**Oral** **Microbiota Composition and Function Changes during Chronic Erythematous Candidiasis**

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**Figure S1.** Shotgun sequences generated from Illumina Hiseq 2000 platform. Reads of low-quality or classified as human sources were indicated.

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**Figure S2.** Co-occurrence network constructed by all taxa presented in salivary samples. Each pair of nodes connected with edge were significantly and highly correlated (Spearman correlation test, *P* <0.05, |r|≥0.6). Solid and dashed lines indicate positive and negative correlations.

**Figure S3.** Mouse oral co-infection model. *C. albicans* (strain SC5314) was cultured in yeast extract peptone dextrose (YPD) medium at 30˚C for 15-18 h. *S. mutans* (strain UA159) was cultured in brain heart infusion (BHI) medium at 37°C under aerobic, static conditions. C57BL/6 mice were maintained under specific pathogen-free (SPF) conditions and fed with 5% sucrose water. Mice aged 6-8 weeks were randomly placed into 2 groups: *C. albicans*-infected group (n=6) and *S. mutans* plus *C. albicans*-infected group (n=6). On the first day, the mice were anesthetized with chloral hydrate (400 mg/kg) and infected with *S. mutans* (3×108 CFU) or PBS sublingually. On the second day, the mice were anesthetized, and a small cotton swab soaked with 100 μl of *C. albicans* suspension (6×108 cfu/ml) was used for infection without immunosuppression. After 2 and 5 days, the mice were screened for *S. mutans*and *C. albicans* infections.For cfu determination, tongues were excised and homogenized. Undiluted and diluted homogenates were plated on chloramphenicol-supplemented Sabouraud dextrose agar or Mitis Salivarius Agar plus Bacitracin plates for *C. albicans* and *S. mutans* cfu counts.

(A) Timeline of the infection model. (B) Co-infection with *S. mutans* induced more weight loss (n=6, \* *P* <0.01, \*\* *P* <0.01). (C) *S. mutans* increased the *C. albicans* burden on mouse tongues (cfu counts on days 2 and 5, n=6, \*\* *P* <0.01). (D) *S. mutans* on mouse tongues were counted on day 2 and 5.