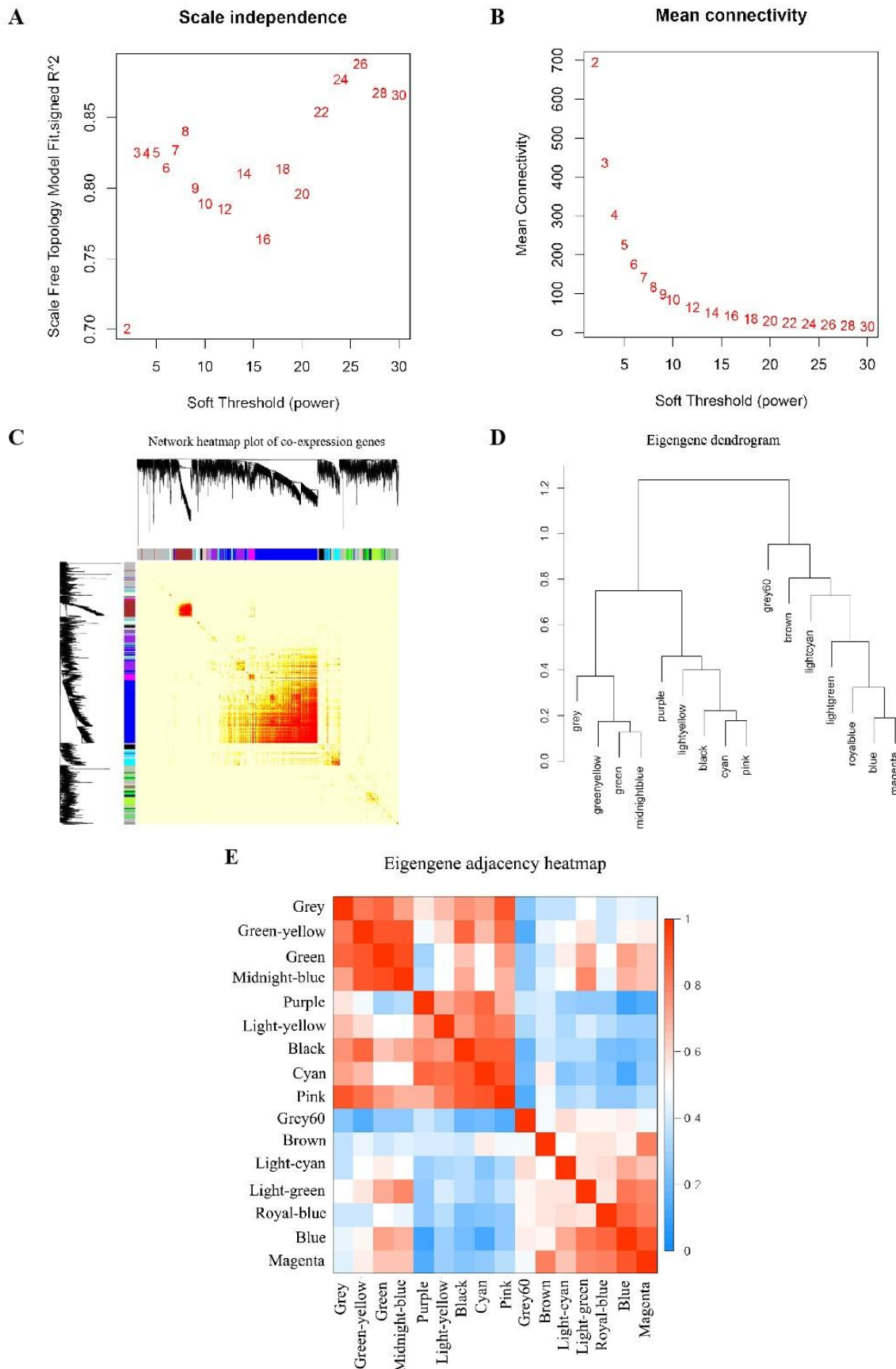


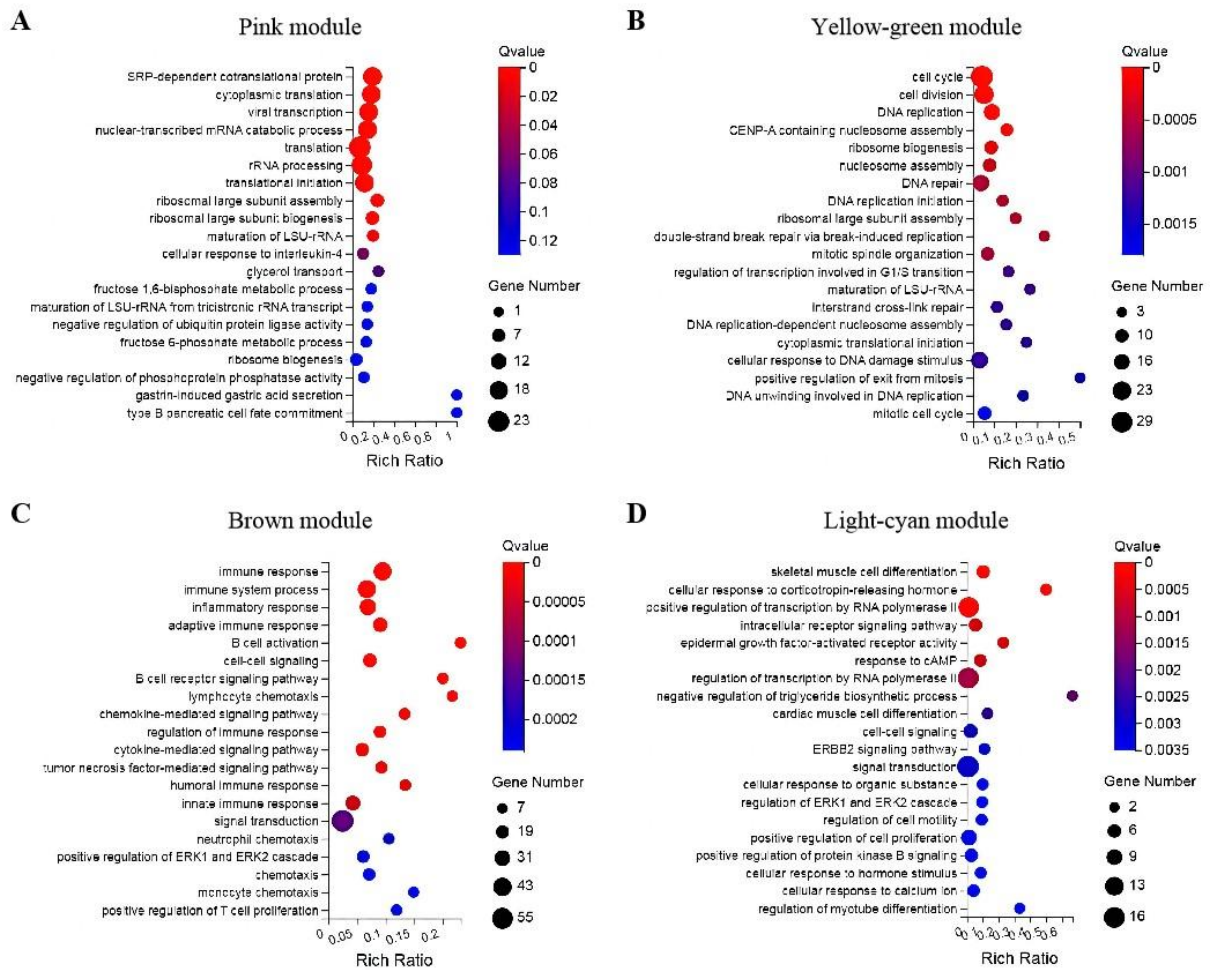
**Supplementary Figure 1 Functional and pathway enrichment analyses .** A: Gene Ontology-cellular component (GO-CC) enrichment analysis based on the 211 differentially expressed genes (DEGs) between the JOD and JC groups. B: Gene Ontology-molecular function (GO-MF) enrichment analysis based on the 211 DEGs between the JOD and JC groups. C: GO-CC enrichment analysis based on the 411 DEGs between the JOD and JO groups. D: GO-MF enrichment analysis based on the 411 DEGs between the JOD and JO groups. E: GO-CC enrichment analysis based on the 129 overlapped DEGs. F: GO-MF enrichment analysis based on the 129 overlapped DEGs. Bubble charts show the top 20 significantly enriched terms. The color of the bubbles represents the *Q* value of each enriched term, and the size of the bubbles represents the number of DEGs enriched in the term. The horizontal axis indicates the rich ratio of the number of DEGs enriched in the term to the total number of human genes annotated to this term.



**Supplementary Figure 2 Identification of modules associated with the clinical traits of ODS.** A: Analysis of the scale-free fit index for various soft-thresholding powers. B: Analysis of the mean connectivity for various soft-thresholding powers. Overall, 22 is considered the most fit power value. C: Interaction relationship analysis of co-expression genes. Different colors of horizontal and vertical axes correspond to

different modules. The degree of connectivity of different modules is indicated by the brightness of yellow.

D: Hierarchical clustering of eigengenes according to their correlation. E: Heatmap plot of the adjacencies in eigengenes.



**Supplementary Figure 3** Gene Ontology - biological process analysis for genes in the pink module (A), the green-yellow module (B), the brown module (C), and the light-cyan module (D). Bubble charts show the top 20 significantly enriched terms. The color of the bubbles represents the  $Q$  value of each enriched term, and the size of the bubbles represents the number of DEGs enriched in the term. The horizontal axis indicates the rich ratio of the number of DEGs enriched in the term to the total number of human genes annotated to this term.

**Supplementary Table 1. Primers used for mRNA detection**

	<b>Forward (5'-3')</b>	<b>Reverse (5'-3')</b>
<b>CDT1</b>	GTGCTGCCCTACAAGTACCA	TGCACTCCTCAAAACGCCTA
<b>NHP2</b>	AAAGGAGAAAAAGGGACCTGGG	AGGCACTCATCGTAAGCCTC
<b>EXOSC5</b>	CTTTGCCTGCGAACAGAACC	TCGAGTGTGGCCTTGTTGAA
<b>EPN3</b>	CAAGTGGACTTTTTGCGGGG	TAAAGGAAGCGGGGCAGTTT
<b>NME1</b>	GCAGCCGGAGTTCAAACCTA	TGCACACCAGGCTGACTTAG
<b>REG3A</b>	ACCATATCCCACCAGAGAGTGA	GCAGGAAAGCAGCATCCAAG
<b>PLA2G2A</b>	CTGTCTCCAAACAGCCTTGTG	GGTGGCTCTCTCAGAGGACT
<b>PRSS2</b>	TTCTGGCTACCACTTCTGCG	TGCGGTGATATTCACACCCTC
<b>DEFA5</b>	GGACTCACGGGTAGCACAAC	CCTTTGCAGGAAATGGACTC
<b>DEFA6</b>	AGCTTATGAGGCTGATGCCC	GTGAAAGCCCTTGTTGAGCC
<b>GADPH</b>	CCTCTGACTTCAACAGCGACAC	TGGTCCAGGGGTCTTACTCC

**Supplementary Table 2. Baseline characteristics of the 66 participants included in this study**

Characteristics	The first cohort for transcriptome analysis			<i>P</i> value	The second cohort for serological tests			<i>P</i> value
	JC group ( <i>n</i> = 6)	JO group ( <i>n</i> = 6)	JOD group ( <i>n</i> = 6)		SC group ( <i>n</i> = 16)	SO group ( <i>n</i> = 16)	SOD group ( <i>n</i> = 16)	
Age (year)	35.33±4.68	36.33±6.15	36.83±9.97	0.94	37.44±7.38	38.13±7.96	37.94±7.99	0.97
Male, n (%)	4 (66.67)	4 (66.67)	2 (33.33)	0.41	9 (56.25)	9 (56.25)	9 (56.25)	1.00
<b>Defecation characteristics</b>								
Diarrhea duration (month)	0	0 (0)	65.00 (12.00-85.50) <sup>a</sup>	0.00	0	0 (0)	65.00 (15.00-85.50) <sup>b</sup>	0.00
Bristol type, n (%)			a	0.00			b	0.00
1-3	0 (0)	0 (0)	0 (0)		0 (0)	0 (0)	0 (0)	
4	6 (100)	6 (100)	0 (0)		16 (100)	16 (100)	0 (0)	
5	0 (0)	0 (0)	1 (16.67)		0 (0)	0 (0)	3 (18.75)	
6	0 (0)	0 (0)	5 (83.33)		0 (0)	0 (0)	13 (81.25)	
7	0 (0)	0 (0)	0 (0)		0 (0)	0 (0)	0 (0)	
Bowel movement per day, n (%)			a	0.00			b	0.00
<3	6 (100)	6 (100)	0 (0)		6 (100)	6 (100)	0 (0)	
3-4	0 (0)	0 (0)	5 (83.33)		0 (0)	0 (0)	12 (75.00)	
≥5	0 (0)	0 (0)	1 (16.67)		0 (0)	0 (0)	4 (25.00)	
Abdominal pain associated with defecation, n (%)	0 (0)	0 (0)	1 (16.67)	0.35	0 (0)	0 (0)	7 (43.75)	0.00
Fecal mucus, n (%)	0 (0)	0 (0)	1 (16.67)	0.35	0 (0)	0 (0)	5 (31.25)	0.00
<b>Obesity-related characteristics</b>								
BMI (kg/m <sup>2</sup> )	23.07±0.49	34.48±4.40	33.67±3.26	0.00	21.81±1.29	34.43±4.89	34.17±4.98	0.00
Weight (kg)	67.62±7.18	98.33±13.37	97.67±5.50	0.00	63.45±7.42	100.88±14.00	101.11±16.07	0.00
Waist circumference (cm)	78.67±2.66	103.00±7.85	100.50±7.42	0.00	71.19±5.67	103.25±11.46	103.13±11.54	0.00
Systolic blood pressure (mmHg)	114.83±9.93	132.67±15.88	135.33±20.67	0.09	114.38±8.43	132.38±17.19	135.25±15.53	0.00

Diastolic blood pressure (mmHg)	68.00±5.18	80.33±17.82	83.83±15.24	0.15	71.25±5.86	79.63±13.53	81.81±12.69	0.03
Total Ch (mg/dl)	133.54±15.52	202.33±19.45	187.60±37.83	0.00	117.76±14.12	190.61±42.92	202.18±35.30	0.00
LDL-Ch (mg/dl)	100.68±13.32	139.09±20.71	121.02±32.82	0.04	75.75±25.64	123.89±41.10	127.34±31.43	0.00
HDL-Ch (mg/dl)	43.84±7.76	39.47±5.32	49.16±12.40	0.21	58.40±13.44	44.73±11.96	50.28±11.39	0.01
Triglycerides (mg/dl)	99.35±33.76	209.90±81.40	144.76±42.41	0.01	86.66±30.02	173.70±68.96	201.95±98.93	0.00
Fasting plasma glucose (mg/dl)	92.55±8.15	91.47±6.34	104.01±27.11	0.38	88.10±10.35	76.29±39.01	93.08±18.28	0.17

### Complications

MetS, n (%)	0 (0)	4 (66.67)	3 (50.00)	0.05	0 (0)	10 (62.50)	9 (56.25)	0.00
Hypertriglyceridemia, n (%)	0 (0)	5 (83.33)	3 (50.00)	0.01	0 (0)	13 (81.25)	13 (81.25)	0.00
Hypertension, n (%)	0 (0)	2 (33.33)	2 (33.33)	0.28	0 (0)	7 (43.75)	8 (50.00)	0.00
Diabetes, n (%)	0 (0)	0 (0)	2 (33.33)	0.11	0 (0)	2 (12.50)	2 (12.50)	0.34
Coronary heart disease, n (%)	0 (0)	0 (0)	0 (0)	1.00	0 (0)	0 (0)	0 (0)	1.00

BMI: body mass index; Ch: cholesterol; LDL: low-density lipoprotein; HDL: high-density lipoprotein; MetS: metabolic syndrome. The cutoff points for the criteria used to define MetS are 3 or more of the following: central obesity (waist circumference > 85 cm in women and > 90 cm in men), hypertriglyceridemia (triglycerides > 150 mg/dl or drug treatment), HDL-Ch < 50 mg/dl, hypertension (systolic BP > 130 mmHg or diastolic BP > 85 mmHg or drug treatment), and diabetes (fasting plasma glucose > 100 mg/dl or drug treatment for elevated blood glucose). <sup>a</sup>*P* < 0.05 vs the JO group. <sup>b</sup>*P* < 0.05 vs the SO group.