Supplemental Information

Acetate Promotes T Cell Effector Function

during Glucose Restriction

Jing Qiu, Matteo Villa, David E. Sanin, Michael D. Buck, David O'Sullivan, Reagan Ching, Mai Matsushita, Katarzyna M. Grzes, Frances Winkler, Chih-Hao Chang, Jonathan D. Curtis, Ryan L. Kyle, Nikki Van Teijlingen Bakker, Mauro Corrado, Fabian Haessler, Francesca Alfei, Joy Edwards-Hicks, Leonard B. Maggi Jr., Dietmar Zehn, Takeshi Egawa, Bertram Bengsch, Ramon I. Klein Geltink, Thomas Jenuwein, Edward J. Pearce, and Erika L. Pearce

SUPPLEMENTARY FIGURES AND TABLES

Figure S1

Figure S2

Figure S3

Table S1

Figure S1 (Related to Figure 1)

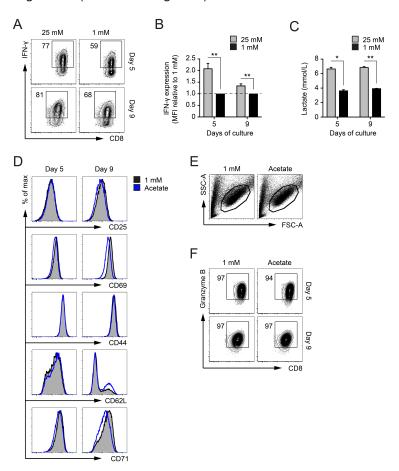


Figure S1. While promoting IFN-γ production, acetate does not affect expression of surface markers, granzyme B, or cell size of glucose-restricted T cells. Related to Figure 1.

A, FACS analysis of IFN- γ production by T cells cultured continuously for 5 or 9 days in 25 mM glucose or switched to 1 mM glucose on day 3 and cultured as described in Fig. 1A. Numbers show percentage of IFN- γ ⁺ cells. FACS plots are representative of n=3 independent experiments. **B**, Quantification of IFN- γ production as MFI of the CD8⁺ population as shown in A. Values were normalized to the 1 mM condition. Mean \pm SEM; Student's t test; n=3 independent experiments. **C**, Quantification of lactate production, as measure of aerobic glycolysis, in the medium of cells cultured for 24 hours in the indicated conditions. Mean \pm SEM; n=3 independent experiments. **D**, FACS analysis of surface expression of the indicated markers on T cells cultured as described in Fig. 1A. FACS plots show representative data of n=2 independent experiments. **E**, FACS analysis of the physical parameters forward scatter (FSC, indicating cell size) and side scatter (SSC, indicating the cell shape complexity) of T cells cultured as in Fig. 1A. Analysis was performed at day 5 post-activation. No previous gating strategy was applied before plotting FSC and SSC. The gate indicates the FSC/SSC gate used throughout the manuscript for further analysis. **F**, FACS analysis of Granzyme B production by T cells cultured as described in Fig. 1A. Numbers show percentage of Granzyme B roduction by T cells cultured as described in Fig. 1A. Numbers show percentage of Granzyme B roduction

Figure S2 (Related to Figure 2)

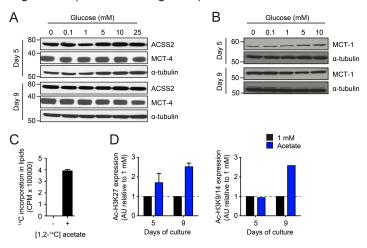


Figure S2. Acetate is incorporated into lipids and histones of glucose-restricted T cells. Related to Figure 2.

A, Western blot analysis of ACSS-2 and MCT-4 in T cells cultured in different glucose concentrations. Data are representative of n=3 (for ACSS2) and n=1 (for MCT-4) independent experiments. **B,** Western blot analysis of MCT-1 in T cells cultured in different glucose concentrations. Data are representative of n=1 experiment. **C,** Quantification of $[1,2^{-14}C]$ acetate-derived ^{14}C incorporation in lipids extracted from T cells cultured in 10 mM glucose media. Mean \pm SEM; n=2 independent experiments. **D,** Quantification of western blots of H3K9/14 and H3K27 acetylation in T cells treated as described in Fig. 1A. Data are representative of n=2 (n=1 for Ac-H3K9/14) independent experiments.

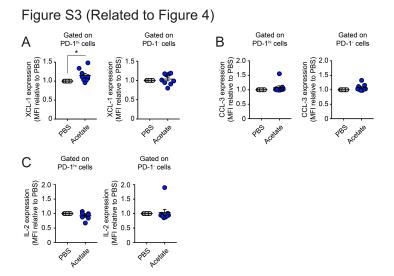


Figure S3. Głłgev'qh'ccetate qp'EF: 'V'egm'lt qo 'J EX/lphgevgf 'r cvlgpw0Related to Figure 4.

A-C, Chemokine and cytokine expression in PBMCs isolated from the blood of patients chronically infected with hepatitis C virus (HCV). Cells were treated overnight with either PBS or 5 mM acetate. Data show MFI of the indicated parameters. Values are normalized to the PBS counterparts. Mean \pm SEM; Paired Student's t test; data from n=9 donors.

Table S1 (Related to Figure 3)

Α	1600020E01Rik	Dlgap1	Gm23701	Myo1d	Slfn10-ps
•	1700072G22Rik	Dmrta2os	Gm2453	Nampt	Smarcd3
	2010111101Rik	Dnah3	Gm24819	Ndfip2	Snx20
	2610306M01Rik	Dnajb6	Gm25283	Nebl	Spcs3
	2900011008Rik	Dnajc5b	Gm25505	Nkx1-1	Spice1
	4921523L03Rik	Dnase1I3	Gm25916	NoI10	Srek1ip1
	4930447M23Rik	Dnmt1	Gm26686	Notch2	St8sia1
	4930519F16Rik	Dock10	Gm26827	Nr4a3	Stk40
	4930555B11Rik	Dock6	Gm27007	Nrros	Stra8
	4930565D16Rik	Dok6	Gm37549	Oma1	Syde2
	5031415H12Rik	E130102H24Rik	Gm38122	Oxsr1	Syne1
	5730508B09Rik	E330017L17Rik	Gm38130	P2ry2	Tbc1d31
	9130204K15Rik	Ebf1	Gm38337	Pak6	Tcof1
	A330074K22Rik	Eci2	Gm42791	Pati2	Tctex1d1
	A930006K02Rik	Efcab2	Gm5544	Pdcd10	Tec
	Abi1	Eif2ak3	Gm7895	Pear1	Tespa1
	Adam32	Emb	Gm8926	Pgk1	Tg
	Add3	Ercc6l2	Gna13	Phipp1	Tmem19
	Akap13	Fam105a	Gng2	Pim3	Tmem229b-ps
	Aldh18a1	Fam178b	Gpr132	Plscr5	Tmem70
	Angel1	Fam49a	H3f3a	Plxdc2	Tnfrsf8
	Ankrd44	Fbln1	Haao	Por	Trav15n-1
	Ankrd50	Fbxl20	Hbs1l	Ppm1h	Trim69
	Aph1a	Fbxo32	Hmgb3	Ppp6r1	Trpm8
	Arhgap10	Fcamr	Hmgcs2	Prex1	Ttc27
	Arl4a	Fcrl5	lfngr1	Prkch	Uba7
	Art2a-ps	Fcrl6	lqsec1	Psmd14	Ubap2
	AsxI1	Fhad1 Fhi2	ltpkb	Ptgs2os2	Ubash3b
	Atg9a		ltpr1	Ptpn1	Ublcp1
	Bbx Bcl9	Focad Foxb2	Katnal1 Katnh1	Ptpn5	Ubr2
	Bci9 Bhihe40		Katnb1 Kcnd3	Ptprj Rab31	Ucp3 Utrn
	Bnine40 Bod1	Frg1 Fuom	Kond3 Konh6	Rabat Ralgapa2	Utm Vps26b
	C230024C17Rik	Fuom	Kdm5a	Raigapaz Raigps2	Vpszeb Wdr7
	Cacna1b	Gad1-os	Khdc1b	Raigps2 Rasgef1b	Wis
	Cacila ib	Gaur-ps Gaint7	Kif1bp	Rassf2	Zcchc9
	Cacui i Camk4	Ganbp1	Kif24	Rbms1	Zdhhc14
	Carnk4	Glyr1	Kirrel3	Rhoh	Zfand4
	Casp3	Gm11684	Kihi30	Rhoa	Zfp330
	Casps Cass4	Gm12536	Larp4b	Ripor2	Zfp365
	Ccdc148	Gm12694	L doc1l	Rnu5a	Zfp407
	Cd226	Gm12709	Lpar4	Rps2-ps5	Zfp521
	Cd220	Gm12862	Lrrc8d	Rps21	Zfp629
	Cdbr4	Gm13217	Maf	Rtcb	Zfp677
	Celf5	Gm14569	Map6	Scube1	Zfp697
	Chsv1	Gm14848	Mcf2I	Serpina12	Zmiz1
	Col15a1	Gm15407	Mepe	Serpinb9	Zzz3
	Col9a3	Gm15848	Mgat5	Sidt1	
	Commd7	Gm16418	Micalcl	Sialeca	
	Cpox	Gm17767	Mirt1	Sik3	
	Crhr2	Gm20388	MIIt3	Sla	
	Dapp1	Gm20661	Mrps5	Slc22a14	
	Def6	Gm21614	Msra	Slc4a10	
	Dera	Gm23218	Mybpc3	Slco4a1	
			, - роо		

В	Gene Ontology Term	Count	p value
_	GO:0035335~peptidyl-tyrosine dephosphorylation	4	0.001630408
	GO:0004721~phosphoprotein phosphatase activity		0.002797221
	GO:0005085~guanyl-nucleotide exchange factor activity		0.004925604
	GO:0006470~protein dephosphorylation	6	0.011846165
	GO:0005089~Rho guanyl-nucleotide exchange factor activity	4	0.038306049
	GO:0016310~phosphorylation	12	0.04000219
	GO:0004672~protein kinase activity	11	0.041832928
	GO:0008270~zinc ion binding	18	0.042151818
	GO:0002250~adaptive immune response	5	0.04865825
	GO:0043407~negative regulation of MAP kinase activity	3	0.06691431
	GO:0004725~protein tyrosine phosphatase activity	4	0.073957904
	GO:0000166~nucleotide binding	27	0.074797927
	GO:0004722~protein serine/threonine phosphatase activity	3	0.098974731

Table S1. Acetate enhances chromatin accessibility of genes associated with T cell signaling. Related to Figure 3.

 $\bf A$, List of the 263 genes associated with the 255 open chromatin peaks resulting from acetate treatment of day 9 glucose-restricted cells, as in Fig. 3B. $\bf B$, Pathway enrichment analysis of the genes indicated in A. Gene ontology terms are listed in order of ascending p value and the number of genes associated to each gene ontology term is indicated.