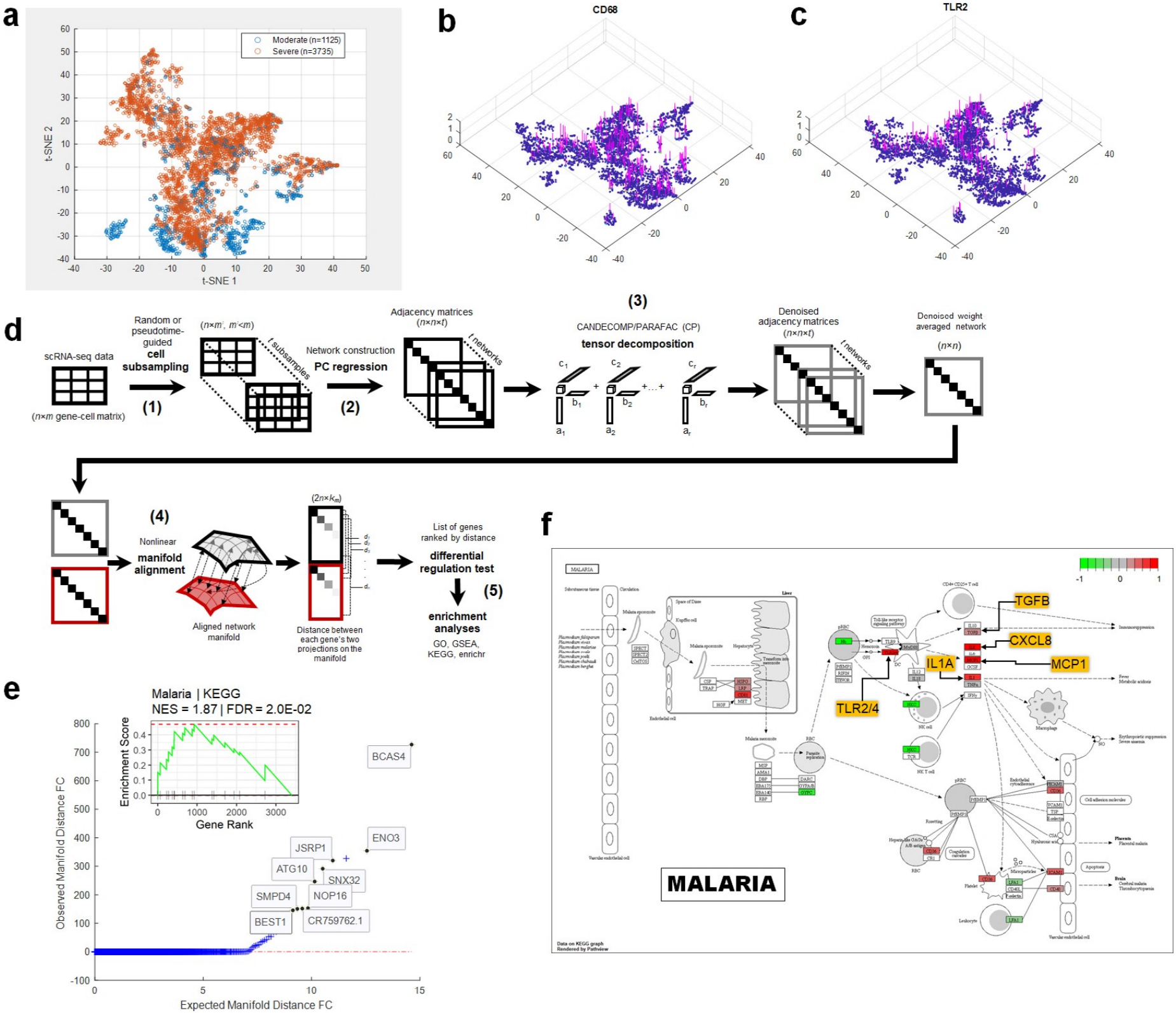
a
Moderate (n=1125)
Severe (n=3735)
t-SNE 1
t-SNE 2
b
CD68
c
TLR2
d
scRNA-seq data
(n×m gene-cell matrix)
Random or pseudotime-guided cell subsampling
(1)
(n×m', m'<m)
t subsamples
Network construction
PC regression
(2)
Adjacency matrices (n×n×t)
t networks
(3)
CANDECOMP/PARAFAC (CP) tensor decomposition
Denoised adjacency matrices (n×n×t)
t networks
Denoised weight averaged network
(n×n)
(4)
Nonlinear manifold alignment
Aligned network manifold
(2n×k_m)
Distance between each gene's two projections on the manifold
List of genes ranked by distance
differential regulation test
(5)
enrichment analyses
GO, GSEA, KEGG, enrichr
e
Malaria | KEGG
NES = 1.87 | FDR = 2.0E-02
Enrichment Score
Gene Rank
Observed Manifold Distance FC
Expected Manifold Distance FC
BCAS4
ENO3
JSRP1
ATG10
SNX32
SMPD4
NOP16
BEST1
CR759762.1
f
MALARIA
TGFB
CXCL8
MCP1
IL1A
TLR2/4