

Expanded View Figures

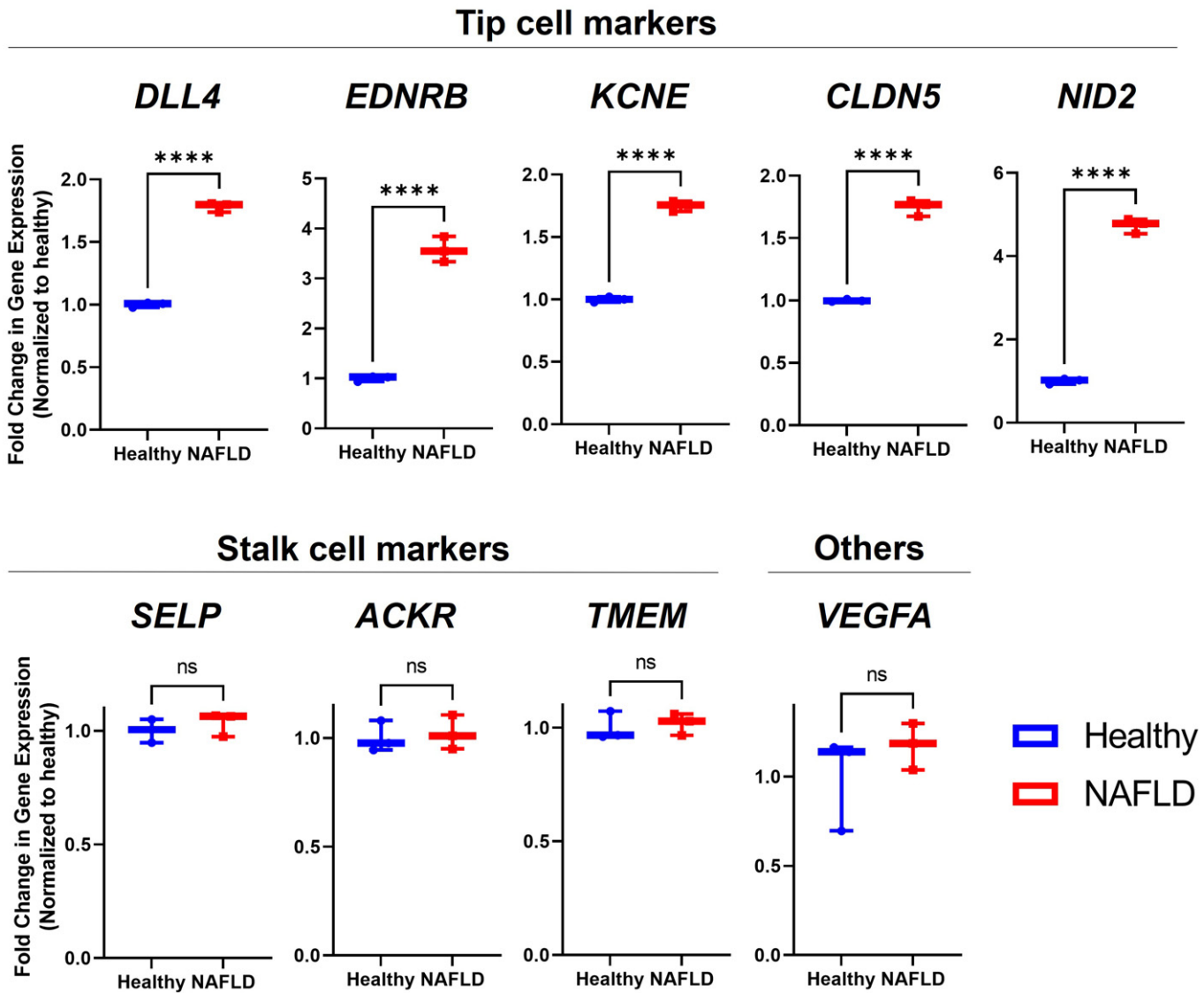


Figure EV1. Gene expressions of tip-stalk markers in sprouting BOECs.
Expressions were determined by qPCR and normalized to monolayers (nonsprouting). Data presented as mean ± SD. *n* = 3 donors; ns—not significant; *****P* < 0.0001 (t-test).

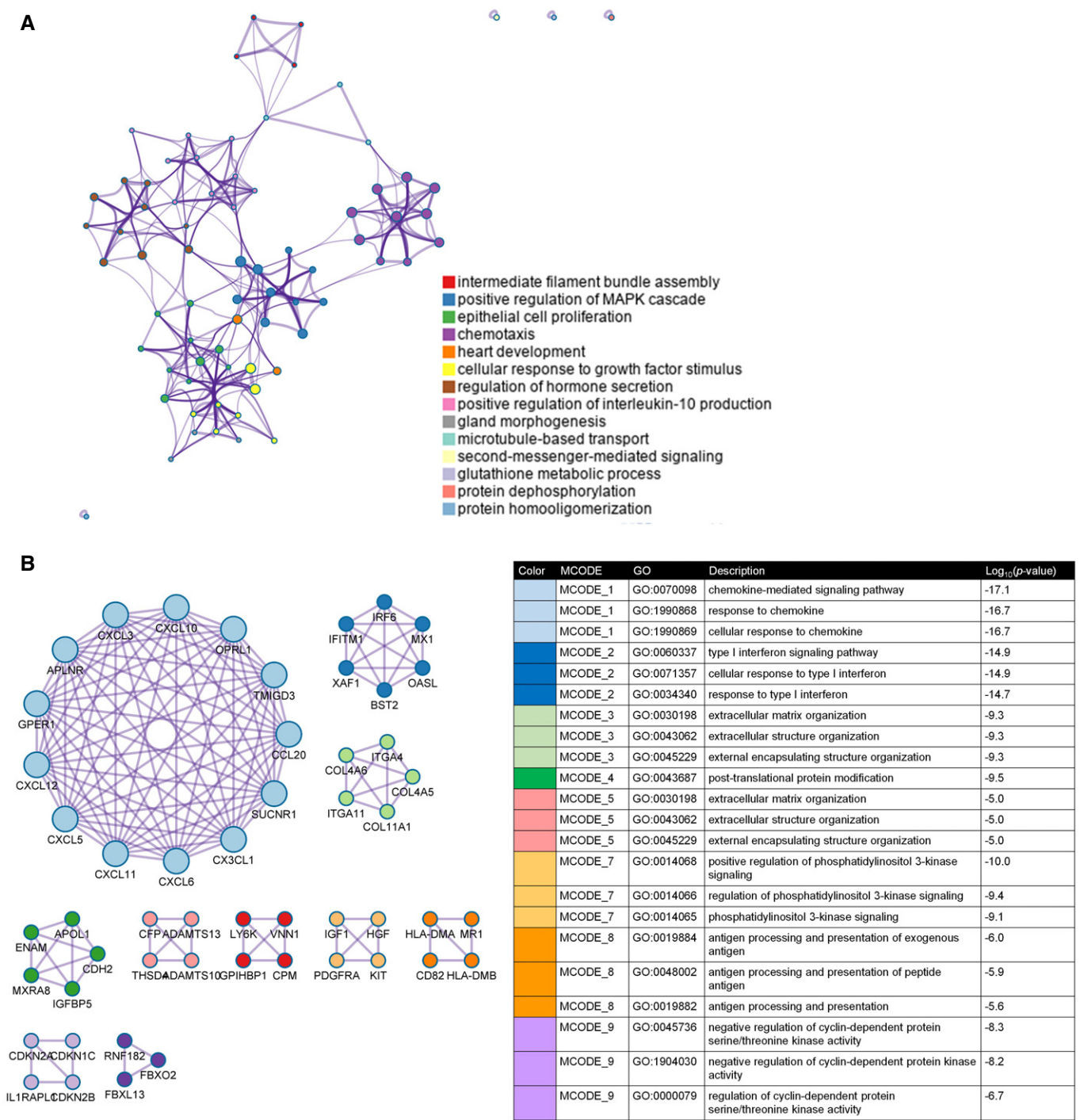


Figure EV2. Transcriptomes of healthy and NAFLD BOECs.
A Metascape enrichment network visualization of interactomes of the downregulated terms in NAFLD BOECs. No identifiable MCODE complexes were found.
B Ten MCODE complexes identified in the upregulated networks in NAFLD BOECs, ranked, and colored by their identities. The identities of the complexes were listed in the table.

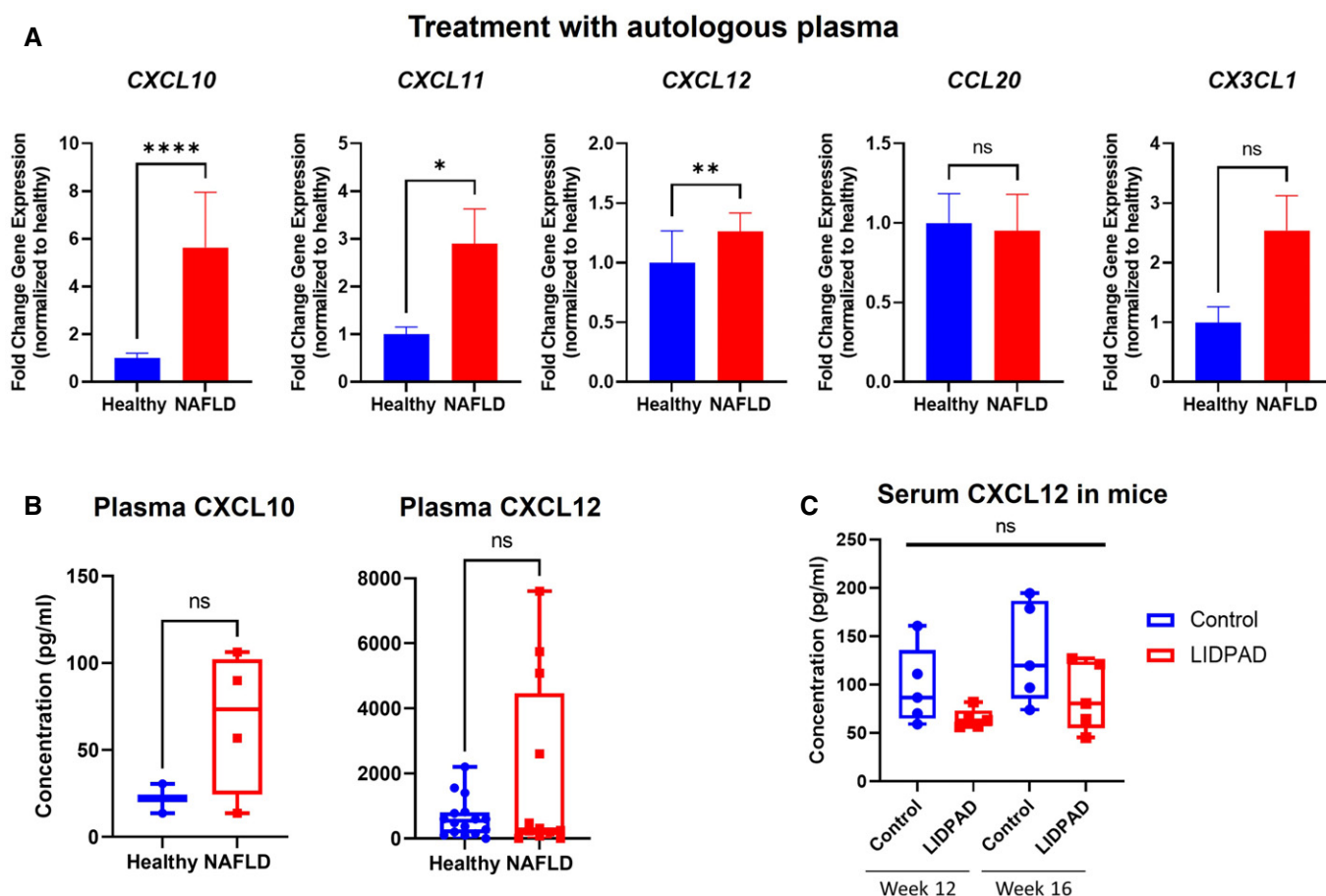


Figure EV3. Human plasma and mouse serum studies.

- A Chemokine expressions in the BOECs treated with autologous plasma. Fold changes in gene expressions of *CXCL10*, *CXCL11*, *CXCL12*, *CCL20*, and *CX3CL1* in NAFLD ($n = 10$) BOECs were normalized to healthy ($n = 12$) BOECs. Results are indicated by mean $\pm$ SD. * $P < 0.05$; ** $P < 0.01$; **** $P < 0.0001$; ns—not significant (Mann–Whitney test).
- B Plasma concentrations of *CXCL10* and *CXCL12* in healthy and NAFLD subjects. Box-whisker plots indicate median (middle line), 25th, 75th percentile (box), and the lowest/highest data points (whiskers). ns—not significant (Mann–Whitney test).
- C Serum *CXCL12* concentrations of wild-type C57BL/6J mice placed on LIDPAD or control diet for 12 and 16 weeks ($n = 5$ mice), determined by ELISA. Data presented as box-whisker plots of median (middle line), 25th, 75th percentile (box), and the lowest/highest data points (whiskers). ns—not significant (two-way ANOVA).