

10

5

5

PECAM TIMP2

ABCC3

AKR1B1

DAB2

-log(p-value)

а

370 Transcripts

d С Up in vLC vs. vM Φ (119) Up in vM Φ vs. vLC (251) HLA-DQB1 ID01* 1115 GADD45A LAMP3 FSCN1 CD163 ECGR2E FCGR MARCKSL1 CD14 FCER1G EBI3 FCGRT TRAF1 CCR7 TRAF5 CCL22 IFNG CSF2 IL17A CCR UBD CSF2 IL1B CCL3L ACCL3L3 BIRC3 CCL3 CSF1 IL1B CCL2 VCAM1 COL13 ANXA6 CD40LG IL3 CSAR1 CXCL1 CCL5 IL4 NGE4 ABP1 CXCL2 GTSB RGL1 CXCL5 СКВ CTSS LAT IL5 TNFSE11 CD300LF MCM5 IL6 TNFSF12 MAP3K14 TNF SLC7A8 TNFRSF4 SLCTBA: TUR SLC16A LAD1 TNFSF11 TNF RBP TLR8 ADORA2A CST7 CD209 .26 HK3 GPR84 CYP27A1 CLEC5A A' CDX2 ASGR1 CLEC10A UPB1 GLS TUBB2B LYBE GERX ANDEPTOTE AQP9 TMEM97 CRIP1PLA2G16

Figure S4: Transcriptional analysis of vLC vs. vM Φ . a. Hierarchical clustering of the 370 transcripts (identified by post-hoc Tukey test) differentially expressed between vLC and vM Φ . **b.** Bar chart representing the IPA canonical pathway enrichment for the 119 transcripts over-expressed in vLC and the 251 transcripts over-expressed vMF. c. Network analysis of the 119 transcripts over-expressed in vLC. d. Network analysis of the 251 transcripts over-expressed in vMo.

b