

Supplementary Materials

Integrated metabolomics and transcriptomics revealed the anti-constipation mechanisms of xylooligosaccharides from corn cobs

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Table S1. Primer sequences used for qPCR.

| Gene | Sequence (5' to 3') | |
|--------------------------------|-----------------------|-----------------------|
| | Forward | Reverse |
| <i>GAPDH</i> | AACGACCCCTTCATTGACCTC | CCTTGACTGTGCCGTTGAACT |
| <i>IL-1α</i> | CCTGTTGTATCAACTGTGTTC | GATGTCCCAACCAGGACAG |
| <i>IL-6</i> | GCCCACCAAGAACGATAGTCA | ACCAGCATCAGTCCAAGAAG |
| <i>IL-1β</i> | TGCCACCTTTTGACAGTGATG | TGATGTGCTGCTGCGAGATT |
| <i>TNF-α</i> | CCTATGTCTCAGCCTCTTCT | CCTGGTATGAGATAGCAAAT |
| <i>Hmgcs2</i> | GGCTATAAAGCTGCGGAGGG | CATGGTGAAAGAGCCAAAGGG |
| <i>Acat1</i> | AATGCTGGAGATTGACCCCC | CGGGCTCCAGACATCCCAAT |
| <i>Cyp11a1</i> | GGTAGTTCTTGGAGCTTCCCC | ATGATCTAGGTGGCTGCTTGG |
| <i>Sult1e1</i> | GCCAAAGATGTGCGCCGTTTC | AACCATACGGAACCTTGCCCT |

| Category | NC | CM | LXOS | MXOS | HXOS |
|--------------------------------|---------------|----------------|----------------|----------------|----------------|
| Feces water content (%) | 49.52±4.93 a | 29.69±5.29 d | 35.08±4.25 c | 41.55±3.82 b | 45.46±4.44 b |
| Feces weight (g) | 0.074±0.017 a | 0.031±0.011c | 0.049±0.020 b | 0.064±0.018 a | 0.066±0.014 a |
| First black stool time (min) | 97.72±8.93 d | 183.75±26.82 a | 161.73±23.07 b | 136.91±15.59 c | 128.47±18.50 c |
| Intestinal propulsion rate (%) | 81.72±8.20 a | 55.12±6.83 c | 66.71±7.07 b | 72.50±9.81 b | 77.73±9.23 ab |
| Gastric emptying rate (%) | 66.16±4.64 a | 22.05±5.90 e | 40.11±4.12 d | 46.54±4.56 c | 51.27±5.39 b |

Table S2. Effects of XOS on defecation-related parameters in constipated mice.

Note: Results are expressed as mean ± SD (n = 10). Means with different letters in the same row are significantly different ($p < 0.05$).

Table S3. Statistics of hepatic RNA-sequencing reads in different groups after filtering.

| Sample ID | Total reads | Total bases | Total giga bases | Q20 rate | Q30 rate | GC content |
|-----------|-------------|-------------|------------------|----------|----------|------------|
| NC01 | 43447400 | 6203466717 | 6.2G | 98.13% | 92.87% | 49.71% |
| NC02 | 42822188 | 6106166260 | 6.11G | 98.44% | 93.59% | 49.50% |
| NC03 | 42278862 | 6005035805 | 6.01G | 98.50% | 93.77% | 50.42% |
| CM01 | 43900210 | 6279900028 | 6.28G | 98.28% | 93.22% | 48.79% |
| CM02 | 45002090 | 6450166882 | 6.45G | 98.46% | 93.63% | 48.97% |
| CM03 | 47855692 | 6853427947 | 6.85G | 98.23% | 93.11% | 49.19% |
| XOS01 | 45049634 | 6446582229 | 6.45G | 98.49% | 93.72% | 49.77% |
| XOS02 | 43534534 | 6220613510 | 6.22G | 98.47% | 93.63% | 49.79% |
| XOS03 | 40597570 | 5795038088 | 5.8G | 98.43% | 93.53% | 49.59% |

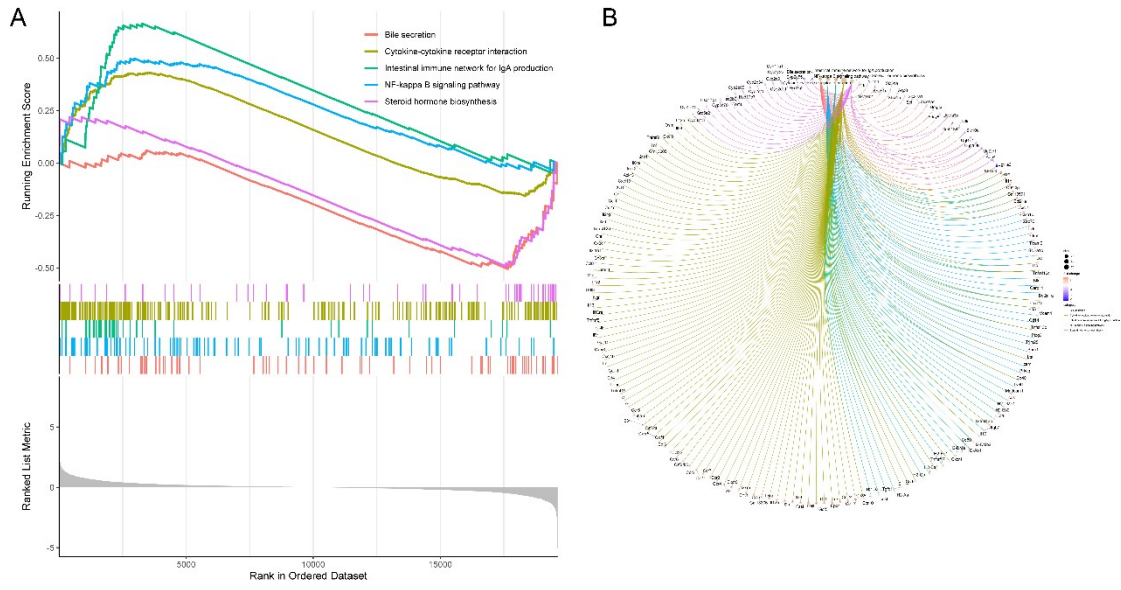


Fig. S1 Gene Set Enrichment Analysis (GSEA). (A) GSEA plot and (B) circular cnetplot.