Salmonella enterica serovar Typhi exposure elicits *ex vivo* cell-type-specific epigenetic changes in human gut cells

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Supplementals

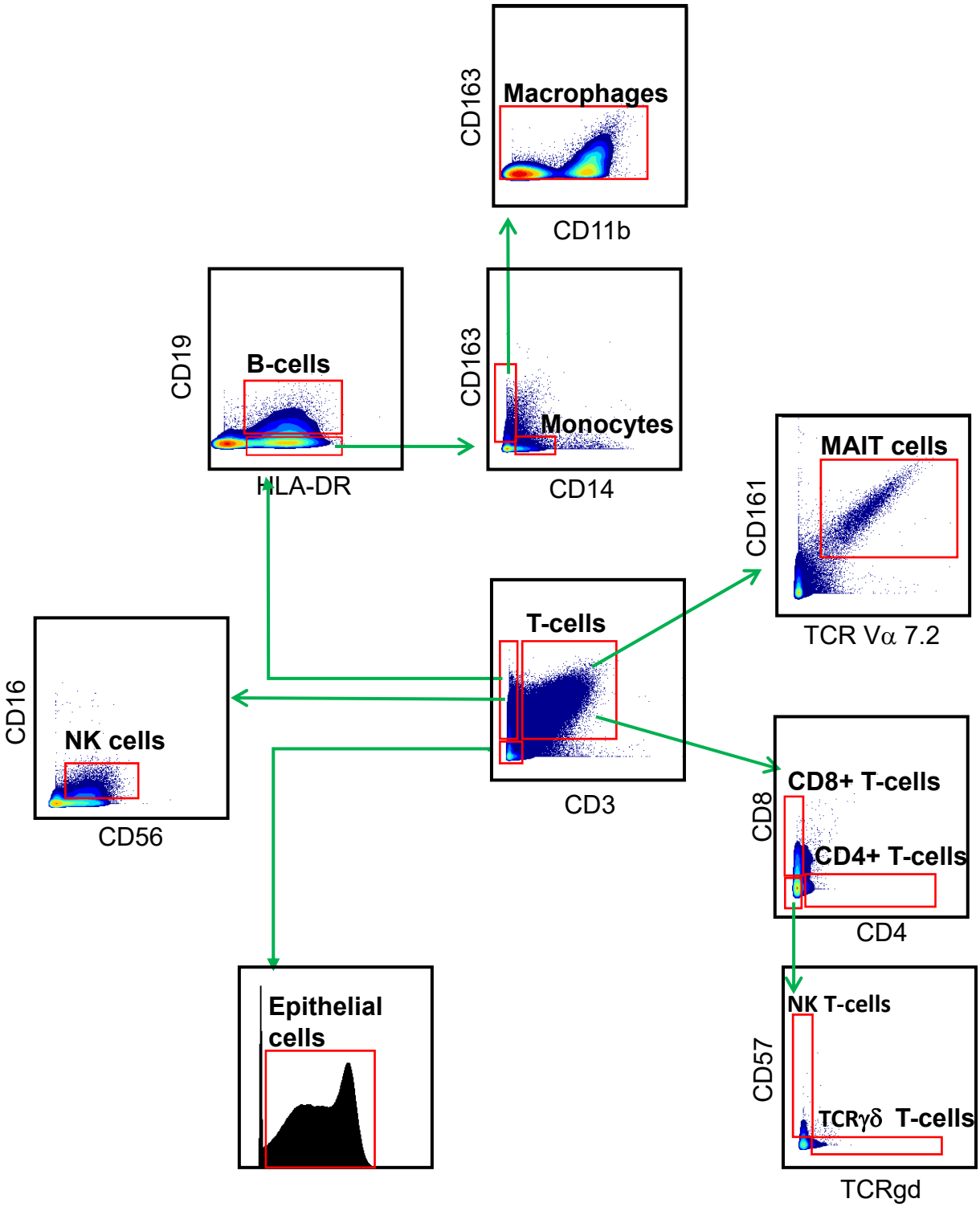
Supplementary table 1. Antibody panel used to evaluate chromatine changes

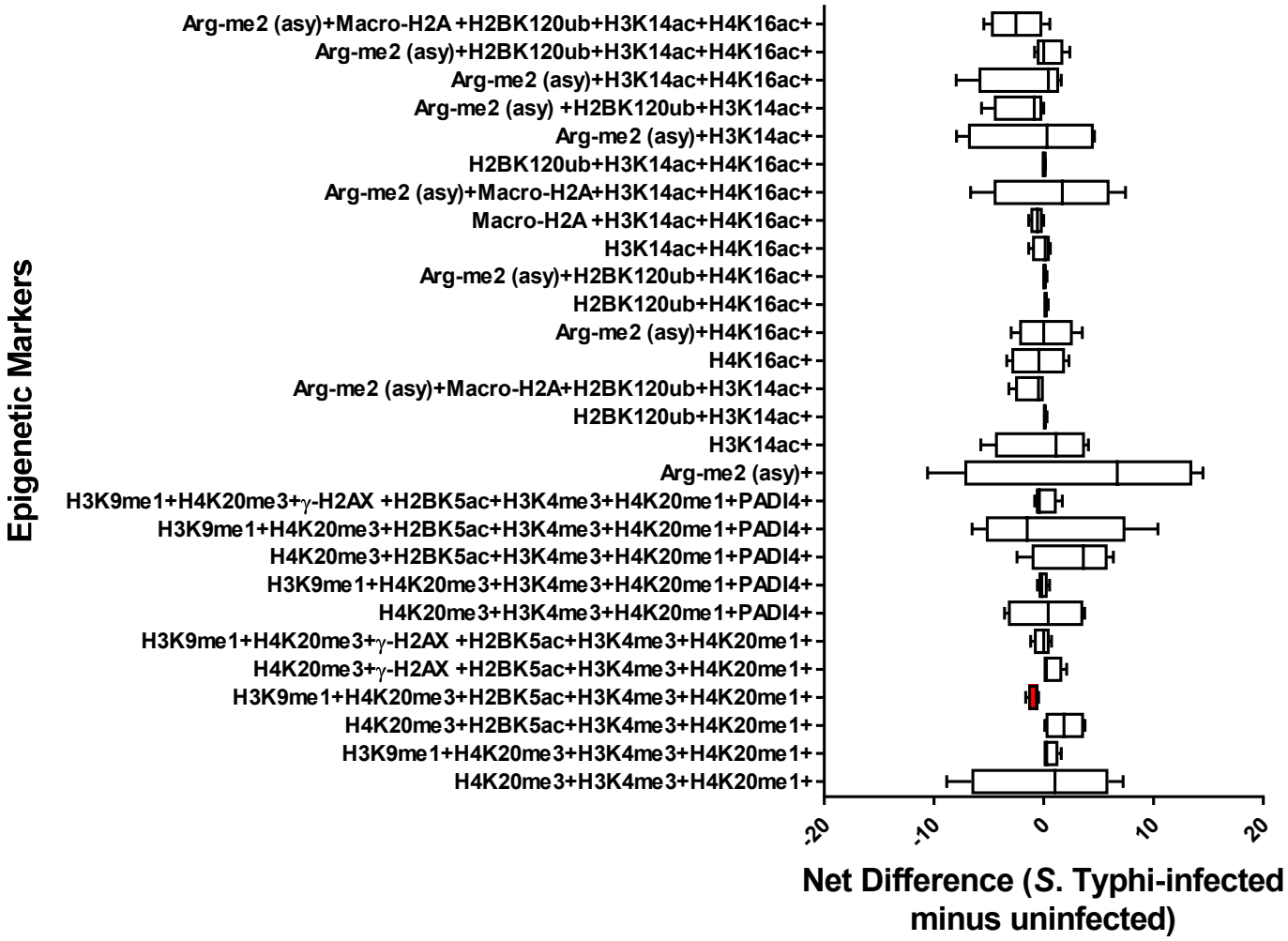
Atomic Mass:		Markers
1	89 Y	CD45
2	114 Cd	CD14
3	141 Pr	EpCAM
4	142 Nd	γ-H2AX
5	143 Nd	HLA-DR
6	144 Nd	CD38
7	145 Nd	CD163
8	146 Nd	CD8
9	148 Nd	CD16
10	149 Sm	CD45RO
11	150 Nd	H3
12	152 Sm	TCR$\gamma\delta$
13	153 Eu	Arg-me2 (asy)
14	154 Sm	H3K9me1
15	155Gd	H2BK5ac
16	156 Gd	H4K20me3
17	159 Tb	CD161
18	160 Gd	H2BK120ub
19	162 Dy	CD69
20	163 Dy	H3K4me3
21	164 Dy	H3K14ac
22	165 Ho	TCR Vα7.2
23	166 Er	H4K16ac
24	167 Er	CCR7
25	169 Tm	CD19
26	170 Er	CD3
27	171 Yb	H4K20me1
28	172 Yb	CD57
29	173 Yb	PADI4
30	174 Yb	CD4
31	175Lu	Macro-H2A
32	176 Yb	CD56
33	209 Bi	CD11b
Atomic Mass:		**Other:**
34	191/193 Ir	DNA content
35	194/195 Pt	Live/dead stain

Supplementary table 2. Epigenetic modifications evaluated in this manuscript

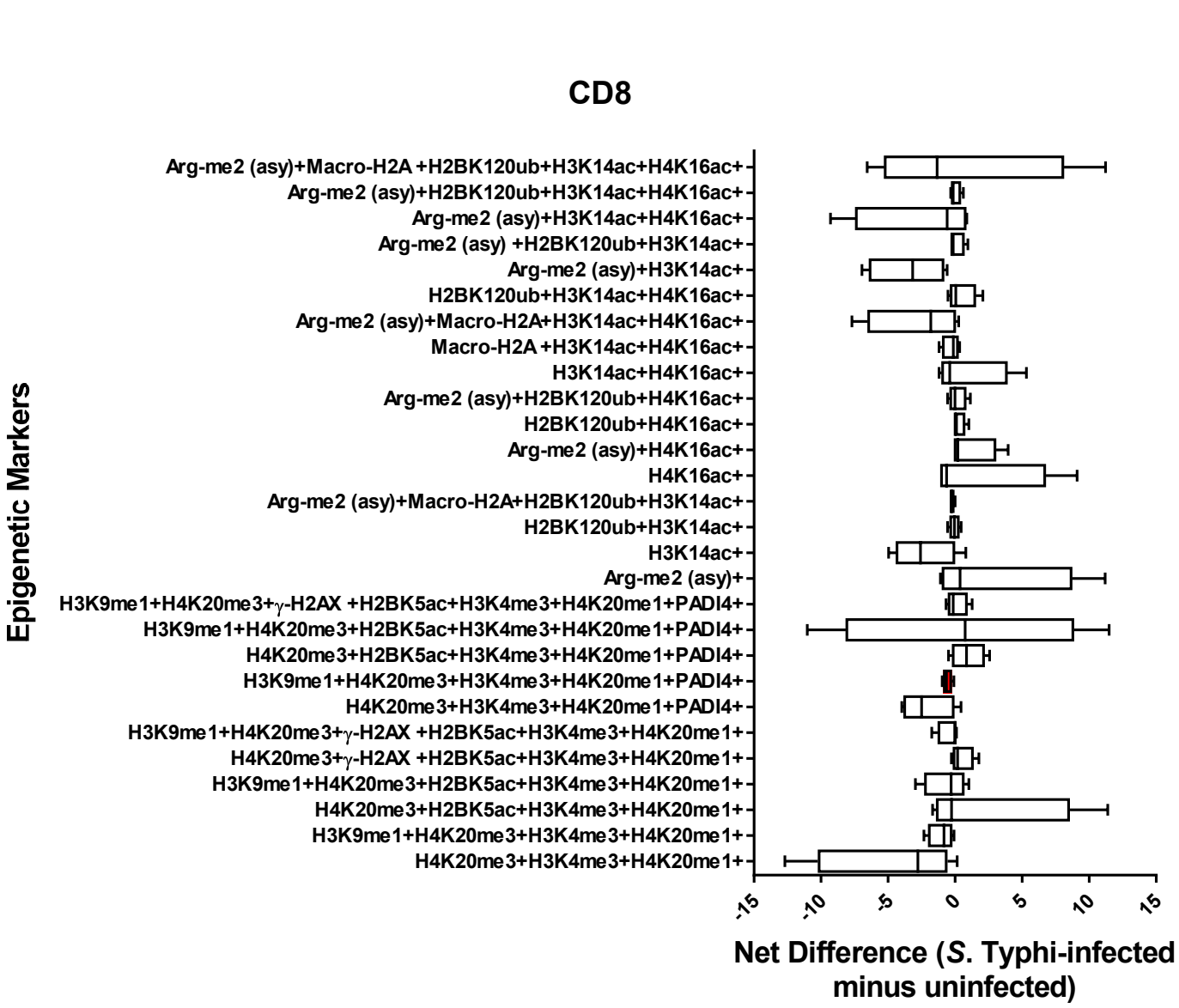
	Antibody		
Chromatine profile	**Clone**	**Vendor**	**Cat. #**
Histones			
H3	D1H2	Cell Signaling Technology	4499S
Histone Variant			
Macro-H2A	14G7	Millipore	MABE61
Post-translational modifications			
Lysine Methylation			
H4K20me1	5E10-D8	BioLegend	828001
H4K20me3	6F8-D9	Biolegend	827701
H3K9me1	7E7.H12	Biolegend	824201
H3K4me3	G.532.8	ThermoFisher	MA5-11199
Acetylation			
H2BK5ac	D5H1S	Cell Signaling Technology	12799S
H3K14ac	D4B9	Cell Signaling Technology	7627S
H4K16ac	E2B8W	Cell Signaling Technology	13534S
Phosphorylation			
γ-H2AX	20E3	Cell Signaling Technology	9718S
Citrullination			
PADI4	OTI4H5	OriGene	CF504813
Ubiquitination			
H2BK120ub	D11	Cell Signaling Technology	5546S
Arginine Methylation			
Arg-me2 (asy)	13522	Cell Signaling Technology	13522S

Supplementary Fig. 1. Gating procedure to identify cell lineage

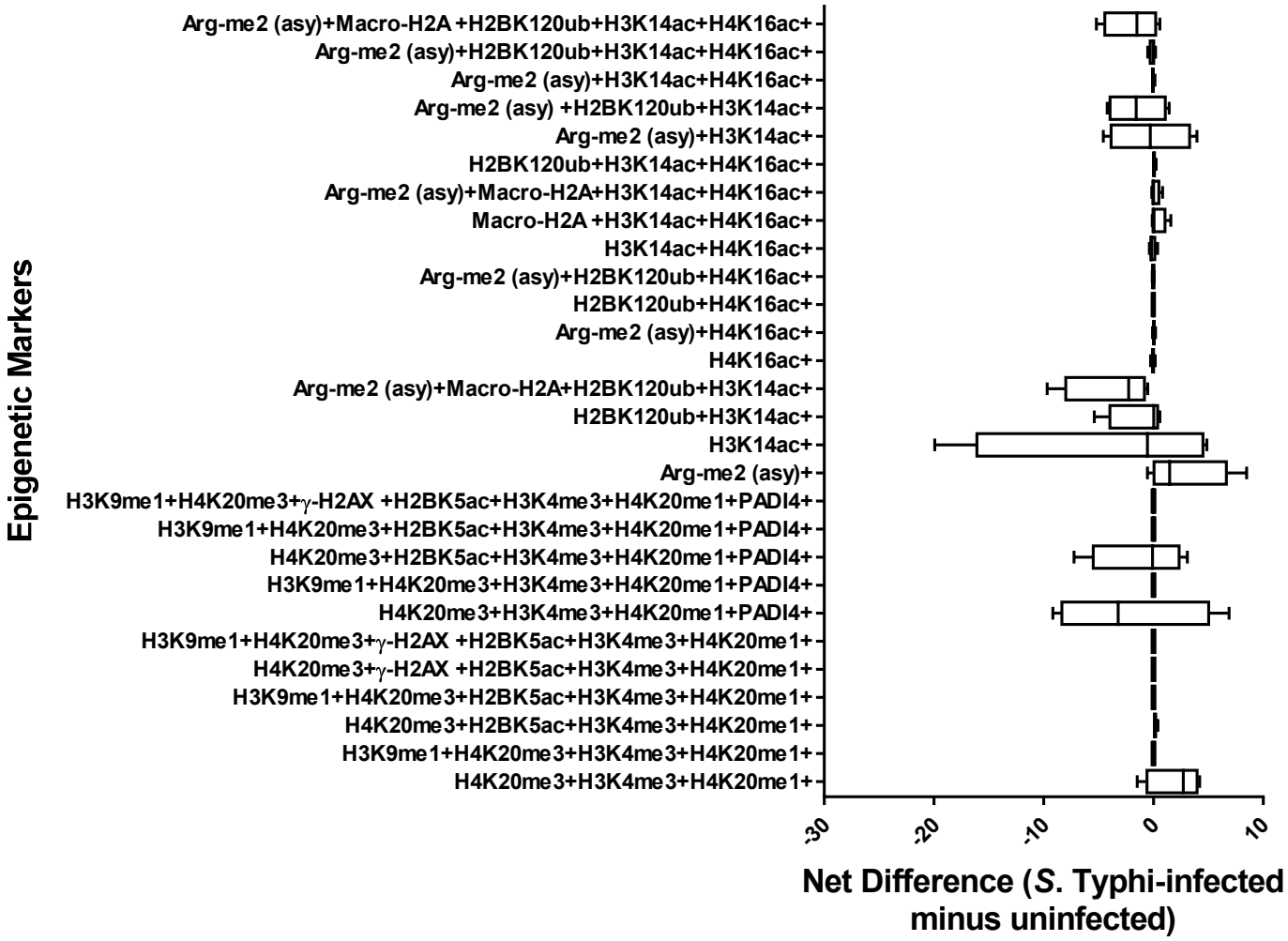




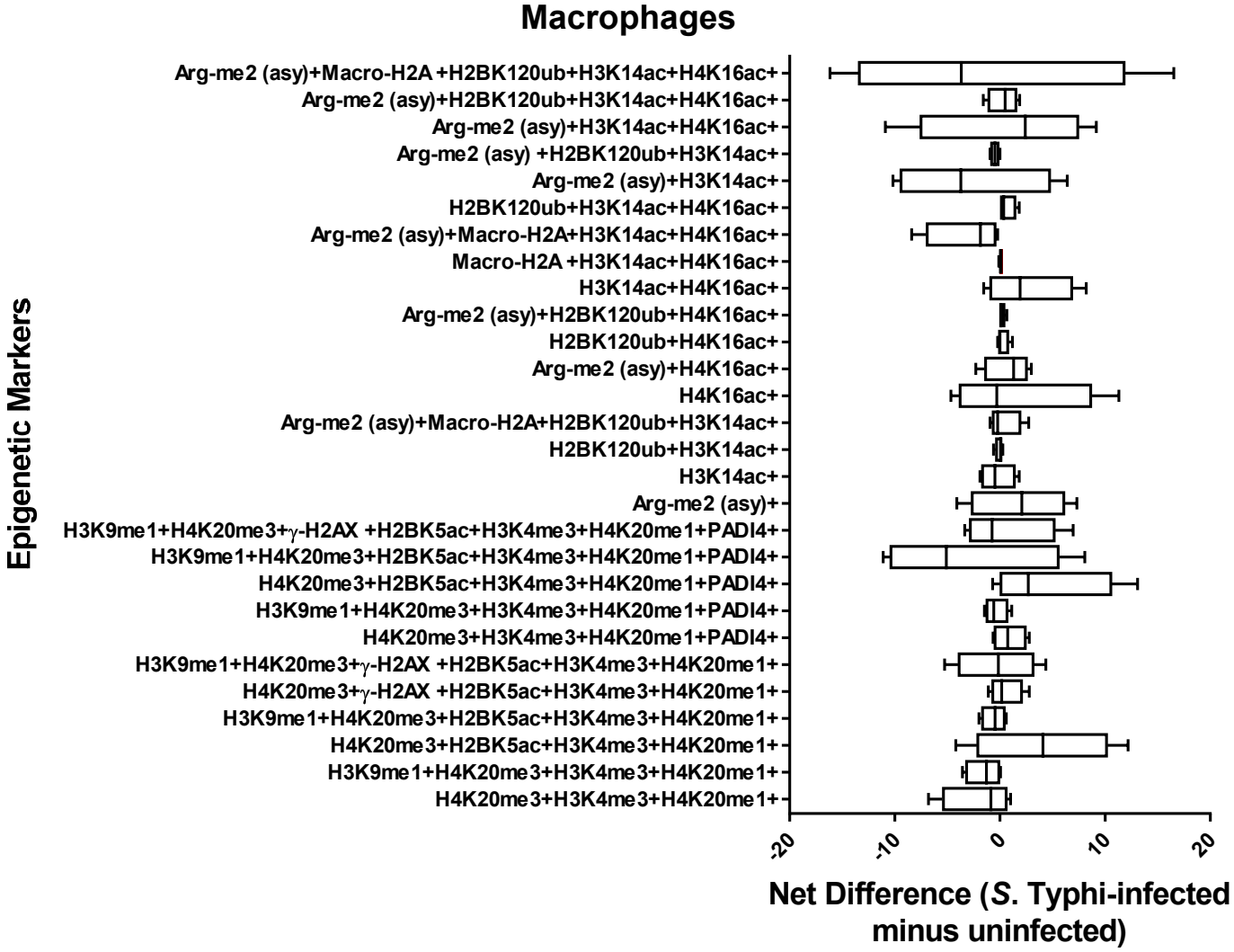
Supplementary Fig. 2. Chromatin profiles of the epigenetic changes in monocytes induced by *S*. Typhi. Cells isolated cells from healthy terminal ileum surgical tissues were exposed to *S*. Typhi strain Ty2 (**Ty2**), and cultured as described in **Fig. 1**. Cells cultured with media only were used as controls (**media**). FCOM data of the 28 combinations within the acceptability criteria for changes of the chromatin marks are shown. Bars represent the net difference (*S*. Typhi-infected minus uninfected cultures). Bar graphs extend from the 25th to 75th percentiles; the line in the middle represents the median of the pooled data. The whiskers delineate the smallest to the largest value. These data are representative of three experiments with terminal ileum segments from 4 different donors, one replicate each. *P* values <0.05 were considered significant (red-colored box).



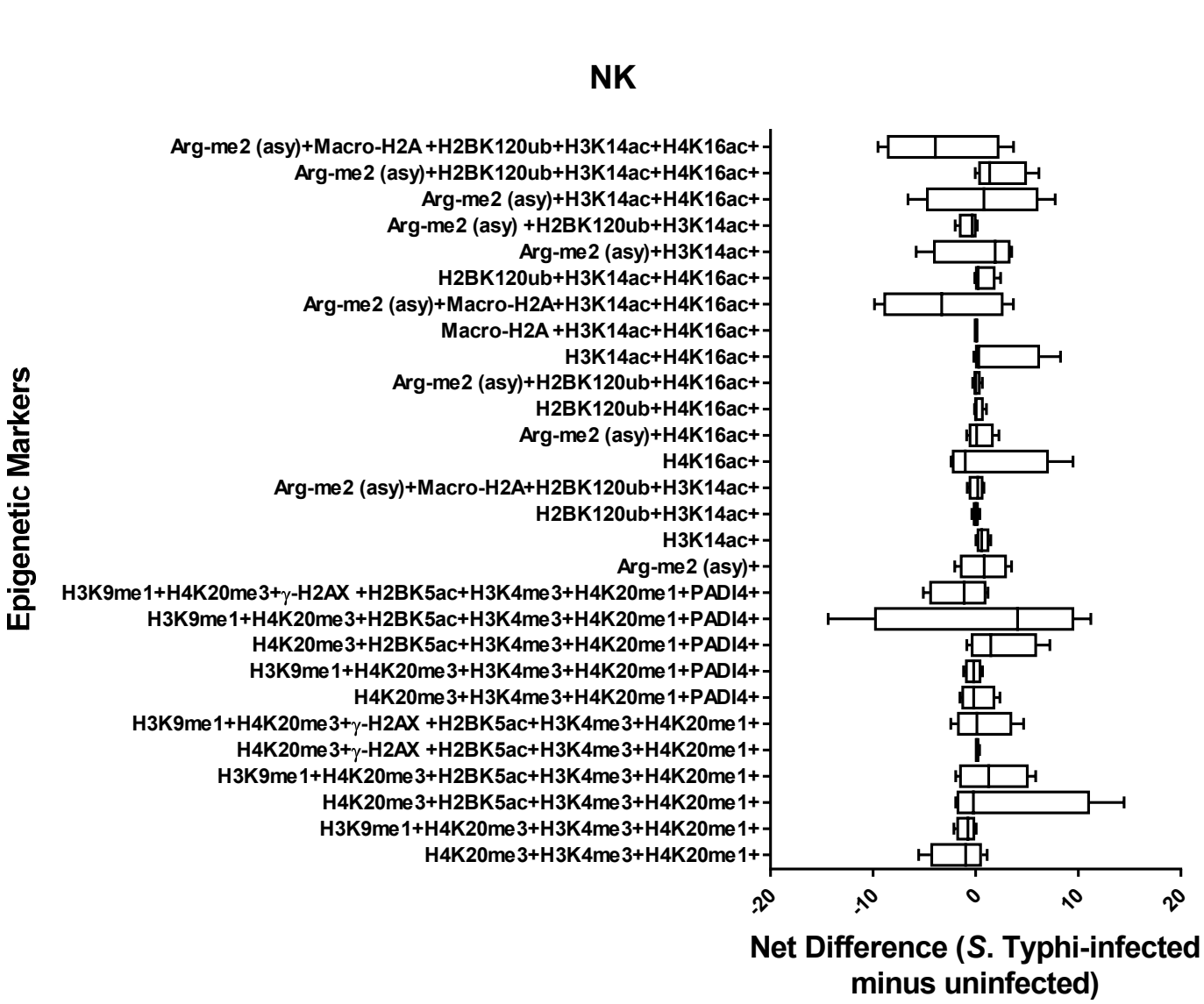
Supplementary Fig. 3. Chromatin profiles of the epigenetic changes in CD8+ T-cells induced by *S*. Typhi. Cells isolated cells from healthy terminal ileum surgical tissues were exposed to *S*. Typhi strain Ty2 (**Ty2**), and cultured as described in **Fig. 1**. Cells cultured with media only were used as controls (**media**). FCOM data of the 28 combinations within the acceptability criteria for changes of the chromatin marks are shown. Bars represent the net difference (*S*. Typhi-infected minus uninfected cultures). Bar graphs extend from the 25th to 75th percentiles; the line in the middle represents the median of the pooled data. The whiskers delineate the smallest to the largest value. These data are representative of three experiments with terminal ileum segments from 4 different donors, one replicate each. *P* values <0.05 were considered significant (red-colored box).



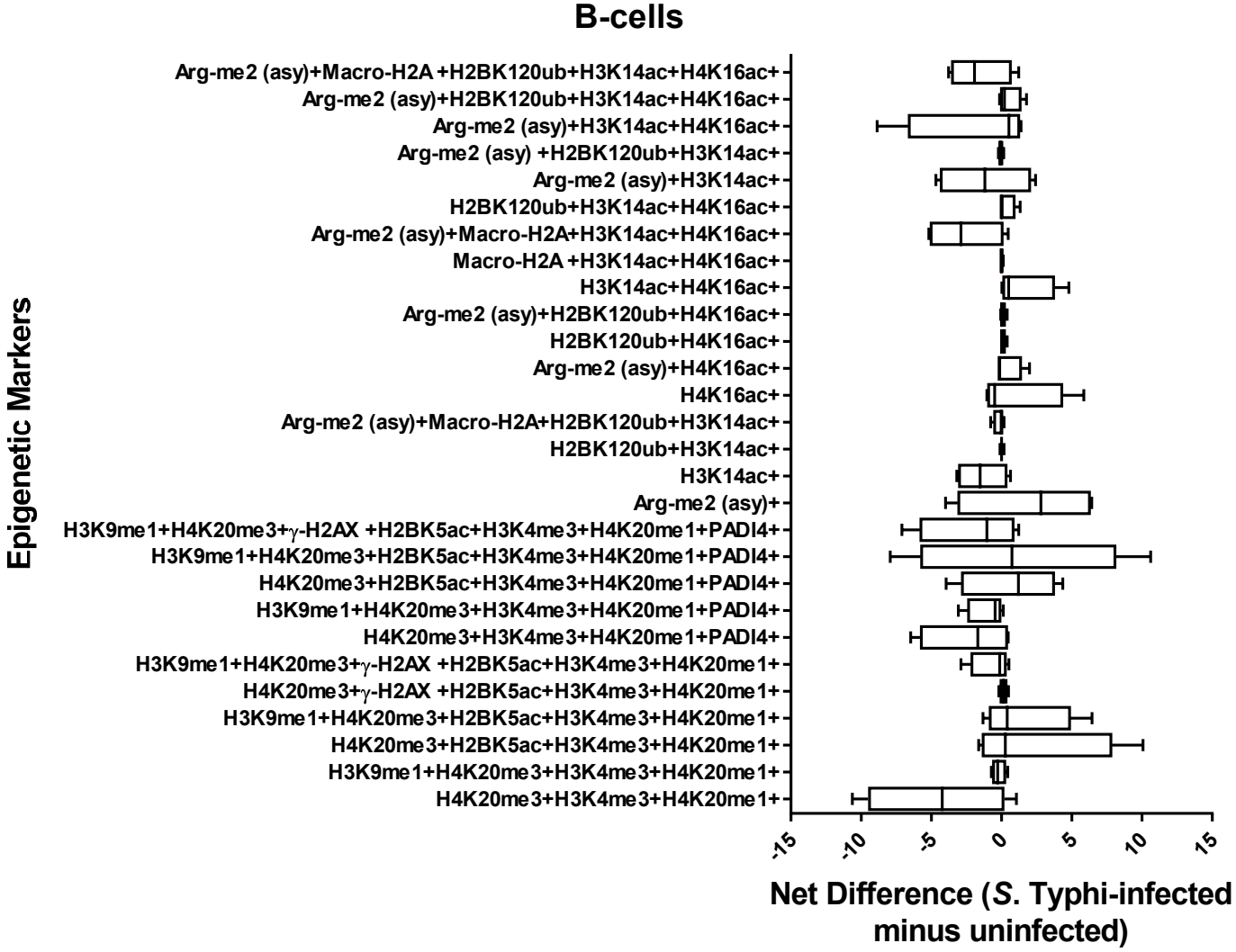
Supplementary Fig. 4. Chromatin profiles of the epigenetic changes in CD3+ T-cells induced by *S*. Typhi. Cells isolated cells from healthy terminal ileum surgical tissues were exposed to *S*. Typhi strain Ty2 (**Ty2**), and cultured as described in **Fig. 1**. Cells cultured with media only were used as controls (**media**). FCOM data of the 28 combinations within the acceptability criteria for changes of the chromatin marks are shown. Bars represent the net difference (*S*. Typhi-infected minus uninfected cultures). Bar graphs extend from the 25th to 75th percentiles; the line in the middle represents the median of the pooled data. The whiskers delineate the smallest to the largest value. These data are representative of three experiments with terminal ileum segments from 4 different donors, one replicate each.



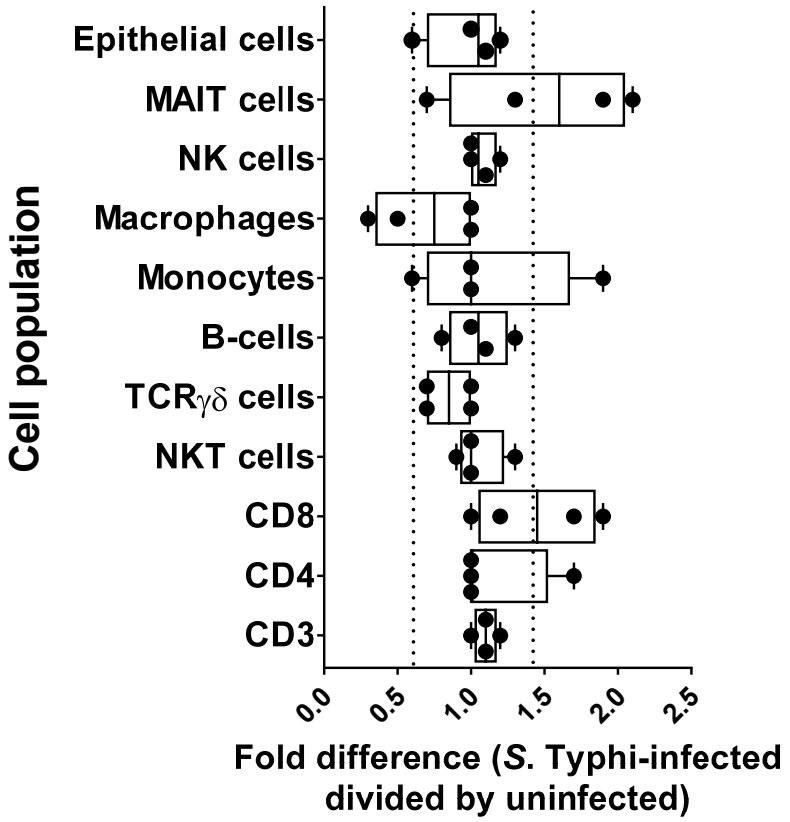
Supplemental Fig. 5. Chromatin profiles of the epigenetic changes in macrophages induced by *S*. Typhi. Cells isolated cells from healthy terminal ileum surgical tissues were exposed to *S*. Typhi strain Ty2 (**Ty2**), and cultured as described in **Fig. 1**. Cells cultured with media only were used as controls (**media**). FCOM data of the 28 combinations within the acceptability criteria for changes of the chromatin marks are shown. Bars represent the net difference (*S*. Typhi-infected minus uninfected cultures). Bar graphs extend from the 25th to 75th percentiles; the line in the middle represents the median of the pooled data. The whiskers delineate the smallest to the largest value. These data are representative of three experiments with terminal ileum segments from 4 different donors, one replicate each.



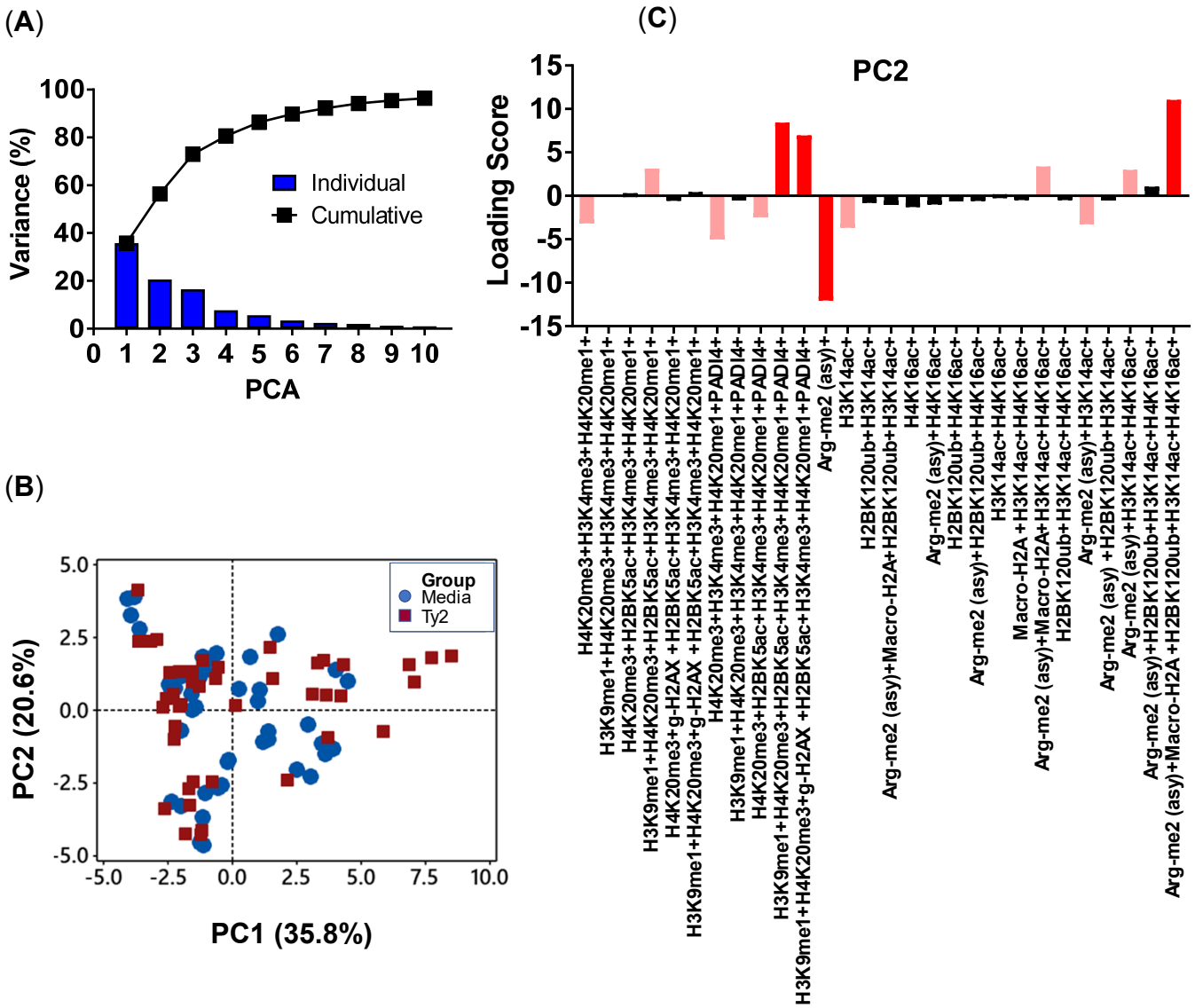
Supplemental Fig. 6. Chromatin profiles of the epigenetic changes in NK cells induced by *S.* Typhi. Cells isolated cells from healthy terminal ileum surgical tissues were exposed to *S*. Typhi strain Ty2 (**Ty2**), and cultured as described in **Fig. 1**. Cells cultured with media only were used as controls (**media**). FCOM data of the 28 combinations within the acceptability criteria for changes of the chromatin marks are shown. Bars represent the net difference (*S*. Typhi-infected minus uninfected cultures). Bar graphs extend from the 25th to 75th percentiles; the line in the middle represents the median of the pooled data. The whiskers delineate the smallest to the largest value. These data are representative of three experiments with terminal ileum segments from 4 different donors, one replicate each.



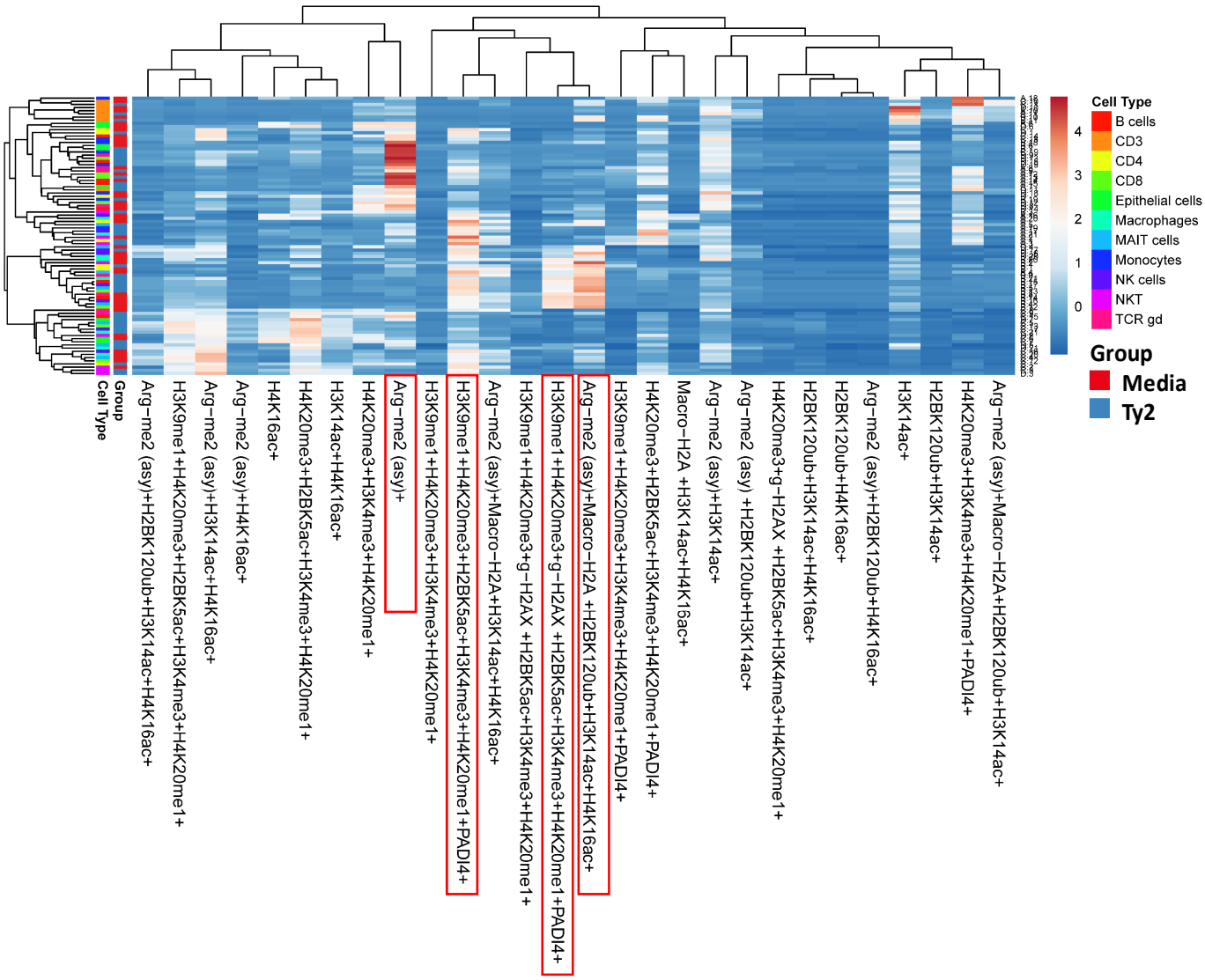
Supplemental Fig. 7. Chromatin profiles of the epigenetic changes in B-cells induced by *S.* Typhi. Cells isolated cells from healthy terminal ileum surgical tissues were exposed to *S*. Typhi strain Ty2 (**Ty2**), and cultured as described in **Fig. 1**. Cells cultured with media only were used as controls (**media**). FCOM data of the 28 combinations within the acceptability criteria for changes of the chromatin marks are shown. Bars represent the net difference (*S*. Typhi-infected minus uninfected cultures). Bar graphs extend from the 25th to 75th percentiles; the line in the middle represents the median of the pooled data. The whiskers delineate the smallest to the largest value. These data are representative of three experiments with terminal ileum segments from 4 different donors, one replicate each, one replicate each.



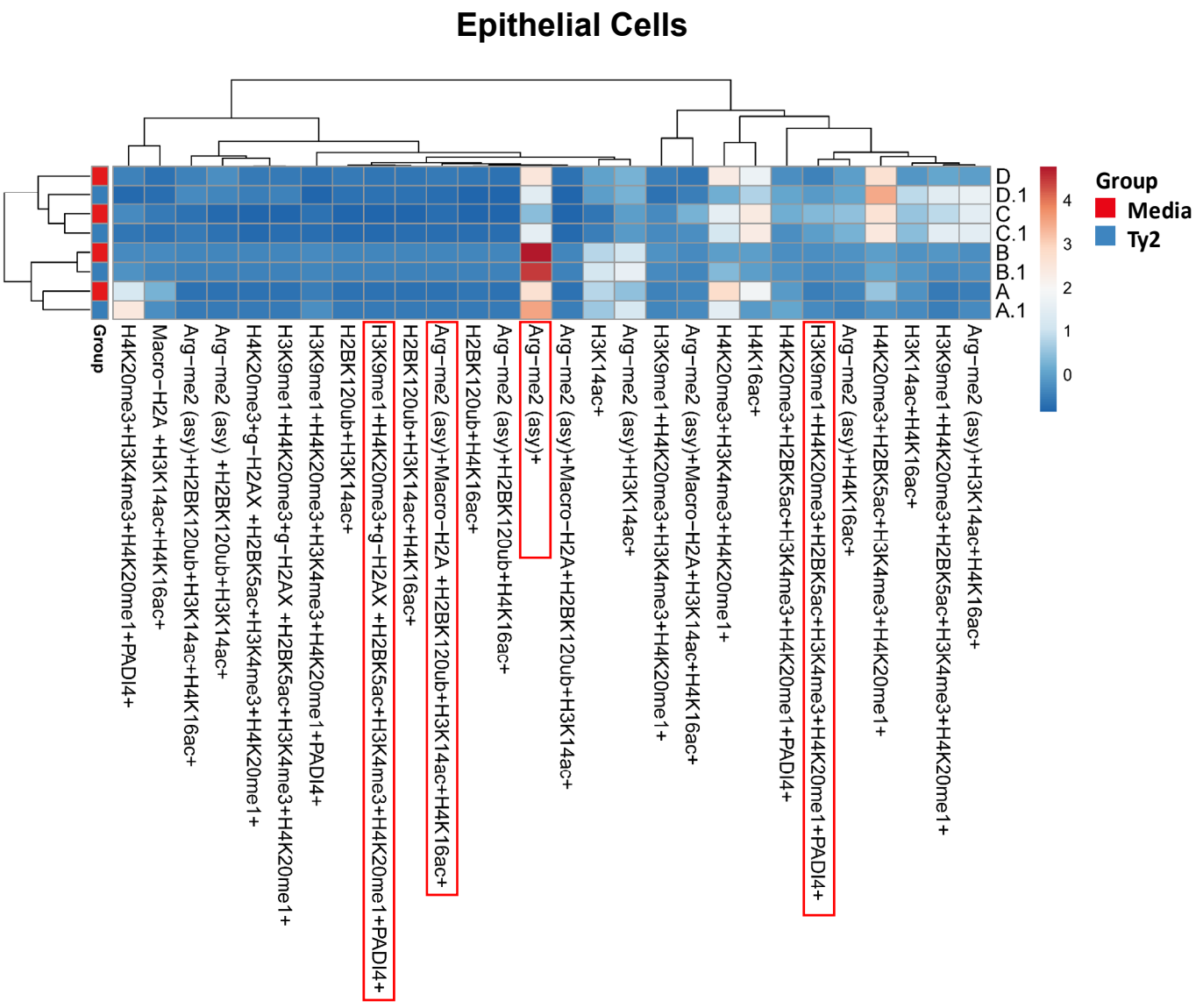
Supplemental Fig. 8. Chromatin profile of H3 histone changes in 11 cell subsets induced by *S*. Typhi. Cells isolated from healthy terminal ileum surgical tissues were exposed to *S*. Typhi strain Ty2 (**Ty2**), and cultured as described in **Fig. 1**. Cells cultured with media only were used as controls (**media**). Bars represent the fold difference (*S*. Typhi-infected divided by uninfected cultures). Bar graphs extend from the 25th to 75th percentiles; the line in the middle represents the median of the pooled data. The whiskers delineate the smallest to the largest value. These data are representative of three experiments with terminal ileum segments from 4 different donors, one replicate each. The doted lines express the data distribution within 95% confidence (± 2SD).



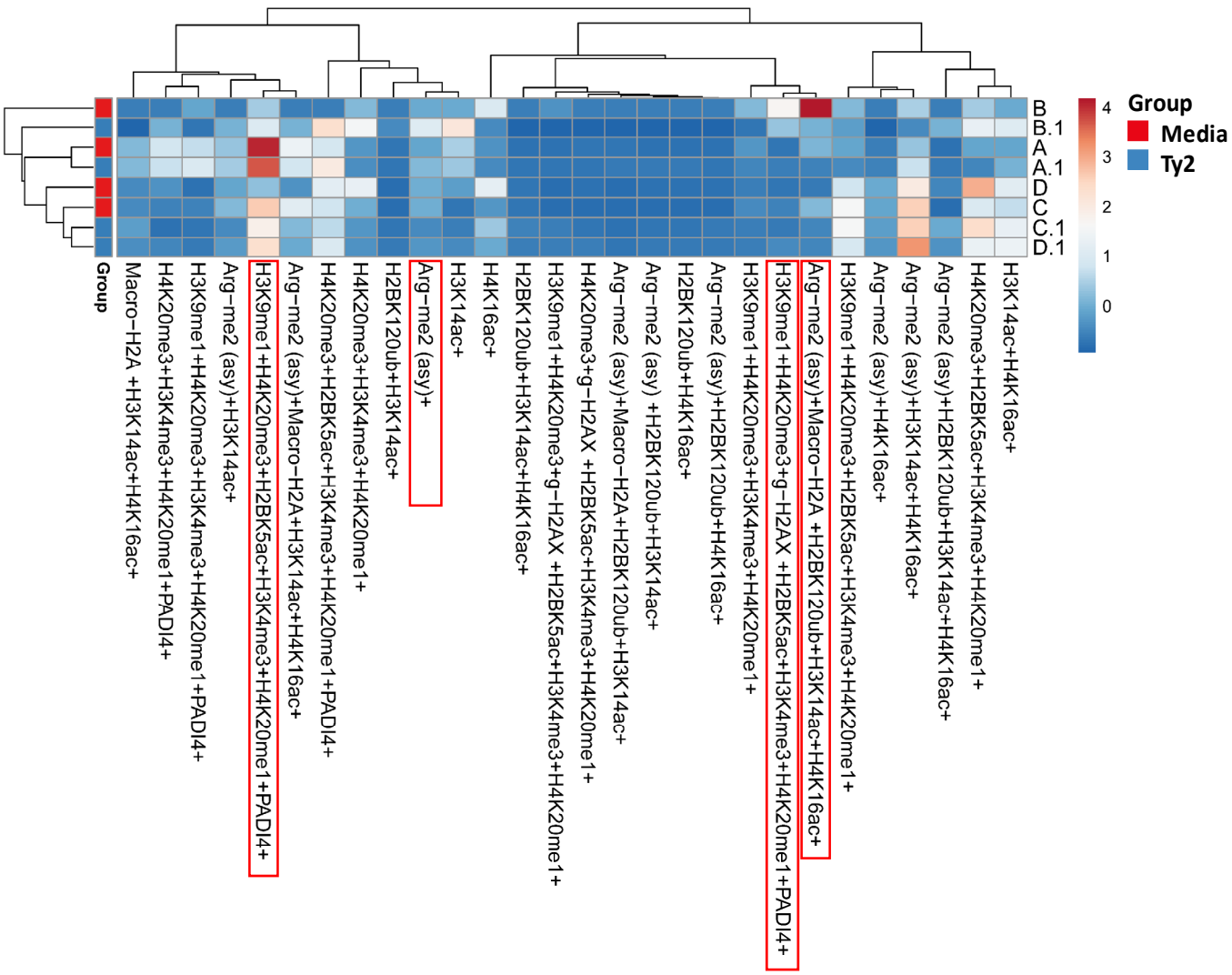
Supplemental Fig. 9. **Principal Component Analysis variances**. (**A**) The percent variation are plotted for each component (bars) and cumulatively (line).(**B**) Ability of PCA to separate FCOM data between media and Ty2 conditions. Each dot represents a single experimental condition, where each PC summarizes the variance of 308 data points for each of the 4 volunteers. (**C**) The principal component analysis parameter loadings (weighting coefficients) for the second component (PC2) is plotted. Colored bars represent the phenotypes with high (●) and moderate (●) variances in PC2.



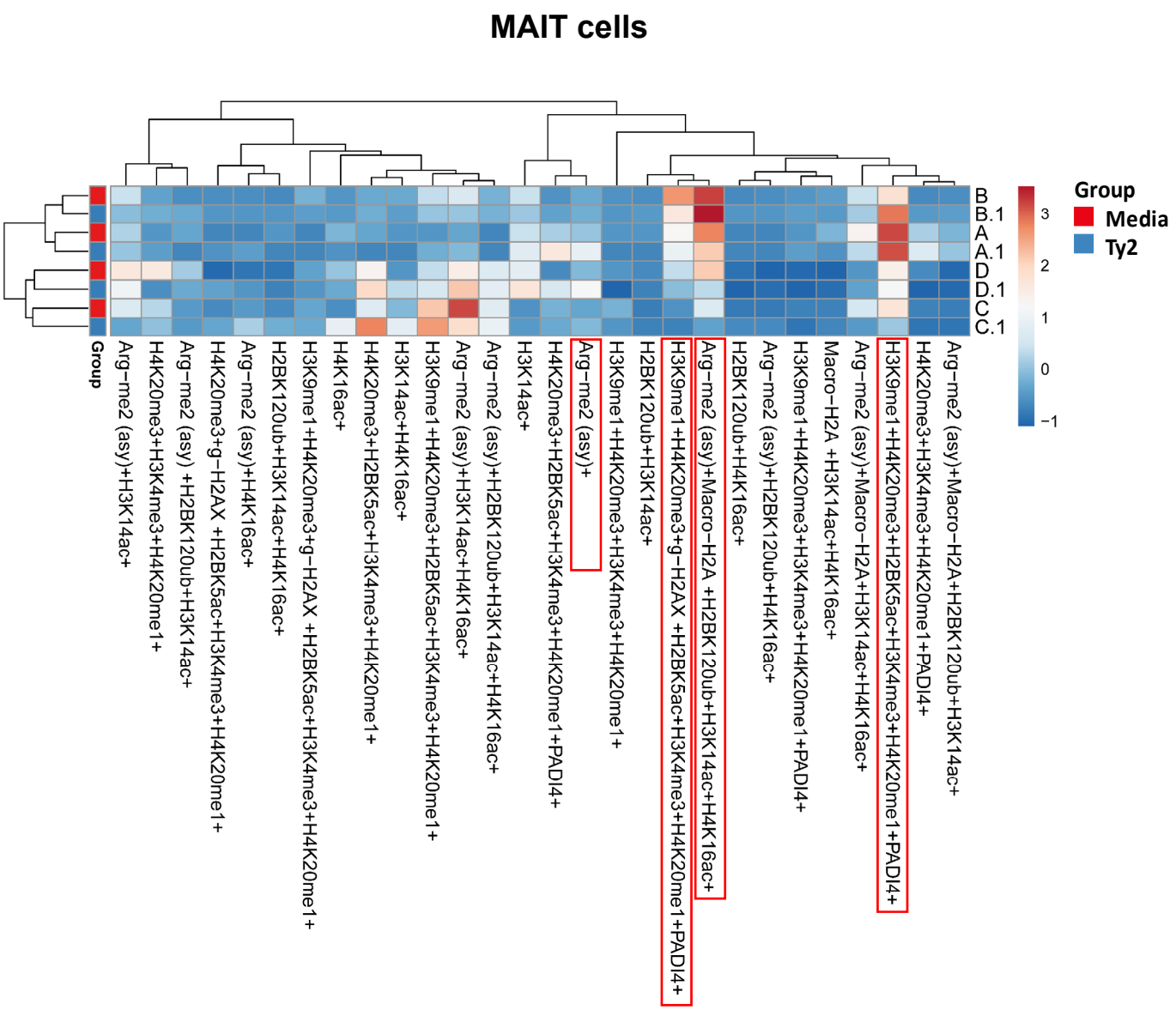
Supplemental Fig. 10. Hierarchical clustering of all cell subsets using principal component analysis. Cells isolated from healthy terminal ileum surgical tissues were exposed to *S*. Typhi strain Ty2 (**Ty2**), and cultured as described in **Fig. 1**. Cells cultured with media only were used as controls (**media**). FCOM data of the 28 combinations (within the acceptability criteria for changes of chromatin marks) were used to perform an unsupervised principal component analysis (PCA). PCA compared sample changes before and after exposure to Ty2. PCA was performed using the ClustVis web tool. Rows were centered and unit variance scaling applied to rows. Rows were clustered using Euclidean distance and average linkage. Columns were clustered using correlation distance and average linkage. Trees ordering for both rows and columns display the tightest cluster first. Red boxes represent the phenotypes with high variances in PC2. These data are representative of three experiments with terminal ileum segments from 4 different donors, one replicate each.



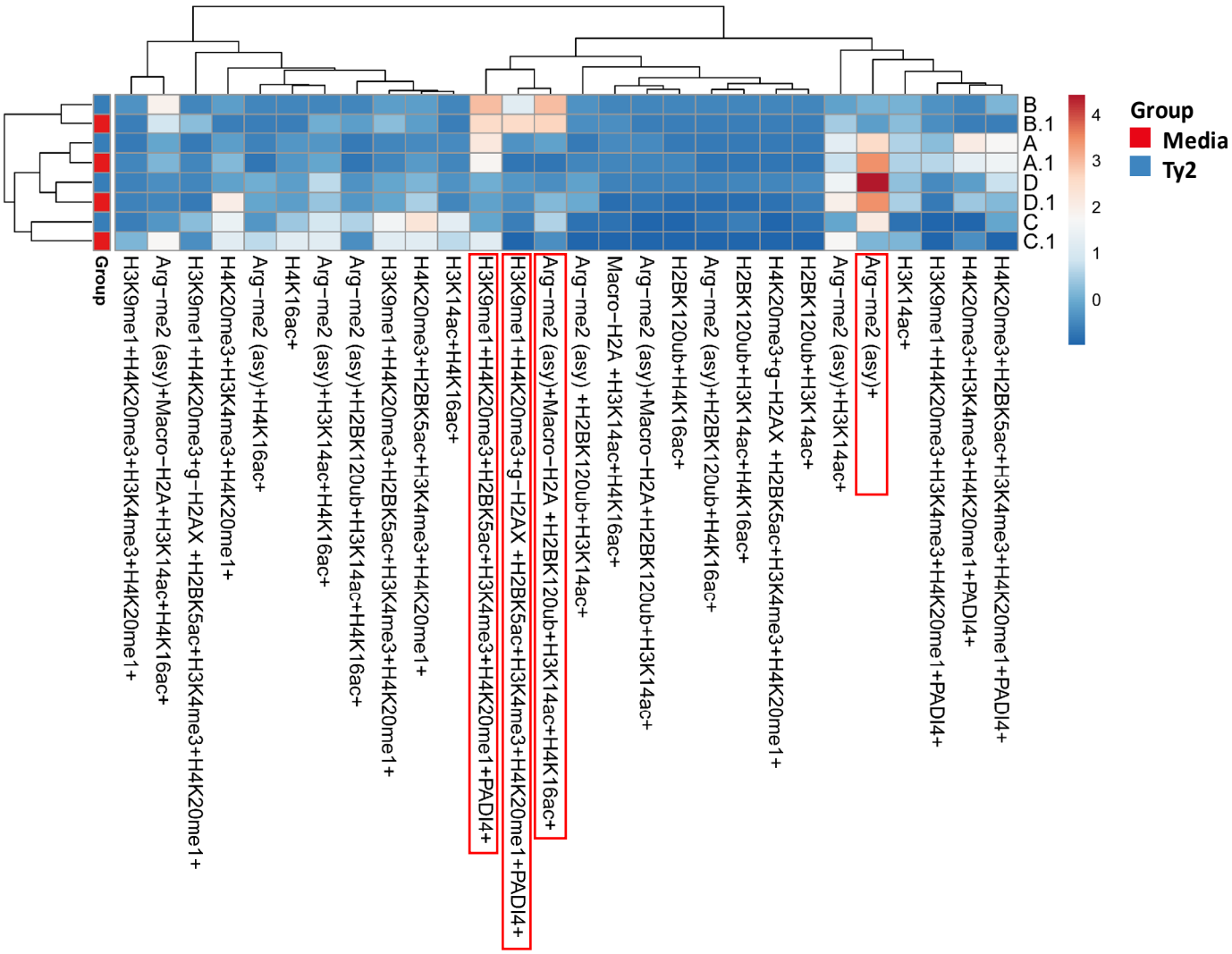
Supplemental Fig. 11. Hierarchical clustering of epithelial cell population using Principal component analysis. Cells isolated from healthy terminal ileum surgical tissues were exposed to *S*. Typhi strain Ty2 (**Ty2**), and cultured as described in **Fig. 1**. Cells cultured with media only were used as controls (**media**). FCOM data of the 28 combinations (within the acceptability criteria for changes of chromatin marks) were used to perform an unsupervised principal component analysis (PCA). PCA compared sample changes before and after exposure to Ty2. PCA was performed using the ClustVis web tool. Rows were centered and unit variance scaling applied to rows. Rows were clustered using Euclidean distance and average linkage. Columns were clustered using correlation distance and average linkage. Trees ordering for both rows and columns display the tightest cluster first. Red boxes represent the phenotypes with high variances in PC2. These data are representative of three experiments with terminal ileum segments from 4 different donors, one replicate each.



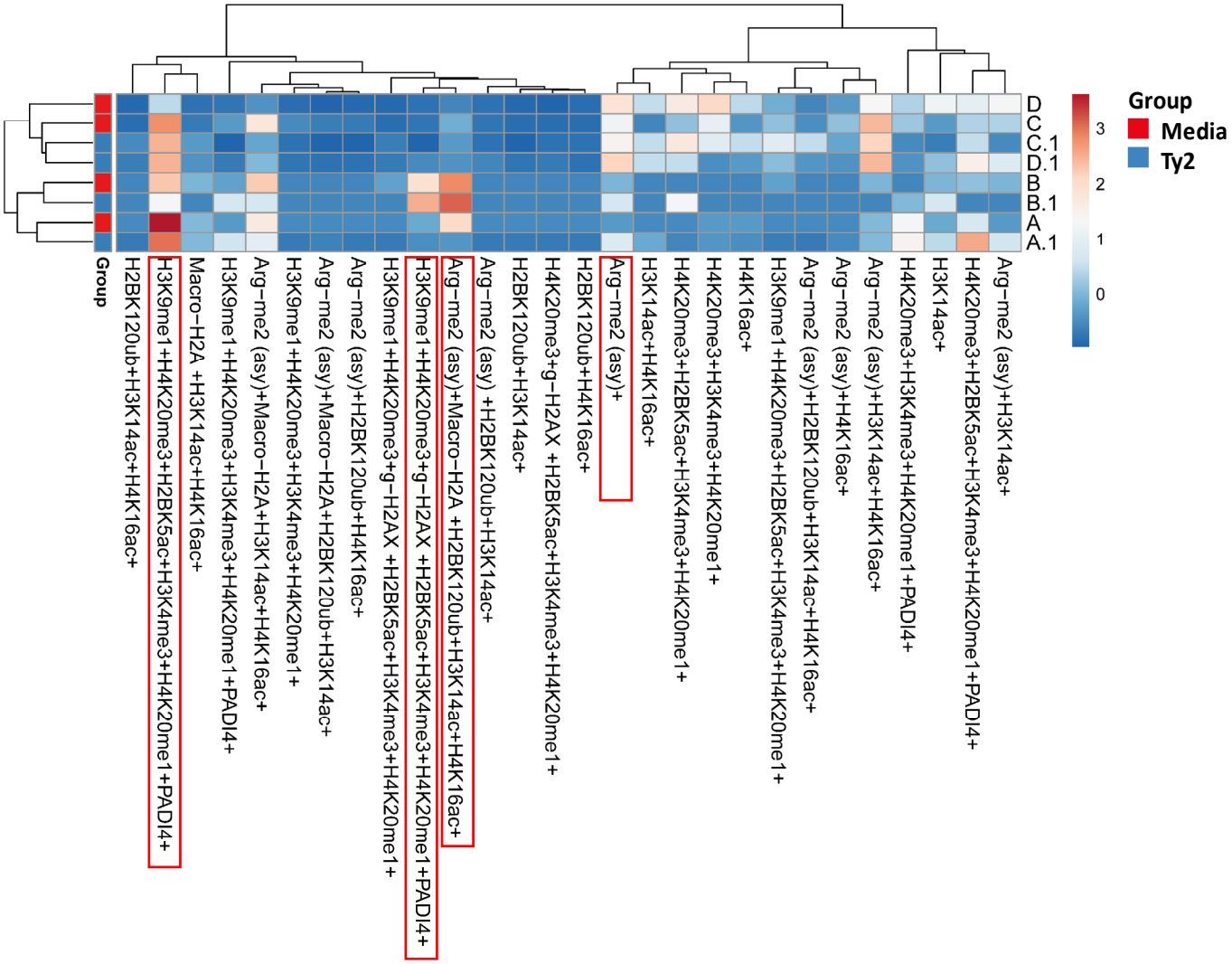
Supplemental Fig. 12. Hierarchical clustering of NKT cell population using Principal component analysis. Cells isolated from healthy terminal ileum surgical tissues were exposed to *S*. Typhi strain Ty2 (**Ty2**), and cultured as described in **Fig. 1**. Cells cultured with media only were used as controls (**media**). FCOM data of the 28 combinations (within the acceptability criteria for changes of chromatin marks) were used to perform an unsupervised principal component analysis (PCA). PCA compared sample changes before and after exposure to Ty2. PCA was performed using the ClustVis web tool. Rows were centered and unit variance scaling applied to rows. Rows were clustered using Euclidean distance and average linkage. Columns were clustered using correlation distance and average linkage. Trees ordering for both rows and columns display the tightest cluster first. Red boxes represent the phenotypes with high variances in PC2. These data are representative of three experiments with terminal ileum segments from 4 different donors, one replicate each.



Supplemental Fig. 13. Hierarchical clustering of MAIT cell population using Principal component analysis. Cells isolated from healthy terminal ileum surgical tissues were exposed to *S*. Typhi strain Ty2 (**Ty2**), and cultured as described in **Fig. 1**. Cells cultured with media only were used as controls (**media**). FCOM data of the 28 combinations (within the acceptability criteria for changes of chromatin marks) were used to perform an unsupervised principal component analysis (PCA). PCA compared sample changes before and after exposure to Ty2. PCA was performed using the ClustVis web tool. Rows were centered and unit variance scaling applied to rows. Rows were clustered using Euclidean distance and average linkage. Columns were clustered using correlation distance and average linkage. Trees ordering for both rows and columns display the tightest cluster first. Red boxes represent the phenotypes with high variances in PC2. These data are representative of three experiments with terminal ileum segments from 4 different donors, one replicate each.



Supplemental Fig. 14. Hierarchical clustering of TCR-γδ cell population using Principal component analysis. Cells isolated from healthy terminal ileum surgical tissues were exposed to *S*. Typhi strain Ty2 (**Ty2**), and cultured as described in **Fig. 1**. Cells cultured with media only were used as controls (**media**). FCOM data of the 28 combinations (within the acceptability criteria for changes of chromatin marks) were used to perform an unsupervised principal component analysis (PCA). PCA compared sample changes before and after exposure to Ty2. PCA was performed using the ClustVis web tool. Rows were centered and unit variance scaling applied to rows. Rows were clustered using Euclidean distance and average linkage. Columns were clustered using correlation distance and average linkage. Trees ordering for both rows and columns display the tightest cluster first. Red boxes represent the phenotypes with high variances in PC2. These data are representative of three experiments with terminal ileum segments from 4 different donors, one replicate each.



Supplemental Fig. 15. Hierarchical clustering of CD4+ T-cell population using Principal component analysis. Cells isolated from healthy terminal ileum surgical tissues were exposed to *S*. Typhi strain Ty2 (**Ty2**), and cultured as described in **Fig. 1**. Cells cultured with media only were used as controls (**media**). FCOM data of the 28 combinations (within the acceptability criteria for changes of chromatin marks) were used to perform an unsupervised principal component analysis (PCA). PCA compared sample changes before and after exposure to Ty2. PCA was performed using the ClustVis web tool. Rows were centered and unit variance scaling applied to rows. Rows were clustered using Euclidean distance and average linkage. Columns were clustered using correlation distance and average linkage. Trees ordering for both rows and columns display the tightest cluster first. Red boxes represent the phenotypes with high variances in PC2. These data are representative of three experiments with terminal ileum segments from 4 different donors, one replicate each.