

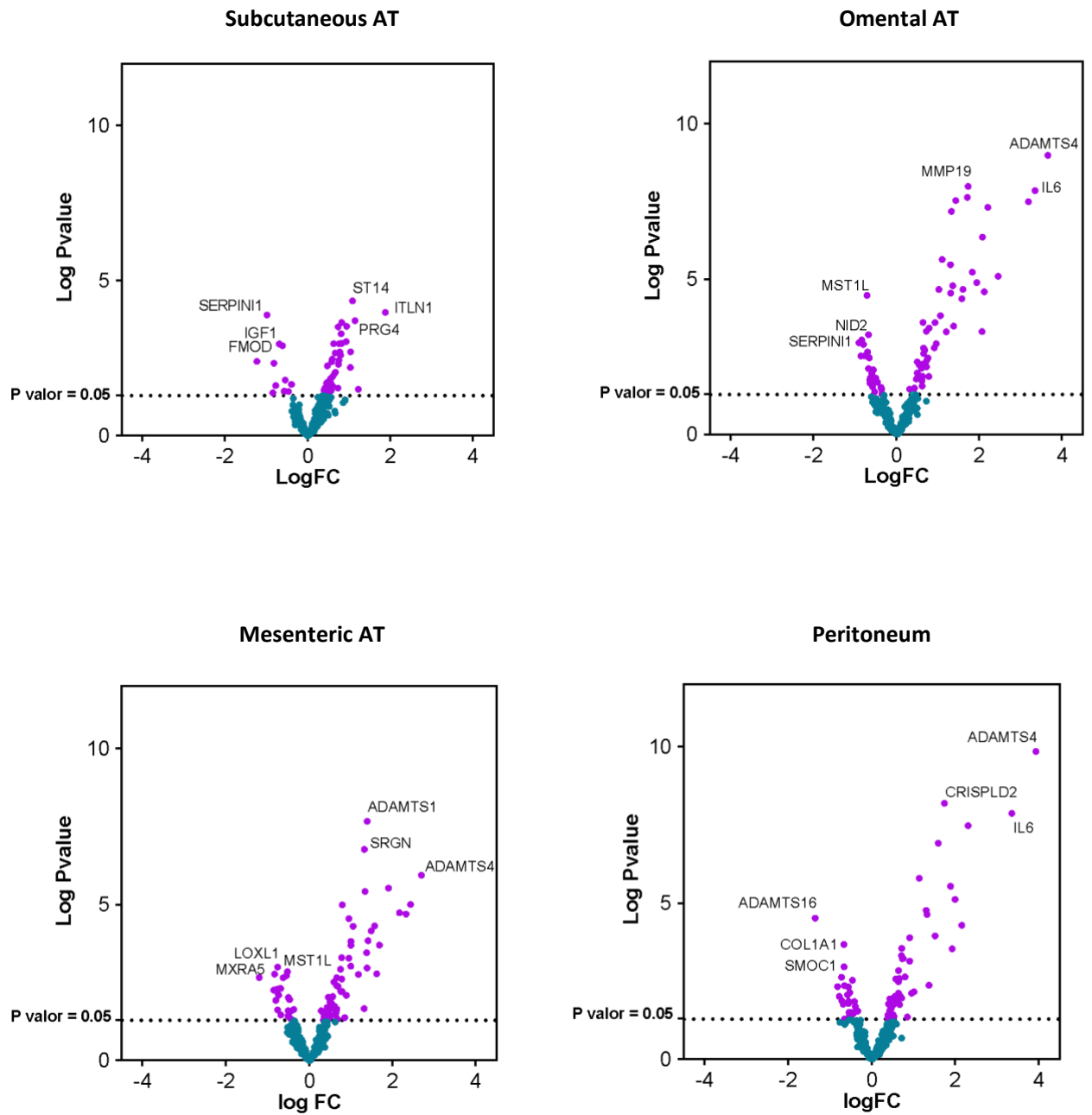


Figure S1: Volcano plots for comparison of gene expression (ECM-related genes) between the Obese group and the Control group in each tissue. Gene symbols are shown for the 3 most statistically significant over-expressed and under-expressed genes in the obese group relative to the non-obese patients in each tissue. Genes are shown in purple if they exceed the previously established expression

and significance threshold (an adjusted p value < 0.05 and a log increase (fold change) > 0.5 for all tissues). (*Log Pvalue*: $-\log_{10} P\text{-value}$, *Log FC*: $\log_2 \text{Fold Change}$).

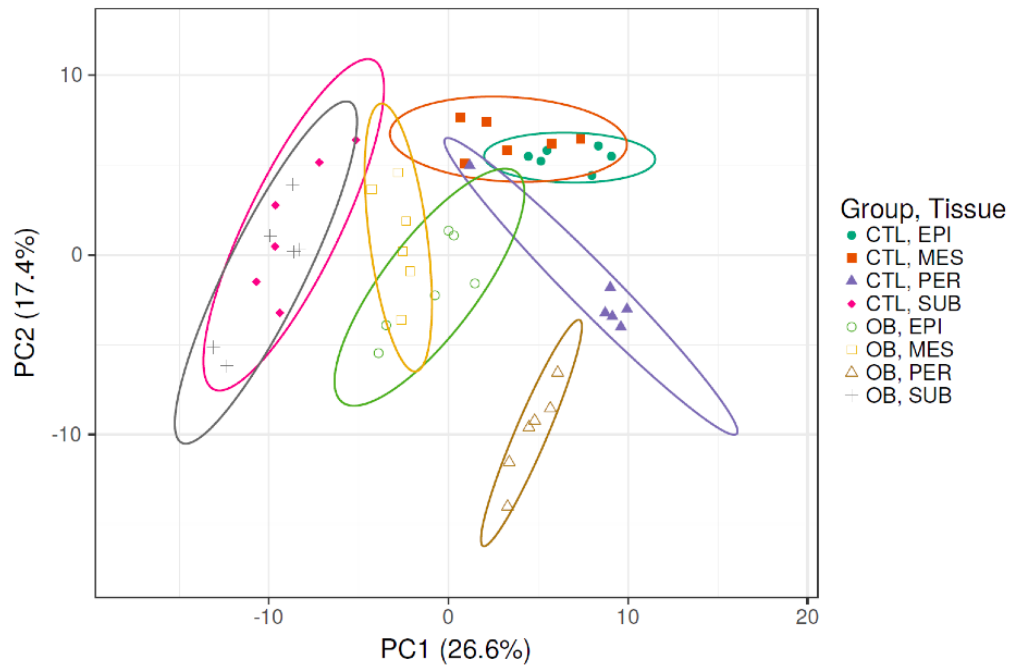
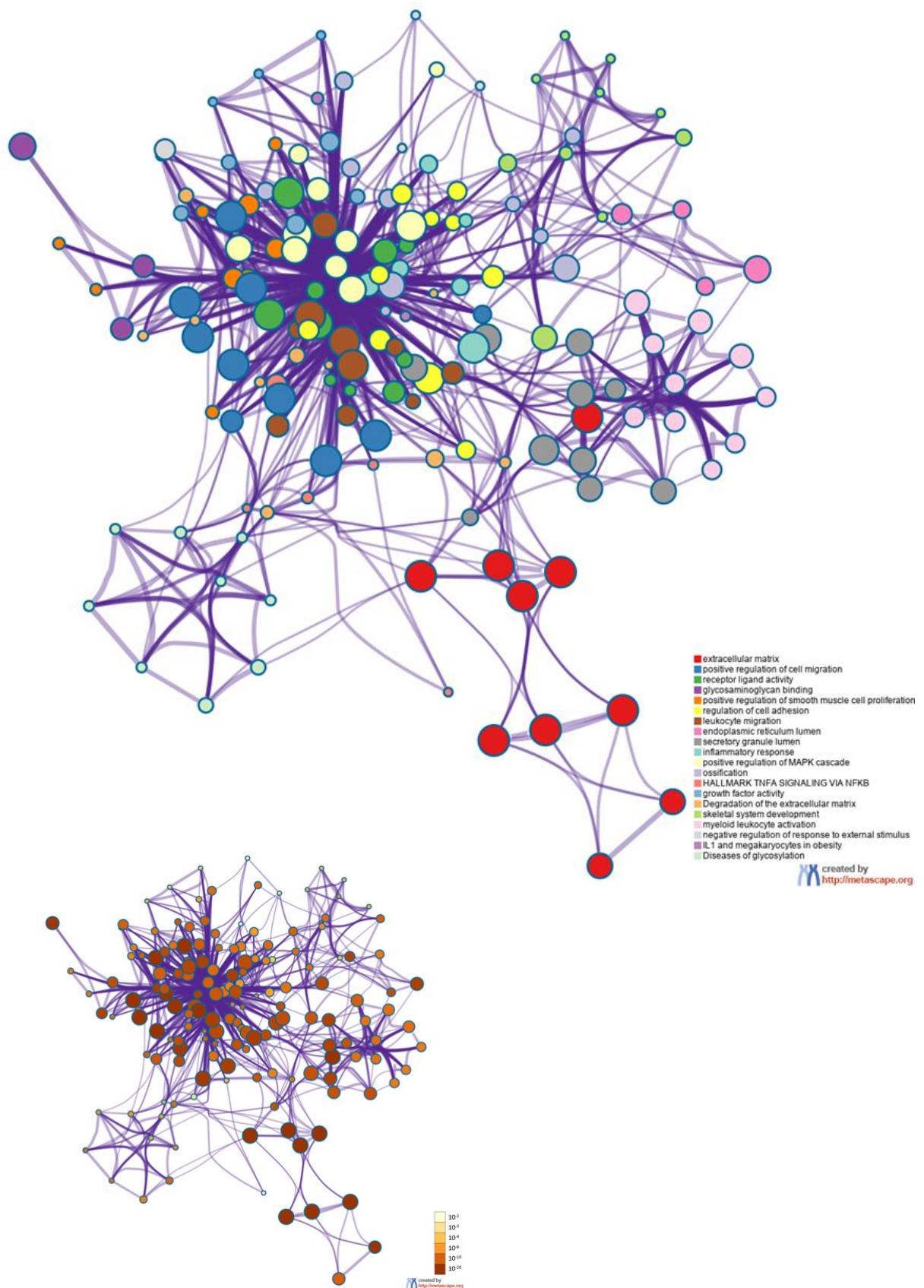
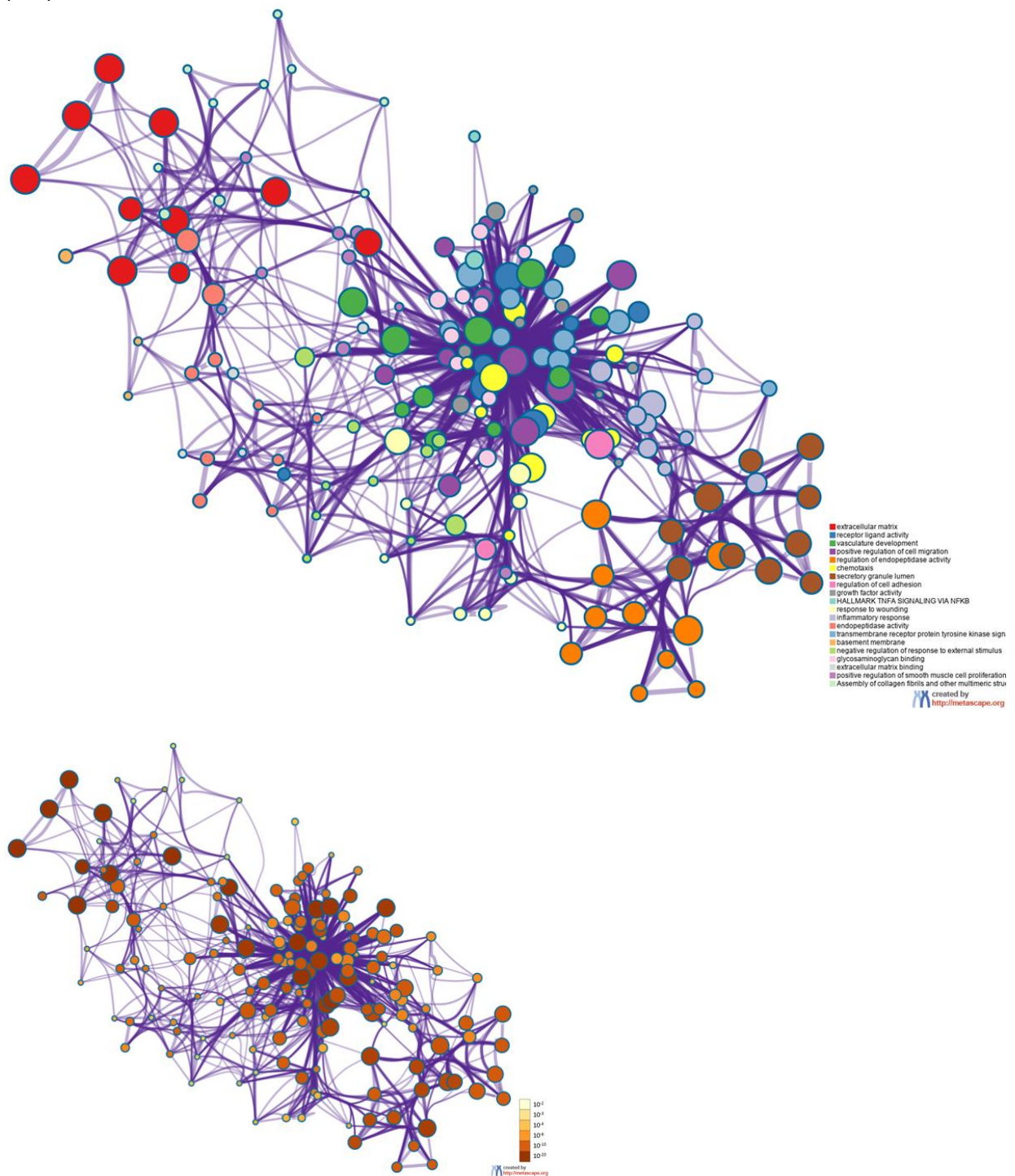


Figure S2: Principal Component Analysis corresponding to the descriptive analysis of the matriosome genes differentially expressed ($p < 0.05$) in the four studied tissues of the Control group and the Obese group. The ellipses represent the area that would include a new observation of a given group with a probability of 0.95. (*CTL*: Control group, *OB*: Obese group, *EPI*: epiploic or omental AT, *MES*: mesentery, *PER*: peritoneum, *SUB*: subcutaneous AT).

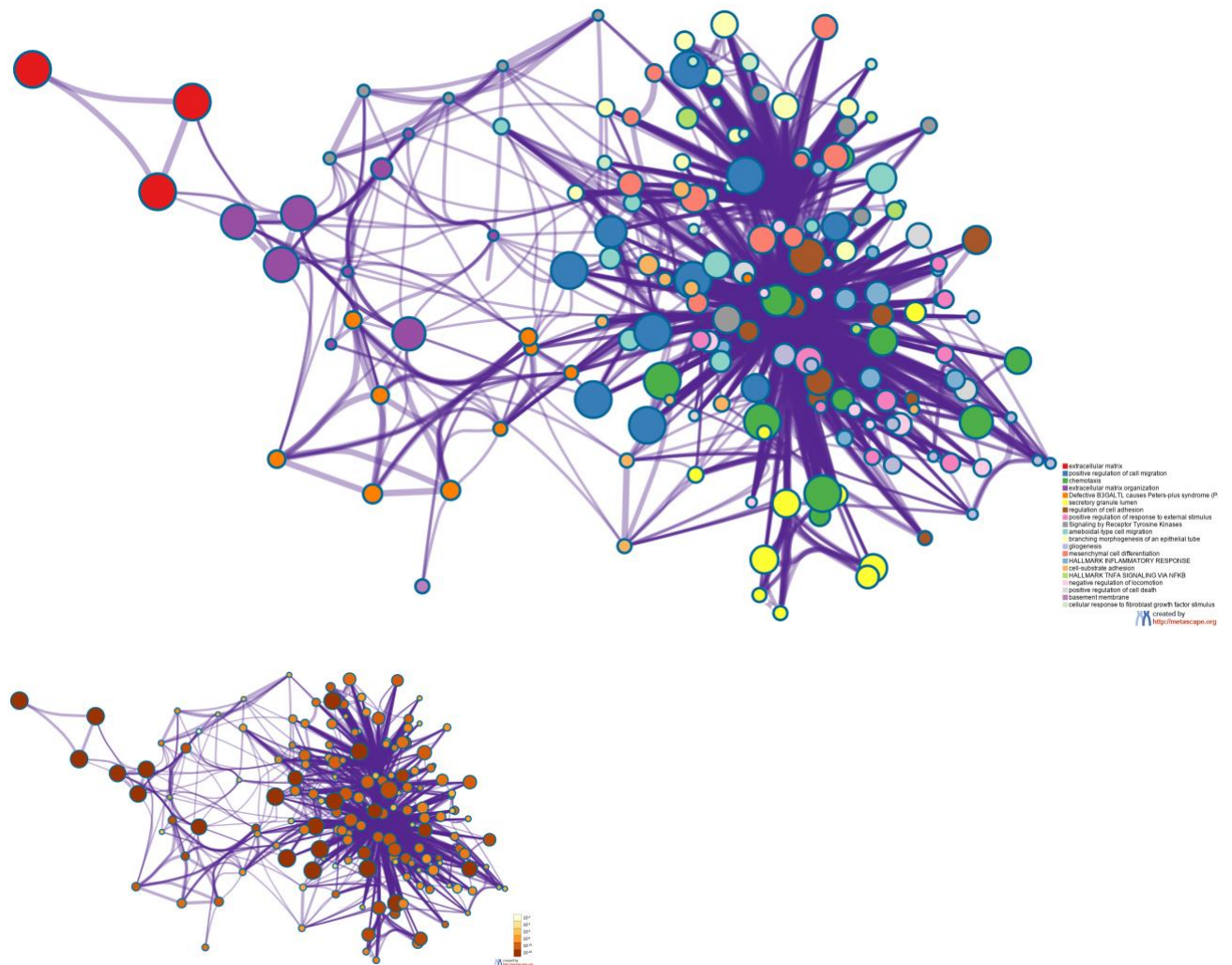
(S3a)



(S3b)



(S3c)



(S3d)

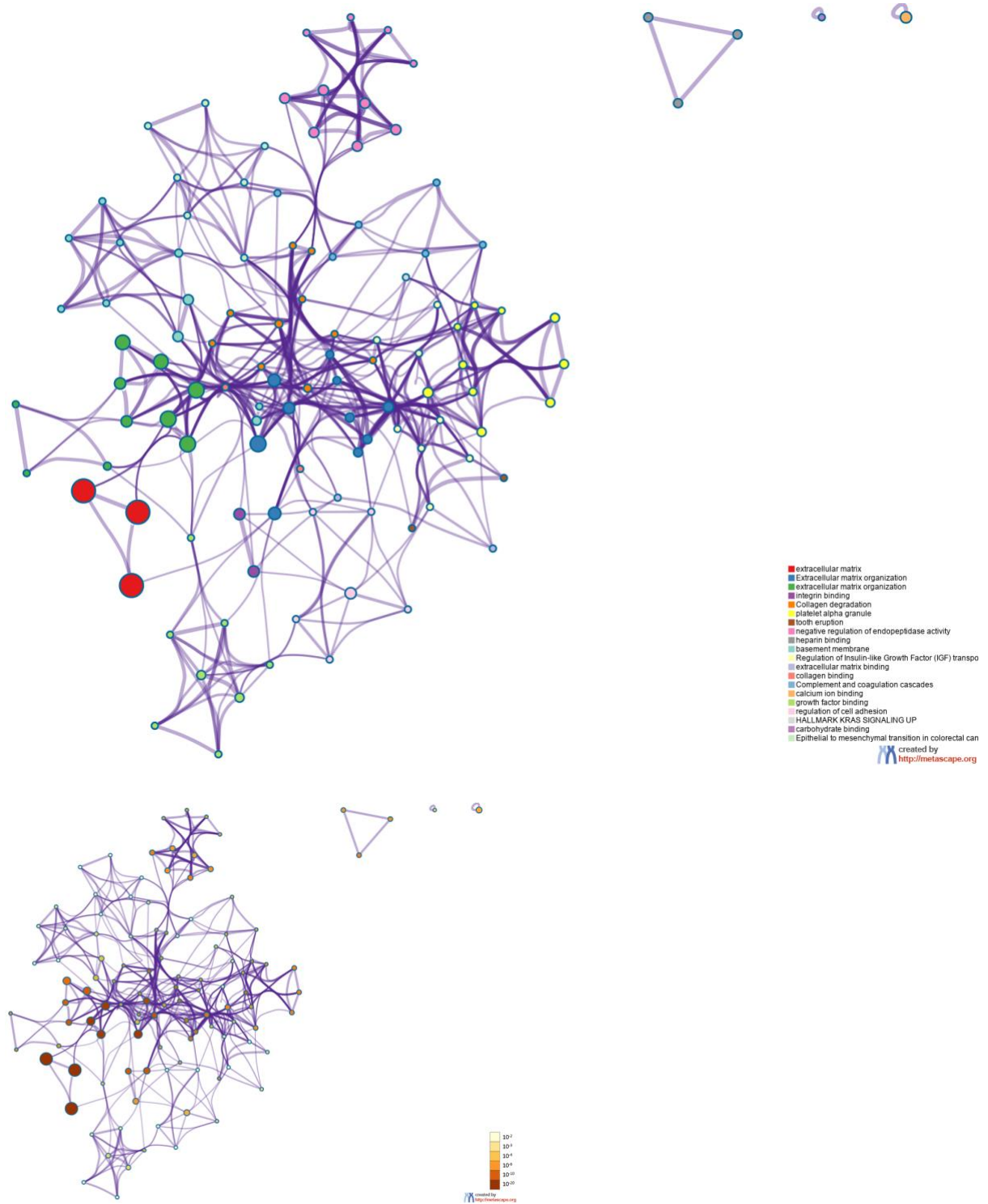


Figure S3: Enrichment map showing the most enriched functional categories in the omentum (S3a), mesentery (S3b), peritoneum (S3c) and subcutaneous tissue (S3d). The size of the nodes represent the number of genes in the category; the connection lines between nodes represent genes or gene groups that overlap between categories.