

**Figure S1: Cytokine milieu during hepatic amebiasis and listeriosis**

A) Cytokine concentration in murine liver lysate at indicated time points after intrahepatic infection of  $2.5 \times 10^5$  *E. histolytica* trophozoites or intravenous infection of  $2 \times 10^4$  *L. monocytogenes* determined by multiplex cytokine assay (LegendPlex, BL). Absolute numbers of pro-inflammatory and anti-inflammatory monocytes on d3 and d5 p.i. from B) *E. histolytica* and C) *L. monocytogenes* infected mice. D) Liver sections from *E. histolytica* infected (d3 p.i.) and naive mice were stained with anti-*E. histolytica* (pool: anti-170kDa Lectin, anti-220kDa Lectin, anti-SOD, anti-peroxiredoxin) and mAbs against CD11b (EPR1344) and Ly6C (ER-MP20). One representative experiment out of 3 (A-D) is shown. Data are expressed as mean  $\pm$  SEM. p values were determined using the Mann-Whitney U test (\*p < 0.05; \*\*p < 0.01; \*\*\*p < 0.001).

A

| Gene          | MeanCount ALA<br>Ly6C <sup>hi</sup> | MeanCount LIS<br>Ly6C <sup>hi</sup> | Log2 FoldChange | padj       |
|---------------|-------------------------------------|-------------------------------------|-----------------|------------|
| IIGP1         | 249,227                             | 24161,955                           | -6.589112667    | 0          |
| GM4951        | 49,9258748                          | 5590,44                             | -6.817560811    | 0          |
| KLHL6         | 997,7453251                         | 5367,57875                          | -2.428462923    | 9.464E-267 |
| F830016B08RIK | 8,233481227                         | 1208,64125                          | -7.208449195    | 1.473E-240 |
| IL18BP        | 119,02244                           | 2709,64875                          | -4.524461161    | 2.809E-228 |
| PLA2G16       | 138,9782702                         | 1722,8375                           | -3.651858069    | 5.373E-225 |
| LY6A          | 414,3645471                         | 25891,21625                         | -5.933574663    | 5.992E-218 |
| WARS          | 927,3850463                         | 3531,69375                          | -1.927610345    | 7.208E-186 |
| AW112010      | 790,5120389                         | 17607,38875                         | -4.458975972    | 5.661E-184 |
| GBP2          | 2285,971974                         | 29539,3175                          | -3.706494048    | 2.123E-176 |
| LAP3          | 245,9667124                         | 2597,11125                          | -3.401025731    | 9.476E-164 |
| GBP6          | 27,67415277                         | 1027,035                            | -5.216537222    | 1.751E-151 |
| GM4841        | 4,55834516                          | 598,79                              | -7.07252909     | 7.654E-126 |
| GLRX          | 1286,863168                         | 6126,465                            | -2.247512811    | 4.659E-119 |
| PSMB9         | 2167,861175                         | 7670,07125                          | -1.822573381    | 4.827E-114 |
| TGTP1         | 129,736205                          | 4691,92                             | -5.236978445    | 7.167E-112 |
| SERPINA3F     | 103,6206307                         | 2881,6275                           | -4.840477368    | 4.521E-106 |
| UPP1          | 115,1120938                         | 3017,54125                          | -4.714344332    | 1.297E-104 |
| IGTP          | 1690,69752                          | 10332,0175                          | -2.633640692    | 6.21E-101  |
| GBP4          | 170,4038873                         | 4706,25625                          | -4.875770858    | 2.262E-100 |

B

| Gene          | MeanCount ALA<br>Ly6C <sup>lo</sup> | MeanCount LIS<br>Ly6C <sup>lo</sup> | Log2<br>FoldChange | padj        |
|---------------|-------------------------------------|-------------------------------------|--------------------|-------------|
| GM4951        | 11,8735096                          | 2208,9975                           | -7.469879617       | 7.14853E-22 |
| IL18BP        | 25,26594539                         | 1073,37875                          | -5.792058644       | 2.29229E-13 |
| F830016B08RIK | 2,816183461                         | 350,4975                            | -7.701683035       | 2.67829E-12 |
| IIGP1         | 140,4051144                         | 8661,08875                          | -5.76518905        | 1.10631E-11 |
| PRM1          | 0                                   | 54,20125                            | -7.000417519       | 2.01085E-10 |
| SPP1          | 177,1890049                         | 2607,13625                          | -4.191041868       | 1.48013E-09 |
| CD209A        | 4094,22731                          | 100,5325                            | 5.284376598        | 4.10385E-09 |
| UPP1          | 24,8934124                          | 1142,89875                          | -6.293533846       | 8.00831E-09 |
| HDC           | 64,10710943                         | 1675,52875                          | -6.319898255       | 1.34919E-08 |
| AA467197      | 17,41170357                         | 310,53625                           | -4.961178145       | 3.00715E-08 |
| GBP2          | 1074,601145                         | 12786,76625                         | -3.761186255       | 3.03927E-08 |
| CXCR2         | 24,45829754                         | 686,3675                            | -6.361284538       | 4.98776E-08 |
| PRSS16        | 19,41762795                         | 97,12                               | -3.658139008       | 6.26113E-08 |
| ASNS          | 49,80068103                         | 300,66                              | -2.882330321       | 1.19752E-07 |
| IL10          | 3,68206119                          | 323,1175                            | -6.545475529       | 2.26944E-07 |
| P2RX3         | 1,006602645                         | 72,13875                            | -6.183108842       | 3.7849E-07  |
| IL1R2         | 126,1450712                         | 2666,46                             | -5.762673771       | 5.71717E-07 |
| MS4A2         | 6,502531354                         | 271,4125                            | -6.082275639       | 6.43744E-07 |
| SULT2B1       | 16,0341714                          | 327,04375                           | -4.426278772       | 1.36361E-06 |
| PRSS34        | 14,34053248                         | 4969,3575                           | -6.279807693       | 3.16683E-06 |

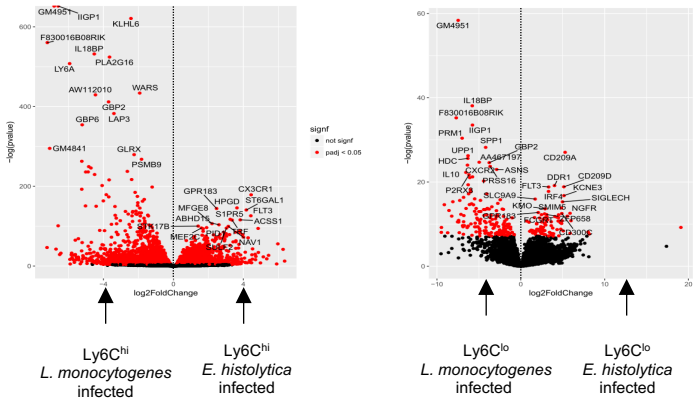
C

| GO-Term number | Enrichment FDR | Genes in list | Functional category                          |
|----------------|----------------|---------------|--|
| 0006955        | 1,5E-59        | 925           | Immune system process                        |
| 0044267        | 2,8E-53        | 1659          | Cellular protein metabolic process           |
| 0006950        | 4,1E-52        | 1269          | Response to stress                           |
| 0002682        | 2,7E-44        | 553           | Regulation of immune system process          |
| 0002684        | 8,1E-37        | 406           | Positive regulation of immune system process |
| 0006955        | 3,3E-36        | 558           | Immune response                              |
| 0009056        | 1,6E-35        | 828           | Catabolic process                            |
| 0044248        | 4,1E-35        | 747           | Cellular catabolic process                   |
| 0006464        | 3,4E-34        | 1265          | Cellular protein modification process        |
| 0036211        | 3,4E-34        | 1265          | Protein modification process                 |
| 0080134        | 3,4E-34        | 525           | Regulation of response to stress             |
| 0034097        | 1,4E-33        | 402           | Response to cytokine                         |
| 0070887        | 2,5E-33        | 1013          | Cellular response to chemical stimulus       |
| 0043412        | 5,0E-33        | 1309          | Macromolecule modification                   |
| 0009893        | 2,6E-31        | 1173          | Positive regulation of metabolic process     |
| 0006952        | 3,2E-31        | 564           | Defense response                             |
| 0001775        | 5,8E-31        | 393           | Cell activation                              |
| 0031347        | 8,7E-31        | 288           | Regulation of defense response               |
| 0006793        | 1,5E-30        | 1058          | Phosphorus metabolic process                 |
| 0071310        | 3,3E-30        | 829           | Cellular response to organic substance       |

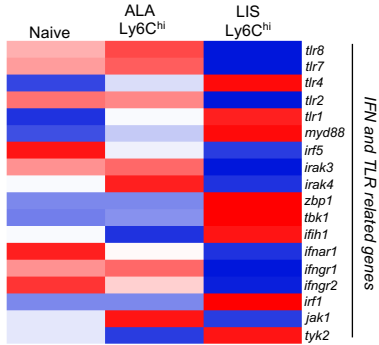
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| GO-Term number | Enrichment FDR | Genes in list | Functional category                    |
|----------------|----------------|---------------|--|
| 0006952        | 2,8E-21        | 67            | Defense response                       |
| 0006955        | 8,7E-20        | 82            | Immune system process                  |
| 0009605        | 2,4E-15        | 76            | Response to external stimulus          |
| 0009617        | 4,5E-15        | 40            | Response to bacterium                  |
| 0043207        | 5,8E-15        | 47            | Response to external biotic stimulus   |
| 0051707        | 5,8E-15        | 47            | Response to other organism             |
| 0006955        | 9,9E-15        | 55            | Immune response                        |
| 0009607        | 1,6E-14        | 47            | Response to biotic stimulus            |
| 0006950        | 3,2E-14        | 92            | Response to stress                     |
| 0035456        | 3,1E-11        | 13            | Response to interferon-beta            |
| 0035458        | 5,7E-11        | 12            | Cellular response to interferon-beta   |
| 0070887        | 3,1E-10        | 74            | Cellular response to chemical stimulus |
| 0034097        | 3,4E-10        | 38            | Response to cytokine                   |
| 0006954        | 5,2E-10        | 32            | Inflammatory response                  |
| 0071345        | 6,0E-10        | 35            | Cellular response to cytokine stimulus |
| 002832         | 2,5E-09        | 9             | Defense response to protozoan          |
| 0071310        | 4,0E-09        | 62            | Cellular response to organic substance |
| 0001562        | 4,4E-09        | 9             | Response to protozoan                  |
| 0002682        | 7,2E-09        | 43            | Regulation of immune system process    |
| 0010033        | 2,0E-08        | 74            | Response to organic substance          |

E

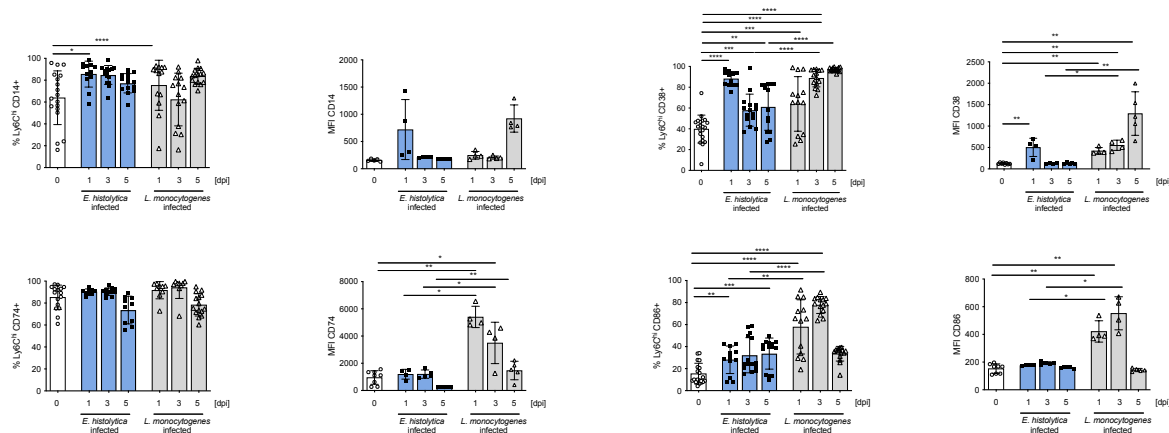


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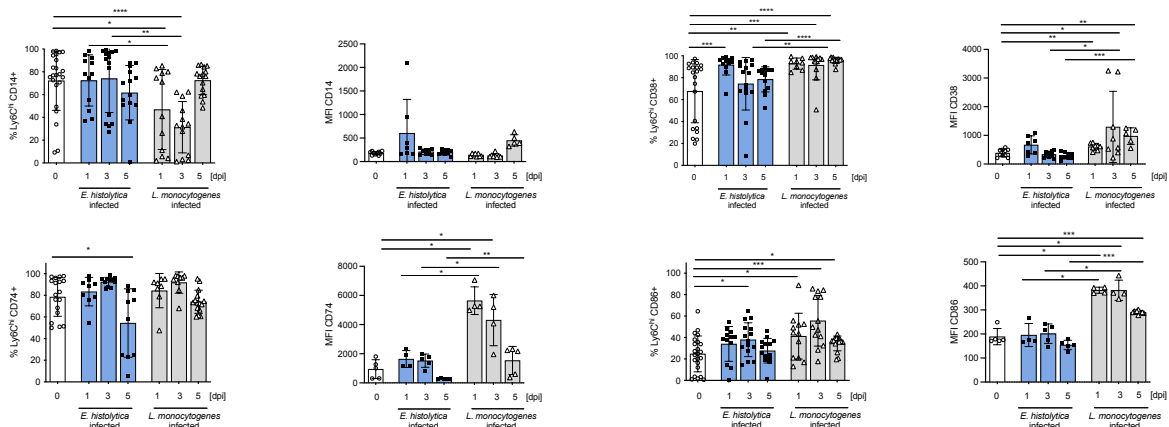


**Figure S2: Comparative analysis of transcriptome and FACS data of liver-specific Ly6C<sup>hi/lo</sup> monocytes from *E. histolytica* and *L. monocytogenes* infected C57BL/6 mice.** 20 most significant regulated genes between A) pro-inflammatory and B) anti-inflammatory monocytes. Most abundant and regulated GO-Term (n=20) comparing significant regulated genes C) from pro-inflammatory and D) anti-inflammatory monocytes; E) Volcano-Plot of regulated genes expressed by Ly6C<sup>hi</sup> and Ly6C<sup>lo</sup> monocytes. Plotting log-p values against log2-fold changes reveals significantly (red) and non-significantly (black) regulated genes. F) Selection of upregulated IFN and TLR related genes.

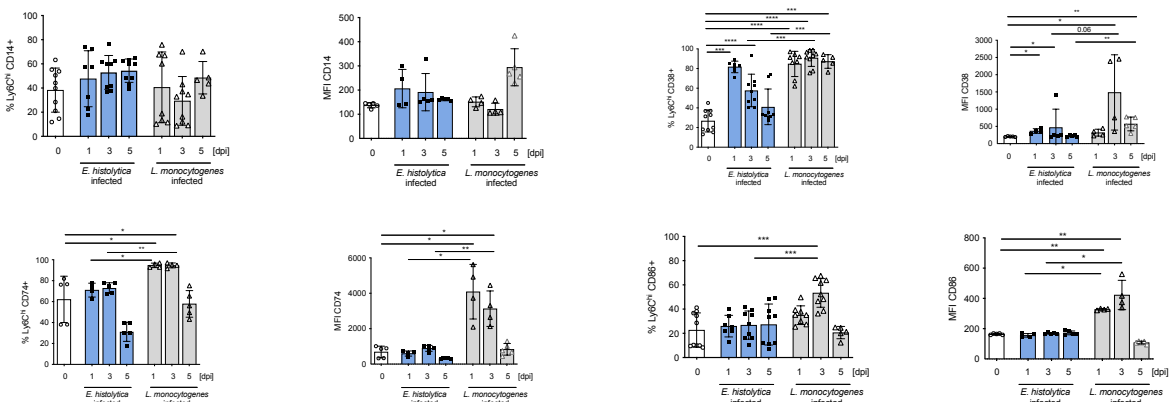
A



B



C



**Figure S3: Expression pattern of CD14, CD38, CD74 and CD86 on Ly6ChI monocytes derived from different organs during the course of infection with *E. histolytica* and *L. monocytogenes*.**

Determination of percentages of positive cells and MFI for selected markers on Ly6ChI monocytes from A) spleen, B) blood and C) bone marrow. Data were pooled from three independent experiments, MFI data in A-C represent one out of three experiments. Data are expressed as the mean  $\pm$  SEM. p values were determined using the Mann-Whitney U test (\*p < 0.05; \*\*p < 0.01; \*\*\*p < 0.001).