Supplementary Table 1:

Search strategies and results.

|  |  |
| --- | --- |
| Pubmed | Results |
| (Bacteroides) [All Fields] AND ((CKD) [All Fields] OR (Chronic kidney disease) [All Fields]) | 55 |
| (Faecalibacterium) [All Fields] AND ((CKD) [All Fields] OR (Chronic kidney disease) [All Fields]) | 15 |
| (Pseudomonas) [All Fields] AND ((CKD) [All Fields] OR (Chronic kidney disease) [All Fields]) | 340 |
| (Eubacterium) [All Fields] AND ((CKD) [All Fields] OR (Chronic kidney disease) [All Fields]) | 4 |
| (Parabacteroides) [All Fields] AND ((CKD) [All Fields] OR (Chronic kidney disease) [All Fields]) | 7 |
| (Alistipes) [All Fields] AND ((CKD) [All Fields] OR (Chronic kidney disease) [All Fields]) | 7 |
| (Ruminococcus) [All Fields] AND ((CKD) [All Fields] OR (Chronic kidney disease) [All Fields]) | 16 |
| (Bifidobacterium) [All Fields] AND ((CKD) [All Fields] OR (Chronic kidney disease) [All Fields]) | 41 |
| (Bacteroides) [All Fields] AND ((Immunoglobulin A nephropathy) [All Fields] OR (IgAN) [All Fields]) | 5 |
| (Faecalibacterium) [All Fields] AND ((Immunoglobulin A nephropathy) [All Fields] OR (IgAN) [All Fields]) | 0 |
| (Pseudomonas) [All Fields] AND ((Immunoglobulin A nephropathy) [All Fields] OR (IgAN) [All Fields]) | 9 |
| (Eubacterium) [All Fields] AND ((Immunoglobulin A nephropathy) [All Fields] OR (IgAN) [All Fields]) | 1 |
| (Parabacteroides) [All Fields] AND ((Immunoglobulin A nephropathy) [All Fields] OR (IgAN) [All Fields]) | 1 |
| (Alistipes) [All Fields] AND ((Immunoglobulin A nephropathy) [All Fields] OR (IgAN) [All Fields]) | 1 |
| (Ruminococcus) [All Fields] AND ((Immunoglobulin A nephropathy) [All Fields] OR (IgAN) [All Fields]) | 2 |
| (Bifidobacterium) [All Fields] AND ((Immunoglobulin A nephropathy) [All Fields] OR (IgAN) [All Fields]) | 3 |
| (Bacteroides) [All Fields] AND ((Idiopathic nephrotic syndrome) [All Fields] OR (INS) [All Fields]) | 7 |
| (Faecalibacterium) [All Fields] AND ((Idiopathic nephrotic syndrome) [All Fields] OR (INS) [All Fields]) | 0 |
| (Pseudomonas) [All Fields] AND ((Idiopathic nephrotic syndrome) [All Fields] OR (INS) [All Fields]) | 26 |
| (Eubacterium) [All Fields] AND ((Idiopathic nephrotic syndrome) [All Fields] OR (INS) [All Fields]) | 1 |
| (Parabacteroides) [All Fields] AND ((Idiopathic nephrotic syndrome) [All Fields] OR (INS) [All Fields]) | 3 |
| (Alistipes) [All Fields] AND ((Idiopathic nephrotic syndrome) [All Fields] OR (INS) [All Fields]) | 1 |
| (Ruminococcus) [All Fields] AND ((Idiopathic nephrotic syndrome) [All Fields] OR (INS) [All Fields]) | 3 |
| (Bifidobacterium) [All Fields] AND ((Idiopathic nephrotic syndrome) [All Fields] OR (INS) [All Fields]) | 3 |
| (Bacteroides) [All Fields] AND ((kidney stone disease) [All Fields] OR (Kidney stones) [All Fields] OR (KS) [All Fields]) | 13 |
| (Faecalibacterium) [All Fields] AND ((kidney stone disease) [All Fields] OR (Kidney stones) [All Fields] OR (KS) [All Fields]) | 3 |
| (Pseudomonas) [All Fields] AND ((kidney stone disease) [All Fields] OR (Kidney stones) [All Fields] OR (KS) [All Fields]) | 73 |
| (Eubacterium) [All Fields] AND ((kidney stone disease) [All Fields] OR (Kidney stones) [All Fields] OR (KS) [All Fields]) | 4 |
| (Parabacteroides) [All Fields] AND ((kidney stone disease) [All Fields] OR (Kidney stones) [All Fields] OR (KS) [All Fields]) | 0 |
| (Alistipes) [All Fields] AND ((kidney stone disease) [All Fields] OR (Kidney stones) [All Fields] OR (KS) [All Fields]) | 0 |
| (Ruminococcus) [All Fields] AND ((kidney stone disease) [All Fields] OR (Kidney stones) [All Fields] OR (KS) [All Fields]) | 2 |
| (Bifidobacterium) [All Fields] AND ((kidney stone disease) [All Fields] OR (Kidney stones) [All Fields] OR (KS) [All Fields]) | 19 |
| (Bacteroides) [All Fields] AND ((Acute kidney injury) [All Fields] OR(AKI) [All Fields]) | 8 |
| (Faecalibacterium) [All Fields] AND ((Acute kidney injury) [All Fields] OR(AKI) [All Fields]) | 2 |
| (Pseudomonas) [All Fields] AND ((Acute kidney injury) [All Fields] OR(AKI) [All Fields]) | 219 |
| (Eubacterium) [All Fields] AND ((Acute kidney injury) [All Fields] OR(AKI) [All Fields]) | 1 |
| (Parabacteroides) [All Fields] AND ((Acute kidney injury) [All Fields] OR(AKI) [All Fields]) | 1 |
| (Alistipes) [All Fields] AND ((Acute kidney injury) [All Fields] OR(AKI) [All Fields]) | 0 |
| (Ruminococcus) [All Fields] AND ((Acute kidney injury) [All Fields] OR(AKI) [All Fields]) | 1 |
| (Bifidobacterium) [All Fields] AND ((Acute kidney injury) [All Fields] OR(AKI) [All Fields]) | 9 |
| (Bacteroides) [All Fields] AND ((Diabetic nephropathy) [All Fields] OR (DN) [All Fields] OR (DKD) [All Fields] OR (diabetic kidney diseases) [All Fields]) | 39 |
| (Faecalibacterium) [All Fields] AND ((Diabetic nephropathy) [All Fields] OR (DN) [All Fields] OR (DKD) [All Fields] OR (diabetic kidney diseases) [All Fields]) | 5 |
| (Pseudomonas) [All Fields] AND ((Diabetic nephropathy) [All Fields] OR (DN) [All Fields] OR (DKD) [All Fields] OR (diabetic kidney diseases) [All Fields]) | 103 |
| (Eubacterium) [All Fields] AND ((Diabetic nephropathy) [All Fields] OR (DN) [All Fields] OR (DKD) [All Fields] OR (diabetic kidney diseases) [All Fields]) | 7 |
| (Parabacteroides) [All Fields] AND ((Diabetic nephropathy) [All Fields] OR (DN) [All Fields] OR (DKD) [All Fields] OR (diabetic kidney diseases) [All Fields]) | 2 |
| (Alistipes) [All Fields] AND ((Diabetic nephropathy) [All Fields] OR (DN) [All Fields] OR (DKD) [All Fields] OR (diabetic kidney diseases) [All Fields]) | 2 |
| (Ruminococcus) [All Fields] AND ((Diabetic nephropathy) [All Fields] OR (DN) [All Fields] OR (DKD) [All Fields] OR (diabetic kidney diseases) [All Fields]) | 3 |
| (Bifidobacterium) [All Fields] AND ((Diabetic nephropathy) [All Fields] OR (DN) [All Fields] OR (DKD) [All Fields] OR (diabetic kidney diseases) [All Fields]) | 66 |

Supplementary Table 2:

Comparison of gut bacteria between patients with kidney diseases and healthy controls at the genus level

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Genus | Significant higher in CKD | | Significant lower or no difference in CKD | | Significant higher in IgAN | | Significant lower or no difference in IgAN | |
| n | Citation | n | Citation | n | Citation | n | Citation |
| Bacteroides | 8 | [1-8] | 4 | [9-12] | 2 | [13, 14] | 2 | [15, 16] |
| Faecalibacterium | 1 | [17] | 8 | [3, 4, 12, 18-21] | 1 | [15] | / | / |
| Pseudomonas | 1 | [22] | / | / | / | / | / | / |
| Eubacterium | 2 | [7, 17] | / | / | / | / | 1 | [13] |
| Parabacteroides | 2 | [6, 23] | / | / | 1 | [13] | / | / |
| Alistipes | 2 | [2, 24] | 1 | [12] | / | / | 2 | [13, 25] |
| Ruminococcus | 7 | [2, 6, 7, 12, 17, 24, 26] | 1 | [1] | 1 | [13] | 1 | [25] |
| Bifidobacterium | 4 | [8, 12, 21, 27] | 1 | [28] | / | / | 3 | [13, 14, 16] |
| Genus | Significant higher in INS | | Significant lower or no difference in INS | | Significant higher in KS | | Significant lower or no difference in KS | |
| n | Citation | n | Citation | n | Citation | n | Citation |
| Bacteroides | / | / | / | / | 4 | [29-32] | / | / |
| Faecalibacterium | / | / | / | / | 1 | [31] | 4 | [29, 32-34] |
| Pseudomonas | / | / | / | / | 1 | [35] | / | / |
| Eubacterium | 1 | [36] | 2 | [37, 38] | 1 | [34] | 1 | [31] |
| Parabacteroides | 2 | [26, 36] | / | / | / | / | / | / |
| Alistipes | / | / | 1 | [38] | / | / | 1 | [32] |
| Ruminococcus | / | / | / | / | / | / | / | / |
| Bifidobacterium | / | / | / | / | / | / | 3 | [29, 30, 34] |
| Genus | Significant higher in AKI | | Significant lower or no difference in AKI | | Significant higher in DN | | Significant lower or no difference in DN | |
| n | Citation | n | Citation | n | Citation | n | Citation |
| Bacteroides | / | / | / | / | 2 | [39, 40] | 1 | [41] |
| Faecalibacterium | / | / | / | / | / | / | 3 | [39, 41, 42] |
| Pseudomonas | / | / | / | / | / | / | / | / |
| Eubacterium | / | / | / | / | / | / | 1 | [39] |
| Parabacteroides | / | / | / | / | / | / | / | / |
| Alistipes | / | / | / | / | 1 | [39] | / | / |
| Ruminococcus | / | / | / | / | 2 | [41, 42] | / | / |
| Bifidobacterium | / | / | / | / | 2 | [39, 42] | / | / |

1. Sato N, Kakuta M, Hasegawa T, Yamaguchi R, Uchino E, Murashita K, et al. Metagenomic profiling of gut microbiome in early chronic kidney disease. *Nephrol Dial Transplant,*2021, 36(9):1675-1684.[DOI:10.1093/ndt/gfaa122]

2. Wu IW, Lin CY, Chang LC, Lee CC, Chiu CY, Hsu HJ, et al. Gut Microbiota as Diagnostic Tools for Mirroring Disease Progression and Circulating Nephrotoxin Levels in Chronic Kidney Disease: Discovery and Validation Study. *Int J Biol Sci,*2020, 16(3):420-434.[DOI:10.7150/ijbs.37421]

3. Hu J, Zhong X, Yan J, Zhou D, Qin D, Xiao X, et al. High-throughput sequencing analysis of intestinal flora changes in ESRD and CKD patients. *BMC Nephrol,*2020, 21(1):12.[DOI:10.1186/s12882-019-1668-4]

4. Jiang S, Xie S, Lv D, Wang P, He H, Zhang T, et al. Alteration of the gut microbiota in Chinese population with chronic kidney disease. *Sci Rep,*2017, 7(1):2870.[DOI:10.1038/s41598-017-02989-2]

5. Shivani S, Kao CY, Chattopadhyay A, Chen JW, Lai LC, Lin WH, et al. Uremic Toxin-Producing Bacteroides Species Prevail in the Gut Microbiota of Taiwanese CKD Patients: An Analysis Using the New Taiwan Microbiome Baseline. *Front Cell Infect Microbiol,*2022, 12:726256.[DOI:10.3389/fcimb.2022.726256]

6. Lun H, Yang W, Zhao S, Jiang M, Xu M, Liu F, et al. Altered gut microbiota and microbial biomarkers associated with chronic kidney disease. *Microbiologyopen,*2019, 8(4):e00678.[DOI:10.1002/mbo3.678]

7. Hu Q, Wu K, Pan W, Zeng Y, Hu K, Chen D, et al. Intestinal flora alterations in patients with early chronic kidney disease: a case-control study among the Han population in southwestern China. *J Int Med Res,*2020, 48(6):300060520926033.[DOI:10.1177/0300060520926033]

8. Gryp T, Huys GRB, Joossens M, Van Biesen W, Glorieux G, &Vaneechoutte M. Isolation and Quantification of Uremic Toxin Precursor-Generating Gut Bacteria in Chronic Kidney Disease Patients. *International journal of molecular sciences,*2020, 21(6).[DOI:10.3390/ijms21061986]

9. Wu IW, Gao SS, Chou HC, Yang HY, Chang LC, Kuo YL, et al. Integrative metagenomic and metabolomic analyses reveal severity-specific signatures of gut microbiota in chronic kidney disease. *Theranostics,*2020, 10(12):5398-5411.[DOI:10.7150/thno.41725]

10. Lohia S, Vlahou A, &Zoidakis J. Microbiome in Chronic Kidney Disease (CKD): An Omics Perspective. *Toxins (Basel),*2022, 14(3).[DOI:10.3390/toxins14030176]

11. Jiang S, Wang B, Sha T, &Li X. Changes in the Intestinal Microbiota in Patients with Stage 5 Chronic Kidney Disease on a Low-Protein Diet and the Effects of Human to Rat Fecal Microbiota Transplantation. *Med Sci Monit,*2020, 26:e921557.[DOI:10.12659/msm.921557]

12. Liu F, Xu X, Chao L, Chen K, Shao A, Sun D, et al. Alteration of the Gut Microbiome in Chronic Kidney Disease Patients and Its Association With Serum Free Immunoglobulin Light Chains. *Front Immunol,*2021, 12:609700.[DOI:10.3389/fimmu.2021.609700]

13. Shah NB, Nigwekar SU, Kalim S, Lelouvier B, Servant F, Dalal M, et al. The Gut and Blood Microbiome in IgA Nephropathy and Healthy Controls. *Kidney360,*2021, 2(8):1261-1274.[DOI:10.34067/kid.0000132021]

14. Zhong Z, Tan J, Tan L, Tang Y, Qiu Z, Pei G, et al. Modifications of gut microbiota are associated with the severity of IgA nephropathy in the Chinese population. *Int Immunopharmacol,*2020, 89(Pt B):107085.[DOI:10.1016/j.intimp.2020.107085]

15. Wu H, Tang D, Zheng F, Li S, Zhang X, Yin L, et al. Identification of a novel interplay between intestinal bacteria and metabolites in Chinese patients with IgA nephropathy via integrated microbiome and metabolome approaches. *Ann Transl Med,*2021, 9(1):32.[DOI:10.21037/atm-20-2506]

16. De Angelis M, Montemurno E, Piccolo M, Vannini L, Lauriero G, Maranzano V, et al. Microbiota and metabolome associated with immunoglobulin A nephropathy (IgAN). *PloS one,*2014, 9(6):e99006.[DOI:10.1371/journal.pone.0099006]

17. Margiotta E, Miragoli F, Callegari ML, Vettoretti S, Caldiroli L, Meneghini M, et al. Gut microbiota composition and frailty in elderly patients with Chronic Kidney Disease. *PloS one,*2020, 15(4):e0228530.[DOI:10.1371/journal.pone.0228530]

18. Guirong YE, Minjie Z, Lixin YU, Junsheng YE, Lin Y, &Lisha S. [Gut microbiota in renal transplant recipients, patients with chronic kidney disease and healthy subjects]. *Nan Fang Yi Ke Da Xue Xue Bao,*2018, 38(12):1401-1408.[DOI:10.12122/j.issn.1673-4254.2018.12.01]

19. Jiang S, Xie S, Lv D, Zhang Y, Deng J, Zeng L, et al. A reduction in the butyrate producing species Roseburia spp. and Faecalibacterium prausnitzii is associated with chronic kidney disease progression. *Antonie Van Leeuwenhoek,*2016, 109(10):1389-1396.[DOI:10.1007/s10482-016-0737-y]

20. Zhao J, Ning X, Liu B, Dong R, Bai M, &Sun S. Specific alterations in gut microbiota in patients with chronic kidney disease: an updated systematic review. *Ren Fail,*2021, 43(1):102-112.[DOI:10.1080/0886022x.2020.1864404]

21. Li Y, Su X, Zhang L, Liu Y, Shi M, Lv C, et al. Dysbiosis of the gut microbiome is associated with CKD5 and correlated with clinical indices of the disease: a case-controlled study. *J Transl Med,*2019, 17(1):228.[DOI:10.1186/s12967-019-1969-1]

22. Wang F, Jiang H, Shi K, Ren Y, Zhang P, &Cheng S. Gut bacterial translocation is associated with microinflammation in end-stage renal disease patients. *Nephrology (Carlton),*2012, 17(8):733-738.[DOI:10.1111/j.1440-1797.2012.01647.x]

23. Hu X, Ouyang S, Xie Y, Gong Z, &Du J. Characterizing the gut microbiota in patients with chronic kidney disease. *Postgrad Med,*2020, 132(6):495-505.[DOI:10.1080/00325481.2020.1744335]

24. Wang X, Yang S, Li S, Zhao L, Hao Y, Qin J, et al. Aberrant gut microbiota alters host metabolome and impacts renal failure in humans and rodents. *Gut,*2020, 69(12):2131-2142.[DOI:10.1136/gutjnl-2019-319766]

25. Chai L, Luo Q, Cai K, Wang K, &Xu B. Reduced fecal short-chain fatty acids levels and the relationship with gut microbiota in IgA nephropathy. *BMC Nephrol,*2021, 22(1):209.[DOI:10.1186/s12882-021-02414-x]

26. Zhang J, Luo D, Lin Z, Zhou W, Rao J, Li Y, et al. Dysbiosis of gut microbiota in adult idiopathic membranous nephropathy with nephrotic syndrome. *Microb Pathog,*2020, 147:104359.[DOI:10.1016/j.micpath.2020.104359]

27. Lin TY, &Hung SC. Association of subjective global assessment of nutritional status with gut microbiota in hemodialysis patients: a case-control study. *Nephrol Dial Transplant,*2021, 36(6):1104-1111.[DOI:10.1093/ndt/gfaa019]

28. Hanifi GR, Samadi Kafil H, Tayebi Khosroshahi H, Shapouri R, &Asgharzadeh M. Bifidobacteriaceae Family Diversity in Gut Microbiota of Patients with Renal Failure. *Arch Razi Inst,*2021, 76(3):521-528.[DOI:10.22092/ari.2020.352271.1557]

29. Stanford J, Charlton K, Stefoska-Needham A, Ibrahim R, &Lambert K. The gut microbiota profile of adults with kidney disease and kidney stones: a systematic review of the literature. *BMC Nephrol,*2020, 21(1):215.[DOI:10.1186/s12882-020-01805-w]

30. Zhao E, Zhang W, Geng B, You B, Wang W, &Li X. Intestinal dysbacteriosis leads to kidney stone disease. *Mol Med Rep,*2021, 23(3).[DOI:10.3892/mmr.2020.11819]

31. Stern JM, Moazami S, Qiu Y, Kurland I, Chen Z, Agalliu I, et al. Evidence for a distinct gut microbiome in kidney stone formers compared to non-stone formers. *Urolithiasis,*2016, 44(5):399-407.[DOI:10.1007/s00240-016-0882-9]

32. Chen F, Bao X, Liu S, Ye K, Xiang S, Yu L, et al. Gut microbiota affect the formation of calcium oxalate renal calculi caused by high daily tea consumption. *Appl Microbiol Biotechnol,*2021, 105(2):789-802.[DOI:10.1007/s00253-020-11086-w]

33. Ticinesi A, Milani C, Guerra A, Allegri F, Lauretani F, Nouvenne A, et al. Understanding the gut-kidney axis in nephrolithiasis: an analysis of the gut microbiota composition and functionality of stone formers. *Gut,*2018, 67(12):2097-2106.[DOI:10.1136/gutjnl-2017-315734]

34. Kim HN, Kim JH, Chang Y, Yang D, Joo KJ, Cho YS, et al. Gut microbiota and the prevalence and incidence of renal stones. *Scientific reports,*2022, 12(1):3732.[DOI:10.1038/s41598-022-07796-y]

35. Yuan C, Jin X, He Y, Liu Y, Xiang L, &Wang K. Association of dietary patterns with gut microbiota in kidney stone and non-kidney stone individuals. *Urolithiasis,*2022, 50(4):389-399.[DOI:10.1007/s00240-022-01325-2]

36. He H, Lin M, You L, Chen T, Liang Z, Li D, et al. Gut Microbiota Profile in Adult Patients with Idiopathic Nephrotic Syndrome. *Biomed Res Int,*2021, 2021:8854969.[DOI:10.1155/2021/8854969]

37. Tsuji S, Suruda C, Hashiyada M, Kimata T, Yamanouchi S, Kitao T, et al. Gut Microbiota Dysbiosis in Children with Relapsing Idiopathic Nephrotic Syndrome. *Am J Nephrol,*2018, 47(3):164-170.[DOI:10.1159/000487557]

38. Tsuji S, Akagawa S, Akagawa Y, Yamaguchi T, Kino J, Yamanouchi S, et al. Idiopathic nephrotic syndrome in children: role of regulatory T cells and gut microbiota. *Pediatr Res,*2021, 89(5):1185-1191.[DOI:10.1038/s41390-020-1022-3]

39. Zhang L, Wang Z, Zhang X, Zhao L, Chu J, Li H, et al. Alterations of the Gut Microbiota in Patients with Diabetic Nephropathy. *Microbiol Spectr,*2022:e0032422.[DOI:10.1128/spectrum.00324-22]

40. He X, Sun J, Liu C, Yu X, Li H, Zhang W, et al. Compositional Alterations of Gut Microbiota in Patients with Diabetic Kidney Disease and Type 2 Diabetes Mellitus. *Diabetes Metab Syndr Obes,*2022, 15:755-765.[DOI:10.2147/dmso.S347805]

41. Wang Y, Ye X, Ding D, &Lu Y. Characteristics of the intestinal flora in patients with peripheral neuropathy associated with type 2 diabetes. *J Int Med Res,*2020, 48(9):300060520936806.[DOI:10.1177/0300060520936806]

42. Chen W, Zhang M, Guo Y, Wang Z, Liu Q, Yan R, et al. The Profile and Function of Gut Microbiota in Diabetic Nephropathy. *Diabetes Metab Syndr Obes,*2021, 14:4283-4296.[DOI:10.2147/dmso.S320169]