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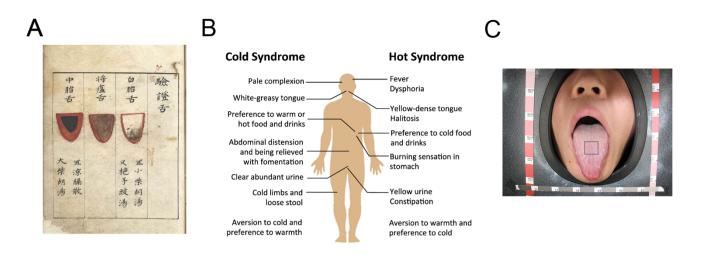
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ERRATUM: Integrating next-generation sequencing and traditional tongue diagnosis to determine tongue coating microbiome

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The labels in Figure 1E and Figure 3B were inadvertently switched for the Cold and Hot Syndrome patients, and therefore published in the wrong order. The correct version of the figures and their labels appear below.





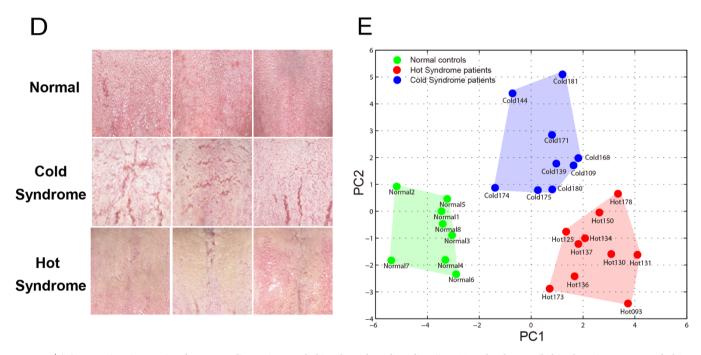


Figure 1 | (A) An ancient instruction for tongue diagnosis recorded in *Shang-han-dian-dian-jin*, a TCM book compiled in the Ming Dynasty of China (1368–1644 AD). (B) Symptoms all over human body used as features for the TCM classification of Cold and Hot Syndromes; the tongue-coating feature is highly important in clinical practice. (C) Sampling images of tongue coating from the centre of the tongue, an area regarded as reflecting conditions of the "spleen-stomach" in the traditional tongue diagnosis. (D) Typical tongue-coating appearances: normal tongue coating of healthy control examples (upper), white-greasy tongue coating of Cold Syndrome examples (middle), and yellow-dense tongue coating of Hot Syndrome examples (lower).

(E) Principal Component Analysis (PCA) of the tongue-coating images. The healthy controls, Cold Syndrome patients and Hot Syndrome patients are distributed in separate regions, indicating that the three classes are distinguishable based on their tongue-coating images.



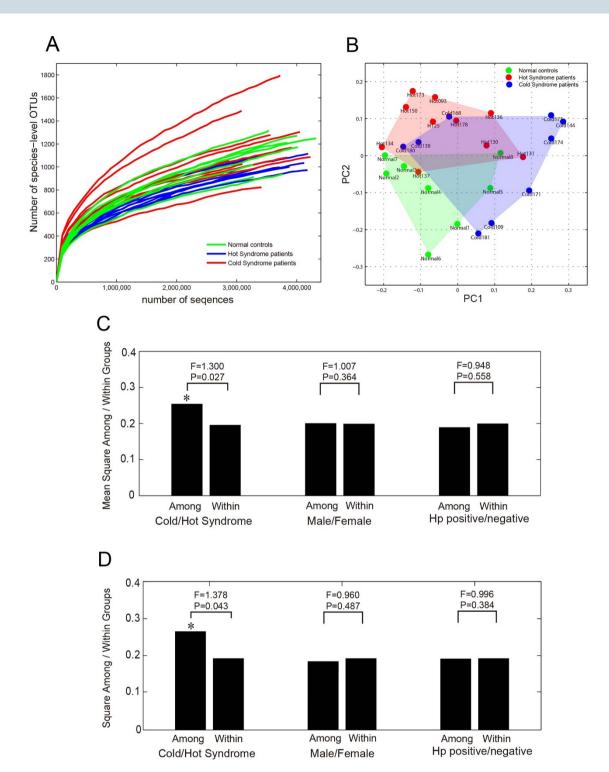


Figure 3 | (A) Alpha diversity rarefaction curves of all 27 samples based on species-level OTUs. (B) PCoA plot of the between-sample Jaccard matrix of all 27 samples. (C) AMOVA results of the between-sample Jaccard distance matrix of the 19 gastritis patients. The F-statistic is the ratio of the mean square among groups within the groups. (D) AMOVA results of the between-sample unweighted Unifrac distance matrix of the 19 gastritis patients.