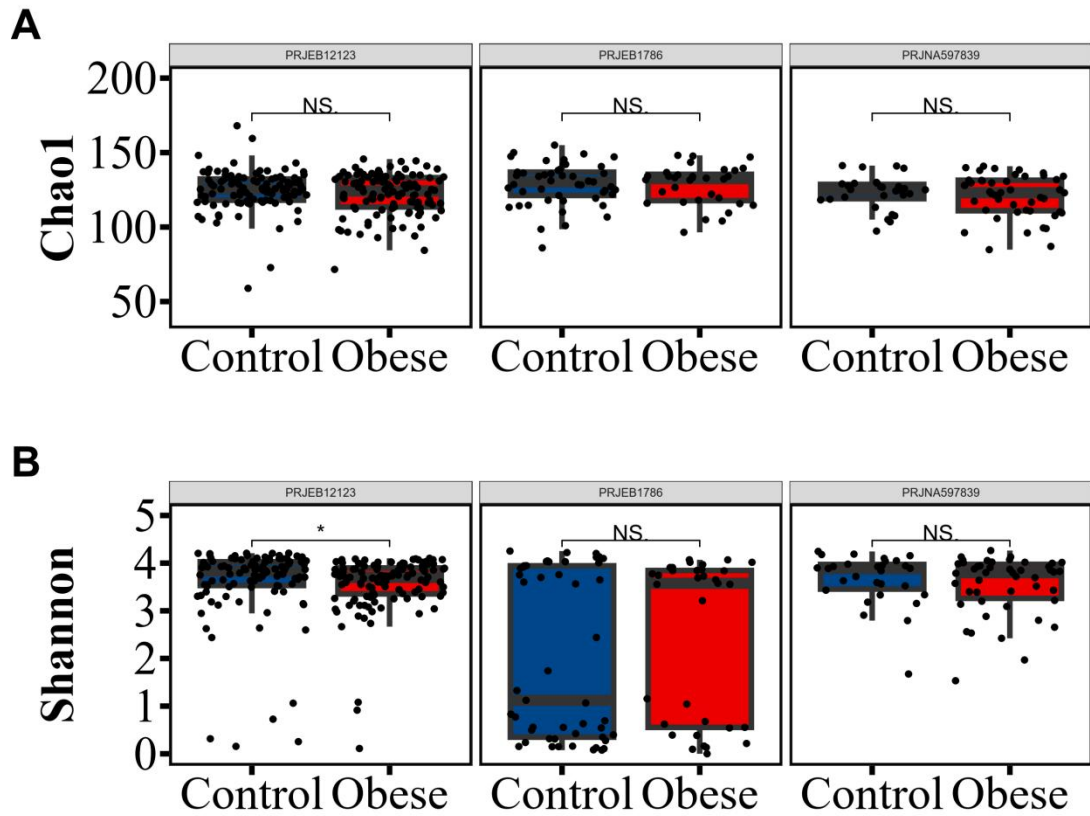
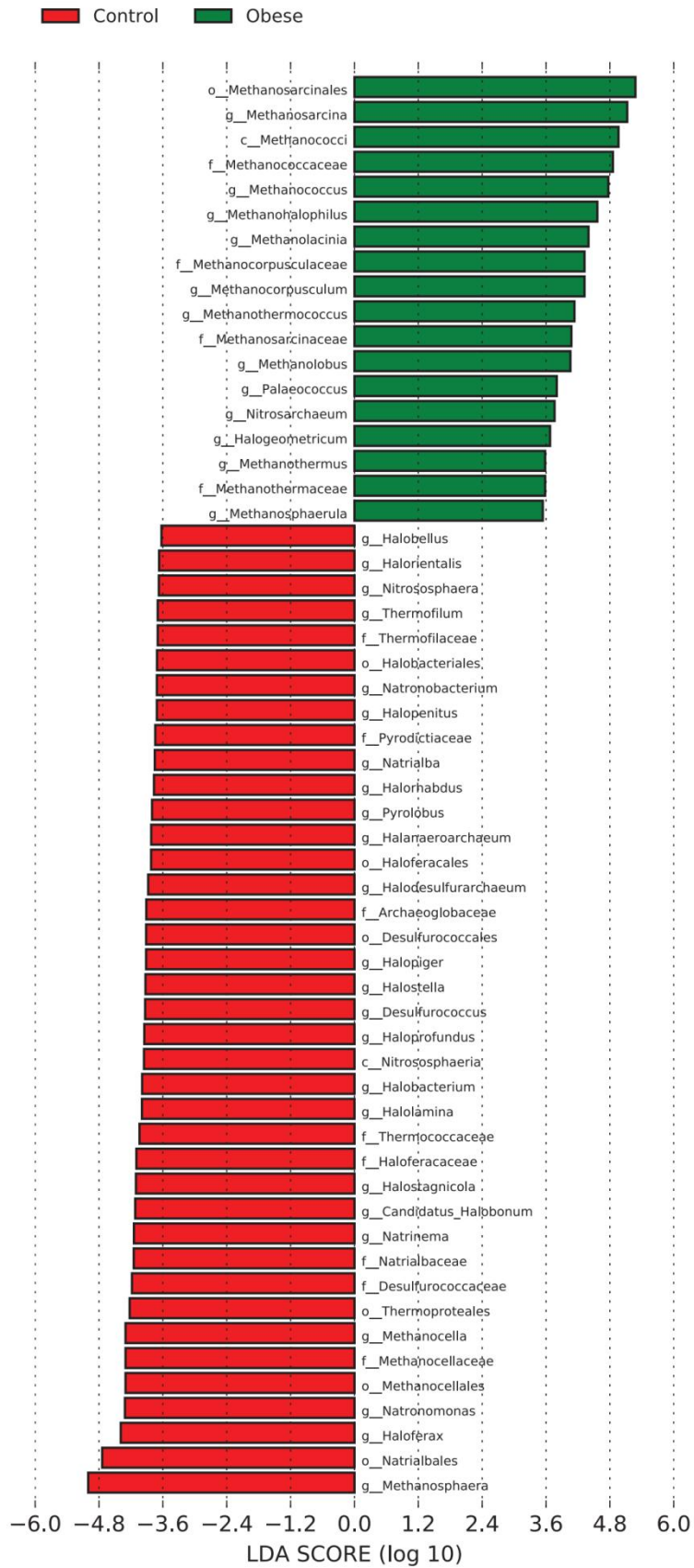


Supplementary Figure S1. Alterations of gut bacteriome in obese subjects. (A) Chao1 richness and (B) Shannon diversity for gut genera between obese subjects and lean controls. Groups were compared using the Wilcoxon rank-sum test. (C) Principal coordinate analysis of gut bacterial genera separates obese subjects from lean controls. Groups were compared using PERMANOVA (permutational multivariate analysis of variance). (D) Relative abundance of gut bacterial phyla in obese subjects and lean controls. (E) Differential bacterial taxa between obese subjects and lean controls. Groups were compared using Linear Discriminant Analysis Effect Size (LEfSe). *** $P < 0.001$, ns ($P > 0.05$).

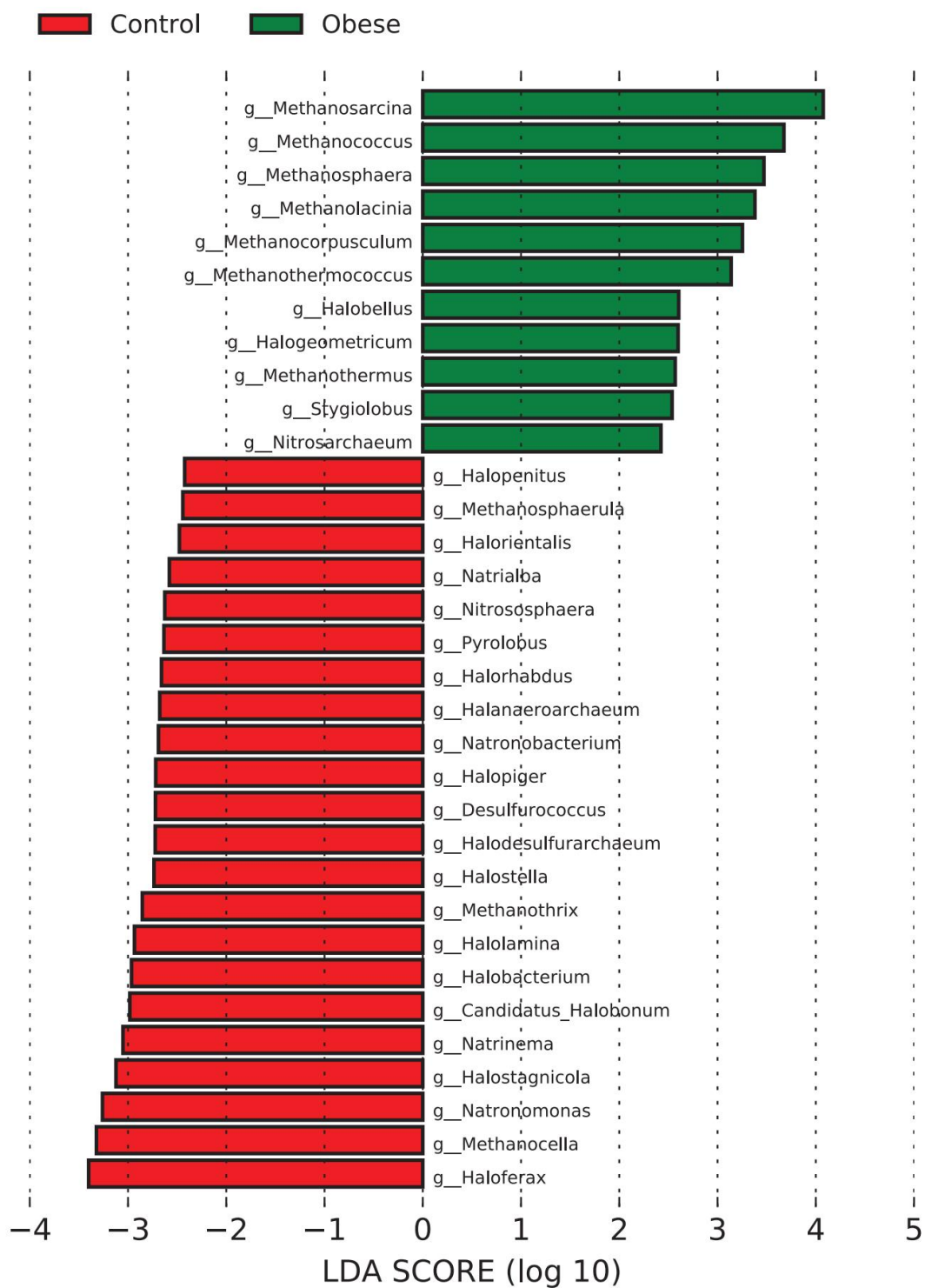


Supplementary Figure S2. Alterations of alpha diversity indices for gut archaea in obese subjects. (A) Chao1 richness and (B) Shannon diversity. Groups were compared using the Wilcoxon rank-sum test. * $P < 0.05$.

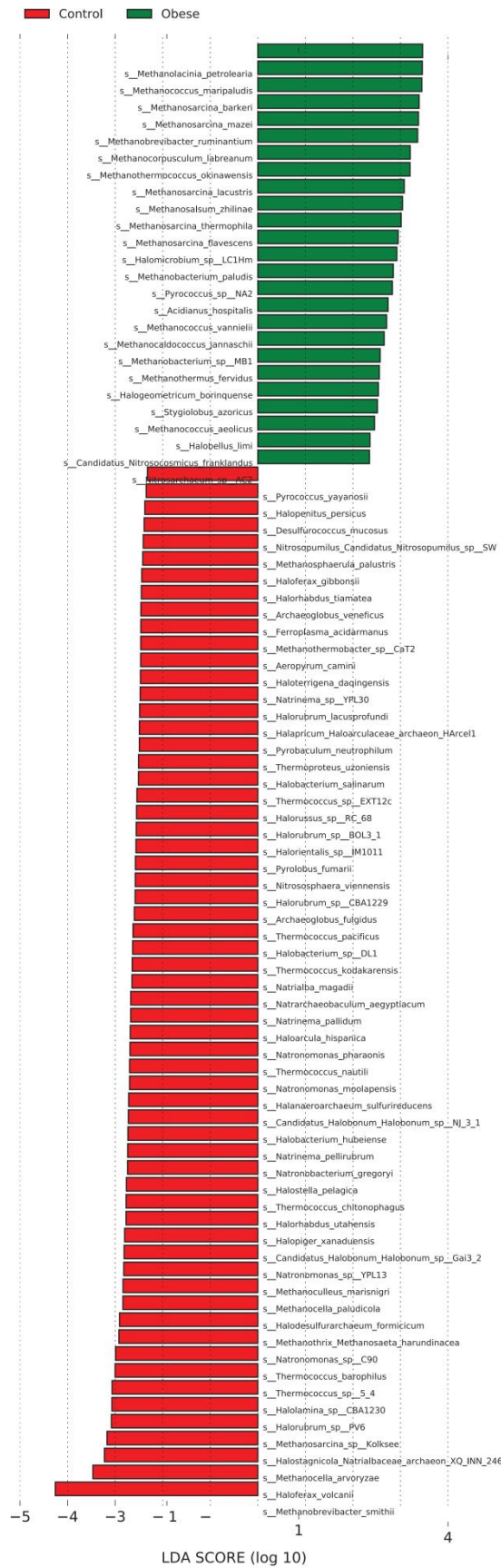


Supplementary Figure S3. Changes of the differential gut archaeal taxa for obese subjects compared with lean controls in the discovery cohort. Groups were compared using Linear

Discriminant Analysis Effect Size (LEfSe). Taxa with an LDA score > 2 were regarded as statistically significant.

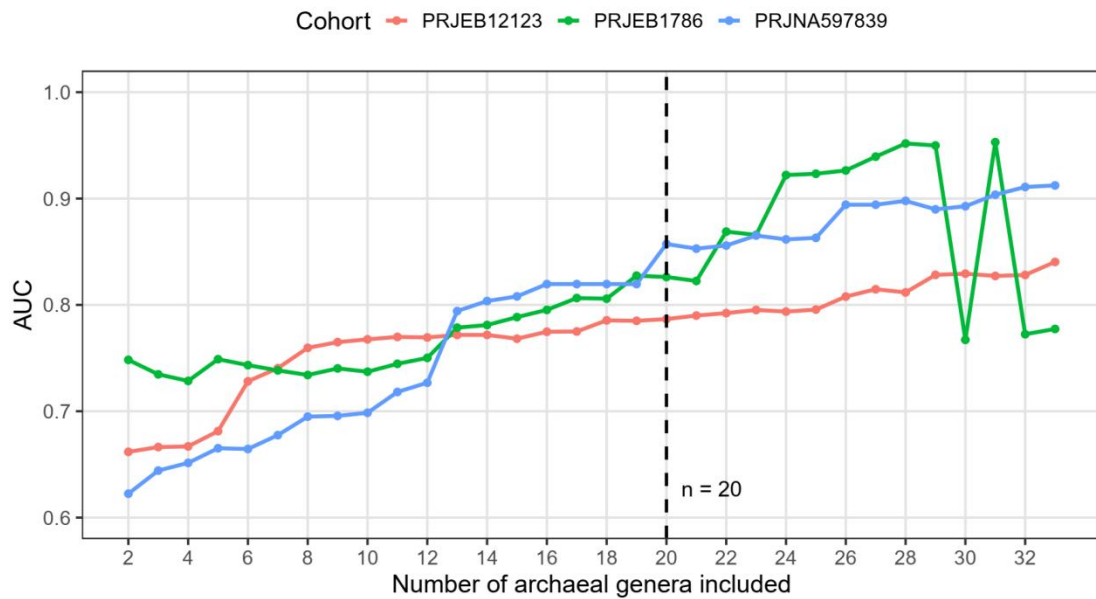


Supplementary Figure S4. Changes of the differential gut archaea for obese subjects compared with lean controls in the discovery cohort at the genus level. Groups were compared using Linear Discriminant Analysis Effect Size (LEfSe).

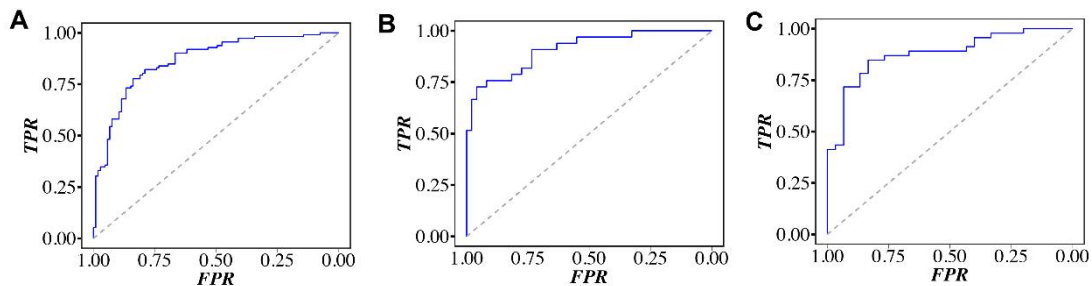


Supplementary Figure S5. Changes in the differential gut archaea for obese subjects compared with lean controls in the discovery cohort at the species level. Groups were compared using Linear Discriminant Analysis Effect Size (LEfSe).

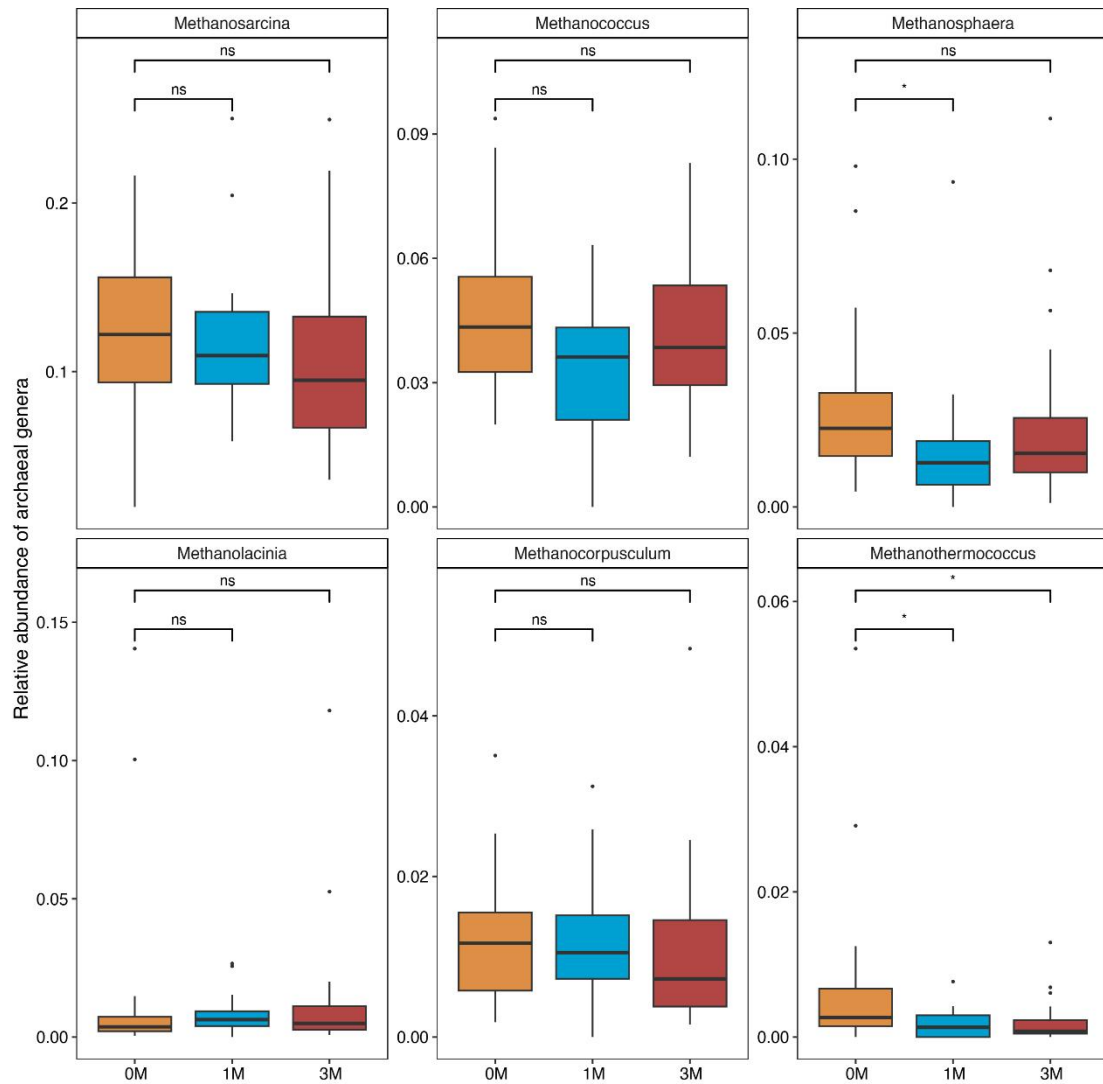
Performance across cohorts using different numbers of archaeal genera



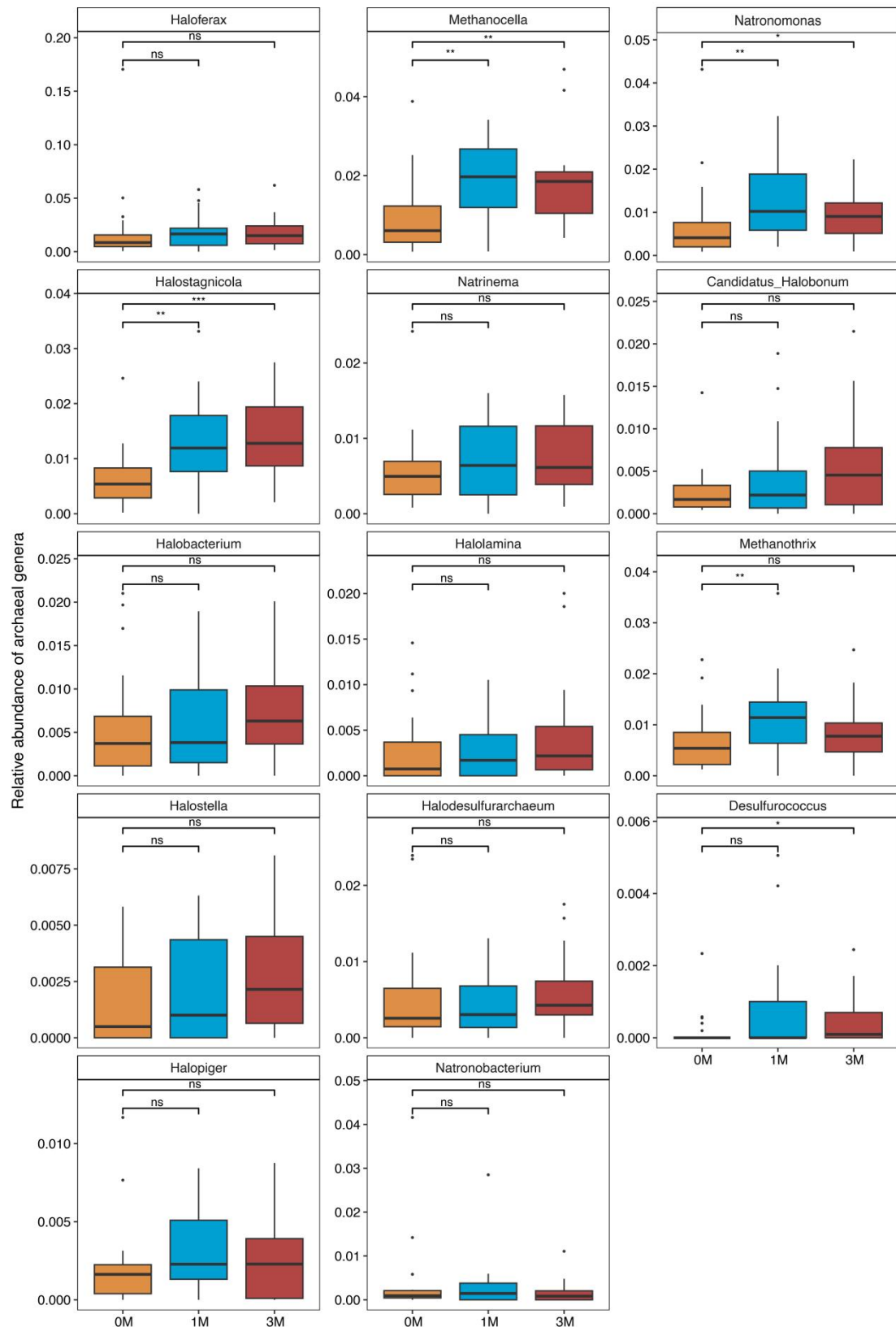
Supplementary Figure S6. Performance of obesity prediction models using different numbers of archaeal genera across three cohorts. Logistic regression models were constructed using increasing numbers of archaeal genera ranked by differential abundance between obese subjects and lean controls.



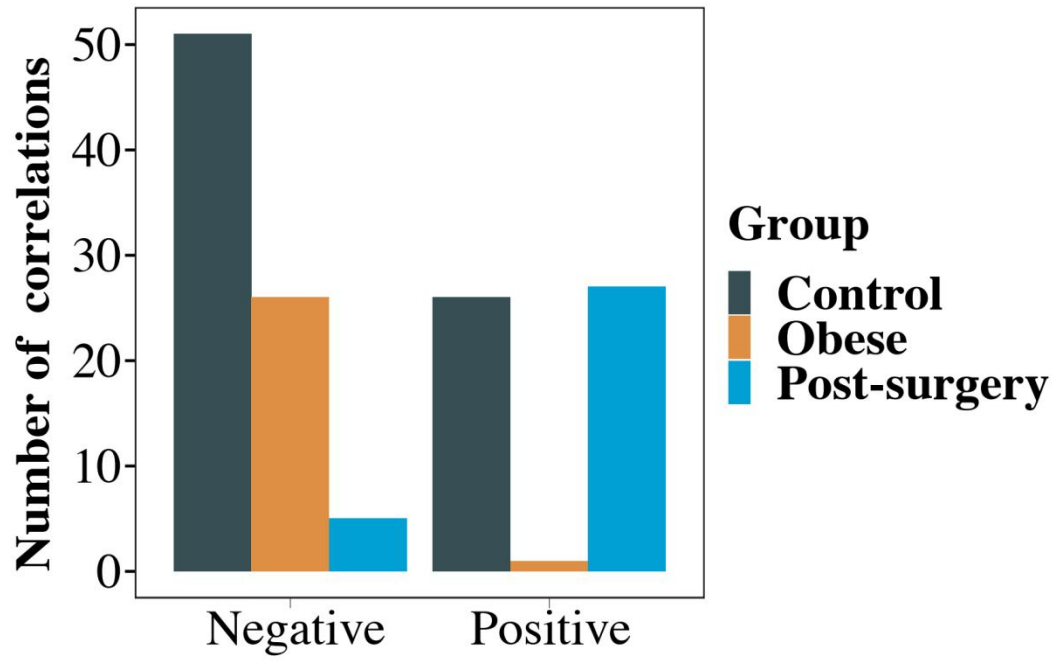
Supplementary Figure S7. Gut archaeal species classify obese subjects from lean controls. Predictive model for (A) discovery cohort. Predictive model for validated cohorts (B) PRJNA597839 and (C) PRJEB1786. Models were trained on the top 20 species filtered by LDA values.



Supplementary Figure S8. Postoperative alterations of archaeal genera that were increased in obese subjects compared with lean controls. Relative abundances of genera originally increased in obesity were evaluated at baseline (0 M), 1 month (1 M), and 3 months (3 M) after bariatric surgery. Groups were compared using the Wilcoxon rank-sum test. * $P < 0.05$.



Supplementary Figure S9. Postoperative alterations of archaeal genera that were decreased in obese subjects compared with lean controls. Relative abundances of genera originally decreased in obesity were evaluated at baseline (0M), 1 month (1M), and 3 months (3M) after bariatric surgery. Groups were compared using the Wilcoxon rank-sum test. * $P < 0.05$, ** $P < 0.01$.



Supplementary Figure S10. Number of correlations between gut archaea and bacteria.

Supplementary Table S1. Summary of cohort design, participant definitions, DNA extraction methods, and sequencing platforms for the three metagenomic datasets.

BioProject ID	Original publication (first author, year)	Geographic region / cohort type	Definition of “obese”	Definition of “lean / healthy control”	DNA extraction method	Sequencing platform / read type	Notes
PRJEB12123	Liu R <i>et al.</i> , <i>Nat Med.</i> 2017 PMID: 28628112	China (Guangzhou & Shenzhen); young-adult community cohort	BMI \geq 30 kg/m ²	BMI 18.5 – 23.0kg/m ²	QIAamp fast DNA stool mini kit (Qiagen)	Illumina HiSeq 2000 (PE 100 bp)	-
PRJNA597839	Nie Y <i>et al.</i> , <i>Comput Struct Biotechnol J.</i> 2020 PMID: 33033580 (PMC7528071)	China (Shanghai); hospital-based bariatric cohort	BMI \geq 30 kg/m ²	BMI 18.5 – 23.9 kg/m ²	PSP Spin Stool DNA Plus Kits (Stratec Molecular GmbH)	Illumina Novaseq 6000 platform (PE 150 bp)	Only 2/30 controls had BMI slightly >23 kg/m ²
PRJEB1786	Karlsson FH <i>et al.</i> , <i>Nature</i> 2013 PMID: 23719380	Sweden; female cohort on glucose tolerance (NGT/IGT/T2D)	BMI \geq 30 kg/m ²	BMI < 25 kg/m ²	NA	Illumina HiSeq 2000 (2 × 100 bp)	22/49 controls BMI 23–25 kg/m ²