

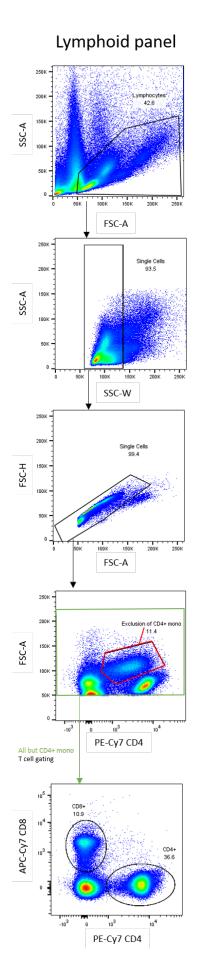
## **Supplementary Material**

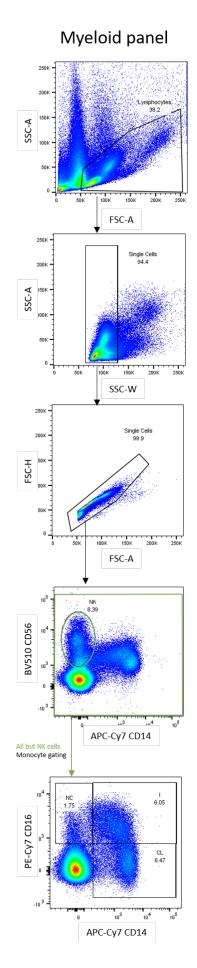
## **1** Supplementary Figures and Tables

## Supplementary Table 1. List of all qRT-PCR primers

Predesigned qPCR assays (IDT)					
Name	Ref Seq	Exon location	Assay ID		
Human					
18S	NR_003286(1)	Exon 1-1	Hs.PT.39a.22214856.g		
TSC22D3 (GILZ)	NM_001015881(3)	Exon 4-5	Hs.PT.58.4331913		
FKBP5	NM_001145775(4)	Exon 7-8	Hs.PT.58.20699604		
Mouse					
TSC22D3 (GILZ)	NM_001077364(1)	Exon 2-5	Mm.PT.58.42845144		
FKBP5	NM_010220(1)	Exon 8-9	Mm.PT.58.45861921		

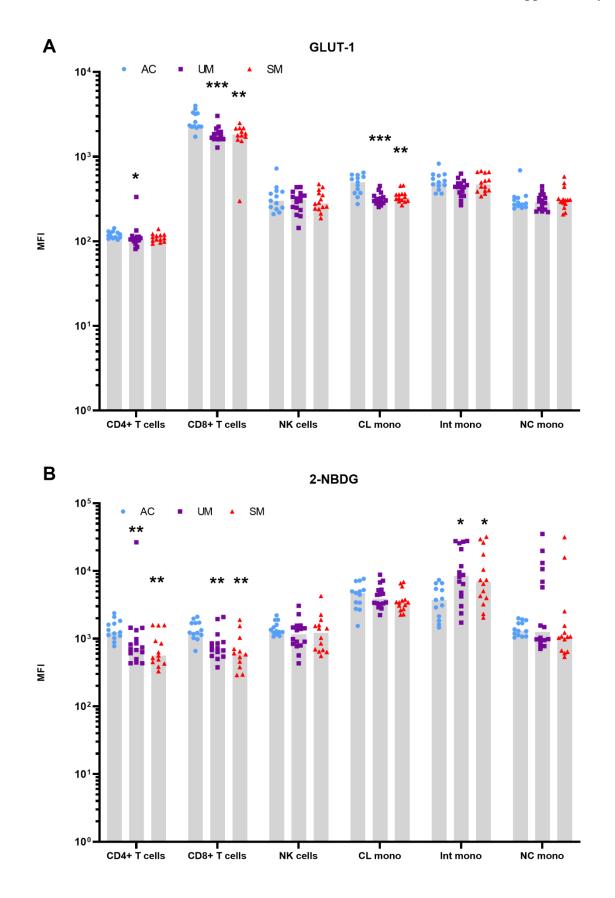
Customized primers					
Name	Forward primer	<b>Reverse primer</b>	6-FAM/ZEN/IBFQ		
			Probe		
GRα	5'- AGAACTGGCAGCGG TTT-3'	5'- GATTGGTGATGATT TCAGCTAAC-3'	5'- ACTCTTGGATTCTAT GCATGAAGTGGTTG A-3'		



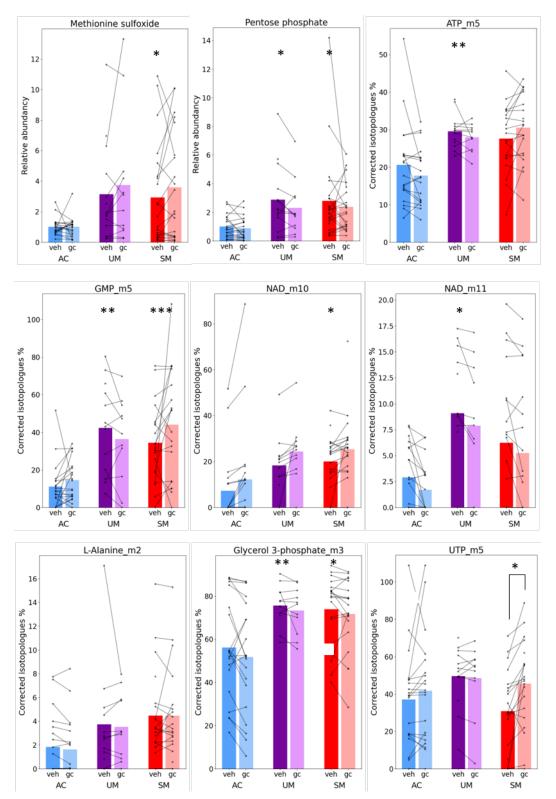


## Supplementary Figure 1. Flow cytometry gating.

PBMCs were isolated and after 2-NBDG incubation, the cells were stained with a lymphoid and a myeloid panel of antibodies. A representative example of the gating performed with the FlowJo v10 software is shown here with the gating of CD4<sup>+</sup> T cells (CD4<sup>+</sup>), CD8<sup>+</sup> T cells (CD8<sup>+</sup>), NK cells (NK), classical (CL), non-classical (NC) and intermediate (I) monocytes.



Supplementary figure 2. Expression of GLUT1 and uptake of 2-NBDG in different cell types. PBMCs were isolated, 2-NBDG uptake was allowed for 30 min and flow cytometry was performed. (A) Median fluorescence intensity (MFI) of GLUT-1 for the indicated subsets. (B) MFI of 2-NBDG for the indicated subsets. (A-B) Each symbol represents data from an individual. Bars represent group medians and analysis was by Mann-Whitney U-test. Asterisks above individual data sets indicate statistical differences compared to the HC group. \* p<0.05, \*\* p<0.01, \*\*\* p<0.001. NK: Natural Killer; CL mono: classical monocyte; Int mono: Intermediate monocyte; NC mono: Non-classical monocyte. AC n=13; UM n=16; SM n=14. For CD4<sup>+</sup> T cells: UM n=15; SM n=13 and for CD8<sup>+</sup> T cells: UM n=15; SM n=11.



**Supplementary figure 3: Relative abundancies and corrected isotopologue percentages of selected metabolites.** PBMCs were isolated and incubated for 24 hours with [U-<sup>13</sup>C]-glucose tracer and vehicle (veh) or 150 nM hydrocortisone (gc). Metabolic extracts were analyzed via mass spectrometry. Each symbol represents data from an individual. Bars represent the mean. Analysis by

t-test for comparison between the veh condition of different groups, indicated by asterisks above individual data sets. Analysis by paired t-test for GC-induced effects, indicated by asterisks above lines. Abundancies: AC n=20; UM n=14; SM n=22 veh. Isotopologues: AC n=20; UM n=13; SM n=20.