

PARP9	poly (ADP-ribose) polymerase family, member 9	0.00196
IFI35	interferon-induced protein 35	0.00202
ECE1	endothelin converting enzyme 1	0.00203
ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)	0.00203
DOCK4	dedicator of cytokinesis 4	0.00204
GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	0.00206
GADD45G	growth arrest and DNA-damage-inducible, gamma	0.00211
IFIT3	interferon-induced protein with tetratricopeptide repeats 3	0.00219
LIMK2	LIM domain kinase 2	0.00223
IFIT2	interferon-induced protein with tetratricopeptide repeats 2	0.00225
DRAP1	DR1-associated protein 1 (negative cofactor 2 alpha)	0.00226
TRIM38	tripartite motif-containing 38	0.00226
CXCL16	chemokine (C-X-C motif) ligand 16	0.00227
FAM129B	family with sequence similarity 129, member B	0.00229
FNDC3B	fibronectin type III domain containing 3B	0.00232
UNC93B1	unc-93 homolog B1 (C. elegans)	0.00247
TANK	TRAF family member-associated NFKB activator	0.00249
CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	0.00249
TRANK1	tetratricopeptide repeat and ankyrin repeat containing 1	0.00253
OASL	2'-5'-oligoadenylate synthetase-like	0.00254
APOL6	apolipoprotein L, 6	0.00255
TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	0.00258
LILRB1	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	0.00261
ANKRD22	ankyrin repeat domain 22	0.00270
UBE2L6	ubiquitin-conjugating enzyme E2L 6	0.00272
BST2	bone marrow stromal cell antigen 2	0.00274
ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	0.00289
STAT1	signal transducer and activator of transcription 1, 91kDa	0.00292
EPSTI1	epithelial stromal interaction 1 (breast)	0.00295
IRF9	interferon regulatory factor 9	0.00302
SLC7A7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	0.00312
MOV10	Mov10, Moloney leukemia virus 10, homolog (mouse)	0.00312
LHFPL2	lipoma HMGIC fusion partner-like 2	0.00319
ODF3B	outer dense fiber of sperm tails 3B	0.00326
TCIRG1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3	0.00326
LAP3	leucine aminopeptidase 3	0.00329
ITGAX	integrin, alpha X (complement component 3 receptor 4 subunit)	0.00331
FMNL2	formin-like 2	0.00333
PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	0.00335

XAF1	XIAP associated factor 1	0.00350
C2	complement component 2	0.00360
FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)	0.00388
PSMB9	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)	0.00396
FBP1	fructose-1,6-bisphosphatase 1	0.00396
GM2A	GM2 ganglioside activator	0.00396
JAK2	Janus kinase 2	0.00403
ZBP1	Z-DNA binding protein 1	0.00403
IFI44	interferon-induced protein 44	0.00411
FCGR1B	Fc fragment of IgG, high affinity Ib, receptor (CD64)	0.00415
ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	0.00415
CXCL10	chemokine (C-X-C motif) ligand 10	0.00418
VAMP5	vesicle-associated membrane protein 5 (myobrevin)	0.00419
NEU1	sialidase 1 (lysosomal sialidase)	0.00420
FBXO6	F-box protein 6	0.00430
GTPBP1	GTP binding protein 1	0.00432
CSF1	colony stimulating factor 1 (macrophage)	0.00433
GSDMD	gasdermin D	0.00443
GCH1	GTP cyclohydrolase 1	0.00445
IFI44L	interferon-induced protein 44-like	0.00453
NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	0.00460
SP110	SP110 nuclear body protein	0.00464
PARP10	poly (ADP-ribose) polymerase family, member 10	0.00467
CD276	CD276 molecule	0.00475
DTX3L	deltex 3-like (Drosophila)	0.00478
TDRD7	tudor domain containing 7	0.00487
TIFA	TRAF-interacting protein with forkhead-associated domain	0.00488
BAZ1A	bromodomain adjacent to zinc finger domain, 1A	0.00509
CCL24	chemokine (C-C motif) ligand 24	0.00513
MT1G	metallothionein 1G	0.00518
PARP14	poly (ADP-ribose) polymerase family, member 14	0.00522
TFEC	transcription factor EC	0.00524
MREG	melanoregulin	0.00524
SAMD9L	sterile alpha motif domain containing 9-like	0.00548
ISG20	interferon stimulated exonuclease gene 20kDa	0.00568
DDX60L	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like	0.00571
FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	0.00574
SIRPA	signal-regulatory protein alpha	0.00578
NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	0.00588
OSM	oncostatin M	0.00614
SLC27A3	solute carrier family 27 (fatty acid transporter), member 3	0.00619

OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa	0.00620
SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	0.00625
IFIH1	interferon induced with helicase C domain 1	0.00627
APOBEC3G	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	0.00635
ETV7	ets variant 7	0.00638
FAM46A	family with sequence similarity 46, member A	0.00672
LOC100288594	hypothetical LOC100288594	0.00678
RALB	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	0.00712
NUB1	negative regulator of ubiquitin-like proteins 1	0.00717
DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	0.00723
LILRB2	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	0.00758
IL15RA	interleukin 15 receptor, alpha	0.00774
FAR2	fatty acyl CoA reductase 2	0.00781
TLR8	toll-like receptor 8	0.00785
ACP5	acid phosphatase 5, tartrate resistant	0.00794
ALPK1	alpha-kinase 1	0.00806
BCL2L1	BCL2-like 1	0.00830
FAS	Fas (TNF receptor superfamily, member 6)	0.00841
LPCAT2	lysophosphatidylcholine acyltransferase 2	0.00869
SNTB1	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	0.00872
HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	0.00898
AIM2	absent in melanoma 2	0.00903
FAM122C	family with sequence similarity 122C	0.00907
STOM	stomatin	0.00935
EMR2	egf-like module containing, mucin-like, hormone receptor-like 2	0.00940
TRIM22	tripartite motif-containing 22	0.00950
PSTPIP2	proline-serine-threonine phosphatase interacting protein 2	0.00961
JAG1	jagged 1	0.00976
TYROBP	TYRO protein tyrosine kinase binding protein	0.00999
PSEN2	presenilin 2 (Alzheimer disease 4)	0.01022
RTP4	receptor (chemosensory) transporter protein 4	0.01034
TLR7	toll-like receptor 7	0.01043
IFI16	interferon, gamma-inducible protein 16	0.01045
CMPK2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	0.01048
TLR1	toll-like receptor 1	0.01070
SOD2	superoxide dismutase 2, mitochondrial	0.01080
DYNLT1	dynein, light chain, Tctex-type 1	0.01081
TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	0.01083
PILRA	paired immunoglobin-like type 2 receptor alpha	0.01083

GSN	gelsolin	0.01132
CD86	CD86 molecule	0.01135
PLSCR1	phospholipid scramblase 1	0.01157
XRN1	5'-3' exoribonuclease 1	0.01161
BCL2L14	BCL2-like 14 (apoptosis facilitator)	0.01189
GK	glycerol kinase	0.01224
C1QB	complement component 1, q subcomponent, B chain	0.01248
GNB4	guanine nucleotide binding protein (G protein), beta polypeptide 4	0.01326
SLC31A1	solute carrier family 31 (copper transporters), member 1	0.01346
SAMD9	sterile alpha motif domain containing 9	0.01385
SCARB2	scavenger receptor class B, member 2	0.01390
LGALS9	lectin, galactoside-binding, soluble, 9	0.01449
CD68	CD68 molecule	0.01461
TFE3	transcription factor binding to IGHM enhancer 3	0.01468
TNFAIP2	tumor necrosis factor, alpha-induced protein 2	0.01532
TLN2	talin 2	0.01540
ZC3H12C	zinc finger CCCH-type containing 12C	0.01547
MLKL	mixed lineage kinase domain-like	0.01593
CTSB	cathepsin B	0.01655
TNFAIP6	tumor necrosis factor, alpha-induced protein 6	0.01728
CARD16	caspase recruitment domain family, member 16	0.01764
IFIT5	interferon-induced protein with tetratricopeptide repeats 5	0.01807
APOL4	apolipoprotein L, 4	0.01848
SAT1	spermidine/spermine N1-acetyltransferase 1	0.01881
SLC43A2	solute carrier family 43, member 2	0.01948
TBC1D2	TBC1 domain family, member 2	0.01966
ARNT2	aryl-hydrocarbon receptor nuclear translocator 2	0.01995
CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	0.02094
CD209	CD209 molecule	0.02115
LACTB	lactamase, beta	0.02199
DNASE2	deoxyribonuclease II, lysosomal	0.02381
STXBP2	syntaxin binding protein 2	0.02406
IRF7	interferon regulatory factor 7	0.02467
GRN	granulin	0.02606
SUCNR1	succinate receptor 1	0.02610
PGD	phosphogluconate dehydrogenase	0.02689

Fig 5b. Down-regulated genes shared by CBD and sarcoidosis peripheral blood mononuclear cells (GDS4587. Koth et al 17)

Symbol	Name	Parametric p-value
TC2N	tandem C2 domains, nuclear	0.00123
RASA4	RAS p21 protein activator 4	0.00187

KLHL3	kelch-like 3 (Drosophila)	0.00418
GPR183	G protein-coupled receptor 183	0.00543
SESN3	sestrin 3	0.00660
AKTIP	AKT interacting protein	0.00720
KRT73	keratin 73	0.00772
GCNT4	glucosaminyl (N-acetyl) transferase 4, core 2	0.00962
NELL2	NEL-like 2 (chicken)	0.00990
TTC3	tetratricopeptide repeat domain 3	0.01002
VSIG1	V-set and immunoglobulin domain containing 1	0.01521
STK38	serine/threonine kinase 38	0.01567
PCYOX1	prenylcysteine oxidase 1	0.01949
ANKRD36B	ankyrin repeat domain 36B	0.02122
PREPL	prolyl endopeptidase-like	0.02250
KLRB1	killer cell lectin-like receptor subfamily B, member 1	0.02355

Table5c. Genes that are up-regulated in sarcoidosis but down-regulated in CBD peripheral blood mononuclear cells(GDS4587. Koth et al 17).

Symbol	Name	Parametric p-value
RNASE3	ribonuclease, RNase A family, 3	0.0001031

Table 5d. Genes that are down-regulated in sarcoidosis but up-regulated in CBD peripheral blood mononuclear cells(GDS4587. Koth et al 17).

Symbol	Name	Parametric p-value
ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2	0.0001985
PFKP	phosphofructokinase, platelet	0.0002113
BCL2	B-cell CLL/lymphoma 2	0.0006361
CCND2	cyclin D2	0.0010465
FAM115C	family with sequence similarity 115, member C	0.0012438
NFE2L3	nuclear factor (erythroid-derived 2)-like 3	0.00135
SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	0.0013568
PGAP1	post-GPI attachment to proteins 1	0.0017591
ACTA2	actin, alpha 2, smooth muscle, aorta	0.0023326
BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	0.0026089
SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	0.0029085
SPP1	secreted phosphoprotein 1	0.0053925
PPM1K	protein phosphatase, Mg2+/Mn2+ dependent, 1K	0.0066405

Table5e. Up-regulated genes found in both CBD peripheral blood transcripts and sarcoidosis lung tissue gene expression (GDS3580. Crouser et al 18).

Symbol	Name	Parametric p-value
CXCL9	chemokine (C-X-C motif) ligand 9	0.00002
FAM26F	family with sequence similarity 26, member F	0.00003
TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	0.00008
CXCL11	chemokine (C-X-C motif) ligand 11	0.00014
GBP4	guanylate binding protein 4	0.00018
CCL8	chemokine (C-C motif) ligand 8	0.00020
STAT1	signal transducer and activator of transcription 1, 91kDa	0.00032
SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	0.00054
BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	0.00070
DOCK4	dedicator of cytokinesis 4	0.00073
SLAMF7	SLAM family member 7	0.00131
DDX60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	0.00139
GNA13	guanine nucleotide binding protein (G protein), alpha 13	0.00141

Table 5f. Down-regulated genes in both CBD peripheral blood transcripts and sarcoidosis lung tissue gene expression (GDS3580. Crouser et al. 18)

Symbol	Name	Parametric p-value
ABCD3	ATP-binding cassette, sub-family D (ALD), member 3	0.00195

Table 5g. Genes that are up-regulated in sarcoidosis lung tissue but down-regulated in CBD peripheral blood cell transcripts (GDS3580. Crouser et al. 18)

Symbol	Name	Parametric p-value
TRERF1	transcriptional regulating factor 1	0.00007
SR140	U2 snRNP-associated SURP domain containing	0.00008
CCNG2	cyclin G2	0.00012
KBTBD6	kelch repeat and BTB (POZ) domain containing 6	0.00016
FYB	FYN binding protein	0.00021
ZNF217	zinc finger protein 217	0.00028

SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	0.00038
STK4	serine/threonine kinase 4	0.00039
TBL1XR1	transducin (beta)-like 1 X-linked receptor 1	0.00084
LPAR6	lysophosphatidic acid receptor 6	0.00121
NKTR	natural killer cell triggering receptor	0.00123
ZNF92	zinc finger protein 92	0.00127
TRERF1	transcriptional regulating factor 1	0.00129
FBXL3	F-box and leucine-rich repeat protein 3	0.00158
PSIP1	PC4 and SFRS1 interacting protein 1	0.00188
IFNGR1	interferon gamma receptor 1	0.00194
SH2D1A	SH2 domain containing 1A	0.00197
RBM12B	RNA binding motif protein 12B	0.00206

Table 5h. Genes that are down-regulated in sarcoidosis lung tissue but up-regulated in CBD peripheral blood transcripts (GDS3580. Crouser et al.18)

Symbol	Name	Parametric p-value
RHBDD2	rhomboid domain containing 2	0.00007