**Physiologic media renders human iPSC-derived macrophages permissive for *M. tuberculosis* by rewiring organelle function and metabolism**

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**Supplementary figures legends**

**Figure S1- Flow cytometry characterization of iPSDM differentiated with M-CSF or GM-CSF and cultured with different media.**

A,B. iPSDM, differentiated with M-CSF (A) or GM-CSF (B) and cultured in X-VIVO15, OXM, or HPLM, were stained for the indicated markers, and surface expression was evaluated by flow cytometry.

**Figure S2- GSEA analysis of GM-CSF vs M-CSF macrophage differentiation (positive enrichment) in different media.**

Top 25 pathways significantly enriched in GSEA (Padj < 0.05) ranked by NES (normalised enrichment score). A-C. Plots show the GSEA results of iPSDM cultured with X-VIVO15 (A), OXM (B) or HPLM (C) and the differential positive enrichment when compared GM-CSF with M-CSF differentiation programs (pathways enriched with GM-CSF differentiation). n = 3 technical replicates.

**Figure S3- GSEA analysis of GM-CSF vs M-CSF macrophage differentiation (negative enrichment) in different media.**

Top 25 pathways significantly enriched in GSEA (Padj < 0.05) ranked by NES (normalised enrichment score). A-C. Plots show the GSEA results of iPSDM cultured with X-VIVO15 (A), OXM (B) or HPLM (C) and the differential negative enrichment when compared GM-CSF with M-CSF differentiation programs (pathways enriched with M-CSF differentiation). n = 3 technical replicates.

**Figure S4- Supplementary data related to Figure 4**

A, B. Density plots show quantifications of lipid droplet (LD) content evaluated as LD area normalised to cell area in iPSDM differentiated with M-CSF (A) and GM-CSF (B) and cultured with the indicated media n= >400 cells per condition analysed. C, D. Density plots show quantifications of lysosomal content evaluated as iABP-positive puncta area normalised to cell area in iPSDM differentiated with M-CSF (C) and GM-CSF (D) and cultured with the indicated media n= >400 cells per condition analysed.

**Table S1.**

Table containing the complete Reactome Pathway enrichment analysis for the comparisons shown in Figure 2.

**Table S2.**

Table containing the complete Reactome Pathway enrichment analysis for the comparisons shown in Figure S3 and S4.

**Table S3**

Table containing the differentially expressed genes and pathway analysis related to Fig. 2E.