<table>
<thead>
<tr>
<th></th>
<th>Gender</th>
<th>Age</th>
<th>MELD score</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Controls</strong> n=14</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>F:36%(5)</td>
<td>46.4±3.4</td>
<td>F:46.8±9.4</td>
<td>NA</td>
</tr>
<tr>
<td>M:64%(9)</td>
<td>M:46.4±2.3</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Alcoholic cirrhosis</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>n=28</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>F:21%(6)</td>
<td>45.7±1.4</td>
<td>F:44.5±2.6</td>
<td>&lt;9  56.6% (15)</td>
</tr>
<tr>
<td>M:79%(22)</td>
<td>M:46±1.7</td>
<td>10–19</td>
<td>35.7% (10)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>20–29</td>
<td>7.1% (2)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>30–39</td>
<td>3.6% (1)</td>
</tr>
<tr>
<td><strong>Hepatitis B cirrhosis</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>n=43</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>F:23%(10)</td>
<td>49.6±1.6</td>
<td>F:49.3±2.9</td>
<td>&lt;9  67.4% (29)</td>
</tr>
<tr>
<td>M:77%(33)</td>
<td>M:49.7±1.9</td>
<td>10–19</td>
<td>27.9% (12)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>20–29</td>
<td>4.7% (2)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>30–39</td>
<td>0</td>
</tr>
</tbody>
</table>

MELD=Model for end stage liver disease, M=male, F=female, NA=not applicable
Table S2.

Subject Characteristics

<table>
<thead>
<tr>
<th></th>
<th>Gender</th>
<th>Age</th>
<th>Alcoholic liver disease</th>
</tr>
</thead>
<tbody>
<tr>
<td>Controls</td>
<td>F:16%(2)</td>
<td>41.2±4.2</td>
<td>F:54±3</td>
</tr>
<tr>
<td>n=8</td>
<td>M:84%(6)</td>
<td></td>
<td>M:37±4.3</td>
</tr>
<tr>
<td>Non-progressive</td>
<td>F:20%(2)</td>
<td>50.9±3.2</td>
<td>F:55±2</td>
</tr>
<tr>
<td>alcoholic liver</td>
<td>M:80%(8)</td>
<td></td>
<td>M:49.9±4</td>
</tr>
<tr>
<td>disease</td>
<td></td>
<td></td>
<td>No liver disease (2)</td>
</tr>
<tr>
<td>n=10</td>
<td></td>
<td></td>
<td>Mild liver disease (8)</td>
</tr>
<tr>
<td>Alcoholic</td>
<td>F:50%(3)</td>
<td>52.7±3.5</td>
<td>F:53±6.8</td>
</tr>
<tr>
<td>hepatitis</td>
<td>M:50%(3)</td>
<td></td>
<td>M:52.3±4.3</td>
</tr>
<tr>
<td>n=6</td>
<td></td>
<td></td>
<td>MELD 22±1.6</td>
</tr>
<tr>
<td>Alcoholic</td>
<td>F:33%(1)</td>
<td>47.5±6.8</td>
<td>F:54</td>
</tr>
<tr>
<td>cirrhosis</td>
<td>M:67%(3)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>n=4</td>
<td></td>
<td></td>
<td>Child Pugh A (2)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Child Pugh C (2)</td>
</tr>
</tbody>
</table>

MELD=Model for end stage liver disease, M=male, F=female, NA=not applicable
Mild liver disease: AST/ALT elevation and/or hepatic steatosis on imaging
Figure S1

A

Total fungi

Fold increase

Control  EtOH

B

Genus

Relative abundance [%]

Control  EtOH

Candida spp.

Fungal Taxa

Candida  parapsilosis
Humicola  albicans
tropicalis  palmiroleophila
Sclerotinia  Unclassified Candida
Guehomyces  Fungal Taxa
Sarcinomyces  parapsilosis
Verticillium  albicans
tropicalis  palmiroleophila
Unclassified Ascomycota  Unclassified Candida
Fusarium  parapsilosis
Aspergillus  albicans
tropicalis  palmiroleophila
Plectosphaerella  Unclassified Ascomycota
Phoma  parapsilosis
Alternaria  tropicalis
Cladosporium  parapsilosis
Mycena  tropicalis
Phaeosphaeria  Unclassified Ascomycota
Unclassified Capnodiales  tropicalis
Debaryomyces  Unclassified Ascomycota
Meyerozyma  tropicalis
Trichosporon  tropicalis
Coprinopsis  tropicalis
Unclassified Genus  tropicalis
Unclassified Genus  tropicalis
... [remaining 52]

C

Plasma 1,3-β-D-glucan

[ng/ml]

Control  EtOH
Figure S1. Changes in the intestinal mycobiota and translocation of fungal products following chronic alcohol feeding. (A and C) C57BL/6 mice were fed an oral control diet (n=4–5) or ethanol diet (n=4–14) for 5 weeks. Total fungi in feces were assessed by qPCR (A), and mean plasma levels of 1,3-β-D-glucan were measured by ELISA (C). (B) ITS sequencing of fecal samples from C57BL/6 mice that were fed an oral control diet (n=9) or ethanol diet (n=9) for 8 weeks. The graph demonstrates the average relative abundance of sequence reads in each fungal genus (left panel) and Candida species (right panel) for control and for ethanol-fed mice. Unpaired Student t test.
Figure S2

A) Liver/Body weight ratio

B) Plasma ethanol

C) Hepatic ADH activity

D) CYP2E1/β-ACTIN

E) Total bacteria

F) Total bacteria

G) Small intestine

H) Plasma LPS

I) Hepatic Irak3

Legend:
- Control
- EtOH
- Control+Ampho B
- EtOH+Ampho B
Figure S2. Absorption and hepatic metabolism of ethanol. C57BL/6 mice were fed an oral control diet (n=5–6) or ethanol diet (n=12–15), and also given vehicle or amphotericin B (Ampho B). (A) Ratio of liver to body weight. (B) Plasma level of ethanol at time of harvesting. (C) Hepatic ADH activity. (D) Immunoblot analysis of hepatic CYP2E1 (n=5 for mice fed a control diet, n=8 for mice fed an ethanol diet). (E) Principal component analysis (PCA) of bacterial microbiomes. (F) Total bacteria in feces were assessed by qPCR. (G) Immunoblot analysis of OCLN (occludin) in the small intestine (n=5 in each group). (H) Plasma LPS. (I) Hepatic expression of Irak3 mRNA. Unpaired Student t test. *P<.05.
Figure S3

A

Mouse liver

![Mouse liver images]

B

CLEC7A

![CLEC7A graph]

C

Human liver

![Human liver images]

D

Hepatic CLEC7A

![Hepatic CLEC7A graph]

E

Duodenal CLEC7A

![Duodenal CLEC7A graph]
Figure S3. Expression of CLEC7A. (A) Immunofluorescence analysis of F4/80 (red) and CLEC7A (green) in non-diseased mouse liver (representative liver sections); nuclei are blue. (B) Expression of Clec7a in primary human hepatocytes (Hep), Kupffer cells (KC), and activated hepatic stellate cells (Act HSC) was measured by qPCR (n=2 independent experiments). (C) Immunofluorescence analysis of CD68 (red) and CLEC7A (green) in non-diseased human liver (representative liver sections); nuclei are blue. (D) Expression of CLEC7A mRNA in hepatic biopsies from controls without alcohol dependency (n=9) and alcohol-dependent patients (n=65). (E) Expression of CLEC7A mRNA in duodenal biopsies from controls without alcohol dependency (n=12) and alcohol-dependent patients (n=110). Scale bars, 50μm. Unpaired Student t test. *P<.05.
Figure S4

A. Liver/Body weight ratio

B. Plasma ethanol

C. Hepatic ADH activity

D. CYP2E1 and β-ACTIN Western blots

E. Plasma LPS

F. Plasma 1,3-β-D-glucan

G. Hepatic Il1b
Figure S4. Absorption and hepatic metabolism of ethanol. C57BL/6 mice were transplanted with bone-marrow from WT (WT) or Clec7a−/− mice (Clec7a−/−) and fed an oral control diet (n=4–5) or ethanol diet (n=6–10). (A) Ratio of liver to body weight. (B) Plasma level of ethanol at time of harvesting. (C) Hepatic ADH activity. (D) Immunoblot analysis of hepatic CYP2E1. (E) Plasma LPS. (F) Plasma 1,3-β-D-glucan. (G) Hepatic expression of Il1b mRNA in WT (n=6) and Clec7a−/− mice (n=3) 2hrs after intraperitoneal injections with carboxymethyl-β-1,3-D-glucan (2mg/mouse). Unpaired Student t test (A–C, E–G). Mann-Whitney U-statistic test (H). *P<.05.
Figure S5

A

- **Cxcl1**
  - **Curdlan**
    - **Fold increase**
      - **Control**
      - **Curdlan**
    - **Fold increase**
      - **WT**
      - **Clec7a^-/-**

- **Cxcl2**
  - **Curdlan**
    - **Fold increase**
      - **Control**
      - **Curdlan**
    - **Fold increase**
      - **WT**
      - **Clec7a^-/-**

- **Tnf**
  - **Curdlan**
    - **Fold increase**
      - **WT**
      - **Clec7a^-/-**

B

- **WT**
  - **Control**
  - **EtOH**
  - **Clec7a^-/-**
  - **Control**
  - **EtOH**

- **Pro-Caspase-1**
- **Cleaved Caspase-1**
- **p20**
- **β-ACTIN**

C

- **Cytotoxicity [%]**
  - **Curdlan**
    - **Control**
    - **Curdlan**

D

- **Control**
- **Curdlan**

E

- **Cytotoxicity [%]**
  - **IL1B**
    - **Control**
    - **IL1B**
Figure S5. Curdlan does not induce hepatocyte death or steatosis. (A) Primary mouse WT and Clec7a−/− Kupffer cells were stimulated with curdlan; graphs show expression of Cxcl1, Cxcl2 and Tnf mRNA (n=4–6 independent experiments). (B) C57BL/6 mice were transplanted with WT (WT) or Clec7a−/− bone-marrow (Clec7aΔBM) and fed an oral control diet or ethanol diet. Hepatic caspase-1, cleaved caspase-1 and β-actin protein. (C–D) Hepatocytes were stimulated with curdlan. Hepatocyte cytotoxicity (C) and lipid accumulation as determined by Oil Red O-staining (D); n=3 independent experiments. (E) Hepatocytes were stimulated with IL1B and hepatocyte cytotoxicity measured; n=3 independent experiments. Unpaired Student t test. *P<.05.
Figure S6

A

Figure S6 A shows the relative abundance of fungal taxa in different conditions: Controls, Non-progressive ALD, Alcoholic hepatitis, and Alcoholic cirrhosis. The y-axis represents the relative abundance [%], and the x-axis lists the conditions.

B

Figure S6 B presents a PCA plot with PC1 and PC2 axes. The plot includes controls, non-progressive ALD, alcoholic hepatitis, and alcoholic cirrhosis.

C

Figure S6 C displays the relative abundance of Candida spp. in different conditions: Controls, Non-progressive ALD, Alcoholic hepatitis, and Alcoholic cirrhosis.
**Figure S6. Intestinal fungal dysbiosis in patients with alcohol abuse.** ITS sequencing of fecal samples from controls (controls, n=8) or alcohol-dependent patients with non-progressive alcoholic liver disease (non-progressive ALD, n=10), alcoholic hepatitis (alcoholic hepatitis, n=6), or alcoholic cirrhosis (alcoholic cirrhosis, n=4). (A) The graph demonstrates the relative abundance of sequence reads in each genus for each individual person. (B) PCA of mycobiomes. (C) *Candida* species composition of human fungal ITS sequences from Fig. 6A divided into four groups: (controls; n=8), alcohol-dependent patients with non-progressive alcoholic liver disease (non-prog. ALD; n=10), alcoholic hepatitis (alcoholic hepatitis; n=6), or alcoholic cirrhosis (alcoholic cirrhosis; n=4).