

SUPPLEMENTARY MATERIAL

ALVEOLAR MACROPHAGES FROM TUBERCULOSIS CONTACTS WITH DIABETES HAVE REDUCED CAPACITY TO CONTAIN M. TUBERCULOSIS

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METHODS

Peripheral blood mononuclear cell isolation

Heparinized whole blood was centrifuged at 800xg for 12min to remove the plasma and to collect the buffy coats. Buffy coats were resuspended in PBS (Lonza) containing 1mM EDTA (Sigma-Aldrich) and 1% human serum albumin (Sigma-Aldrich), layered onto Ficoll-Paque-Plus (GE Healthcare) and centrifuged at 600xg for 30min at RT. PBMCs were collected, and washed twice with RPMI-HEPES, first by centrifuging at 600xg for 4min at 4°C and then at 150xg for 8min at 4°C to remove excess platelets. The PBMCs were then resuspended in RPMI containing 2mM glutamine, 100UI penicillin (Sigma-Aldrich) and 20% autologous plasma and cultured in Teflon jars (Savillex) at a concentration of 1x10⁶cells/ml at 37°C with 5% CO₂ for 5 days to allow for differentiation of monocytes into MDMs [1, 2]

Mycobacterial growth inhibition assay

Colony forming units (CFUs) were assessed at 2h, day 1 and day 3 post infection (p.i.) after lysing the cells with 0.05% SDS (Sigma-Aldrich) and plating the lysates on 7H11 agar plates. Cell viability and monolayer density were assessed at each time point after removing non-viable/non-adhering cells, lysing adherent cells with cetyltrimethylammonium bromide (CTAB; Sigma-Aldrich) and counting nuclei using a hemocytometer.

Cytokine quantification using Luminex

IL-1α, IL-1β, IL-1RA, IL-6, IL-8, IL-10, IL-12p40, IFN-α2, CXCL10 (IP-10), CSF2 (GM-CSF), CCL2 (MCP-1), CCL3 (MIP-1α) and TNF-α concentrations were measured using the Bio-Plex platform (Bio-Plex™, Bio-Rad Laboratories). All samples, quality controls (QCs) and standards were run in duplicate. To account for inter- and intra-plate variation, samples were randomized across plates. The data generated were analyzed using the Bio-Plex Manager v6.1 software and a five-parameter logistic curve regression model was used to determine the concentrations of all the analytes. The concentrations of all analytes in the QCs were within the expected ranges. Values below and above

the standard curve range which fell within the detection limit of the assay, were extrapolated by the Bio-Plex Manager Software. For analytes with out-of-range values, 10% was added to the highest or subtracted from the lowest value measured for that analyte and the value used to replace the missing data point.

FACS and CyTOF analysis

MDMs were first stained with the Zombie aqua (BV510) fixable viability dye (1:100; BioLegend) for 30min at 4°C. Cells were washed with FACS buffer (2% FBS), resuspended in blocking buffer (1:1 ratio of FACS buffer and human AB serum) and incubated on ice for 30min. After the blocking step, antibodies and isotype controls (supplementary table S1) were added, and the cells incubated for 30min at 4°C. Cells were fixed with 2% paraformaldehyde before flow cytometric analysis on the FACSCanto II flow cytometer (BD Biosciences). Post-acquisition analysis was performed using FlowJo™ v10.1 software (BD Life Sciences).

HAMs from each participant were barcoded, using the Fluidigm Cell-ID 20-Plex Pd Barcoding kit, and pooled prior to staining. Each participant had five samples consisting of the cells that were fixed and stored immediately after being isolated as well as uninfected and *Mtb*-infected HAMs cultured for 1 and 3 days. Briefly, barcoding reagents were prepared weekly and stored at 4°C. Fixed cells were thawed and transferred to Maxpar PBS and centrifuged at 800xg for 5min. After resuspending the pellets in 1ml Maxpar cell staining buffer (CSB) the HAMs were counted, centrifuged, and resuspended in 800µl of Maxpar barcode perm buffer (BPB). Eppendorf tubes containing 10µl of barcodes were allowed to reach RT prior to adding 100µl BPB. Barcodes were then added to the cells and incubated for 45min at RT. Cells were mixed gently every 15min. After washing the cells twice with CSB the pellets were resuspended in 100µl CSB and pooled into a single FACS tube. The antibody cocktail was subsequently prepared in a 0.1µm filter column and spun at 12,000xg for 1min. Cells were then stained for 45min at 4°C. After washing the cells with cell staining buffer, DVS fix/perm solution (Fluidigm) was added, and the cells incubated for 20min at RT. Cells were washed with CyPBS and the DNA labeled with a nucleic acid intercalator, iridium (1:6000), overnight at 4°C. The following day the cells were washed twice with milliQ double distilled water and spun at 800xg for 10min at 4°C. The cells were diluted in EQ™ four element calibration beads (1:10 EQ four Beads in MilliQ water), before acquisition on the CyTOF® 2 mass cytometer with DVS CyTOF 2 v6.0 software. The acquisition rate was kept at <400 cells/second and the mass range adjusted to 102-192. Post-acquisition, the data were normalized using the Matlab-based Normalizer v0.3 software and analyzed in FlowJo™ v10.1 software. In FlowJo™ the beads were removed from the pooled samples and the samples deconvoluted using a Boolean gating strategy.

RNA isolation and sequencing

Isolated RNA was quantified using the Qubit RNA High Sensitivity Assay Kit (ThermoFisher) and Qubit 4 fluorometer (ThermoFisher). Prior to RNA sequencing (RNA-Seq), RNA quality was assessed with the Fragment analyzer (Agilent Technologies, Santa Clara, CA, USA). Samples with an RNA integrity number (RIN) higher than 7 were used for RNA-Seq. RNA-Seq libraries were prepared from 15-500ng of total RNA using the NEBNext Poly(A) mRNA magnetic isolation module (New England Biolabs, Ipswich, MA, USA). RNA sequencing was done at the Genome Sequencing Facility at UT Health, San Antonio, using the HiSeq 3000 platform (Illumina), with 50bp single read sequencing with approximately 25M reads per sample.

RNA sequencing data preprocessing and analysis

Low-quality sequences and adapters were trimmed. Trimmed reads were mapped to the human hg38 reference genome. The reads were assigned to the transcripts using the EM algorithm. The TMM normalization [3] in EdgeR [4, 5] and multi-factorial statistics based on a negative binomial Generalized Linear Model (GLM) were carried out for differential expression analysis. The metadata of the samples used for RNA-Seq with the donor ID, sample descriptions and comparisons are included in supplementary table S3. The Benjamini-Hochberg (1995) procedure was used to control the false discovery rate (FDR) [6]. Genes with FDR-adjusted p-value <0.1 and log2 fold changes (LFC) of >1 or <-1 were considered differentially expressed. Gene Set Enrichment Analysis (GSEA) [7], KOBAS analysis [8] and the Gene Ontology (GO) resource [9, 10] were used to identify over-represented GO terms and biological pathways. Pathway and network analyses were performed using Ingenuity Pathway Analysis (IPA) (Qiagen, Redwood City, CA, USA).

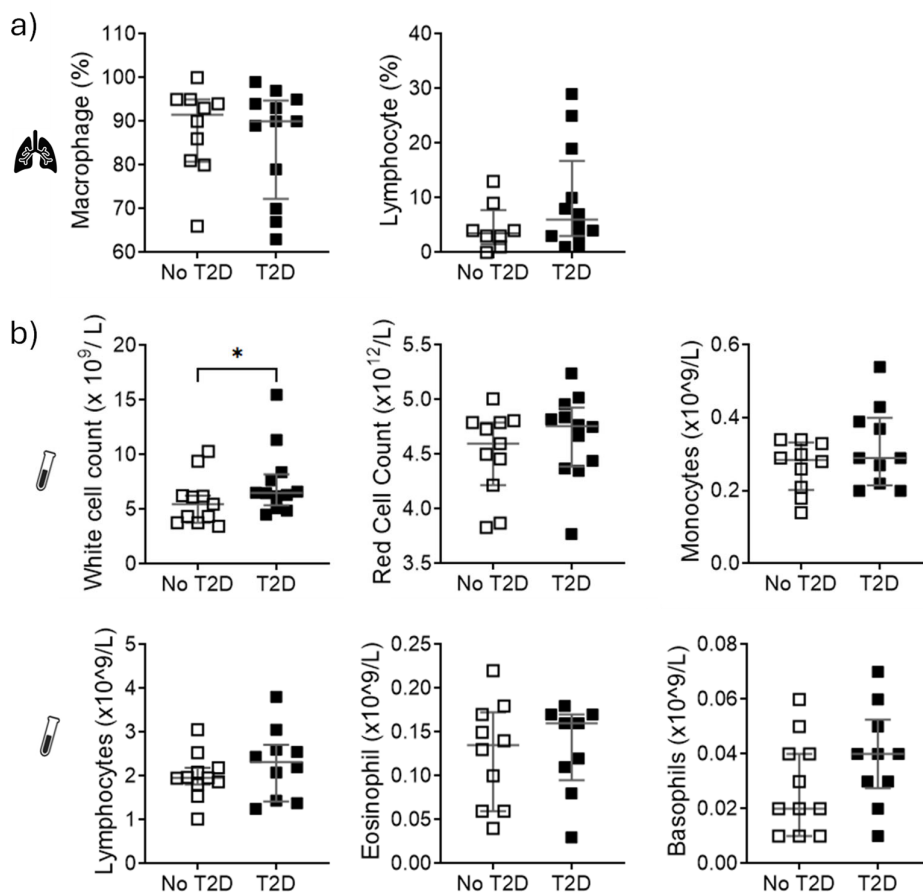
DNA extraction and methylation profiling

Genomic DNA (gDNA) was isolated, using the DNeasy Blood & Tissue kit (Qiagen), according to the manufacturer's instructions. Red blood cells (RBCs) were lysed using the eBioscience RBC Lysis Buffer (ThermoFisher), and the leukocytes used as input material. The eluted gDNA was quantified using a Nanodrop 2000c spectrophotometer (ThermoFisher) and utilized for subsequent DNA methylation analysis with the Illumina Infinium HumanMethylationEPIC BeadChip (Illumina). The DNA samples were shipped to the University of Southern California Norris Comprehensive Cancer Center, Molecular Genomics Core, Los Angeles where the DNA methylation analysis was performed. Briefly, 250-1000ng gDNA was bisulfite converted using the Zymo EZ DNA Methylation Kit (Zymo Research). DNA samples from four BALs with low DNA yields were recovered using the Infinium Restoration Kit prior to bisulfite conversion (Illumina). The resulting bisulfite converted DNA was amplified, enzymatically fragmented, precipitated and hybridized onto Illumina Infinium HumanMethylationEPIC BeadChips following the Infinium protocol [11]. The BeadChips were

105 scanned using the Illumina iScan system and raw methylation data from 865,860 CpG sites
106 exported as IDAT files.

107 **Methylation data preprocessing and analysis**

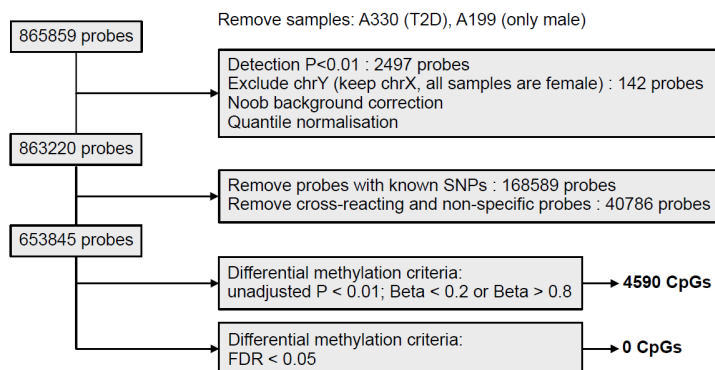
108 Analysis of methylation arrays was carried out following the Bioconductor
109 'methylationArrayAnalysis' workflow, using the IlluminaHumanMethylationEPICanno.ilm10b4.hg19
110 annotation set for Illumina MethylationEPIC arrays. Probes were excluded where detection p-value
111 was <0.01 , where they were located on the Y chromosome, or were annotated as containing SNPs
112 or known to be cross-reacting (supplementary figure S2a). Probes on the X chromosome were
113 retained as only females were included in this analysis. Background correction was carried out via
114 the Noob method and probe intensities were quantile normalized. Differentially methylated
115 positions (DMPs) were retained with uncorrected $p < 0.01$ and beta values >0.8 and <0.2 . Gene set
116 enrichment testing was carried out via the "gsameth" function in the missMethyl package [12] using
117 hallmark and GO gene sets from the MSigDB Molecular Signatures Database [13]. The Hallmark
118 (H) gene sets represent well-defined biological states or processes, whereas the GO (C5) set
119 consists of genes annotated by the same ontology term.



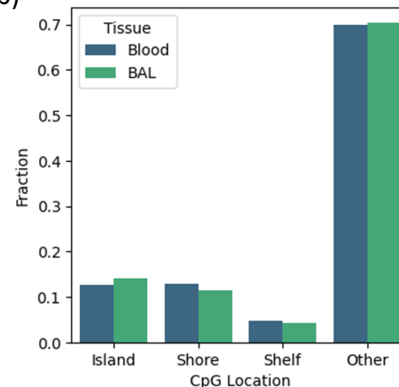
Supplementary figure S1. Blood counts and differential cell counts from whole blood and BALF.

a) Percentage of cell types in BALF. Percentages were calculated from the differential counts done on the cytospins. b) Absolute cell numbers in whole blood determined by a reference laboratory. Blood was collected on the same day of the bronchoscopy. Data are presented as medians with interquartile ranges.

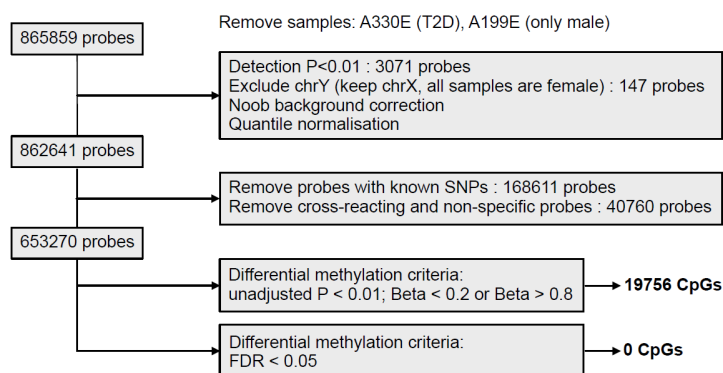
a) **Blood: pT2D vs non-T2D**



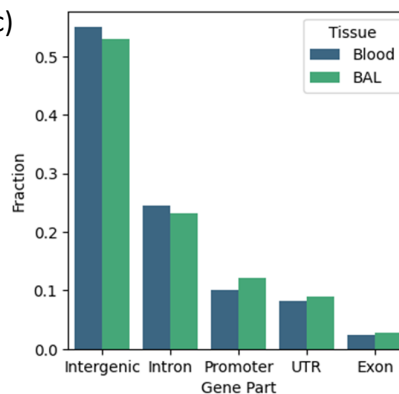
b)



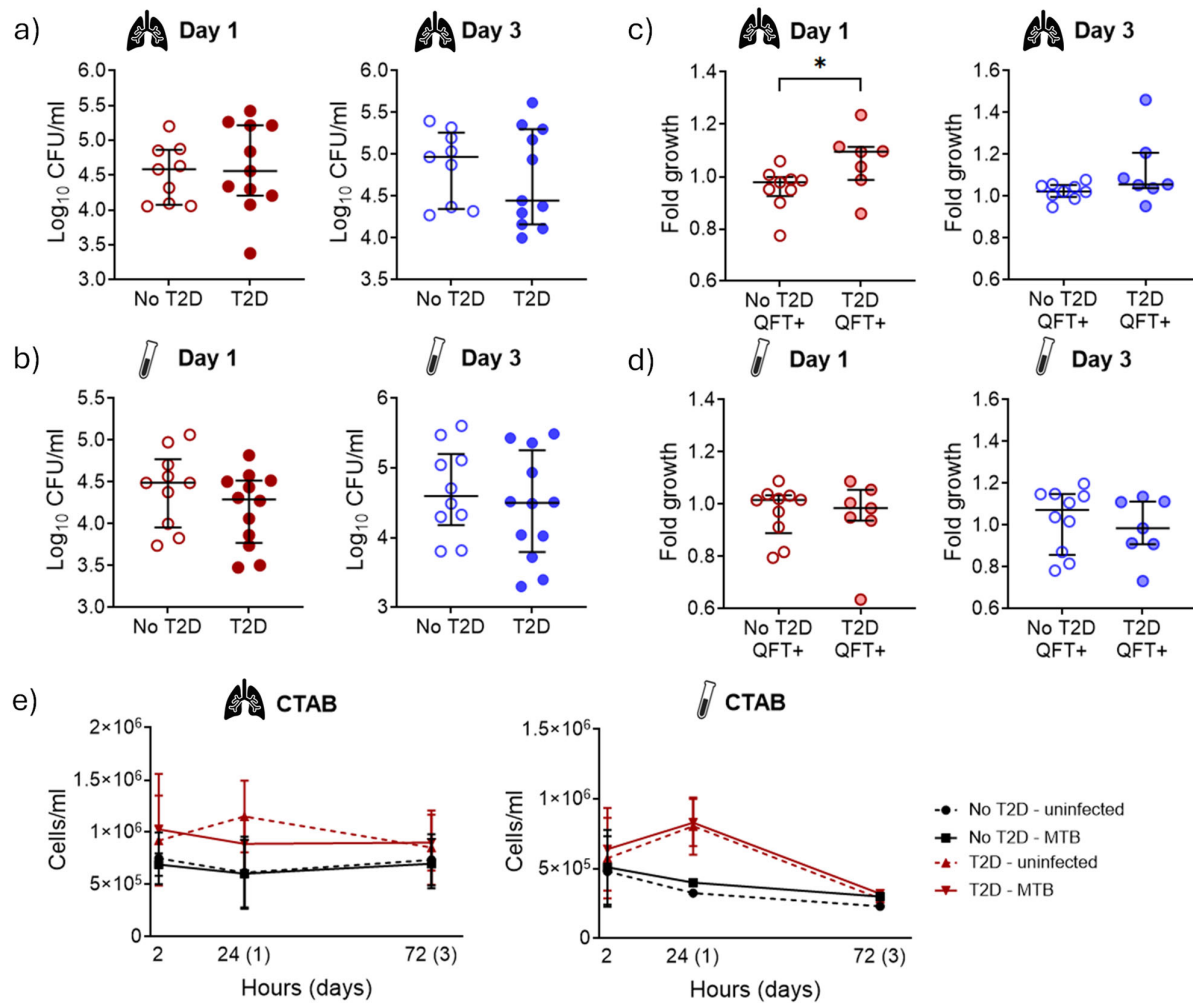
BAL: pT2D vs non-T2D



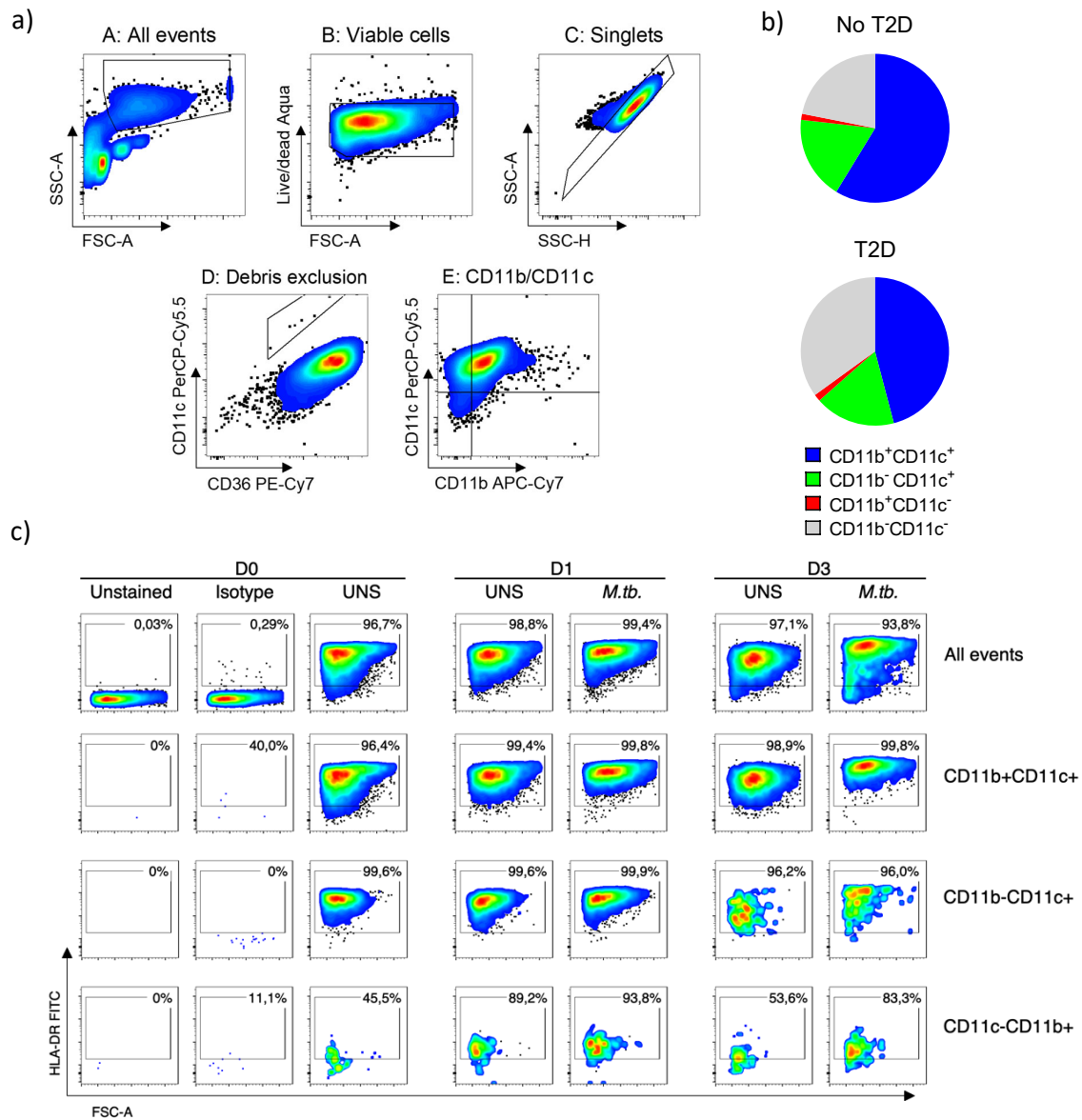
c)



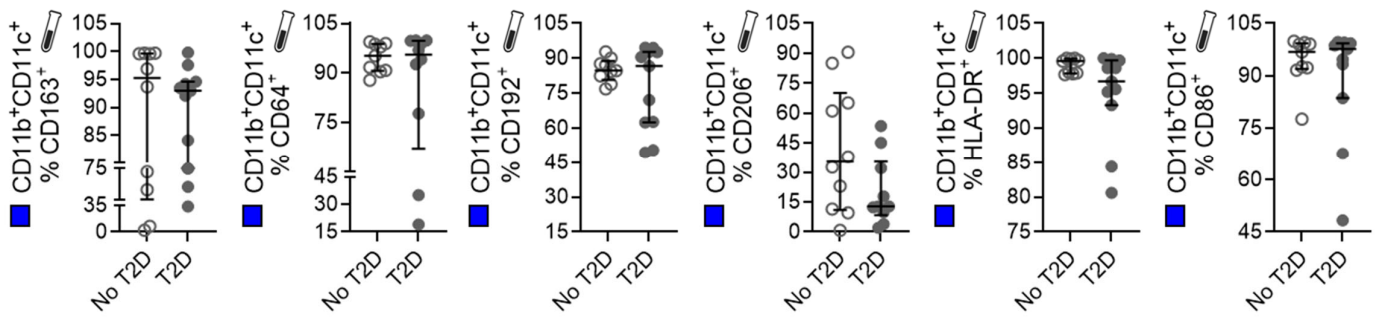
Supplementary figure S2. a) Filtering criteria for the identification of CpGs differentially methylated between T2D patients and no T2D controls. A total of 653,845 probes were derived from whole blood leucocytes and 653,270 probes from BAL cells, after correcting the data and removing probes with known SNPs and cross-reacting and non-specific probes. 4,590 CpGs from the whole blood leucocyte dataset and 19,758 CpGs from the BAL cell dataset were selected for further analysis within each sample type. A summary of differentially methylated positions across b) genomic locations relative to CpG islands and c) gene annotations, University of California Santa Cruz (UCSC) refGene. Noob – normal-exponential out-of-band; FDR – false discovery rate; UTR – untranslated region.



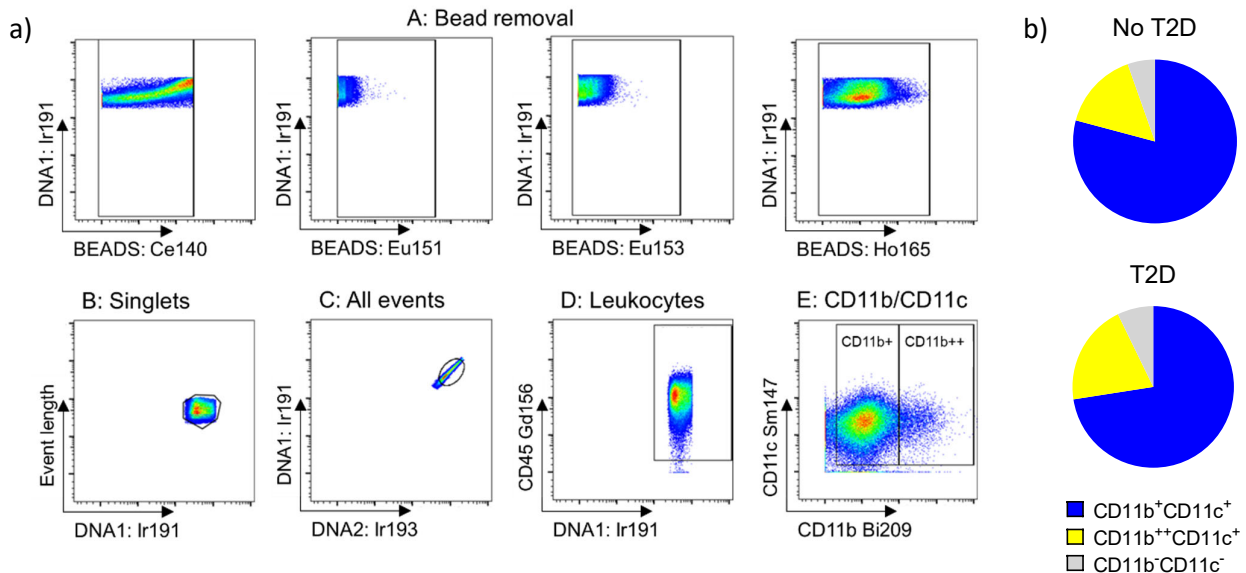
Supplementary figure S3. Raw colony forming units (CFUs) and cell numbers remain consistent during the infection assay of MDMs and HAMs. HAMs and MDMs from contacts of TB patients with and without T2D were infected with *M.tb* H₃₇R_v (MOI 1:1) for 2h and subsequently cultured for 1 and 3 days. Number of bacilli, presented as $\log_{10}$ CFU/ml, 1 and 3 days p.i. in a) HAMs and b) MDMs. *M.tb* fold growth of c) HAMs and d) MDMs of QFT+ individuals. The number of viable cells present in the wells of 96-well culture plates for the c) HAM and d) MDM stimulation assays. The number of viable cells were determined by washing the wells to remove non-viable/non-adhering cells. Cetyltrimethylammonium bromide (CTAB) was added to each well and the total number of nuclei counted using a hemocytometer. Data are presented as medians with interquartile ranges (a-d) or mean $\pm$ SD (e).



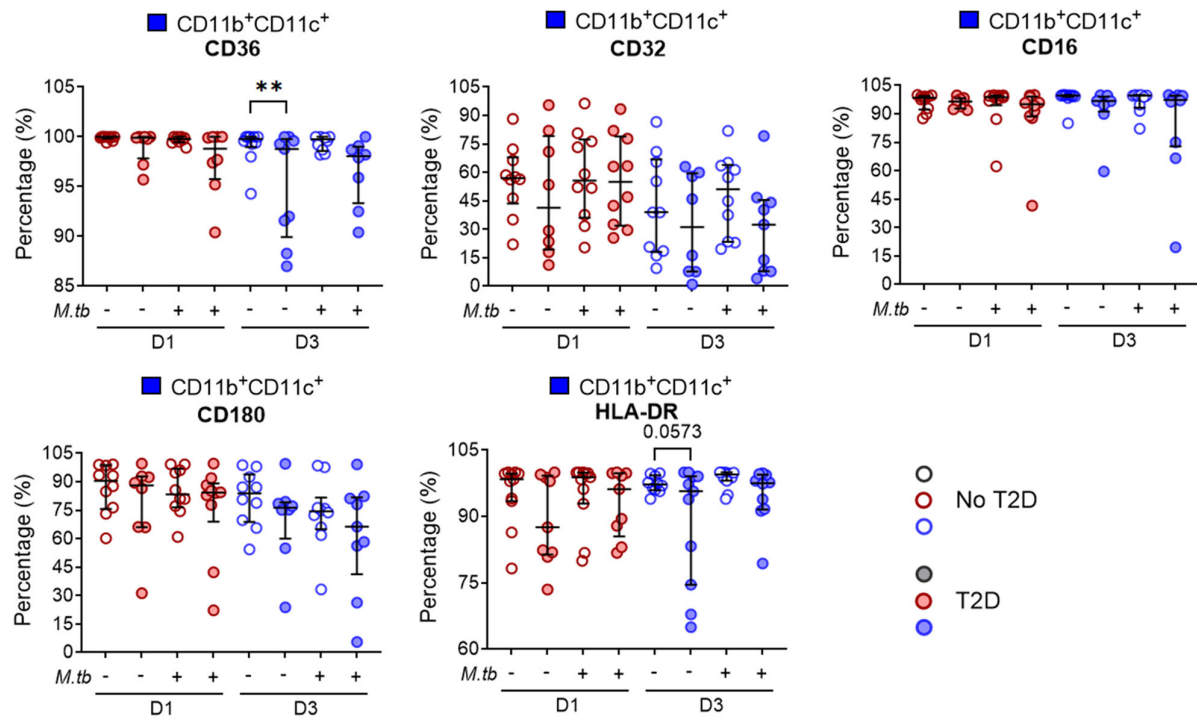
Supplementary figure S4. Characterization of MDM populations using flow cytometry. MDMs retrieved from the Teflon jars (D0) and not yet infected with *M.tb* (UNS) as well as uninfected (UNS) and *M.tb*-infected (*M.tb*) MDMs cultured for 1 (D1) and 3 (D3) days were stained for flow cytometric analysis. a) The gating strategy used to define MDM populations. b) Pie charts indicating the percentage of CD11b and CD11c expressing MDMs. c) Example of the gating strategy used to assess the frequency of the different MDM subsets expressing individual markers, e.g HLA-DR. Unstained and isotype controls were included to define negative cell populations and to assess if non-specific binding occurred.



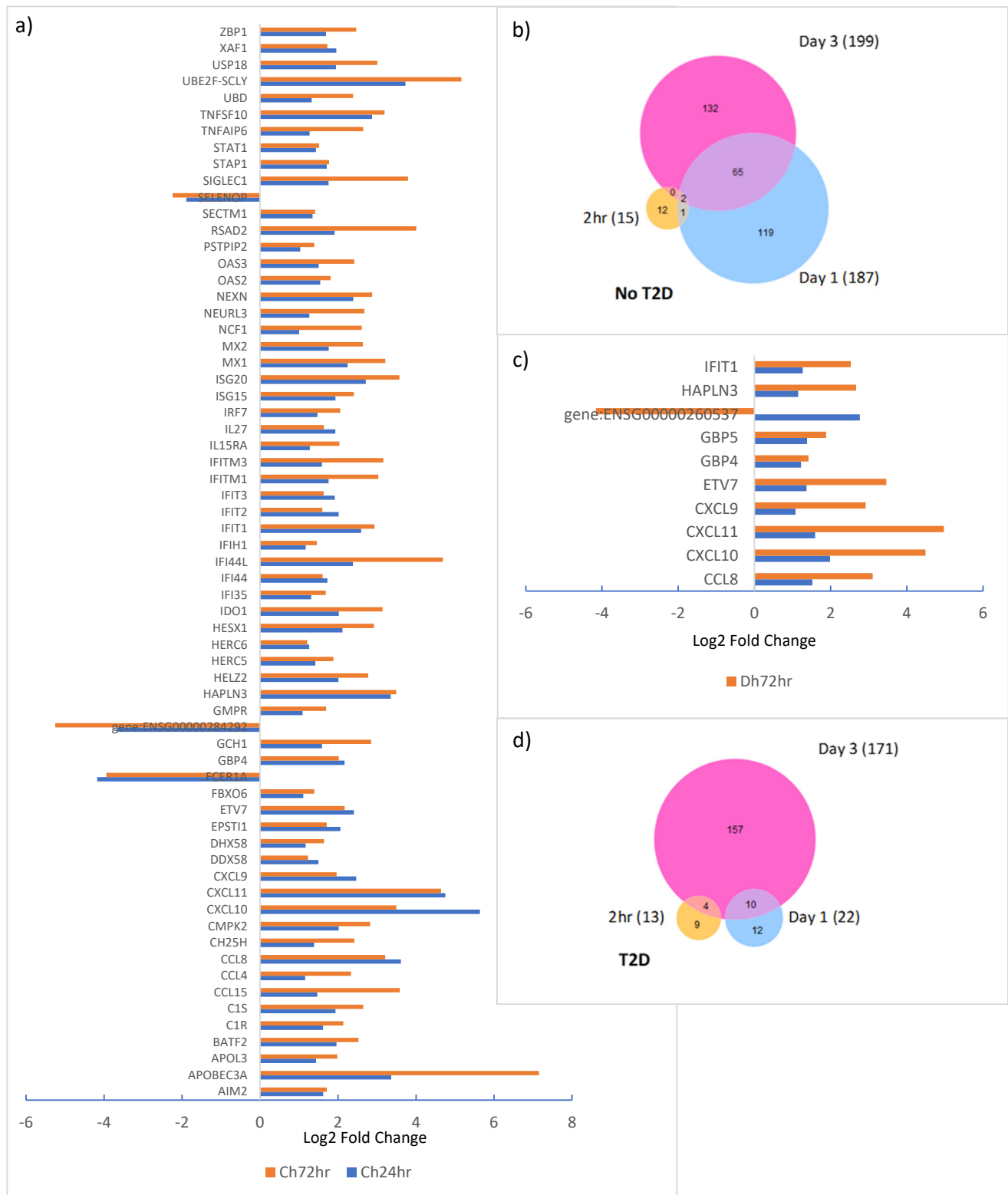
153 **Supplementary figure S5.** Frequencies of MDMs expressing CD163, CD64, CD192, CD206,
 154 HLA-DR and CD86 are not affected by T2D. PBMCs were cultured in Teflon jars for 5 days to allow
 155 monocytes to differentiate into MDMs. After 5 days the PBMCs were stained for flow cytometric
 156 analysis. Data are presented as medians with interquartile ranges.



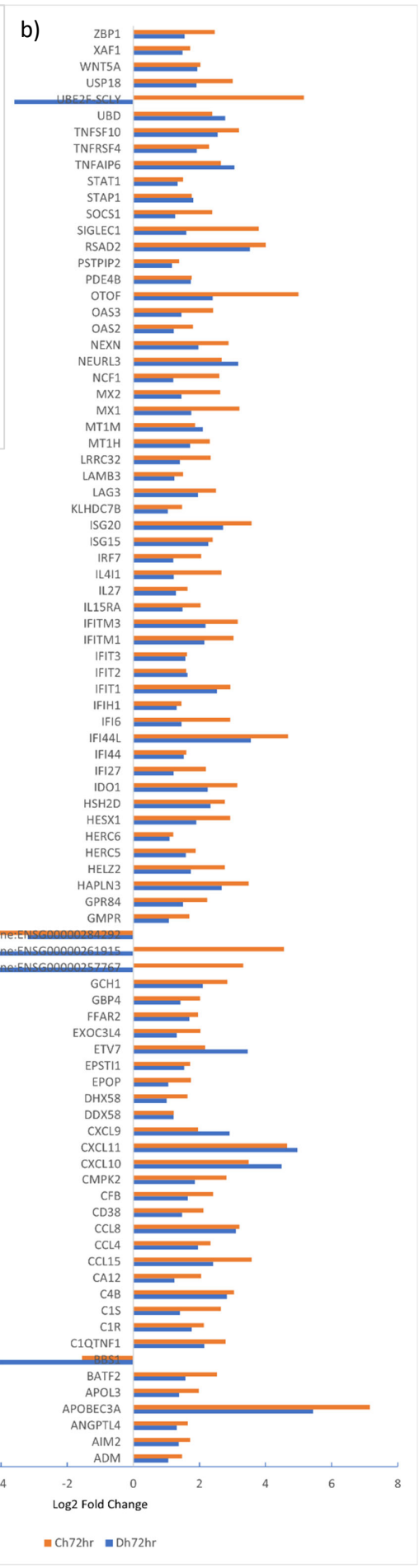
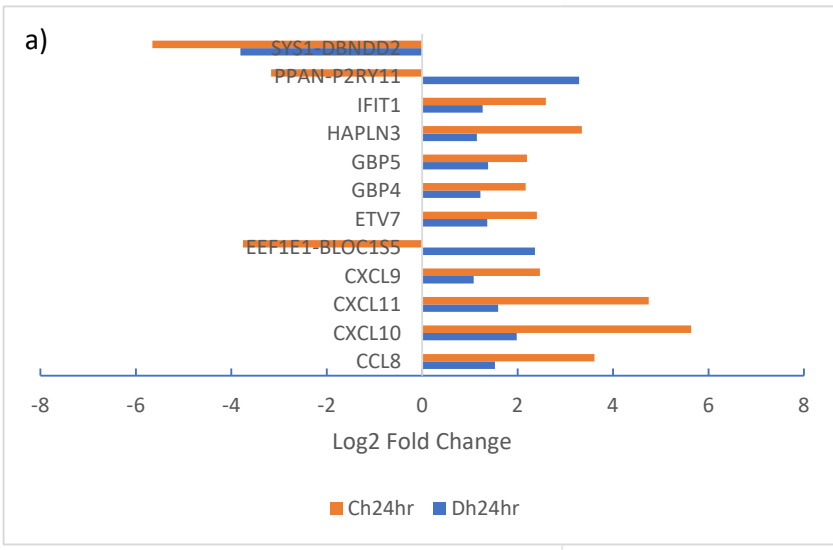
157 **Supplementary figure S6.** Characterization of HAM populations using CyTOF. Isolated HAMs,
 158 not yet infected with *M.tb* as well as uninfected and *M.tb*-infected HAMs cultured for 1 and 3 days
 159 were fixed, cryopreserved and subsequently stained for CyTOF analysis. a) The gating strategy
 160 applied to normalized and deconvoluted data to define CD11b and CD11c expressing HAM
 161 populations. b) Pie charts indicating the percentage of the HAM subsets (included in the two
 162 rectangular gates) of the total number of cells.



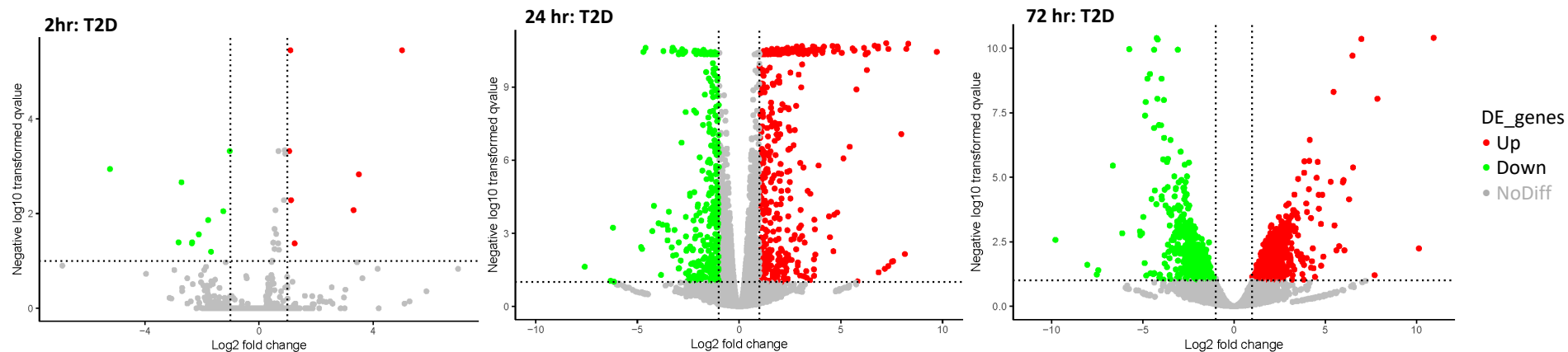
Supplementary figure S7. Characterization of cultured MDMs using flow cytometry. Uninfected and *M.tb*-infected MDMs were cultured for 1 (D1) and 3 (D3) days. At each time point, cells were stained for flow cytometric analysis. MDMs were classified as CD11b⁺CD11c⁺ cells and the frequency expressing different cell surface markers assessed at both time points. Data are presented as medians with interquartile ranges.



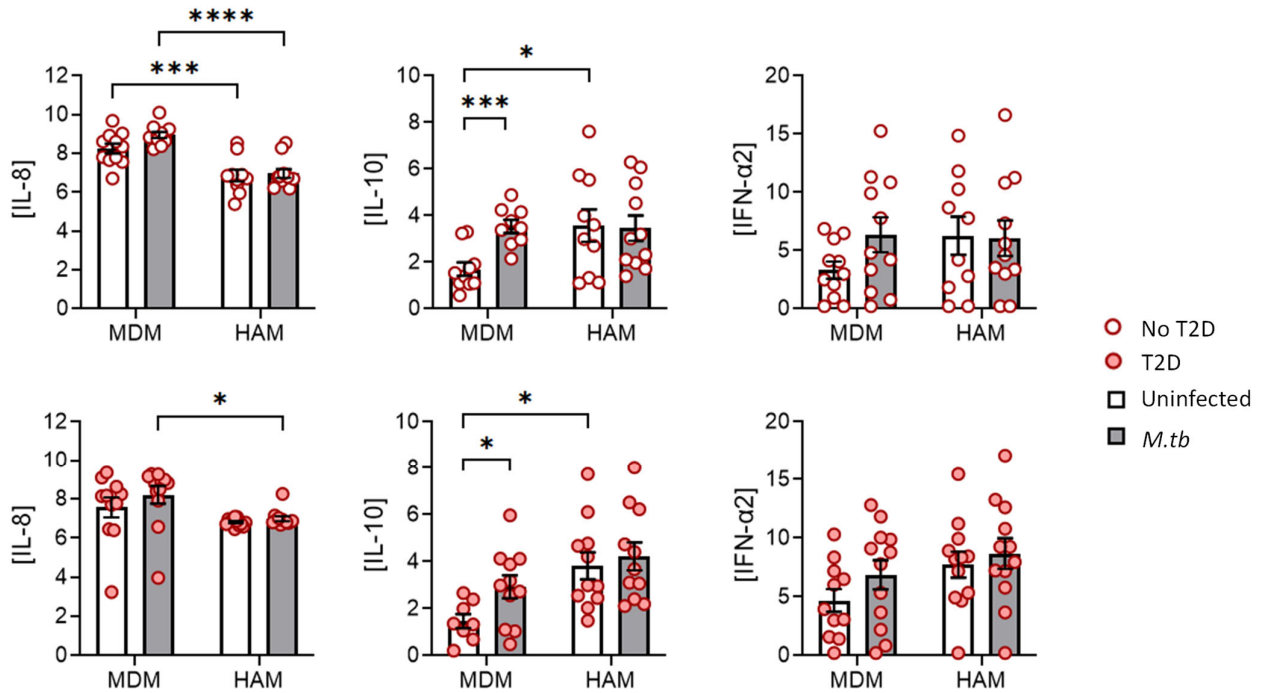
Supplementary figure S8. Lists of genes commonly expressed in HAMs between culture time points. a) Upon assessing the number of DEGs between uninfected and *M.tb*-infected HAMs, 65 genes were found to be co-expressed in HAMs of no T2D controls cultured for 1 and 3 days. b) Ten genes were co-expressed in HAMs from T2D patients cultured for 1 and 3 days.



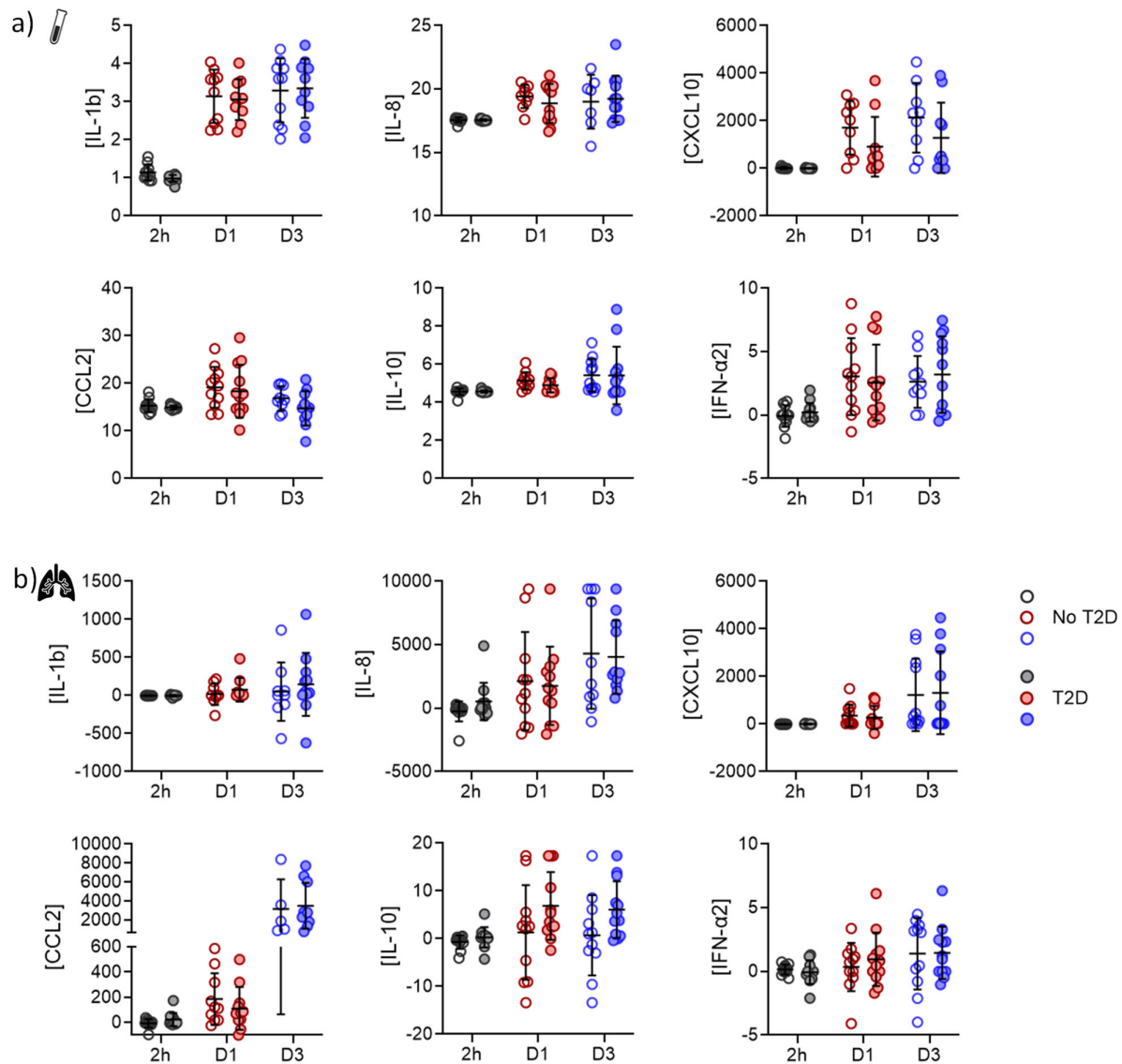
174 **Supplementary figure S9.** Lists of genes commonly expressed between HAMs of the two patient
175 groups. Upon assessing the number of DEGs between uninfected and *M.tb*-infected HAMs, a) 12
176 genes were found to be co-expressed in HAMs of no T2D controls and T2D patients at day 1 and
177 b) 88 genes were co-expressed at day 3.



178 **Supplementary figure S10.** *M.tb*-induced alterations in gene expression in T2D MDMs closely resemble the gene expression in no T2D HAMs.
 179 Differential expression analysis of *M.tb*-infected MDMs of T2D patients compared to uninfected MDMs. Genes were deemed significantly differentially
 180 expressed based on an FDR<0.1 and log2 fold changes (LFC) of >1 or <-1. Green corresponds to genes whose expression was significantly
 181 downregulated upon *M.tb* infection and red corresponds to genes whose expression was significantly upregulated.



Supplementary figure S11. Cytokine/chemokine profiles in HAMs and MDMs. Culture supernatants from both infected and uninfected cells were collected at 2h, day 1 (shown in this figure) and 3 p.i. and the cytokine concentrations measured using the Luminex platform. The data are presented as mean±SEM.



Supplementary figure S12. Cytokine/chemokine concentrations measured in MDM and HAM culture supernatants. Culture supernatants from both infected and uninfected a) MDMs and b) HAMs were collected at 2h, day 1 and 3 p.i. and the cytokine/chemokine concentrations measured using the Luminex platform. Cytokine/chemokine concentrations measured in infected culture supernatants were corrected for the concentration measured in the uninfected samples at each time point. Data are presented as medians with interquartile ranges.

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Supplementary Table S1. Antibodies for MDM FACS analysis.

Antibody	Fluorophore	Supplier
Panel 1		
Anti-CD11b	APC-Cy7	Biolegend
Anti-CD11c	PerCP-Cy5.5	Biolegend
Anti-HLA-DR	FITC	Biolegend
Anti-CD206	APC	Biolegend
Anti-CD36	PE-Vio770	Miltenyi
Anti-CD163	PE	Ebioscience
Anti-CD86	BV421	Biolegend
Viability marker (1:100)	BV510	Biolegend
Panel 2		
Anti-CD11b	APC-Cy7	Biolegend
Anti-CD11c	PerCP-Cy5.5	Biolegend
Anti-CD16	FITC	BD bioscience
Anti-CD32	APC	BD bioscience
Anti-CD192 (CCR2)	PE-Cy7	Biolegend
Anti-CD180	PE	BD bioscience
Anti-CD64	BV421	BD bioscience
Viability marker (1:100)	BV510	Biolegend
Isotypes control		
Mouse IgG1, K	PerCP-Cy5.5	BD bioscience
Mouse IgG2a, K	FITC	BD bioscience

Supplementary Table S2. Antibodies for HAM CyTOF analysis.

Probe	Palladium (Pd)	Supplier
CD192 (CCR2)*	141Pr	Fluidigm
HLA-DR	143Nd	Fluidigm
CD8a	144Nd	Fluidigm
CD4	145Nd	Fluidigm
CD64	146Nd	Fluidigm
CD11c	147Sm	Fluidigm
CD16	148Nd	Fluidigm
CD86	150Nd	Fluidigm
CD36	152Sm	Fluidigm
TCR Va7.2	153Eu	Fluidigm
CD163	154Sm	Fluidigm
CD45RA	155Gd	Fluidigm
CD45	156Gd	Fluidigm
CD284 (TLR4)	158Gd	Fluidigm
CCR7	159Tb	Fluidigm
CD26	161Dy	Fluidigm
CD80 (B7-1)	162Dy	Fluidigm
CD161	164Dy	Fluidigm
CD209*	165Ho	Fluidigm
CD206 (MMR)	168Er	Fluidigm
CD32	169Tm	Fluidigm
CD3	170Er	Fluidigm
CD180*	171Yb	Fluidigm
CD282 (TLR2)	176Yb	Fluidigm
CD11b (Mac-1)	209Bi	Fluidigm

*Antibodies conjugated in-house with palladium labels using the X8 Maxpar conjugation kit from Fluidigm.

Supplementary Table S3. Metadata for the RNA-seq analysis with sample descriptions and group comparisons.

Sample No.	Donor type (No.)	Species (for data analysis reference genome)	Sample definition	Sample Symbol (D for diabetic or C for Control, donor number, h for ham or m for mdmd. 2/24/72 for 2/24/72h, +/- for +/- TB infected)	Group Name
13	Diabetic (D2)	human	HAM 2hr, TB	D2h.2+	Dh.2+ (7 samples: Diabetic, hAM, 2h TB infected)
21	Diabetic (D3)	human	HAM 2hr, TB	D3h.2+	
49	Diabetic (D6)	human	HAM 2hr, TB	D6h.2+	
71	Diabetic (D8)	human	HAM 2hr, TB	D8h.2+	
83	Diabetic (D9)	human	HAM 2hr, TB	D9h.2+	
95	Diabetic (D10)	human	HAM 2hr, TB	D10h.2+	
103	Diabetic (D11)	human	HAM 2hr, TB	D11h.2+	Dh.2- (8 samples: Diabetic, hAM, 2h uninfected)
14	Diabetic (D2)	human	HAM 2hr, no TB	D2h.2-	
22	Diabetic (D3)	human	HAM 2hr, no TB	D3h.2-	
50	Diabetic (D6)	human	HAM 2hr, no TB	D6h.2-	
58	Diabetic (D7)	human	HAM 2hr, no TB	D7h.2-	
72	Diabetic (D8)	human	HAM 2hr, no TB	D8h.2-	
84	Diabetic (D9)	human	HAM 2hr, no TB	D9h.2-	
96	Diabetic (D10)	human	HAM 2hr, no TB	D10h.2-	
104	Diabetic (D11)	human	HAM 2hr, no TB	D11h.2-	Dh.24+ (6 samples: Diabetic, hAM, 24h TB infected)
39	Diabetic (D5)	human	HAM 24hr, TB	D5h.24+	
51	Diabetic (D6)	human	HAM 24hr, TB	D6h.24+	
59	Diabetic (D7)	human	HAM 24hr, TB	D7h.24+	
73	Diabetic (D8)	human	HAM 24hr, TB	D8h.24+	
85	Diabetic (D9)	human	HAM 24hr, TB	D9h.24+	
97	Diabetic (D10)	human	HAM 24hr, TB	D10h.24+	Dh.24- (6 samples: Diabetic, hAM, 24h uninfected)
40	Diabetic (D5)	human	HAM 24hr, no TB	D5h.24-	
52	Diabetic (D6)	human	HAM 24hr, no TB	D6h.24-	
60	Diabetic (D7)	human	HAM 24hr, no TB	D7h.24-	
74	Diabetic (D8)	human	HAM 24hr, no TB	D8h.24-	

86	Diabetic (D9)	human	HAM 24hr, no TB	D9h.24-	
98	Diabetic (D10)	human	HAM 24hr, no TB	D10h.24-	
17	Diabetic (D2)	human	HAM 72hr, TB	D2h.72+	Dh.72+ (7 samples: Diabetic, hAM, 72h TB infected)
41	Diabetic (D5)	human	HAM 72hr, TB	D5h.72+	
61	Diabetic (D7)	human	HAM 72hr, TB	D7h.72+	
75	Diabetic (D8)	human	HAM 72hr, TB	D8h.72+	
87	Diabetic (D9)	human	HAM 72hr, TB	D9h.72+	
99	Diabetic (D10)	human	HAM 72hr, TB	D10h.72+	
107	Diabetic (D11)	human	HAM 72hr, TB	D11h.72+	
18	Diabetic (D2)	human	HAM 72hr, no TB	D2h.72-	Dh.72- (6 samples: Diabetic, hAM, 72h uninfected)
42	Diabetic (D5)	human	HAM 72hr, no TB	D5h.72-	
62	Diabetic (D7)	human	HAM 72hr, no TB	D7h.72-	
88	Diabetic (D9)	human	HAM 72hr, no TB	D9h.72-	
100	Diabetic (D10)	human	HAM 72hr, no TB	D10h.72-	
108	Diabetic (D11)	human	HAM 72hr, no TB	D11h.72-	
19	Diabetic (D2)	human	MDM 2hr, TB	D2m.2+	Dm.2+ (6 samples: Diabetic, mdm, 2h TB infected)
31	Diabetic (D4)	human	MDM 2hr, TB	D4m.2+	
53	Diabetic (D6)	human	MDM 2hr, TB	D6m.2+	
63	Diabetic (D7)	human	MDM 2hr, TB	D7m.2+	
77	Diabetic (D8)	human	MDM 2hr, TB	D8m.2+	
89	Diabetic (D9)	human	MDM 2hr, TB	D9m.2+	
20	Diabetic (D2)	human	MDM 2hr, no TB	D2m.2-	Dm.2- (5 samples: Diabetic, mdm, 2h uninfected)
32	Diabetic (D4)	human	MDM 2hr, no TB	D4m.2-	
54	Diabetic (D6)	human	MDM 2hr, no TB	D6m.2-	
78	Diabetic (D8)	human	MDM 2hr, no TB	D8m.2-	
90	Diabetic (D9)	human	MDM 2hr, no TB	D9m.2-	
33	Diabetic (D4)	human	MDM 24hr, TB	D4m.24+	Dm.24+ (3 samples: Diabetic, mdm, 24h TB infected)
45	Diabetic (D5)	human	MDM 24hr, TB	D5m.24+	
91	Diabetic (D9)	human	MDM 24hr, TB	D9m.24+	
34	Diabetic (D4)	human	MDM 24hr, no TB	D4m.24-	Dm.24- (3 samples: Diabetic, mdm, 24h uninfected)
46	Diabetic (D5)	human	MDM 24hr, no TB	D5m.24-	
92	Diabetic (D9)	human	MDM 24hr, no TB	D9m.24-	
11	Diabetic (D1)	human	MDM 72hr,TB	D1m.72+	

47	Diabetic (D5)	human	MDM 72hr, TB	D5m.72+	Dm.72+ (3 samples: Diabetic, mdm, 72h TB infected)
81	Diabetic (D8)	human	MDM 72hr, TB	D8m.72+	
12	Diabetic (D1)	human	MDM 72hr, no TB	D1m.72-	Dm.72- (3 samples: Diabetic, mdm, 72h uninfected)
48	Diabetic (D5)	human	MDM 72hr, no TB	D5m.72-	
82	Diabetic (D8)	human	MDM 72hr, no TB	D8m.72-	
109	Control, healthy (C1)	human	HAM 2hr, TB	C1h.2+	Ch.2+ (8 samples: Control healthy, hAM, 2h TB infected)
121	Control, healthy (C2)	human	HAM 2hr, TB	C2h.2+	
141	Control, healthy (C3)	human	HAM 2hr, TB	C3h.2+	
149	Control, healthy (C4)	human	HAM 2hr, TB	C4h.2+	
161	Control, healthy (C5)	human	HAM 2hr, TB	C5h.2+	
169	Control, healthy (C6)	human	HAM 2hr, TB	C6h.2+	
177	Control, healthy (C7)	human	HAM 2hr, TB	C7h.2+	
183	Control, healthy (C9)	human	HAM 2hr, TB	C9h.2+	Ch.2- (4 samples: Control healthy, hAM, 2h uninfected)
122	Control, healthy (C2)	human	HAM 2hr, no TB	C2h.2-	
142	Control, healthy (C3)	human	HAM 2hr, no TB	C3h.2-	
170	Control, healthy (C6)	human	HAM 2hr, no TB	C6h.2-	
178	Control, healthy (C7)	human	HAM 2hr, no TB	C7h.2-	Ch.24+ (5 samples: Control healthy, hAM, 24h TB infected)
111	Control, healthy (C1)	human	HAM 24hr, TB	C1h.24+	
123	Control, healthy (C2)	human	HAM 24hr, TB	C2h.24+	
143	Control, healthy (C3)	human	HAM 24hr, TB	C3h.24+	
151	Control, healthy (C4)	human	HAM 24hr, TB	C4h.24+	
163	Control, healthy (C5)	human	HAM 24hr, TB	C5h.24+	Ch.24- (5 samples: Control healthy, hAM, 24h uninfected)
112	Control, healthy (C1)	human	HAM 24hr, no TB	C1h.24-	
124	Control, healthy (C2)	human	HAM 24hr, no TB	C2h.24-	
144	Control, healthy (C3)	human	HAM 24hr, no TB	C3h.24-	
152	Control, healthy (C4)	human	HAM 24hr, no TB	C4h.24-	
164	Control, healthy (C5)	human	HAM 24hr, no TB	C5h.24-	Ch.72+ (4 samples: Control healthy, hAM, 72h TB infected)
113	Control, healthy (C1)	human	HAM 72hr, TB	C1h.72+	
125	Control, healthy (C2)	human	HAM 72hr, TB	C2h.72+	
145	Control, healthy (C3)	human	HAM 72hr, TB	C3h.72+	
181	Control, healthy (C8)	human	HAM 72hr, TB	C8h.72+	Ch.72- (4 samples: Control healthy, hAM, 72h uninfected)
114	Control, healthy (C1)	human	HAM 72hr, no TB	C1h.72-	
126	Control, healthy (C2)	human	HAM 72hr, no TB	C2h.72-	

146	Control, healthy (C3)	human	HAM 72hr, no TB	C3h.72-		
182	Control, healthy (C8)	human	HAM 72hr, no TB	C8h.72-		
115	Control, healthy (C1)	human	MDM 2hr, TB	C1m.2+	Cm.2+	(1 sample: Control healthy, mdm, 2h TB infected)
116	Control, healthy (C1)	human	MDM 2hr, no TB	C1m.2-	Cm.2-	(1 sample: Control healthy, mdm, 2h uninfected)

Group of comparisons (B vs A meaning A is the control)	
Dh.2- vs Ch.2-	
Dm.2- vs Cm.2-	
Dh.2+ vs Dh.2-	
Dh.24+ vs Dh.24-	
Dh.72+ vs Dh.71-	
Ch.2+ vs Ch.2-	
Ch.24+ vs Ch.24-	
Ch.72+ vs Ch.71-	
Dm.2+ vs Dm.2-	
Dm.24+ vs Dm.24-	
Dm.72+ vs Dm.71-	
Cm.2+ vs Cm.2-	

Supplementary Table S4. Relationship between host characteristics and *M.tb* association (2h p.i.) and control (Day 3 CFU fold growth) in monocyte-derived macrophages (MDMs) and human alveolar macrophages (HAMs).

	MDMs		HAMs	
	Spearman r	p-value	Spearman r	p-value
2 hr				
BMI (kg/m ²)	0,1947	0,3733	0,1468	0,5038
HbA1c (%)	-0,2437	0,2624	-0,3171	0,1403
Total CHL (mmol/L)	0,2763	0,2020	0,1972	0,3670
Triglycerides (mmol/L)	0,2228	0,3069	0,1454	0,5079
HDL (mmol/L)	-0,1417	0,5191	-0,0903	0,6821
LDL (mmol/L)	0,3632	0,0885	0,3213	0,1349
Insulin (mIU/L)	-0,1035	0,6733	0,1370	0,5761
Cortisol (nmol/L)	-0,0831	0,7133	-0,1113	0,6218
Day 3 (fold-growth)				
BMI (kg/m ²)	-0,2836	0,2009	0,1105	0,6524
HbA1c (%)	-0,2353	0,2918	-0,0756	0,7585
Total CHL (mmol/L)	-0,2108	0,3343	0,1838	0,4012
Triglycerides (mmol/L)	-0,1327	0,5462	-0,0242	0,1911
HDL (mmol/L)	0,4053	0,0550	0,2827	0,1911
LDL (mmol/L)	0,0009	0,9968	0,0079	0,9714
Insulin (mIU/L)	0,3171	0,1859	0,0403	0,8697
Cortisol (nmol/L)	-0,0600	0,7910	0,1423	0,5275

P<0.05 was considered statistically significant.

BMI – body mass index, CHL – cholesterol, HDL – high-density lipoprotein, LDL – low-density lipoprotein

Supplementary Table S5. Differentially expressed genes in HAMs of no T2D controls 2h p.i. with *M.tb*.

Name	Chromosome	Region	Identifier	Ch.2+ vs. Ch.2- Max group means	Ch.2+ vs. Ch.2- Fold change	Ch.2+ vs. Ch.2- Log fold change	Ch.2+ vs. Ch.2- P-value	Ch.2+ vs. Ch.2- FDR p-value
Upregulated genes (8)								
gene:ENSG00000276612	21	complement (5116343..5133805)	ENSG00000276612	0.551295236	248.2235852	7.955496391	0.000202569	0.058402209
gene:ENSG00000205236	7	complement (102582523..102642869)	ENSG00000205236	0.073227114	19.45095289	4.281768928	0.000220967	0.061346962
gene:ENSG00000288684	9	complement (32455323..32552603)	ENSG00000288684	0.529520804	6.764609347	2.758006622	4.84944E-05	0.024234266
gene:ENSG00000203546	14	complement (31334312..31457441)	ENSG00000203546	0.273184332	3.815115011	1.93172655	1.23375E-06	0.000973491
BSCL2	11	complement (62689289..62709845)	ENSG00000168000	3.023635442	2.657123696	1.409865391	2.33361E-13	3.49855E-09
gene:ENSG00000144785	12	complement (56285916..56316059)	ENSG00000144785	3.950587755	2.472871571	1.306187315	5.24856E-10	2.62288E-06
MT1B	16	56651886..56653204	ENSG00000169688	6.628713146	2.43147769	1.281833354	1.14722E-06	0.000955503
KYAT1	9	complement (128832942..128882494)	ENSG00000171097	0.731012239	2.165810069	1.114906731	0.000422073	0.098870657
Downregulated genes (7)								
PDCD6-AHRR	5	271670..438291	ENSG00000288622	0.203082011	-25.87701661	-4.693599392	2.17799E-07	0.00029684
PPAN-P2RY11	19	10106223..10114780	ENSG00000243207	0.529655583	-5.243175623	-2.39044087	8.37152E-07	0.00089647
NPIP8	16	28637654..28658744	ENSG00000255524	0.471782064	-3.844717456	-1.94287758	0.000342851	0.087790888
UPK3BL1	7	complement (102637025..102642791)	ENSG00000267368	2.562209508	-3.453953076	-1.788248483	0.000134854	0.047971839
gene:ENSG00000271793	6	complement (85504776..85678733)	ENSG00000271793	0.156084941	-3.071547727	-1.618965801	0.000279816	0.074092213
FRK	6	complement (115931149..116060891)	ENSG00000111816	0.077461126	-2.935950141	-1.553827468	0.000281701	0.074092213
gene:ENSG00000285238	12	complement (6556886..6607367)	ENSG00000285238	3.025762064	-2.371867428	-1.246023375	6.79587E-07	0.000783721

C: control; h: HAM; 2: 2 hr p.i.; +: *M.tb* infected; -: *M.tb* uninfected

Supplementary Table S6. Differentially expressed genes in HAMs of no T2D controls 1 day p.i. with *M.tb.*

Name	Chromosome	Region	Identifier	Ch.24+ vs.	Ch.24+ vs.	Ch.24+ vs.	Ch.24+ vs.	Ch.24+ vs.
				Ch.24- Max group means				
Upregulated genes (144)								
		complement (155763043..155854442						
gene:ENSG00000284952	3	)	ENSG00000284952	0.133393851	88.29728287	6.464297138	0.00106624	0.025007872
H2AC19	1	149851061..149851624	ENSG00000272196	0.657932658	60.03645418	5.907766867	0.00403651	0.070132563
		complement						
CXCL10	4	(76021118..76023497)	ENSG00000169245	62.80218953	49.83852498	5.639189466	3.29538E-36	4.81521E-32
		complement						
gene:ENSG00000286192	7	(1815804..2242215)	ENSG00000286192	0.090166313	28.8250714	4.849252276	4.26757E-05	0.001717843
		complement						
CXCL11	4	(76033682..76041415)	ENSG00000169248	4.640550124	26.90370125	4.749732759	6.48941E-25	1.18529E-21
		complement						
gene:ENSG00000272897	20	(35632340..35674544)	ENSG00000272897	1.371621227	21.25633509	4.409820971	2.07481E-08	2.21293E-06
FAM72D	1	145095974..145112696	ENSG00000215784	0.264022142	18.45718639	4.20611074	7.07343E-06	0.000355179
SAPCD1	6	31762996..31764851	ENSG00000228727	0.25204942	16.43401932	4.038613463	0.001423801	0.031673323
UBE2F-SCLY	2	237967014..238099412	ENSG00000258984	0.285905029	13.24701494	3.727595397	2.10982E-06	0.000128693
CCL8	17	34319435..34321402	ENSG00000108700	9.032362663	12.23842508	3.61334601	5.16389E-21	5.31415E-18
		complement						
CBSL	21	(6444869..6468040)	ENSG00000274276	0.220665295	11.99566774	3.584441563	0.002361106	0.046474466
gene:ENSG00000249590	22	30409255..30428990	ENSG00000249590	0.157786742	11.48863714	3.52213576	0.004530129	0.075433306
GOLGA6D	15	75282835..75295807	ENSG00000140478	0.155743176	11.12996655	3.476377352	0.000287005	0.008523817
APOBEC3A	22	38952741..38992778	ENSG00000128383	2.403681064	10.26991805	3.360352764	2.33005E-11	4.53956E-09
		complement						
C1QTNF3-AMACR	5	(33987174..34124528)	ENSG00000273294	0.148377956	10.26921117	3.36025346	0.00025818	0.007892306
		complement						
HAPLN3	15	(88877294..88895597)	ENSG00000140511	1.413738964	10.18847323	3.348865971	1.40542E-12	3.31227E-10
		complement						
gene:ENSG00000263620	17	(8150816..8162975)	ENSG00000263620	0.599984078	9.887674891	3.305631308	0.003337771	0.060510557

TNFRSF6B	20 63696652..63698684 complement	ENSG00000243509	0.315485374	9.150812957	3.193899918	0.001002997	0.023714865
gene:ENSG00000267120	19 (35739252..35745432) complement (172505508..172523475	ENSG00000267120	0.273628113	8.71412651	3.123356058	0.000151254	0.005000275
TNFSF10	3)	ENSG00000121858	4.702352862	7.320083679	2.871860141	7.07722E-16	3.6933E-13
PDGFRL	8 17576433..17644071	ENSG00000104213	0.264214444	7.258087186	2.859589387	0.000487764	0.013200585
ISG20	15 88635670..88656483	ENSG00000172183	8.883612928	6.540793371	2.709465639	1.80396E-32	1.31797E-28
IFIT1	10 89392546..89406487	ENSG00000185745	27.13228006	6.029845577	2.592121055	9.99951E-11	1.73944E-08
OR2I1P	6 29550407..29557721	ENSG00000237988	0.046957446	5.93071589	2.568206261	0.001820455	0.038495648
ACOD1	13 76948511..76958638 complement	ENSG00000102794	2.353768539	5.540075476	2.469905631	4.00375E-12	9.14106E-10
CXCL9	4 (76001275..76007509) complement	ENSG00000138755	1.942540835	5.531615288	2.467700824	1.96572E-08	2.11199E-06
IFNG	12 (68154768..68159740) complement	ENSG00000111537	0.845467076	5.45887354	2.448603276	8.2126E-05	0.002955726
ANKRD22	10 (88819896..88851844) complement	ENSG00000152766	1.533040157	5.445960989	2.445186648	1.81947E-13	5.77959E-11
ETV7	6 (36354091..36387800)	ENSG00000010030	1.725750727	5.297517435	2.405316431	2.16005E-20	1.75348E-17
NEXN	1 77888513..77943895	ENSG00000162614	4.221094149	5.247002851	2.391493574	8.43919E-17	4.74283E-14
IFI44L	1 78619902..78646145	ENSG00000137959	9.95257337	5.20741575	2.380567593	3.99024E-08	3.93956E-06
MX1	21 41420020..41470071 complement	ENSG00000157601	63.58998135	4.741232555	2.245262158	5.4657E-13	1.40114E-10
SIK1	21 (43414483..43427131) complement	ENSG00000142178	0.219360028	4.730565671	2.242012708	0.001959553	0.040671856
GBP5	1 (89258950..89272804) complement	ENSG00000154451	9.347391218	4.580766147	2.195588914	1.04208E-08	1.1896E-06
GBP4	1 (89181144..89198942) complement	ENSG00000162654	13.56487241	4.499958625	2.169911737	3.93303E-31	1.91565E-27
HESX1	3 (57197838..57227606) complement	ENSG00000163666	1.387571101	4.336157196	2.116417059	2.60866E-06	0.000150185
TRIL	7 (28953358..28958330)	ENSG00000255690	0.078918519	4.288984102	2.100635968	0.00578037	0.08994969

	complement							
EPSTI1	13 (42886388..42992271)	ENSG00000133106	17.958443	4.168879016	2.059659505	7.4863E-26	1.82316E-22	
CCL13	17 34356480..34358610	ENSG00000181374	1.566283112	4.126712243	2.044992842	1.25203E-05	0.000593985	
IDO1	8 39902275..39928790	ENSG00000131203	10.39992456	4.053319468	2.019103888	3.29293E-25	6.87376E-22	
	complement							
CMPK2	2 (6840570..6866635)	ENSG00000134326	16.26845357	4.051796791	2.018561821	8.55502E-13	2.11875E-10	
IFIT2	10 89283694..89309271	ENSG00000119922	53.51508963	4.045272551	2.016236908	1.11397E-15	5.39843E-13	
	complement							
HELZ2	20 (63558086..63574239)	ENSG00000130589	9.51684186	4.026743285	2.0096135	1.33276E-20	1.21715E-17	
	complement							
GBP7	1 (89131742..89176009)	ENSG00000213512	0.771569607	4.012001163	2.004322024	1.10425E-09	1.60876E-07	
NNMT	11 114257787..114313536	ENSG00000166741	0.245907229	3.904710033	1.965215417	0.003291441	0.059893566	
	complement							
BATF2	11 (64987945..64997018)	ENSG00000168062	6.600997934	3.88959468	1.959619825	1.06523E-26	3.11304E-23	
XAF1	17 6755447..6775647	ENSG00000132530	19.46154051	3.881538561	1.95662862	9.88361E-22	1.11092E-18	
USP18	22 18150170..18177397	ENSG00000184979	23.90617084	3.857020357	1.94748676	3.39451E-10	5.45061E-08	
ISG15	1 1001138..1014540	ENSG00000187608	162.3822301	3.824498153	1.935270451	7.62771E-20	5.86611E-17	
C1S	12 6988259..7071032	ENSG00000182326	3.089980039	3.819176569	1.93326162	4.54502E-24	6.64119E-21	
	complement							
IL27	16 (28499362..28512051)	ENSG00000197272	4.329770792	3.818625825	1.933053562	6.40814E-14	2.2838E-11	
IFIT3	10 89327307..89377473	ENSG00000119917	61.96065856	3.778485652	1.917808144	4.17532E-22	5.08415E-19	
RSAD2	2 6865557..6898239	ENSG00000134321	34.6586787	3.767492559	1.913604662	1.22856E-07	1.00853E-05	
	complement							
TRIM31	6 (30102897..30113090)	ENSG00000204616	0.154721782	3.74239465	1.903961704	0.004137301	0.071122632	
FBXO40	3 121593379..121630295	ENSG00000163833	0.044141113	3.651021227	1.868300057	0.004976882	0.081163163	
	complement							
AMT	3 (49416778..49422685)	ENSG00000145020	0.170646498	3.531321566	1.820208201	0.001872083	0.039302985	
	complement							
CCL14	17 (35983288..35987004)	ENSG00000276409	0.098722331	3.502116747	1.808227178	0.003900289	0.068383084	
MX2	21 41361999..41409393	ENSG00000183486	13.39512094	3.392177002	1.762211451	1.63615E-07	1.30641E-05	
	complement							
SIGLEC1	20 (3686970..3712600)	ENSG00000088827	24.88285898	3.382583437	1.758125521	1.91646E-11	3.83607E-09	

	complement							
TMEM150C	4 (82483170..82562357)	ENSG00000249242	0.083421914	3.379411079	1.756771854	0.003519476	0.063255323	
IFITM1	11 310041..315272	ENSG00000185885	1.131149187	3.376573235	1.755559849	2.262E-05	0.000995551	
RSPO3	6 127118671..127199481	ENSG00000146374	0.980263277	3.376099877	1.755357585	1.35279E-09	1.90067E-07	
IFI44	1 78649796..78664078	ENSG00000137965	39.65961671	3.312274562	1.727822266	5.25806E-13	1.39263E-10	
CTRC	1 15438442..15449242	ENSG00000162438	0.10038898	3.293639723	1.719682754	0.004439226	0.074558587	
STAP1	4 67558727..67607337	ENSG00000035720	1.621360454	3.267851057	1.708342229	0.000190841	0.006169402	
	complement							
ZBP1	20 (57603846..57620576)	ENSG00000124256	1.039250465	3.232713277	1.692745554	6.34764E-08	5.86597E-06	
CALHM6	6 116461370..116463771	ENSG00000188820	4.213241361	3.086333435	1.625893933	0.000116687	0.004011839	
VAMP5	2 85584431..85593406	ENSG00000168899	22.6027922	3.082169893	1.623946387	2.02875E-13	6.17584E-11	
	complement							
	(159062484..159147096							
AIM2	1)	ENSG00000163568	6.502567835	3.07831272	1.6221398	7.80698E-16	3.93364E-13	
	complement							
C1R	12 (7080214..7092540)	ENSG00000159403	0.882042152	3.068187607	1.6173867	9.73027E-08	8.36345E-06	
	complement							
GCH1	14 (54842008..54902826)	ENSG00000131979	15.61963065	3.009402784	1.589477213	3.41212E-09	4.33547E-07	
	complement							
IFITM3	11 (319676..329475)	ENSG00000142089	35.14490424	3.008864565	1.58921917	5.3372E-13	1.39263E-10	
	complement							
GBP1	1 (89051882..89065360)	ENSG00000117228	101.1965331	2.994154153	1.5821485	5.38982E-15	2.31635E-12	
FCRL6	1 159800511..159816257	ENSG00000181036	0.503157423	2.986042424	1.578234663	4.62258E-05	0.00181086	
GIMAP8	7 150450630..150479393	ENSG00000171115	1.817143579	2.933250465	1.552500265	6.22936E-14	2.27558E-11	
OAS2	12 112978395..113011723	ENSG00000111335	30.76299521	2.913462652	1.542734817	2.00973E-13	6.17584E-11	
	complement							
RCAN2	6 (46220736..46491972)	ENSG00000172348	0.921865225	2.883477714	1.527809872	7.88401E-07	5.53852E-05	
OAS3	12 112938051..112976460	ENSG00000111331	26.56670023	2.833951597	1.502815118	1.89257E-10	3.17864E-08	
	complement							
DDX58	9 (32455302..32526208)	ENSG00000107201	12.58762404	2.819736621	1.495560413	5.94081E-11	1.07169E-08	
	complement							
XIRP1	3 (39183210..39192596)	ENSG00000168334	0.126804744	2.805011332	1.488006599	0.005019415	0.08138454	

	complement							
IRF7	11 (612553..615983)	ENSG00000185507	29.19598667	2.772384021	1.471127109	5.45526E-21	5.31415E-18	
	complement							
CCL15	17 (35996440..36001553)	ENSG00000275718	19.32061683	2.768023373	1.468856125	1.27401E-06	8.27371E-05	
	complement							
APOL3	22 (36140330..36166177)	ENSG00000128284	5.749211119	2.707055705	1.436724575	1.69421E-19	1.17885E-16	
	complement							
	(190908460..191020960							
STAT1	2)	ENSG00000115415	57.18211787	2.704910797	1.435581018	2.84572E-22	3.78015E-19	
	complement							
	(139390592..139395104							
PROB1	5)	ENSG00000228672	0.108178358	2.686630599	1.42579797	0.004556397	0.075656896	
	complement							
EXOC3L1	16 (67184379..67190185)	ENSG00000179044	0.352749806	2.679428721	1.421925437	0.00023547	0.007399329	
HERC5	4 88457119..88506163	ENSG00000138646	20.28466003	2.672112258	1.417980618	1.92806E-08	2.08687E-06	
CCL17	16 57404767..57416063	ENSG00000102970	2.320869918	2.663415159	1.413277326	0.001213628	0.027882907	
	complement							
ITIH4	3 (52812962..52830688)	ENSG00000055955	0.963785695	2.64631705	1.403985919	3.58743E-07	2.68818E-05	
	complement							
CH25H	10 (89205629..89207317)	ENSG00000138135	1.88593253	2.616406083	1.387586474	2.82483E-05	0.001210453	
CCL4L2	17 36210924..36212878	ENSG00000276070	126.6487646	2.586662639	1.371091905	0.000957481	0.023048955	
	complement							
STIMATE-MUSTN1	3 (52833121..52897562)	ENSG00000248592	2.430333237	2.568557835	1.360958559	0.000140763	0.00469594	
	complement							
SECTM1	17 (82321024..82334074)	ENSG00000141574	10.20428055	2.539028476	1.344276575	3.60627E-11	6.84347E-09	
	complement							
	(168216291..168318883							
DDX60	4)	ENSG00000137628	4.028235718	2.527885218	1.337930957	4.81216E-18	3.05718E-15	
	complement							
UBD	6 (29555515..29559732)	ENSG00000213886	2.709361687	2.50345082	1.323918114	6.76284E-05	0.002501738	
PSMB9	6 32844136..32859851	ENSG00000240065	96.83705753	2.486643863	1.3141999	1.57247E-24	2.553E-21	
IFI35	17 43006740..43014456	ENSG00000068079	93.39061517	2.48074864	1.310775563	1.53147E-27	5.59448E-24	
ANXA3	4 78551747..78610451	ENSG00000138772	0.371561804	2.467033512	1.302777313	0.005408103	0.086081926	

TMEM171	5 73120569..73131809 complement	ENSG00000157111	1.015402187	2.456795019	1.296777492	0.000663014	0.017029393
TAP1	6 (32845209..32853816) complement	ENSG00000168394	107.2632997	2.443304434	1.288833633	2.03739E-20	1.7512E-17
PLEKHA4	19 (48837097..48868617) complement	ENSG00000105559	1.864216509	2.438400213	1.285934934	1.25747E-08	1.39198E-06
IL15RA	10 (5943639..5978187)	ENSG00000134470	5.824781875	2.423605421	1.277154838	9.9536E-20	7.2721E-17
TNFAIP6	2 151357592..151380046 complement	ENSG00000123610	108.691453	2.413185932	1.270939077	0.001126392	0.02612515
NEURL3	2 (96497646..96508109)	ENSG00000163121	0.924296246	2.405530774	1.266355256	7.02377E-05	0.002572215
HERC6	4 88378739..88443097	ENSG00000138642	6.002293928	2.400037422	1.263056901	4.55894E-13	1.2456E-10
STON1	2 48529383..48598513 complement	ENSG00000243244	1.447742645	2.398879537	1.262360712	6.59038E-08	5.94436E-06
CCL1	17 (34360328..34363233)	ENSG00000108702	5.162197428	2.360284944	1.238961039	0.001435937	0.031812689
NLRC5	16 56989485..57083531 complement	ENSG00000140853	4.623732159	2.344264148	1.229135139	1.67957E-17	1.02258E-14
SAMD9L	7 (93130056..93148385) complement	ENSG00000177409	27.55764647	2.342216546	1.227874464	1.4943E-14	5.90128E-12
MEFV	16 (3242027..3256633)	ENSG00000103313	1.131043043	2.312370042	1.209372287	4.36403E-07	3.18836E-05
SGIP1	1 66533267..66751139	ENSG00000118473	0.042294082	2.309927539	1.207847596	0.006527439	0.098025628
SLAMF7	1 160739057..160754821	ENSG00000026751	49.66667079	2.279021694	1.188414657	4.16545E-09	5.11475E-07
gene:ENSG00000284057	11 93741664..93812378 complement	ENSG00000284057	1.975848621	2.259572165	1.176049634	4.17857E-08	4.07048E-06
DHX58	17 (42101404..42112714) complement (162267074..162318684	ENSG00000108771	7.59651013	2.250367846	1.170160844	2.08585E-17	1.21913E-14
IFIH1	2) complement	ENSG00000115267	31.24539014	2.249647373	1.16969888	4.1003E-13	1.15218E-10
MCOLN2	1 (84925583..84997113)	ENSG00000153898	0.915860428	2.244206326	1.166205319	3.05201E-05	0.001303978
CCL4	17 36103827..36105621 complement	ENSG00000275302	383.349054	2.22820268	1.155880468	0.006240249	0.094685894
APOL4	22 (36189124..36204840)	ENSG00000100336	5.974057884	2.228160667	1.155853265	1.97152E-07	1.55718E-05
C4A	6 31982057..32002681	ENSG00000244731	0.51575197	2.221588086	1.151591345	6.30898E-05	0.002363764

TNFSF13B	13	108251240..108308484	ENSG00000102524	17.31771409	2.220289927	1.150748077	2.39894E-13	7.01068E-11
CIITA	16	10866222..10943021	ENSG00000179583	4.57103909	2.207032886	1.142108127	1.01625E-09	1.49994E-07
LAP3	4	17577198..17607972	ENSG00000002549	162.287691	2.195711393	1.134688437	1.01139E-16	5.47349E-14
		complement						
CD69	12	(9752486..9760901)	ENSG00000110848	0.863619404	2.188881535	1.130193876	0.000364542	0.010424053
RTP4	3	187368385..187372076	ENSG00000136514	6.374604513	2.184712607	1.12744351	7.37973E-14	2.50773E-11
		complement						
		(122527924..122564577						
PARP9	3	)	ENSG00000138496	22.25832596	2.181025507	1.125006643	7.18036E-15	2.91443E-12
FBXO6	1	11664200..11674354	ENSG00000116663	27.16847696	2.1610225	1.111714093	4.88611E-19	3.24527E-16
		complement						
JAK3	19	(17824780..17848071)	ENSG00000105639	0.369384243	2.15728853	1.109219145	1.17649E-05	0.000563633
GMPR	6	16238587..16295549	ENSG00000137198	17.21283563	2.127559444	1.089199441	6.45288E-08	5.89309E-06
		complement						
		(139448560..139462743						
ECSCR	5	)	ENSG00000249751	7.405064329	2.100191383	1.070520802	1.49486E-06	9.49688E-05
CCL2	17	34255218..34257203	ENSG00000108691	105.6951374	2.085261919	1.060228605	2.19159E-13	6.53542E-11
gene:ENSG00000285816	11	65261928..65326543	ENSG00000285816	0.930991328	2.078316596	1.055415441	6.80534E-06	0.000344082
IL15	4	141636583..141733987	ENSG00000164136	1.152821514	2.075330203	1.0533409	6.66119E-12	1.42588E-09
ITK	5	157142933..157255185	ENSG00000113263	0.514711441	2.05932397	1.042170811	0.000582443	0.015252079
		complement						
PSTPIP2	18	(45983536..46072272)	ENSG00000152229	13.11274943	2.045842319	1.032694955	2.90731E-06	0.000162952
		complement						
CCL3L1	17	(36194869..36196758)	ENSG00000276085	250.0432597	2.031905458	1.022833277	0.004213233	0.071934738
		complement						
CYP27B1	12	(57762334..57768986)	ENSG00000111012	3.252820986	2.026824731	1.019221338	5.30435E-06	0.000277804
		complement						
		(230165186..230225729						
SP110	2	)	ENSG00000135899	9.953133088	2.026671631	1.019112357	6.89046E-14	2.39722E-11
		complement						
		(100333790..100376805						
WARS1	14	)	ENSG00000140105	175.7686729	2.020704824	1.014858595	3.95575E-13	1.13336E-10
HS3ST3B1	17	14301081..14349404	ENSG00000125430	1.863629264	2.016338003	1.011737501	2.45672E-05	0.001072949

	complement						
NT5C3A	7 (33014130..33062796)	ENSG00000122643	21.9721045	2.010895356	1.007838008	2.72457E-08	2.86413E-06
TRIM22	11 5689697..5737089	ENSG00000132274	30.08608233	2.009055404	1.00651735	2.0528E-15	9.37358E-13
FPR2	19 51752026..51770531	ENSG00000171049	3.825878541	2.006850227	1.004932951	3.95857E-09	4.98644E-07
	complement						
GBP2	1 (89106132..89150456)	ENSG00000162645	29.06386412	2.004502762	1.003244405	4.31929E-10	6.78639E-08
NCF1	7 74773962..74789376	ENSG00000158517	170.5080842	2.002127655	1.001533963	1.00186E-06	6.8407E-05
Downregulated genes (43)							
gene:ENSG00000268173	19 18153158..18178117	ENSG00000268173	0.12746664	-119.720386	-6.903525025	0.000213444	0.006809713
SYS1-DBNDD2	20 45363200..45410610	ENSG00000254806	0.184319904	-50.32292838	-5.653143973	0.002603021	0.04933249
	complement						
C16orf46	16 (81053497..81077267)	ENSG00000166455	0.100532987	-43.79717251	-5.452765829	0.0029971	0.055788049
PDCD6-AHRR	5 271670..438291	ENSG00000288622	0.264963919	-28.764301	-4.846207507	1.65702E-10	2.8154E-08
	complement						
OR2A4	(131699644..131701401 6)	ENSG00000180658	0.51892578	-19.5060684	-4.285851116	2.70364E-05	0.001165355
	complement						
URGCP-MRPS24	7 (43866558..43906589)	ENSG00000270617	0.517544414	-18.47937859	-4.207844339	0.000301729	0.008906788
FCER1A	1 159289714..159308224	ENSG00000179639	0.215386795	-18.10971233	-4.178691724	0.002339938	0.046266806
	complement						
gene:ENSG00000285953	7 (92131774..92245924)	ENSG00000285953	0.434282883	-15.55260159	-3.959084024	2.63092E-05	0.001137367
gene:ENSG00000257921	12 57772660..57797554	ENSG00000257921	0.564247353	-14.49425732	-3.857409507	1.96034E-11	3.87088E-09
	complement						
EEF1E1-BLOC1S5	6 (8015726..8102530)	ENSG00000265818	0.714704276	-13.52197107	-3.757233561	5.66422E-05	0.002135504
gene:ENSG00000284292	7 99325879..99394653	ENSG00000284292	1.619933492	-12.79510488	-3.677520068	1.153E-07	9.5725E-06
PPAN-P2RY11	19 10106223..10114780	ENSG00000243207	0.503407933	-8.961097516	-3.163675438	0.000284731	0.008490799
gene:ENSG00000285446	6 116399395..116463696	ENSG00000285446	0.590913653	-8.627167696	-3.108887	0.000609239	0.015784039
	complement						
SLC40A1	(189560590..189583758 2)	ENSG00000138449	0.069149299	-6.879271544	-2.782255804	0.001036677	0.02443214
	complement						
KLF1	19 (12884422..12887201)	ENSG00000105610	0.11118697	-6.133469638	-2.616703422	0.004454487	0.074729

	complement (118133377..118152888						
SCN4B	11)	ENSG00000177098	0.049103058	-5.895200587	-2.559540902	0.00386123	0.06797625
	complement						
AMIGO3	3 (49716829..49719684)	ENSG00000176020	0.257526295	-4.767083049	-2.253106759	0.000200708	0.006445592
	complement						
gene:ENSG00000288684	9 (32455323..32552603)	ENSG00000288684	0.522711185	-4.369555671	-2.127486583	0.000642999	0.016570559
	complement						
gene:ENSG00000284969	11 (33698261..33722467)	ENSG00000284969	1.603105809	-4.199113462	-2.070084771	0.003112417	0.057205828
	complement						
SELENOP	5 (42799880..42887392)	ENSG00000250722	1.499013891	-3.710078865	-1.891449855	1.0669E-07	9.01131E-06
	complement						
FNDG5	1 (32862268..32872482)	ENSG00000160097	0.441878841	-3.574916576	-1.837909576	3.66462E-06	0.000196866
HAMP	19 35280716..35285143	ENSG00000105697	0.934643591	-3.35771282	-1.747478844	0.00091709	0.022260003
TMEM37	2 119429901..119438504	ENSG00000171227	0.985328546	-3.317960145	-1.730296557	4.72293E-07	3.43341E-05
PCSK9	1 55039447..55064852	ENSG00000169174	0.174342187	-2.943409629	-1.557488333	0.006016609	0.092433325
	complement (111499429..111503633						
ADORA3	1)	ENSG00000282608	1.456768273	-2.870528838	-1.52131655	6.87015E-06	0.000346161
gene:ENSG00000249319	7 66087761..66152277	ENSG00000249319	1.912131266	-2.693545827	-1.429506611	0.000325327	0.009488373
	complement						
ADAMTS1	21 (26835755..26845409)	ENSG00000154734	0.933658253	-2.655242979	-1.408843887	2.77409E-10	4.60626E-08
	complement						
ANGPT4	20 (869900..916334)	ENSG00000101280	0.866184781	-2.574001416	-1.364012847	1.18613E-05	0.000566399
	complement (129645259..129654956						
APLN	X)	ENSG00000171388	0.531562116	-2.54518166	-1.347768631	0.000446211	0.012301957
CEACAM3	19 41796587..41811554	ENSG00000170956	0.541425101	-2.510644371	-1.328057687	0.001616114	0.034778584
ADAMTS15	11 130448645..130476645	ENSG00000166106	1.379049892	-2.486127106	-1.313900058	1.74338E-13	5.66093E-11
TLCD4	1 95117355..95197607	ENSG00000152078	0.180968569	-2.473959981	-1.306822164	0.000379964	0.010759767
ADCY1	7 45574140..45723116	ENSG00000164742	0.833372379	-2.470767964	-1.30495953	1.09401E-12	2.66428E-10
	complement						
MRO	18 (50795120..50825402)	ENSG00000134042	0.158240635	-2.432736596	-1.282580121	0.004349651	0.073561453

complement								
gene:ENSG00000283189	3	(49416777..49429314)	ENSG00000283189	0.763214384	-2.407593115	-1.267591596	0.000139179	0.00465374
MERTK	2	111898607..112029561	ENSG00000153208	1.997927851	-2.243136404	-1.165517353	4.30163E-10	6.78639E-08
FBLIM1	1	15756607..15786594	ENSG00000162458	0.195297092	-2.233731426	-1.159455733	0.006067541	0.092836554
complement								
gene:ENSG00000261611	16	(71447600..71489311)	ENSG00000261611	0.244004545	-2.083473222	-1.058990558	0.0024167	0.047209655
ADORA1	1	203090654..203167405	ENSG00000163485	0.666766169	-2.058643203	-1.041693809	0.00059855	0.015562299
complement								
(118193725..118225094								
JAML	11	)	ENSG00000160593	28.00028971	-2.021585653	-1.015487331	6.44823E-12	1.40629E-09
PRR15	7	29563835..29567293	ENSG00000176532	0.548299794	-2.014892604	-1.010702944	0.004989753	0.081282348
ADRB2	5	148826611..148828623	ENSG00000169252	0.785601777	-2.003208496	-1.002312586	0.000862067	0.02106442
GAPT	5	58491435..58497090	ENSG00000175857	1.118348454	-2.000960755	-1.000692872	3.08992E-05	0.001316322

C: control; h: HAM; 24: 24 hr p.i.; +: *M.tb* infected; -: *M.tb* uninfected

Supplementary Table S7. Differentially expressed genes in HAMs of no T2D controls 3 days p.i. with *M.tb.*

Name	Chromosome	Region	Identifier	Ch.72+ vs.	Ch.72+ vs.	Ch.72+ vs.	Ch.72+ vs.	Ch.72+ vs.
				Ch.72- Max group means				
Upregulated genes (170)								
APOBEC3A	22	38952741..38992778	ENSG00000128383	2.391490737	142.1445661	7.151215139	3.13851E-11	4.5844E-08
UBE2F-SCLY	2	237967014..238099412	ENSG00000258984	0.588012039	35.81553534	5.162513601	1.0368E-06	0.00036058
OTOF	2	complement (26457203..26558756)	ENSG00000115155	0.111657834	31.93924313	4.99725822	2.65727E-05	0.00548107
PPAN-P2RY11	19	10106223..10114780	ENSG00000243207	0.260005852	28.34496613	4.82502064	0.000195266	0.02524116
IFI44L	1	78619902..78646145	ENSG00000137959	13.9906292	25.80294506	4.689463834	3.42266E-37	4.9995E-33
CXCL11	4	complement (76033682..76041415)	ENSG00000169248	3.931193637	24.97047932	4.64215161	6.61637E-12	1.0738E-08
gene:ENSG00000261915	17	complement (7312661..7319174)	ENSG00000261915	0.479037054	23.53330535	4.556632062	4.21223E-06	0.00109872
RTEL1-TNFRSF6B	20	63659300..63698684	ENSG00000026036	0.259379246	21.38268335	4.418371006	1.17019E-05	0.00258984
gene:ENSG00000277117	21	5022493..5040666	ENSG00000277117	2.308514015	19.84477935	4.310687616	7.40565E-09	4.917E-06
RSAD2	2	6865557..6898239	ENSG00000134321	16.00564282	16.03971317	4.003576438	2.60012E-16	1.899E-12
SIGLEC1	20	complement (3686970..3712600)	ENSG00000088827	45.85060106	13.88405628	3.795357213	2.29864E-15	9.4438E-12
GRM3	7	86643909..86864879	ENSG00000198822	0.676374073	13.42805722	3.747178685	3.54422E-08	1.7852E-05
CCL15	17	complement (35996440..36001553)	ENSG00000275718	11.31565826	12.00248203	3.58526087	6.44732E-07	0.00025453
ISG20	15	88635670..88656483	ENSG00000172183	11.67377258	11.9101737	3.574122549	3.97264E-11	5.2753E-08
CXCL10	4	complement (76021118..76023497)	ENSG00000169245	15.43670373	11.27222165	3.49469998	1.57237E-08	9.5698E-06
HAPLN3	15	complement (88877294..88895597)	ENSG00000140511	1.199423991	11.24548905	3.491274498	1.35981E-07	6.4073E-05
EBI3	19	4229523..4237528	ENSG00000105246	17.66902272	11.00493193	3.460078316	2.5184E-07	0.00011496
KRT23	17	complement (40922700..40937646)	ENSG00000108244	2.464646757	10.27937873	3.361681168	1.21917E-06	0.00040673
gene:ENSG00000257767	12	111753890..111791418	ENSG00000257767	1.202415686	10.01314839	3.32382376	0.000756139	0.0673471
MINAR2	5	129748094..129766732	ENSG00000186367	0.835207074	9.881940551	3.304794377	1.28652E-05	0.00280481
TBC1D3D	17	38003976..38014902	ENSG00000274419	0.25417635	9.810361104	3.294306241	0.001128749	0.08912237

MX1	21 41420020..41470071	ENSG00000157601	58.92566613	9.254018607	3.21008	9.5765E-11	1.076E-07
CCL8	17 34319435..34321402	ENSG00000108700	2.076140726	9.246790801	3.20895275	2.3494E-06	0.00068935
	complement						
TNFSF10	3 (172505508..172523475)	ENSG00000121858	5.610957503	9.151921038	3.194074605	4.84808E-13	1.0117E-09
PTGIR	19 complement (46620468..46625089)	ENSG00000160013	3.345893786	9.021111149	3.173305144	1.70235E-06	0.00053901
N4BP3	5 178113532..178126081	ENSG00000145911	0.796671115	8.961813085	3.163790637	3.59212E-05	0.00655876
IFITM3	11 complement (319676..329475)	ENSG00000142089	55.49362729	8.937586571	3.159885311	1.29028E-13	3.1412E-10
IDO1	8 39902275..39928790	ENSG00000131203	7.792875044	8.830788437	3.142542251	6.6545E-09	4.6287E-06
PTCHD4	6 complement (47856673..48111197)	ENSG00000244694	0.030384527	8.349174802	3.061633615	0.000754405	0.0673471
C4B	6 32014795..32035418	ENSG00000224389	0.322389896	8.257145278	3.045643088	2.9624E-06	0.00083215
IFITM1	11 310041..315272	ENSG00000185885	3.075527978	8.189406857	3.033758964	3.1694E-06	0.0008735
USP18	22 18150170..18177397	ENSG00000184979	16.17522388	8.043199009	3.007769416	6.88705E-15	2.012E-11
IFIT1	10 89392546..89406487	ENSG00000185745	30.12772061	7.656465309	2.93667851	2.58611E-15	9.4438E-12
HESX1	3 complement (57197838..57227606)	ENSG00000163666	1.388203293	7.583549194	2.922873205	1.73433E-06	0.00053901
IFI6	1 complement (27666064..27672212)	ENSG00000126709	1441.857048	7.581173156	2.922421117	2.71741E-09	2.2052E-06
NEXN	1 77888513..77943895	ENSG00000162614	1.974158029	7.342435989	2.876258783	3.37774E-09	2.5968E-06
GCH1	14 complement (54842008..54902826)	ENSG00000131979	16.09649386	7.19177007	2.846346897	8.70337E-09	5.5274E-06
CMPK2	2 complement (6840570..6866635)	ENSG00000134326	10.85800812	7.077035494	2.823145155	6.99344E-13	1.2769E-09
C1QTNF1	17 79022814..79049788	ENSG00000173918	0.738731492	6.894191811	2.785381438	0.000496733	0.04935899
HELZ2	20 complement (63558086..63574239)	ENSG00000130589	7.908044446	6.838254142	2.773628041	1.61366E-10	1.6836E-07
HSH2D	19 16134028..16158575	ENSG00000196684	0.377960976	6.82415311	2.770650016	0.000138374	0.01962358
IGFBP4	17 40443450..40457725	ENSG00000141753	2.299958711	6.695305056	2.74314979	8.14242E-07	0.00029734
RUFY4	2 218034960..218090581	ENSG00000188282	0.214138631	6.591878458	2.720689642	0.001323768	0.09865449
NEURL3	2 complement (96497646..96508109)	ENSG00000163121	2.639953362	6.381156301	2.673817872	4.6526E-05	0.00787107
IL4I1	19 complement (49889654..49929539)	ENSG00000104951	39.63911597	6.347763801	2.666248447	2.70566E-09	2.2052E-06

LRG1	19 complement (4536402..4540036)	ENSG00000171236	2.193013953	6.305442597	2.656597641	2.84489E-08	1.5444E-05
C1S	12 6988259..7071032	ENSG00000182326	5.425181116	6.261527938	2.646514746	7.34289E-10	7.1505E-07
TNFAIP6	2 151357592..151380046	ENSG00000123610	799.2822023	6.259497117	2.646046757	0.000258804	0.0312426
MX2	21 41361999..41409393	ENSG00000183486	15.68062259	6.216729659	2.636155843	7.68441E-11	9.3539E-08
NCF1	7 74773962..74789376	ENSG00000158517	263.8969924	6.091468537	2.606790076	7.34343E-07	0.00027504
GPR35	2 240605430..240631259	ENSG00000178623	4.172565077	6.041498524	2.594906438	2.04188E-08	1.193E-05
PLEKHG6	12 6310436..6328506	ENSG00000008323	3.047756612	6.013233636	2.588141014	4.64367E-06	0.00114966
EXPH5	11 (108505435..108593768)	ENSG00000110723	0.082914594	5.881568703	2.556200995	0.001287913	0.09697185
BATF2	11 complement (64987945..64997018)	ENSG00000168062	3.741642412	5.752297788	2.524138364	4.46515E-08	2.1741E-05
LAG3	12 6772512..6778455	ENSG00000089692	0.857053094	5.656078993	2.499802269	0.000186777	0.02435935
SLC2A6	9 (133471094..133479127)	ENSG00000160326	40.68079278	5.590061004	2.482864027	4.43355E-07	0.00018503
ZBP1	20 complement (57603846..57620576)	ENSG00000124256	1.368425855	5.53468351	2.468500822	4.46198E-06	0.00112373
CH25H	10 complement (89205629..89207317)	ENSG00000138135	1.206669853	5.351450873	2.419930085	0.000500687	0.04941575
CFB	6 31945650..31952084	ENSG00000243649	29.96104527	5.348686692	2.419184698	5.51429E-07	0.00022374
OAS3	12 112938051..112976460	ENSG00000111331	20.02884034	5.337819098	2.416250412	2.04098E-09	1.8633E-06
ISG15	1 1001138..1014540	ENSG00000187608	190.1056583	5.291158774	2.40358371	2.85477E-08	1.5444E-05
SOCS1	16 complement (11254417..11256204)	ENSG00000185338	2.736046162	5.250036336	2.392327408	6.61502E-05	0.01050277
UBD	6 complement (29555515..29559732)	ENSG00000213886	1.737050845	5.223704743	2.385073354	0.000346993	0.03959785
LRRC32	11 complement (76657524..76670747)	ENSG00000137507	1.279410529	5.080821382	2.345061747	2.37124E-05	0.00501982
CCL4	17 36103827..36105621	ENSG00000275302	182.0497434	5.033088979	2.331444103	0.000156285	0.02153641
MT1H	16 56669814..56671129	ENSG00000205358	41.71205099	4.954649026	2.308782865	0.00021448	0.02721312
DUSP15	20 complement (31847637..31870664)	ENSG00000149599	0.50498271	4.923837028	2.299783012	0.000599473	0.0561314
CELF4	18 complement (37243040..37565827)	ENSG00000101489	0.337066413	4.909431131	2.295555865	0.000351669	0.03964689

TNFRSF4	1 complement (1211340..1214153)	ENSG00000186827	1.467862017	4.882282269	2.287555707	0.001353298	0.09933483
GPR84	12 complement (54362445..54364487)	ENSG00000139572	10.87588744	4.717529095	2.238031415	5.15397E-06	0.00125473
GP1BA	17 4932277..4935023	ENSG00000185245	2.774552528	4.652365946	2.217964581	8.39967E-05	0.01291516
IFI27	14 94104836..94116698	ENSG00000165949	51.56794608	4.577820729	2.194660967	4.325E-09	3.1588E-06
ETV7	6 complement (36354091..36387800)	ENSG00000010030	0.827362376	4.501437458	2.170385775	0.000167957	0.02271619
CRISPLD2	16 84819985..84920768	ENSG00000103196	0.196627135	4.475590055	2.162077898	0.000488916	0.04891507
CD300E	17 complement (74609885..74623738)	ENSG00000186407	0.443867431	4.452836298	2.154724574	0.000519391	0.0505783
SPATC1	8 144012280..144047114	ENSG00000186583	1.079084504	4.405692886	2.13936893	9.58116E-05	0.01457834
C1R	12 complement (7080214..7092540)	ENSG00000159403	2.666204791	4.397072951	2.136543468	2.35967E-06	0.00068935
TNIP3	4 (121131408..121227466)	ENSG00000050730	5.650665385	4.389020268	2.133898932	4.51625E-05	0.00783134
CD38	4 15778275..15853232	ENSG00000004468	0.940310966	4.328826886	2.113976107	9.86867E-06	0.00228812
SYT14	1 209900923..210171389	ENSG00000143469	0.198335522	4.269695257	2.094133103	0.001334074	0.09891786
IRF7	11 complement (612553..615983)	ENSG00000185507	33.30131118	4.157670933	2.055775578	2.96632E-08	1.5475E-05
CA12	15 complement (63321378..63381846)	ENSG00000074410	16.01199309	4.128198141	2.045512217	1.03612E-05	0.00236477
IL15RA	10 complement (5943639..5978187)	ENSG00000134470	20.14319247	4.100278388	2.035721865	4.36771E-06	0.00111928
EXOC3L4	14 103100144..103110559	ENSG00000205436	0.667468994	4.075775064	2.027074434	0.000826273	0.07184151
WNT5A	3 complement (55465715..55490539)	ENSG00000114251	0.86884985	4.069416038	2.024821782	0.000236232	0.0294926
gene:ENSG00000256349	11 66509079..66533613	ENSG00000256349	1.189675677	4.069056361	2.024694263	2.85423E-05	0.00579052
GBP4	1 complement (89181144..89198942)	ENSG00000162654	8.918219824	4.053193262	2.019058967	2.86134E-07	0.00012665
APOL3	22 complement (36140330..36166177)	ENSG00000128284	8.843511352	3.947802389	1.981049776	1.88211E-06	0.00057275
CXCL9	4 complement (76001275..76007509)	ENSG00000138755	2.21858041	3.90048592	1.963653865	0.000149121	0.02092402
FFAR2	19 35443907..35451767	ENSG00000126262	0.832679412	3.883359594	1.957305305	0.000617799	0.05747889
gene:ENSG00000259753	17 47253897..47344292	ENSG00000259753	0.605025654	3.83218283	1.938166392	0.000533864	0.05130367
ICAM1	19 10271093..10286615	ENSG00000090339	67.21367376	3.828530999	1.936790939	1.10786E-05	0.00248961

FCAR	19 54874235..54891420	ENSG00000186431	0.804448836	3.711249902	1.89190515	0.000253885	0.03090417
HERC5	4 88457119..88506163	ENSG00000138646	19.08678338	3.682834949	1.880816742	6.99758E-07	0.00026898
CCL5	17 complement (35871491..35880793)	ENSG00000271503	18.62322734	3.660541657	1.872057142	0.00027564	0.03273394
MT1M	16 56632659..56633981	ENSG00000205364	12.15406923	3.659978632	1.871835226	0.000697528	0.06378085
LY6E	8 143017982..143023832	ENSG00000160932	300.6908979	3.656288395	1.87037987	5.30601E-05	0.00865397
CFP	X complement (47623172..47630305)	ENSG00000126759	8.322525606	3.606778708	1.85071091	4.55715E-05	0.00783134
JUP	17 complement (41754604..41786931)	ENSG00000173801	6.337922717	3.568974595	1.835509632	3.16163E-05	0.00604495
SEMA4A	1 156147366..156177752	ENSG00000196189	7.197557155	3.526717743	1.818326116	9.63452E-06	0.00226986
OAS2	12 112978395..113011723	ENSG00000111335	30.45013739	3.50148615	1.807967381	1.22518E-06	0.00040673
CMKLR1	12 (108288044..108339317)	ENSG00000174600	5.343463705	3.468581892	1.794345947	3.19445E-05	0.00604495
STAP1	4 67558727..67607337	ENSG00000035720	2.156571082	3.415107138	1.771930839	0.000895994	0.07698696
TMEM176A	7 150800403..150805118	ENSG00000002933	9.775381875	3.410271838	1.769886743	0.00012882	0.01844781
PDE4B	1 65792514..66374579	ENSG00000184588	4.681587587	3.400409193	1.765708366	0.000713269	0.06431313
SOCS3	17 complement (78356778..78360077)	ENSG00000184557	23.48187073	3.400298947	1.765661591	0.000405074	0.04384722
TIFAB	5 (135444226..135452351)	ENSG00000255833	2.069445432	3.350230486	1.744260352	4.2648E-05	0.00769086
EPOP	17 complement (38671703..38674957)	ENSG00000273604	3.520956829	3.344706784	1.741879742	5.33208E-05	0.00865397
LAMP3	3 (183122215..183163839)	ENSG00000078081	3.706826977	3.331874531	1.736334074	0.000566726	0.05340754
XAF1	17 6755447..6775647	ENSG00000132530	18.22453475	3.312824625	1.728061832	3.3482E-06	0.00090569
EPSTI1	13 complement (42886388..42992271)	ENSG00000133106	21.14566844	3.280402582	1.713872878	2.6041E-06	0.00074584
AIM2	1 (159062484..159147096)	ENSG00000163568	8.953318774	3.280244831	1.713803499	0.00021611	0.02721312
GMPR	6 16238587..16295549	ENSG00000137198	14.99578876	3.239777574	1.695894769	0.000122165	0.01784463
IFI35	17 43006740..43014456	ENSG00000068079	89.14778778	3.215563335	1.685071505	4.81437E-05	0.0079913

	complement							
TRAF1	9 (120902393..120929173)	ENSG00000056558	27.28013441	3.2140466	1.684390847	0.000405242	0.04384722	
TRPM2	21 44350163..44443081	ENSG00000142185	4.67000632	3.19657264	1.676525879	8.16556E-05	0.01268877	
IL32	16 3065297..3082192	ENSG00000008517	3.478457537	3.178399721	1.668300572	0.000249182	0.03058658	
ANGPTL4	19 8363289..8374370	ENSG00000167772	11.99979974	3.139870625	1.650705115	0.000423859	0.04519525	
AGRN	1 1020120..1056118	ENSG00000188157	22.53067142	3.125420392	1.644050256	0.000467129	0.04771576	
DHX58	17 complement (42101404..42112714)	ENSG00000108771	9.466932826	3.116827814	1.640078457	4.45366E-05	0.00783134	
IL27	16 complement (28499362..28512051)	ENSG00000197272	8.299176376	3.106730073	1.635396899	0.000167929	0.02271619	
IFIT3	10 89327307..89377473	ENSG00000119917	53.01456635	3.09871808	1.631671505	3.0197E-05	0.0059448	
BCL3	19 44747705..44760044	ENSG00000069399	13.04759415	3.087273165	1.62633314	0.000178876	0.02353914	
	complement							
ADAM8	10 (133262420..133276868)	ENSG00000151651	23.92759015	3.054453385	1.610914223	4.36693E-05	0.00777899	
IFI44	1 78649796..78664078	ENSG00000137965	43.06461125	3.03968825	1.603923368	2.29765E-05	0.00493555	
IFIT2	10 89283694..89309271	ENSG00000119922	45.81069691	3.026385026	1.597595543	4.68805E-05	0.00787107	
GPX3	5 151020438..151028992	ENSG00000211445	75.51416451	3.015508587	1.592401343	0.000446473	0.04625266	
ALOX15B	17 8039034..8049134	ENSG00000179593	15.24937881	3.007491452	1.588560637	3.22795E-05	0.00604495	
	complement							
TMEM176B	7 (150791285..150801360)	ENSG00000106565	18.17964727	2.936230496	1.553965225	0.000315577	0.03687704	
DDIT4	10 72273919..72276036	ENSG00000168209	73.00737203	2.936032527	1.553867951	0.000352851	0.03964689	
P2RY6	11 73264498..73305103	ENSG00000171631	0.604589089	2.922613878	1.54725924	0.001023212	0.08396666	
CAVIN1	17 complement (42402449..42423256)	ENSG00000177469	3.734707128	2.907370103	1.539714736	0.00042823	0.04532719	
MYO1G	7 complement (44962662..44979088)	ENSG00000136286	41.47067594	2.902837841	1.537463982	0.000623769	0.05766707	
SCARF1	17 complement (1633858..1645744)	ENSG00000074660	6.891631085	2.888294282	1.530217743	0.000126308	0.01826707	
	complement							
STAT1	2 (190908460..191020960)	ENSG00000115415	56.43578394	2.859132218	1.515577338	0.000247829	0.03058658	
PDE6G	17 complement (81650459..81663112)	ENSG00000185527	8.572940014	2.856126121	1.514059688	0.000150409	0.02092402	
NFKB2	10 102394110..102402524	ENSG00000077150	40.67971332	2.856020518	1.514006344	0.000437472	0.04590148	

	complement						
LAMB3	1 (209614870..209652425)	ENSG00000196878	2.402164952	2.845592071	1.508728859	0.000805758	0.0705906
PLEKHG3	14 64704102..64750249	ENSG00000126822	1.799426616	2.817842641	1.494591049	0.000478762	0.04823046
ADA	20 complement (44619522..44652233)	ENSG00000196839	22.14213029	2.808651621	1.489877687	0.001314504	0.09846649
ZSWIM4	19 13795460..13832230	ENSG00000132003	3.702801936	2.807954238	1.489519424	0.000355704	0.03966233
	complement						
SLC9A9	3 (143265222..143848485)	ENSG00000181804	1.275022877	2.80346646	1.48721181	0.001057813	0.0863211
RELB	19 45001449..45038198	ENSG00000104856	14.1096592	2.80318975	1.487069405	0.000215788	0.02721312
ZC3H12A	1 37474580..37484377	ENSG00000163874	36.8231363	2.797446676	1.484110631	0.000380598	0.0418
CLU	8 complement (27596917..27614700)	ENSG00000120885	0.770083075	2.795392434	1.483050831	0.000262917	0.03147889
C3	19 complement (6677704..6730562)	ENSG00000125730	51.43648097	2.791752435	1.481171013	0.001156194	0.09031299
PDGFB	22 complement (39223359..39244982)	ENSG00000100311	8.195520635	2.789257549	1.479881153	0.000111101	0.01655967
KLHDC7B	22 50545899..50551023	ENSG00000130487	1.21294241	2.77810305	1.474100115	0.000983261	0.08114403
ADM	11 10305073..10307397	ENSG00000148926	112.6780601	2.777356913	1.473712587	0.000702885	0.06378085
POU2F2	19 complement (42086110..42196585)	ENSG00000028277	1.010456544	2.763901086	1.466705985	0.000423889	0.04519525
	complement						
IFIH1	2 (162267074..162318684)	ENSG00000115267	28.62743949	2.741717608	1.455079984	9.76317E-05	0.01470213
PLEKHA7	11 complement (16777297..17014414)	ENSG00000166689	0.333764358	2.705256579	1.435765432	0.001067023	0.08658888
VEGFA	6 43770184..43786487	ENSG00000112715	21.03997777	2.694579638	1.430060226	0.000915189	0.07789774
	complement						
GPR132	14 (105049395..105065445)	ENSG00000183484	4.673309601	2.670188229	1.416941445	0.000519259	0.0505783
MVB12B	9 126326829..126507041	ENSG00000196814	0.884872256	2.655957776	1.409232211	0.001268985	0.09693739
SECTM1	17 complement (82321024..82334074)	ENSG00000141574	16.5752321	2.655745246	1.409116762	0.001083686	0.08697471
ATF5	19 49928702..49933935	ENSG00000169136	25.60582537	2.637244378	1.399031264	0.000454335	0.04673572
FBXO6	1 11664200..11674354	ENSG00000116663	20.33497825	2.623832274	1.3916755	0.000875817	0.07569857
SIPA1L1	14 71320449..71741229	ENSG00000197555	2.783984953	2.623175308	1.391314227	0.000478772	0.04823046

PSTPIP2	18 complement (45983536..46072272)	ENSG00000152229	15.66555594	2.618304308	1.388632782	0.000345142	0.03959785
MYO7B	2 127535802..127637729 complement	ENSG00000169994	1.898201327	2.607828257	1.382848861	0.000703	0.06378085
OASL	12 (121017763..121039242)	ENSG00000135114	26.94545181	2.568960558	1.36118474	0.00037484	0.04147949
NLRP3	1 247416156..247449108	ENSG00000162711	3.124612119	2.536740443	1.342975912	0.000525926	0.05087547
TUT1	11 complement (62575045..62591637)	ENSG00000149016	13.19479075	2.535302569	1.342157932	0.000807053	0.0705906
PML	15 73994673..74047827	ENSG00000140464	7.587998034	2.527492032	1.337706544	0.001077137	0.08692672
AXL	19 41219223..41261766	ENSG00000167601	20.93450459	2.408487263	1.268127295	0.00126657	0.09693739
MDK	11 46380756..46383837	ENSG00000110492	14.10999033	2.3995783	1.26278089	0.001280819	0.09693739
DDX58	9 complement (32455302..32526208)	ENSG00000107201	9.956195083	2.347431262	1.231082913	0.000555777	0.05271584
HERC6	4 88378739..88443097	ENSG00000138642	4.388682258	2.312803603	1.209642761	0.000957575	0.08038674
C1RL	12 complement (7089587..7109238)	ENSG00000139178	6.667041925	2.271789234	1.183828995	0.00115178	0.09031299

Downregulated genes (29)

TBC1D3C	17 complement (38057693..38068634)	ENSG00000278299	0.422915962	-154.9694855	-7.275840357	0.001215313	0.09437584
gene:ENSG00000284292	7 99325879..99394653	ENSG00000284292	0.317735898	-38.1112214	-5.25214394	3.02232E-05	0.0059448
FCER1A	1 159289714..159308224	ENSG00000179639	0.587087942	-15.37616652	-3.94262396	0.000329279	0.03817285
gene:ENSG00000284976	9 137217452..137219361	ENSG00000284976	0.340429573	-10.13969693	-3.341942626	0.000917863	0.07789774
GGTLC2	22 226444475..22647903	ENSG00000100121	0.276031396	-8.8258492	-3.141735097	0.000978087	0.08114403
SPTLC3	20 13008972..13169103	ENSG00000172296	0.286881791	-6.183312695	-2.628379966	0.000295397	0.03479729
RPS4Y1	Y 2841602..2932000	ENSG00000129824	53.11352812	-5.449250465	-2.446057803	0.00043994	0.04590148
gene:ENSG00000288684	9 complement (32455323..32552603)	ENSG00000288684	0.386720255	-5.335858754	-2.415720477	0.000922593	0.07789774
DLGAP5	14 complement (55148112..55191608)	ENSG00000126787	0.662435862	-5.221086695	-2.384350115	3.61546E-06	0.0009602
SELENOP	5 complement (42799880..42887392)	ENSG00000250722	3.719647729	-4.737447542	-2.244109968	2.9722E-07	0.00012769
DDX3Y	Y 12904108..12920478	ENSG00000067048	10.23927869	-4.724051399	-2.240024662	0.000974728	0.08114403
PCLAF	15 complement (64364304..64387687)	ENSG00000166803	0.737130915	-4.414633059	-2.142293527	6.24781E-05	0.01002876

HMMR	5	163460203..163491941	ENSG00000072571	0.845608046	-4.339199491	-2.117428914	8.35109E-06	0.00199974
TOP2A	17	complement (40388525..40417896)	ENSG00000131747	1.397675687	-4.201898322	-2.071041252	9.98764E-07	0.00035583
DDIAS	11	82899975..82958277	ENSG00000165490	1.589055468	-4.148963438	-2.052750944	1.66752E-06	0.00053901
FAM111B	11	59107185..59127412	ENSG00000189057	0.803077095	-4.134906343	-2.047854652	2.66417E-05	0.00548107
BUB1B	15	40161023..40221123	ENSG00000156970	0.52425038	-4.061629128	-2.022058511	0.000176956	0.02349817
ANLN	7	36389821..36453791	ENSG00000011426	0.832834678	-4.060854586	-2.021783367	3.05237E-05	0.0059448
CDK1	10	60778331..60794852	ENSG00000170312	1.664609843	-3.737229797	-1.901969276	7.85385E-05	0.01233561
CEP55	10	93496612..93529092	ENSG00000138180	1.077027938	-3.734825292	-1.901040758	3.55193E-05	0.00655876
KITLG	12	complement (88492793..88580851)	ENSG00000049130	0.309700635	-3.427388031	-1.777109535	0.000174387	0.02336951
RGS18	1	192158462..192185815	ENSG00000150681	1.093364275	-3.094520122	-1.629715703	0.001221129	0.09437584
		complement						
RGPD6	2	(110513802..110577222)	ENSG00000183054	0.963212192	-3.080479796	-1.623155074	0.000118243	0.01744616
FAM161A	2	complement (61824848..61854143)	ENSG00000170264	0.320129598	-3.049766827	-1.608698944	0.00127457	0.09693739
gene:ENSG00000267022	19	44025354..44087318	ENSG00000267022	0.565082046	-2.989967246	-1.58012968	0.001343101	0.09908423
BBS1	11	66510606..66533613	ENSG00000174483	0.680710917	-2.935468942	-1.553590993	0.001103497	0.08760207
		complement						
DYNLT2B	3	(196291219..196318299)	ENSG00000213123	3.292906786	-2.87710938	-1.524620069	0.000774692	0.06858137
CENPF	1	214603195..214664571	ENSG00000117724	0.573643044	-2.865684114	-1.518879589	0.000538011	0.05136425
		complement						
MKI67	10	(128096659..128126423)	ENSG00000148773	0.797436518	-2.616811051	-1.387809757	0.001095053	0.08740678

C: control; h: HAM; 72: 72 hr p.i.; +: *M.tb* infected; -: *M.tb* uninfected

Supplementary Table S8. Differentially expressed genes in HAMs of T2D patients 2 hr p.i. with *M.tb*.

Name	Chromosome	Region	Identifier	Dh.2+ vs. Dh.2- Max group means	Dh.2+ vs. Dh.2- Fold change	Dh.2+ vs. Dh.2- Log fold change	Dh.2+ vs. Dh.2- P-value	Dh.2+ vs. Dh.2- FDR p-value
Upregulated genes (5)								
SAPCD1	6	31762996..31764851	ENSG00000228727	0.3512515	20.0208407	4.323430652	1.018E-05	0.0219035
gene:ENSG00000284820	2	complement(219209772..219222738)	ENSG00000284820	0.1512328	16.4533928	4.040313203	4.3583E-06	0.0109407
gene:ENSG00000268193	19	complement(18907013..18934397)	ENSG00000268193	0.6070482	13.6131476	3.766928779	1.3715E-05	0.0258223
gene:ENSG00000267022	19	44025354..44087318	ENSG00000267022	0.2031901	4.69990042	2.232630189	0.00010525	0.0880722
SPTY2D1OS	11	18588781..18610255	ENSG00000247595	0.191122	3.1682381	1.663680759	0.00016258	0.0997247
Downregulated genes (8)								
gene:ENSG00000285953	7	complement(92131774..92245924)	ENSG00000285953	0.2075605	-96.674131	-6.595057989	4.7174E-05	0.0507526
H2AC19	1	149851061..149851624	ENSG00000272196	1.940041	-12.398514	-3.632095362	2.3927E-05	0.0342661
TRIM39-RPP21	6	30328907..30346854	ENSG00000248167	0.7115485	-10.138478	-3.34176919	1.6944E-06	0.0063804
gene:ENSG00000276612	21	complement(5116343..5133805)	ENSG00000276612	0.6353608	-10.100585	-3.336366947	2.73E-05	0.0342661
CORO7-PAM16	16	complement(4340251..4420494)	ENSG00000103426	0.5861566	-7.1633824	-2.840640965	2.4663E-05	0.0342661
gene:ENSG00000248751	22	complement(30285238..30299482)	ENSG00000248751	0.4724047	-4.5275883	-2.178742783	2.8589E-06	0.008612
SULT1A4	16	29459913..29464966	ENSG00000213648	0.8349066	-4.1061048	-2.037770438	1.1444E-07	0.0005746
BPIFA1	20	33235995..33243311	ENSG00000198183	1.7965313	-2.1718387	-1.118916936	0.00011877	0.0941532

D: Diabetes; h: HAM; 2: 2 hr p.i.; +: *M.tb* infected; -: *M.tb* uninfected

Supplementary Table S9. Differentially expressed genes in HAMs of T2D patients 1 day p.i. with *M.tb*.

Name	Chromosome	Region	Identifier	Dh.24+ vs.		Dh.24+ vs.		Dh.24+ vs.	
				Dh.24- Max group means	Dh.24+ vs. Dh.24- Fold change	Dh.24- Log fold change	Dh.24+ vs. Dh.24- P-value	Dh.24+ vs. Dh.24- FDR p-value	
Upregulated genes (18)									
gene:ENSG00000288725	16	complement(56430556..56501497)	ENSG00000288725	0.128109617	93.46368941	6.546334083	0.00032959	0.08751344	
gene:ENSG00000288534	11	57712582..57818431	ENSG00000288534	0.881032482	33.77221982	5.077765105	6.1466E-11	5.2452E-07	
COMMD3-BMI1	10	22316388..22329542	ENSG00000269897	0.854288332	23.41855656	4.54958025	5.0268E-07	0.00057195	
gene:ENSG00000251357	22	23862188..23895223	ENSG00000251357	0.451701247	11.61783529	3.538269377	0.00011811	0.04247021	
PPAN-P2RY11	19	10106223..10114780	ENSG00000243207	0.206089215	9.79315172	3.291773236	0.00018204	0.06213773	
KIAA0408	6	complement(127438406..127459389)	ENSG00000189367	0.038905104	8.973499628	3.16567074	0.00022906	0.07332626	
gene:ENSG00000260537	16	70299194..70372582	ENSG00000260537	0.700234014	6.808997618	2.767442428	5.6448E-07	0.00060212	
gene:ENSG00000285839	1	complement(52020153..52033350)	ENSG00000285839	0.35128847	5.831885319	2.54396235	4.8569E-05	0.02125469	
EEF1E1-BLOC1S5	6	complement(8015726..8102530)	ENSG00000265818	1.568842876	5.142130592	2.36236625	0.00030385	0.08364318	
CXCL10	4	complement(76021118..76023497)	ENSG00000169245	28.34560963	3.954103579	1.983350664	2.6438E-12	4.5121E-08	
CXCL11	4	complement(76033682..76041415)	ENSG00000169248	1.868801559	3.019341839	1.594234103	3.3704E-08	9.5872E-05	
CCL8	17	34319435..34321402	ENSG00000108700	3.359760063	2.874268787	1.523194982	1.6062E-07	0.0002492	
GBP5	1	complement(89258950..89272804)	ENSG00000154451	32.66722147	2.606144571	1.381917117	6.8256E-10	2.3298E-06	
ETV7	6	complement(36354091..36387800)	ENSG00000010030	1.347720394	2.580702409	1.367763788	3.1987E-06	0.00218371	
IFIT1	10	89392546..89406487	ENSG00000185745	3.633132044	2.411938173	1.270192926	4.007E-05	0.01799691	
GBP4	1	complement(89181144..89198942)	ENSG00000162654	16.82956969	2.334723738	1.22325185	1.0457E-10	5.9489E-07	
HAPLN3	15	complement(88877294..88895597)	ENSG00000140511	3.73451828	2.21498681	1.147298107	5.2282E-08	0.00012747	
CXCL9	4	complement(76001275..76007509)	ENSG00000138755	5.177016627	2.114063419	1.080018656	3.4349E-10	1.4656E-06	
Downregulated genes (4)									
gene:ENSG00000259753	17	47253897..47344292	ENSG00000259753	0.42183672	-26.0515545	-4.703297556	4.4247E-07	0.00055047	
H4C12	6	complement(27831174..27831560)	ENSG00000273542	1.302032792	-20.20817726	-4.336867294	0.00012988	0.04523816	
SYS1-DBNDD2	20	45363200..45410610	ENSG00000254806	1.022592949	-14.02644616	-3.810077619	1.2698E-06	0.00100259	
TBCE_2	1	235367360..235452443	ENSG00000284770	0.711104434	-2.242029913	-1.164805527	6.2686E-05	0.02547301	

D: Diabetes; h: HAM; 24: 24 hr p.i.; +: *M.tb* infected; -: *M.tb* uninfected

Supplementary Table S10. Differentially expressed genes in HAMs of T2D patients 3 days p.i. with *M.tb*.

Name	Chromosome	Region	Identifier	Dh.72+ vs.		Dh.72+ vs.		Dh.72+ vs.
				Dh.72-	Dh.72+ vs.	Dh.72-	Dh.72+ vs.	Dh.72+ vs.
				Max group	Dh.72-	Log fold	Dh.72-	Dh.72-
				means	Fold change	change	P-value	FDR p-value
Upregulated genes (144)								
CCL15-CCL14	17	complement(35983656..36001621)	ENSG00000275688	0.462935881	134.4460767	7.070883846	0.000793523	0.04565518
APOBEC3A	22	38952741..38992778	ENSG00000128383	0.719812304	43.17171777	5.432014593	1.75071E-09	5.7288E-07
CXCL11	4	complement(76033682..76041415)	ENSG00000169248	1.125180214	31.38281205	4.971902726	7.75687E-15	6.7687E-12
C11orf96	11	43925342..43943878	ENSG00000187479	0.195795153	28.24064865	4.819701321	0.00020359	0.01473632
CXCL10	4	complement(76021118..76023497)	ENSG00000169245	22.0829256	22.44605165	4.488389786	8.01656E-50	1.2592E-45
RHCG	15	complement(89471398..89496589)	ENSG00000140519	0.232204906	16.41186742	4.0366675	8.18013E-05	0.00713807
OR2I1P	6	29550407..29557721	ENSG00000237988	0.376018347	14.2611045	3.834013815	1.12928E-12	6.5695E-10
gene:ENSG00000286192	7	complement(1815804..2242215)	ENSG00000286192	0.069214506	13.32197381	3.735735945	0.00216131	0.09639885
gene:ENSG00000261147	15	90249556..90272208	ENSG00000261147	0.067651291	12.6312573	3.658926346	0.000398208	0.02595294
ACOD1	13	76948511..76958638	ENSG00000102794	0.228868622	12.5539455	3.650068945	6.26308E-05	0.00565169
IFI44L	1	78619902..78646145	ENSG00000137959	8.886936742	11.71408478	3.550172335	3.23777E-31	2.5428E-27
RSAD2	2	6865557..6898239	ENSG00000134321	21.07922105	11.4541657	3.517800475	3.54247E-24	9.2736E-21
ETV7	6	complement(36354091..36387800)	ENSG00000010030	1.393512207	11.00006999	3.459440798	1.78446E-15	1.6487E-12
NEURL3	2	complement(96497646..96508109)	ENSG00000163121	0.731413445	8.990406019	3.168386271	5.04991E-06	0.0006009
CCL8	17	34319435..34321402	ENSG00000108700	1.267285352	8.583917835	3.101636267	8.5973E-07	0.00012861
NIPAL4	5	157460213..157474722	ENSG00000172548	0.072474293	8.54134793	3.094463763	0.001781967	0.08455997
TNFAIP6	2	151357592..151380046	ENSG00000123610	120.0409391	8.376935453	3.066422557	6.75072E-08	1.4934E-05
gene:ENSG00000269179	19	complement(49909501..49958391)	ENSG00000269179	0.89355538	7.782969481	2.9603207	0.00029837	0.02055482
CXCL9	4	complement(76001275..76007509)	ENSG00000138755	6.382677595	7.562347486	2.918834142	4.50894E-29	1.7705E-25
C4B	6	32014795..32035418	ENSG00000224389	0.272296813	7.126773934	2.833249162	5.94311E-06	0.00069663
GIMAP5	7	150722253..150750033	ENSG00000196329	0.732899675	6.999558979	2.807264025	6.2495E-07	9.8161E-05
UBD	6	complement(29555515..29559732)	ENSG00000213886	8.2806693	6.860466365	2.778306652	1.8668E-17	2.4435E-14
PTGES	9	complement(129738331..129753042)	ENSG00000148344	1.395633996	6.860309224	2.778273606	4.63308E-08	1.0702E-05
ISG20	15	88635670..88656483	ENSG00000172183	5.673167139	6.533497851	2.707855577	1.00694E-08	2.7747E-06
HAPLN3	15	complement(88877294..88895597)	ENSG00000140511	1.904189384	6.360138284	2.669058133	1.05096E-29	5.5025E-26
TNFSF10	3	complement(172505508..172523475)	ENSG00000121858	3.881269741	5.85053997	2.548569783	1.45771E-11	7.6321E-09
IFIT1	10	89392546..89406487	ENSG00000185745	20.62636734	5.771130517	2.528853959	6.32851E-13	3.9761E-10

CCL15	17	complement(35996440..36001553)	ENSG00000275718	13.81931524	5.35332372	2.420434896	2.00571E-08	5.2506E-06
OTOF	2	complement(26457203..26558756)	ENSG00000115155	0.113727793	5.293954373	2.404345761	0.000117376	0.0094591
MAS1	6	159890988..159917447	ENSG00000130368	0.063243876	5.262051768	2.395625442	0.000312573	0.02134601
LTA	6	31572054..31574324	ENSG00000226979	0.336354387	5.109776636	2.353260228	0.000873674	0.04972026
HSH2D	19	16134028..16158575	ENSG00000196684	0.561150974	5.017217466	2.326887472	2.58625E-06	0.00032498
ISG15	1	1001138..1014540	ENSG00000187608	133.9233269	4.834494894	2.273365165	2.48278E-19	4.333E-16
gene:ENSG00000285283	11	31812391..32104665	ENSG00000285283	5.802628643	4.791881433	2.260592212	0.000134843	0.01058987
IDO1	8	39902275..39928790	ENSG00000131203	3.207097101	4.782326233	2.257712549	5.94296E-08	1.3528E-05
CFH	1	196652043..196747504	ENSG00000000971	0.193309413	4.711456343	2.236173075	7.73869E-05	0.00682875
IFITM3	11	complement(319676..329475)	ENSG00000142089	43.80369035	4.558436675	2.188539134	1.34576E-11	7.2889E-09
IFITM1	11	310041..315272	ENSG00000185885	3.455821592	4.447397521	2.152961363	3.71031E-08	8.8935E-06
C1QTNF1	17	79022814..79049788	ENSG00000173918	0.099198284	4.427544725	2.146506881	0.001188238	0.06284059
MT1M	16	56632659..56633981	ENSG00000205364	20.64839635	4.304985576	2.106008404	4.4455E-09	1.2696E-06
GCH1	14	complement(54842008..54902826)	ENSG00000131979	7.250978703	4.27915041	2.09732439	2.8606E-08	7.247E-06
ANKRD22	10	complement(88819896..88851844)	ENSG00000152766	0.308245008	4.261398636	2.091327016	3.02459E-05	0.00290508
GOS2	1	209675412..209676390	ENSG00000123689	72.20056021	4.1136335	2.040413264	1.79676E-05	0.00185669
CCL20	2	227805739..227817564	ENSG00000115009	65.20227019	3.951917888	1.982552971	0.000129294	0.0102567
NEXN	1	77888513..77943895	ENSG00000162614	2.884526936	3.925241056	1.972781255	1.11892E-09	3.7393E-07
CCL4	17	36103827..36105621	ENSG00000275302	57.88242158	3.86043995	1.948765272	3.03325E-05	0.00290508
LAG3	12	6772512..6778455	ENSG00000089692	0.679392308	3.857289699	1.947587503	9.5744E-07	0.00014055
WNT5A	3	complement(55465715..55490539)	ENSG00000114251	0.78341029	3.844790289	1.94290491	2.49528E-05	0.00244958
CALHM6	6	116461370..116463771	ENSG00000188820	3.302514028	3.828568693	1.936805143	4.43079E-08	1.0387E-05
TNFRSF4	1	complement(1211340..1214153)	ENSG00000186827	1.11988127	3.775553672	1.916688226	0.000368929	0.02434776
USP18	22	18150170..18177397	ENSG00000184979	14.8531963	3.757151953	1.909639465	2.59264E-11	1.2726E-08
HESX1	3	complement(57197838..57227606)	ENSG00000163666	0.709158062	3.735505884	1.901303634	0.000509245	0.0317409
SYNM	15	99098217..99135593	ENSG00000182253	0.459326453	3.70979064	1.891337771	0.001150731	0.06147802
GBP5	1	complement(89258950..89272804)	ENSG00000154451	12.02720549	3.684446464	1.881447891	8.78334E-16	8.6225E-13
OSM	22	complement(30262829..30266851)	ENSG00000099985	1.182630242	3.64273456	1.865021872	0.000212939	0.01534235
CMPK2	2	complement(6840570..6866635)	ENSG00000134326	13.82565588	3.629346243	1.859709698	7.88317E-18	1.2382E-14
CP	3	complement(149162410..149221829)	ENSG00000047457	9.226815154	3.577193184	1.838828032	2.95661E-08	7.3713E-06
STAP1	4	67558727..67607337	ENSG00000035720	1.015704115	3.522223206	1.816486337	0.00017224	0.01300658
SLAMF7	1	160739057..160754821	ENSG00000026751	27.42319823	3.501838363	1.808112494	2.39094E-07	4.3166E-05
CXCL8	4	73740541..73743716	ENSG00000169429	624.575088	3.487359871	1.802135248	0.001295363	0.0660593

EREG	4	74365145..74388749	ENSG00000124882	1.860367476	3.477300192	1.797967619	0.000446402	0.02850262
C1R	12	complement(7080214..7092540)	ENSG00000159403	2.636826209	3.408178044	1.769000704	2.86958E-10	1.1268E-07
MX1	21	41420020..41470071	ENSG00000157601	53.55042461	3.374198913	1.754545025	9.98471E-18	1.4257E-14
HELZ2	20	complement(63558086..63574239)	ENSG00000130589	5.202945417	3.336344277	1.738268168	3.53493E-17	4.271E-14
PDE4B	1	65792514..66374579	ENSG00000184588	1.825523311	3.320057065	1.731208039	5.55191E-06	0.00065567
MT1H	16	56669814..56671129	ENSG00000205358	24.16926066	3.27968305	1.713556399	3.91945E-09	1.1616E-06
MARCKS	6	113857345..113863475	ENSG00000277443	8.033404359	3.278580425	1.713071285	1.29763E-05	0.00140565
MMP1	11	complement(102789401..102798160)	ENSG00000196611	12.81857201	3.276681003	1.712235228	0.001136258	0.06112055
FFAR2	19	35443907..35451767	ENSG00000126262	1.626909378	3.234644722	1.693607262	9.33116E-08	1.9542E-05
CFB	6	31945650..31952084	ENSG00000243649	13.71886775	3.138733488	1.650182534	6.10761E-08	1.3705E-05
CCL4L2	17	36210924..36212878	ENSG00000276070	12.15705943	3.132006494	1.647087204	0.000501927	0.03140943
IFIT2	10	89283694..89309271	ENSG00000119922	35.69638754	3.116502119	1.639927694	2.58563E-08	6.6578E-06
MT1G	16	complement(56666730..56668065)	ENSG00000125144	245.5588009	3.087466405	1.626423439	1.20083E-07	2.4495E-05
SIGLEC1	20	complement(3686970..3712600)	ENSG00000088827	32.29875672	3.045459497	1.606659917	7.55655E-26	2.3738E-22
HERC5	4	88457119..88506163	ENSG00000138646	13.61723891	3.01663588	1.592940568	3.38302E-14	2.5303E-11
SGPP2	2	222424543..222562621	ENSG00000163082	0.38378832	3.007070421	1.588358654	0.002120987	0.09545659
BATF2	11	complement(64987945..64997018)	ENSG00000168062	3.720709845	2.982180174	1.576367424	4.22576E-07	7.2886E-05
IFIT3	10	89327307..89377473	ENSG00000119917	51.16849393	2.967443289	1.569220459	2.1239E-10	8.5539E-08
LGALS2	22	complement(37570248..37582616)	ENSG00000100079	10.86145984	2.945031111	1.558282875	1.13583E-10	5.0973E-08
ZBP1	20	complement(57603846..57620576)	ENSG00000124256	0.836845681	2.922574681	1.547239891	0.000339395	0.02273664
RCAN2	6	complement(46220736..46491972)	ENSG00000172348	0.526058093	2.917167797	1.544568373	2.29916E-05	0.00229213
EPSTI1	13	complement(42886388..42992271)	ENSG00000133106	20.85701598	2.904316314	1.538198588	7.93898E-16	8.3132E-13
GCNT4	5	complement(75025346..75052558)	ENSG00000176928	0.195274568	2.885918866	1.529030741	0.001449578	0.07205227
IFI44	1	78649796..78664078	ENSG00000137965	40.61275524	2.869111606	1.520604089	6.97538E-10	2.548E-07
GPR84	12	complement(54362445..54364487)	ENSG00000139572	4.083769262	2.831710687	1.501673874	0.000418859	0.02707413
IL2RA	10	complement(6010689..6062370)	ENSG00000134460	1.680977838	2.822447498	1.496946745	0.001863227	0.08762188
IL15RA	10	complement(5943639..5978187)	ENSG00000134470	5.43720811	2.811998616	1.491595884	7.51497E-08	1.617E-05
XAF1	17	6755447..6775647	ENSG00000132530	13.06909822	2.81006918	1.490605648	4.67078E-17	5.2403E-14
CD38	4	15778275..15853232	ENSG00000004468	1.596051495	2.776716892	1.473380091	2.28465E-07	4.2218E-05
IFI6	1	complement(27666064..27672212)	ENSG00000126709	884.4711222	2.762099256	1.465765164	1.39292E-10	6.0774E-08
IL3RA	X	1336616..1382689	ENSG00000185291	10.41745687	2.751012961	1.459962937	2.32194E-07	4.2408E-05
OAS3	12	112938051..112976460	ENSG00000111331	22.91260779	2.742162754	1.455314201	2.13829E-19	4.1983E-16
MX2	21	41361999..41409393	ENSG00000183486	12.83564395	2.740821019	1.45460812	6.35331E-07	9.8803E-05

HEY1	8 complement(79762371..79767857)	ENSG00000164683	0.466206133	2.723051136	1.445224075	0.001967694	0.09037107
GBP4	1 complement(89181144..89198942)	ENSG00000162654	10.71069585	2.675780158	1.419959589	3.07051E-11	1.4615E-08
C1S	12 6988259..7071032	ENSG00000182326	6.776707434	2.670135941	1.416913194	8.62623E-10	3.0109E-07
LRRC32	11 complement(76657524..76670747)	ENSG00000137507	1.037577737	2.64590962	1.403763782	0.001585742	0.07759268
SOD2	6 complement(159669069..159762529)	ENSG00000112096	51.82273703	2.636401174	1.398569918	4.90212E-06	0.00058777
PPFIA4	1 203026498..203078740	ENSG00000143847	0.246768345	2.634311283	1.397425832	0.000979474	0.05398104
APOL3	22 complement(36140330..36166177)	ENSG00000128284	8.975870319	2.601366753	1.379269812	1.22096E-11	6.8491E-09
AIM2	1 complement(159062484..159147096)	ENSG00000163568	6.494129081	2.583944911	1.369575312	2.37023E-09	7.4458E-07
gene:ENSG00000288640	7 112450460..112490941	ENSG00000288640	0.453007241	2.563557135	1.358147052	0.000666139	0.03963273
STAT1	2 complement(190908460..191020960)	ENSG00000115415	79.38070403	2.544070079	1.347138412	4.47529E-20	1.0042E-16
VAMP5	2 85584431..85593406	ENSG00000168899	32.15818706	2.506683499	1.325779849	3.49936E-08	8.5882E-06
ANGPTL4	19 8363289..8374370	ENSG00000167772	7.861631408	2.496798923	1.32007964	0.000104831	0.00866621
EXOC3L4	14 103100144..103110559	ENSG00000205436	0.867001434	2.491416284	1.316966098	0.000420829	0.02708998
IFIH1	2 complement(162267074..162318684)	ENSG00000115267	21.95793409	2.474689771	1.307247679	2.5932E-13	1.6971E-10
IL27	16 complement(28499362..28512051)	ENSG00000197272	5.56611948	2.446624806	1.290792878	1.6151E-05	0.00169123
gene:ENSG00000286001	5 218298..314955	ENSG00000286001	0.414504961	2.442451679	1.28833002	0.000690536	0.04077538
GBP1	1 complement(89051882..89065360)	ENSG00000117228	97.22581229	2.423074672	1.276838865	1.04087E-13	7.1082E-11
SOCS1	16 complement(11254417..11256204)	ENSG00000185338	1.960661233	2.40507018	1.266078993	0.000956172	0.05332095
MT1E	16 56625475..56627112	ENSG00000169715	40.63140155	2.395097179	1.260084193	7.97934E-07	0.00012051
CA12	15 complement(63321378..63381846)	ENSG00000074410	6.860509601	2.380994003	1.251563987	7.46839E-09	2.0947E-06
MT2A	16 56608584..56609497	ENSG00000125148	523.3962979	2.380300778	1.251143886	1.4036E-06	0.00019893
MEFV	16 complement(3242027..3256633)	ENSG00000103313	0.657912955	2.368561842	1.24401134	0.000410204	0.0266243
HES4	1 complement(998962..1000172)	ENSG00000188290	2.242620303	2.360355297	1.23900404	0.001237507	0.06403969
NDP	X complement(43948776..43973395)	ENSG00000124479	1.406453611	2.355196881	1.235847666	0.000953777	0.05332095
LAMB3	1 complement(209614870..209652425)	ENSG00000196878	2.685181894	2.349814178	1.232546674	0.00016969	0.0130016
IL4I1	19 complement(49889654..49929539)	ENSG00000104951	32.83648194	2.343206969	1.228484389	3.09289E-09	9.5255E-07
OAS2	12 112978395..113011723	ENSG00000111335	25.24887692	2.335466065	1.223710482	9.26742E-14	6.6165E-11
IFI27	14 94104836..94116698	ENSG00000165949	91.83851296	2.329211024	1.219841352	7.99145E-13	4.8278E-10
DDX58	9 complement(32455302..32526208)	ENSG00000107201	7.183110654	2.322142298	1.215456381	4.26913E-07	7.2886E-05
NCF1	7 74773962..74789376	ENSG00000158517	174.6397335	2.303423466	1.203779664	1.73542E-05	0.00180518
IRF7	11 complement(612553..615983)	ENSG00000185507	25.52544441	2.302529761	1.203219804	7.19074E-10	2.5669E-07
TAP1	6 complement(32845209..32853816)	ENSG00000168394	77.16860029	2.292936261	1.197196251	2.5339E-14	1.99E-11
MT1X	16 56682470..56684196	ENSG00000187193	55.99330374	2.291039187	1.196002136	3.54883E-09	1.072E-06

MT1F	16	56657731..56660698	ENSG00000198417	41.61409999	2.261993652	1.177594881	2.12515E-07	4.0494E-05
PSTPIP2	18	complement(45983536..46072272)	ENSG00000152229	9.615222702	2.245208484	1.166849416	2.26269E-07	4.2218E-05
SAMD9L	7	complement(93130056..93148385)	ENSG00000177409	20.63446254	2.242509774	1.165114273	9.34426E-11	4.3168E-08
NT5C3A	7	complement(33014130..33062796)	ENSG00000122643	14.00627827	2.217141812	1.14870105	7.88254E-07	0.0001202
TNFSF13B	13	108251240..108308484	ENSG00000102524	19.65128752	2.188001488	1.129613719	1.9149E-09	6.1382E-07
ASCL2	11	complement(2268498..2270588)	ENSG00000183734	3.082804916	2.18412436	1.127055003	2.08541E-07	4.0439E-05
HERC6	4	88378739..88443097	ENSG00000138642	5.088391189	2.131163588	1.091641339	3.2605E-07	5.6903E-05
H2AC18	1	complement(149842188..149842736)	ENSG00000203812	21.85113578	2.112139112	1.078704858	1.06216E-06	0.00015306
GMPR	6	16238587..16295549	ENSG00000137198	16.49933127	2.109276508	1.076748232	1.41586E-07	2.8512E-05
PLEKHA4	19	complement(48837097..48868617)	ENSG00000105559	1.123265798	2.096669233	1.068099283	0.00137346	0.06914405
EPOP	17	complement(38671703..38674957)	ENSG00000273604	3.651195647	2.090286532	1.063700718	0.000182585	0.01352765
ADM	11	10305073..10307397	ENSG00000148926	34.83671122	2.086698671	1.061222284	0.000198503	0.01450182
RTP4	3	187368385..187372076	ENSG00000136514	6.928414581	2.086228952	1.060897495	1.17292E-07	2.4241E-05
KLHDC7B	22	50545899..50551023	ENSG00000130487	2.734640229	2.063218772	1.044896804	6.03879E-10	2.2584E-07
SAMD9	7	complement(93099513..93118023)	ENSG00000205413	8.151163581	2.054154025	1.038544362	2.32356E-06	0.00029944
H4C14	1	149832659..149839767	ENSG00000270882	1.097728649	2.036353574	1.02598808	0.001966363	0.09037107
DHX58	17	complement(42101404..42112714)	ENSG00000108771	9.338727952	2.020661668	1.014827783	9.84091E-07	0.00014312
DDX60	4	complement(168216291..168318883)	ENSG00000137628	4.037195509	2.019847192	1.014246153	4.10198E-09	1.1931E-06

Downregulated genes (27)

gene:ENSG00000261915	17	complement(7312661..7319174)	ENSG00000261915	0.456462831	-214.4526338	-7.744515225	0.000196116	0.01439439
gene:ENSG00000257767	12	111753890..111791418	ENSG00000257767	1.156705755	-169.2896929	-7.403350328	0.000751156	0.04386027
gene:ENSG00000248751	22	complement(30285238..30299482)	ENSG00000248751	0.30642131	-24.18583403	-4.596090384	7.87999E-05	0.00691458
TRIM39-RPP21	6	30328907..30346854	ENSG00000248167	0.447463158	-19.42770075	-4.280043264	0.00017771	0.01329188
gene:ENSG00000276612	21	complement(5116343..5133805)	ENSG00000276612	1.01879941	-19.26754923	-4.268101172	1.68945E-10	6.9832E-08
gene:ENSG00000260537	16	70299194..70372582	ENSG00000260537	1.928482072	-17.86494985	-4.159059959	2.27925E-11	1.1548E-08
BBS1	11	66510606..66533613	ENSG00000174483	0.229229066	-16.82793681	-4.072786401	7.62013E-07	0.00011734
C10orf105	10	complement(71711701..71737824)	ENSG00000214688	0.109411136	-13.28752025	-3.731999985	0.000109071	0.0089695
UBE2F-SCLY	2	237967014..238099412	ENSG00000258984	0.360375988	-12.06462464	-3.592711126	0.00017462	0.01312322
CORO7-PAM16	16	complement(4340251..4420494)	ENSG00000103426	2.266968693	-11.1762588	-3.482365429	8.60691E-15	7.1152E-12
gene:ENSG00000284292	7	99325879..99394653	ENSG00000284292	0.28133845	-9.160108204	-3.19536464	0.000690535	0.04077538
gene:ENSG00000256966	9	complement(37512547..37592469)	ENSG00000256966	0.449494486	-8.499042431	-3.087300305	0.001211057	0.06340693
gene:ENSG00000131152	16	complement(87302876..87334273)	ENSG00000131152	0.530329369	-8.172933202	-3.030853943	0.001912778	0.08915135

SPECC1L-ADORA2A	22	24270898..24442356	ENSG00000258555	0.110945536	-6.466921119	-2.693079013	0.002096681	0.09517826
MROH7-TTC4	1	54641786..54742308	ENSG00000271723	0.131713714	-6.329667512	-2.662129719	0.000615351	0.03703189
gene:ENSG00000263020	6	31666102..31673546	ENSG00000263020	0.347734693	-5.364018933	-2.423314329	0.000354421	0.023489
NPIPA8	16	complement(18317942..18336736)	ENSG00000214940	0.664360242	-3.407761467	-1.768824355	0.002235169	0.09861742
RAB4B-EGLN2	19	40778242..40808418	ENSG00000171570	8.964335615	-3.014710459	-1.592019449	9.3086E-06	0.00102965
gene:ENSG00000285976	6	63572472..63583587	ENSG00000285976	2.219782916	-2.859250055	-1.515636796	5.76829E-10	2.2098E-07
CBSL	21	complement(6444869..6468040)	ENSG00000274276	4.220662007	-2.791646985	-1.481116518	0.001105267	0.05965783
gene:ENSG00000268173	19	18153158..18178117	ENSG00000268173	0.397169895	-2.637928461	-1.39940544	0.000969789	0.05382501
ARPC4-TTL3	3	9793082..9835401	ENSG00000250151	0.903435284	-2.603042676	-1.380198964	1.86702E-05	0.00190424
gene:ENSG00000285000	5	77030902..77152155	ENSG00000285000	2.534671139	-2.220875307	-1.151128394	0.000577551	0.03502546
gene:ENSG00000256861	12	complement(122207779..122266423)	ENSG00000256861	4.445409892	-2.159171352	-1.11047774	0.000479847	0.03039097
ADAMTS1	21	complement(26835755..26845409)	ENSG00000154734	0.921472779	-2.123596122	-1.086509412	9.0826E-05	0.00771138
CFAP298-TCP10L	21	complement(32402511..32612865)	ENSG00000265590	0.11134487	-2.115240983	-1.080822034	0.002242654	0.0986705
gene:ENSG00000268790	19	complement(16577642..16660115)	ENSG00000268790	3.922367843	-2.035268934	-1.025219441	1.42042E-05	0.00151772

D: Diabetes; h: HAM; 72: 72 hr p.i.; +: *M.tb* infected; -: *M.tb* uninfected