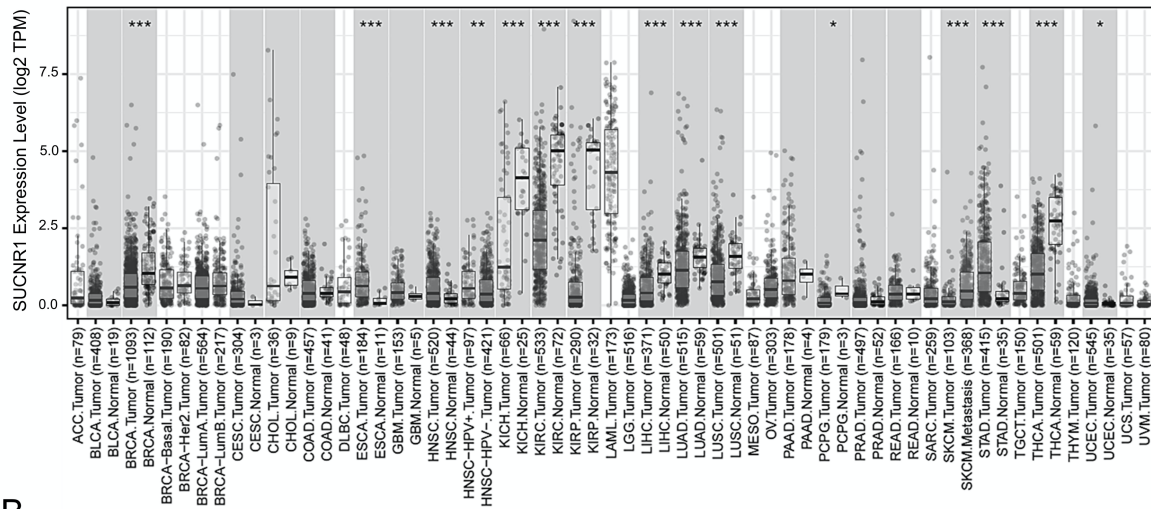


Supplementary Materials

A



B

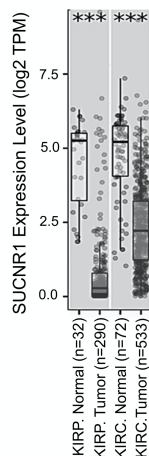


Figure S1: Differential SUCNR1 expression among cancers. (A) Box plots for differential expression of SUCNR1 (Log2 TPM) between normal and tumor tissues of all TCGA tumors. **(B)** Box plots for differential expression of SUCNR1 (Log2 TPM) between normal and tumor tissues of clear cell or papillary RCC. Data available on TIMER2.0 platform. Wilcoxon test; * for p-value < 0.05; ** for p-value < 0.01, *** or **** for p-value < 0.001.

ACC: Adrenocortical Carcinoma, BLCA: Bladder Urothelial Carcinoma, BRCA: Breast Invasive Carcinoma, CESC: Cervical and Endocervical Cancer, CHOL: Cholangiocarcinoma, COAD: Colon Adenocarcinoma, DLBC: Diffuse Large B-cell Lymphoma, ESCA: Esophageal Carcinoma, GBM: Glioblastoma Multiforme, HNSC: Head and Neck Cancer, KICH: Kidney Chromophobe, KIRC: Kidney Renal Clear Cell Carcinoma, KIRP: Kidney Renal Papillary Cell Carcinoma, LAML: Acute Myeloid Leukemia, LGG: Lower Grade Glioma, LIHC: Liver Hepatocellular Carcinoma, LUAD: Lung Adenocarcinoma, LUSC: Lung Squamous Cell Carcinoma, MESO: Mesothelioma, OV: Ovarian Serous Cystadenocarcinoma, PAAD: Pancreatic Adenocarcinoma, PCPG: Pheochromocytoma and Paraganglioma, PRAD: Prostate Adenocarcinoma, READ: Rectum Adenocarcinoma, SARC: Sarcoma, SKCM: Skin Cutaneous Melanoma, STAD: Stomach Adenocarcinoma, TGCT: Testicular Germ Cell Tumors, THCA: Thyroid Carcinoma, THYM: Thymoma, UCEC: Uterine Corpus Endometrial Carcinoma, UCS: Uterine Carsinosarcoma, UVM: Uveal Melanoma

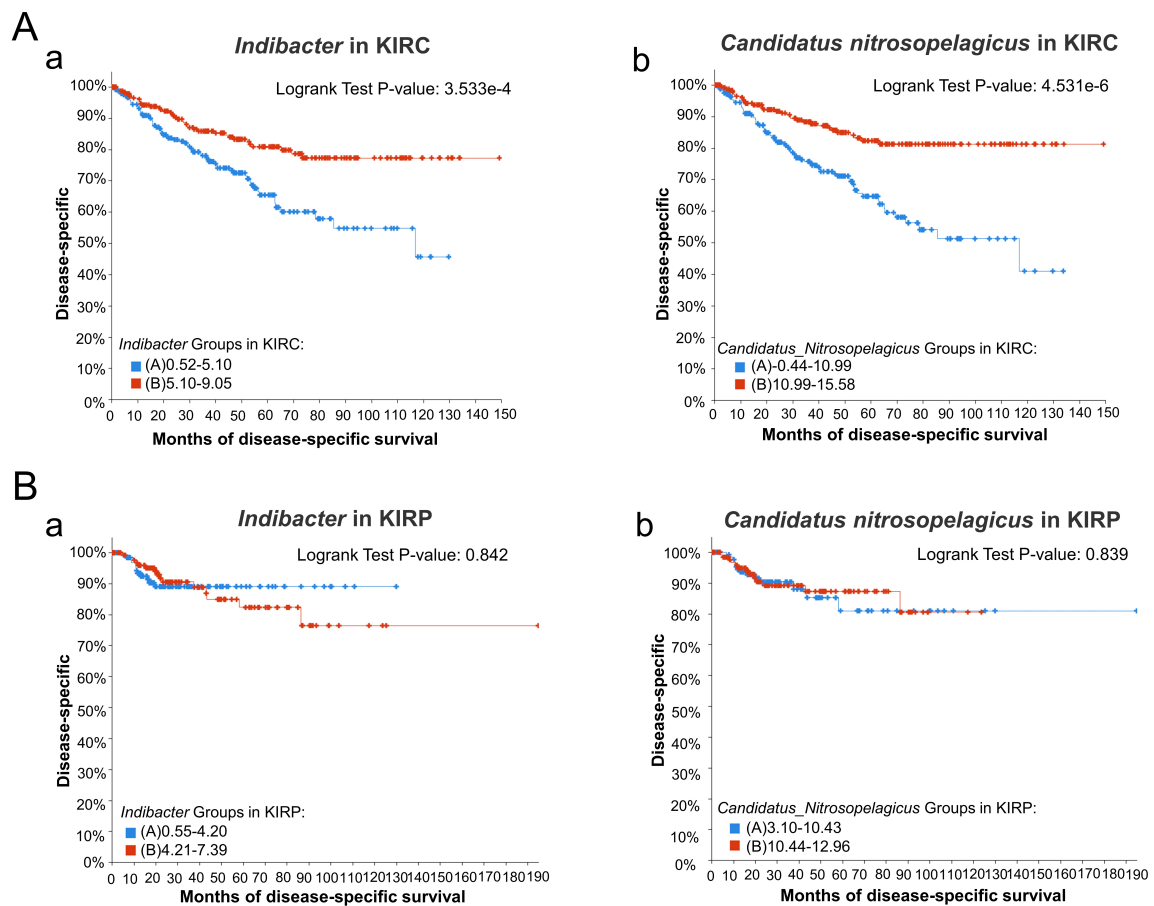


Figure S2: *Indibacter* and *Candidatus nitrosopelagicus* are beneficial in clear cell RCC. (A) Kaplan-Meier curves of low signature group A and high signature group B of a) *Indibacter* (Logrank test, $p=3.533e-4$) and b) *Candidatus nitrosopelagicus* (Logrank test, $p=4.531e-6$) in clear cell RCC. **(B)** Kaplan-Meier curves of low signature group A and high signature group B of a) *Indibacter* (Logrank test, $p=0.842$) and b) *Candidatus nitrosopelagicus* (Logrank test, $p=0.839$) in papillary RCC. Data available on cBioPortal platform.

Microbiome Signature	mean in (A)	mean in (B)	p-Value	q-Value	Higher in
<i>Pseudorhodofera</i>	0.66	0.03	2.69E-04	0.0105	(A)
<i>Azorhizobium</i>	0.88	0.59	3.69E-04	0.014	(A)
<i>Anoxybacillus</i>	0.13	-0.44	4.47E-04	0.0155	(A)
<i>Bacteroides</i>	18.98	18.75	4.48E-04	0.0155	(A)
<i>Altererythrobacter</i>	3.59	3.13	4.66E-04	0.0155	(A)
<i>Draconibacterium</i>	2.05	1.83	6.22E-04	0.0194	(A)
<i>Selenomonas</i>	10.36	10	7.86E-04	0.0226	(A)
<i>Avastrovirus</i>	3.4	2.98	9.92E-04	0.0274	(A)
<i>Isoptericola</i>	1.82	1.47	1.06E-03	0.0288	(A)
<i>Diaphorobacter</i>	-0.41	-0.74	1.14E-03	0.0302	(A)

<i>Alicyclophilus</i>	0.54	-0.02	1.24E-03	0.0323	(A)
<i>Rubrivivax</i>	-0.04	-0.62	1.63E-03	0.0395	(A)
<i>Sediminibacterium</i>	-0.04	-0.53	1.74E-03	0.0414	(A)
<i>Gemmata</i>	13.84	13.72	1.86E-03	0.0435	(A)
<i>Segniliparus</i>	2.38	2.05	1.89E-03	0.0435	(A)
<i>Tannerella</i>	1.46	1.03	1.92E-03	0.0435	(A)
<i>Ramlibacter</i>	4.32	3.85	2.16E-03	0.0475	(A)
<i>Kineococcus</i>	1.15	0.83	2.29E-03	0.048	(A)
<i>Magnetospirillum</i>	4.91	4.66	2.42E-03	0.0492	(A)
<i>Simplexvirus</i>	5.99	6.84	1.72E-14	2.42E-11	(B)
<i>Candidatus nitrosopelagicus</i>	10.36	11.21	1.14E-11	8.01E-09	(B)
<i>Alpharetrovirus</i>	7.56	8.26	2.09E-09	9.80E-07	(B)
<i>Lachnoclostridium</i>	12.24	12.83	7.55E-09	2.65E-06	(B)
<i>Chitinivibrio</i>	8.57	9.4	1.27E-08	3.57E-06	(B)
<i>Maricaulis</i>	3.54	4.24	2.04E-08	4.79E-06	(B)
<i>Campylobacter</i>	16.69	17.17	3.12E-08	6.28E-06	(B)
<i>Indibacter</i>	4.54	5.15	4.54E-08	7.97E-06	(B)
<i>Desulfotalea</i>	5.36	6.03	5.78E-08	9.02E-06	(B)
<i>Aeromonas</i>	16.85	17.33	8.52E-08	1.20E-05	(B)
<i>Riemerella</i>	12.65	12.96	1.57E-07	2.01E-05	(B)
<i>Plantibacter</i>	4.58	5.34	1.79E-07	2.09E-05	(B)
<i>Tunalikevirus</i>	3.98	4.65	2.49E-07	2.69E-05	(B)
<i>Lawsonia</i>	11.12	11.35	4.50E-07	4.52E-05	(B)
<i>Kamptonema</i>	9.09	9.43	4.83E-07	4.53E-05	(B)
<i>Ichnovirus</i>	11.88	12.13	1.72E-06	1.51E-04	(B)
<i>Omegapapillomavirus</i>	4.26	4.91	2.02E-06	1.67E-04	(B)
<i>Lysinimicrobium</i>	3.31	3.85	2.44E-06	1.91E-04	(B)
<i>Bulleidia</i>	3.59	4.11	2.60E-06	1.93E-04	(B)
<i>Mastigocoleus</i>	2.79	3.35	2.79E-06	1.96E-04	(B)
<i>Prevotella</i>	13.51	13.71	3.10E-06	2.07E-04	(B)

<i>Vibrio</i>	15.67	15.89	7.80E-06	4.99E-04	(B)
<i>Coprobacillus</i>	4	4.44	8.72E-06	5.33E-04	(B)
<i>Haliangium</i>	5.54	5.85	1.01E-05	5.94E-04	(B)
<i>Gammaretrovirus</i>	11.54	12.15	1.16E-05	6.52E-04	(B)
<i>Sorangium</i>	9.9	10.19	2.46E-05	1.33E-03	(B)
<i>Microtetraspora</i>	0.04	0.51	2.77E-05	1.44E-03	(B)
<i>Apibacter</i>	3.7	4.05	3.54E-05	1.78E-03	(B)
<i>Entomoplasma</i>	1.66	2.12	5.12E-05	2.48E-03	(B)
<i>Scardovia</i>	2.14	2.72	9.30E-05	4.36E-03	(B)
<i>Alkalibacterium</i>	1.37	1.81	9.79E-05	4.44E-03	(B)
<i>Mannheimia</i>	12.95	13.15	1.21E-04	5.31E-03	(B)
<i>Frankia</i>	5.73	6.05	1.25E-04	5.32E-03	(B)
<i>Treponema</i>	9.88	10.07	2.13E-04	8.82E-03	(B)
<i>Succinimonas</i>	13.09	13.6	2.61E-04	0.0105	(B)
<i>Mycetocola</i>	1.92	2.28	3.95E-04	0.0146	(B)
<i>Rhodobacter</i>	1.52	1.89	4.63E-04	0.0155	(B)
<i>Chromobacterium</i>	4.54	4.94	4.73E-04	0.0155	(B)
<i>Microvirga</i>	13.39	13.61	4.90E-04	0.0157	(B)
<i>Candidatus_Stoquefichus</i>	10.2	10.42	6.73E-04	0.0206	(B)
<i>Ornithobacterium</i>	10.88	11.08	7.71E-04	0.0226	(B)
<i>Gloeobacter</i>	1.96	2.29	7.77E-04	0.0226	(B)
<i>Neorickettsia</i>	5.57	5.99	8.71E-04	0.0245	(B)
<i>Flectobacillus</i>	2.74	3.07	1.32E-03	0.0338	(B)
<i>Flavonifractor</i>	5.04	5.37	1.40E-03	0.0352	(B)
<i>Catenuloplanes</i>	1.7	2.04	1.49E-03	0.0367	(B)
<i>Rhadinovirus</i>	7.66	8.03	2.01E-03	0.0449	(B)
<i>Prymnesiovirus</i>	8.13	8.34	2.23E-03	0.048	(B)
<i>Arenibacter</i>	4.16	4.34	2.26E-03	0.048	(B)
<i>Iflavivirus</i>	2.1	2.48	2.36E-03	0.0488	(B)

Table S1: SUCNR1 associated microbiome signature in clear cell RCC. A table showing the mean of microbiota signature (log CPM) in low expressing SUCNR1 group A and high expressing SUCNR1

group B in clear cell RCC. Data available on cBioPortal platform. Student's t-test p-values and Benjamini-Hochberg q-values are displayed.

Microbiome Signature	mean in (A)	mean in (B)	p-Value	q-Value	Higher in
<i>Indibacter</i>	3.52	4.26	1.93E-06	2.72E-03	(B)
<i>Candidatus nitrosopelagicus</i>	9.73	10.51	2.13E-05	0.0104	(B)
<i>Lachnoclostridium</i>	11.51	12.21	2.22E-05	0.0104	(B)
<i>Algicola</i>	6.07	6.64	5.94E-05	0.0149	(B)
<i>Apibacter</i>	3.66	4.21	6.20E-05	0.0149	(B)
<i>Desulfotalea</i>	4.87	5.54	6.37E-05	0.0149	(B)
<i>Luteibacter</i>	15.34	15.62	1.41E-04	0.0284	(B)
<i>Paludibacter</i>	8.02	8.59	1.93E-04	0.0338	(B)
<i>Flavonifractor</i>	3.46	4.02	2.31E-04	0.0361	(B)

Table S2: SUCNR1 associated microbiome signature in papillary RCC. A table showing the mean of microbiota signature (log CPM) in low expressing SUCNR1 group A and high expressing SUCNR1 group B in papillary RCC. Data available on cBioPortal platform. Student's t-test p-values and Benjamini-Hochberg q-values are displayed.