

Oral Microbiome in Patients with Oesophageal Squamous Cell Carcinoma

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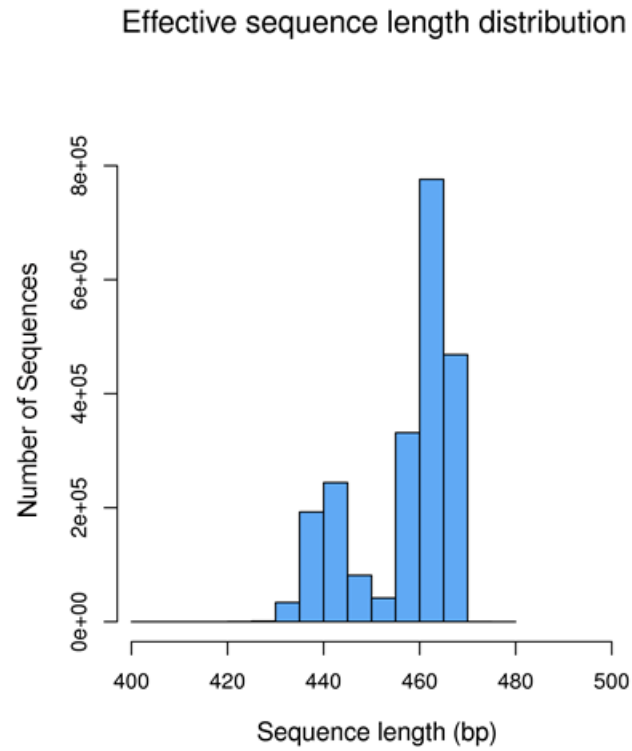
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Supplementary Fig. S1. After optimizing the sequencing raw data, effective sequence length distribution statistics were obtained. The abscissa is the sequence length (bp), and the ordinate is the sequence number.

Supplementary Table S1. Sequencing data

Sample	#PE reads	#Nochimaera	AvgLen (bp)	GC (%)
Control10	56725	50328	454.21	52.54
Control11	65787	58060	457.46	52.5
Control12	70287	62686	457.48	52.33
Control13	68421	57795	459.47	52.37
Control14	75225	65128	457.18	52.76
Control15	67889	57478	456.08	52.18
Control16	86015	75677	456.83	52.44
Control17	64035	58547	457.4	53.11
Control18	56573	45935	457.18	53.37
Control19	61671	55042	456.23	53.25
Control1	48398	45289	458.89	52.26
Control20	51519	46643	457.95	53.49
Control21	55466	51092	458.82	51.95
Control2	51623	46686	457.08	52.51
Control3	50354	44843	458.32	52.51
Control4	49518	44719	455.88	51.97
Control5	58924	53904	459.54	52.17
Control6	59177	55054	457.59	52.13
Control7	50973	45338	457.98	52.94
Control8	67001	60825	458.07	52.77
Control9	67007	61045	456.59	51.93
ESCC10	54363	49872	456.43	52.63
ESCC11	55655	51507	459.7	52.71
ESCC12	63178	57329	457.55	53
ESCC13	59349	56292	458.55	51.83
ESCC14	53250	44208	455.97	52.98
ESCC15	62701	55176	455.6	52.86
ESCC16	51728	48206	454.18	53
ESCC17	76104	70487	461.73	53.78
ESCC18	73663	64587	456.74	52.77
ESCC19	54864	50196	459.53	52.45
ESCC1	67686	57907	454.47	52.63
ESCC20	69151	63068	455.92	52.45
ESCC2	50099	41905	456.96	52.94
ESCC3	48471	38519	454.54	52.48
ESCC4	51918	43161	457.4	53.24

ESCC5	50249	42021	458.83	52.82
ESCC6	50709	45297	460.23	52.48
ESCC7	50119	45157	456.82	53.73
ESCC8	50875	44230	457.09	52.41
ESCC9	66485	62665	458.21	52.84

Supplementary Table S2. Alpha diversity analysis

Sample	Ace	Chao1	Shannon	Simpson	Goods_coverage
Control1	193.723	189.12	4.407	0.9	1
Control2	209.779	206	4.731	0.911	0.999
Control3	187.843	186.059	4.61	0.911	0.999
Control4	201.349	212.833	4.933	0.941	0.999
Control5	177.833	183	3.987	0.876	0.999
Control6	180.511	176.2	4.464	0.875	1
Control7	182.08	190.273	4.771	0.937	0.999
Control8	221.369	228.083	4.833	0.921	0.999
Control9	199.577	199.125	5.829	0.965	1
Control10	183.806	185.545	5.087	0.943	1
Control11	196.575	194.875	5.211	0.952	0.999
Control12	193.857	195.071	4.925	0.936	0.999
Control13	150.072	146.4	4.061	0.898	0.999
Control14	176.997	181.6	5.021	0.943	1
Control15	188.193	183.714	5.077	0.948	1
Control16	205.785	223.545	4.016	0.844	0.999
Control17	174.506	176.615	4.722	0.932	0.999
Control18	157.692	158	4.379	0.919	0.999
Control19	164.074	161.882	4.708	0.934	1
Control20	194.734	196	3.64	0.861	0.999
Control21	198.772	204.2	4.523	0.916	0.999
ESCC1	198.092	193.667	5.457	0.961	0.999
ESCC2	147.017	147.1	5.157	0.953	1
ESCC3	203.796	198.438	5.462	0.963	0.999
ESCC4	195.863	192.5	4.589	0.919	0.999
ESCC5	99.827	93.8	3.831	0.888	1
ESCC6	191.711	194.067	4.098	0.883	0.999
ESCC7	195.778	191.056	3.944	0.826	0.999
ESCC8	157.216	152.176	3.919	0.853	0.999
ESCC9	180.435	182.364	4.362	0.883	1
ESCC10	206.762	205.5	5.14	0.933	1
ESCC11	174.713	177.25	4.166	0.852	0.999
ESCC12	140.47	133.077	4.931	0.943	1
ESCC13	158.031	155.55	2.884	0.643	0.999
ESCC14	148.77	147.909	4.995	0.945	1
ESCC15	217.387	215.5	5.682	0.968	0.999
ESCC16	180.199	184.375	5.351	0.941	0.999

ESCC17	163.614	180.111	1.997	0.466	0.999
ESCC18	202.916	199.056	4.978	0.936	0.999
ESCC19	223.431	221.2	4.829	0.91	0.999
ESCC20	215.606	216.769	5.189	0.921	0.999

Supplementary Table S3. Beta diversity analysis. PCoA analysis

Sample	Axis.1	Axis.2	Axis.3
Control1	-0.204	-0.028	-0.049
Control2	-0.162	0.274	-0.045
Control3	-0.115	-0.055	-0.002
Control4	-0.149	0.11	0.021
Control5	-0.247	0.027	0.112
Control6	-0.178	-0.227	-0.115
Control7	0.073	0.128	0.077
Control8	-0.083	0.136	-0.031
Control9	-0.095	0.071	-0.087
Control10	0.071	0.06	0.026
Control11	0.029	-0.071	0.131
Control12	-0.031	-0.114	0.059
Control13	-0.103	0.087	0.164
Control14	0.004	-0.101	0.126
Control15	-0.077	0.009	0.039
Control16	-0.119	-0.215	-0.033
Control17	0.111	0.103	0.029
Control18	0.457	-0.029	0.16
Control19	0.149	-0.144	0.122
Control20	0.298	0.066	0.195
Control21	-0.216	-0.193	0.018
ESCC1	-0.079	0.117	-0.056
ESCC2	0.163	0.082	0.018
ESCC3	0.086	-0.071	0.044
ESCC4	0.013	0.065	0.043
ESCC5	0.01	-0.043	0.095
ESCC6	-0.231	0.121	0.078
ESCC7	0.473	-0.002	-0.003
ESCC8	-0.136	-0.18	-0.191
ESCC9	-0.077	0.073	0.128
ESCC10	-0.11	-0.06	-0.035
ESCC11	-0.108	0.188	0.047
ESCC12	0.174	0.087	0.029
ESCC13	-0.042	0.409	-0.249
ESCC14	0.13	-0.256	0.081
ESCC15	0.061	-0.078	0.035
ESCC16	0.164	0.03	-0.283

ESCC17	0.379	-0.085	-0.453
ESCC18	0.04	0.066	-0.059
ESCC19	-0.208	-0.147	-0.018
ESCC20	-0.116	-0.208	-0.167

Supplementary Table S4. Metastats group difference analysis

Taxon	Group p1_m ean	Group 1_varia nce	Group 1_stan dard	Group p2_m ean	Group 2_varia nce	Group 2_stan dard	P_ Val ue	Q_ Val ue
Streptococcus	0.183 471	0.0064 94	0.01758 5	0.197 938	0.0202 62	0.03183	0.7 142 86	1
Neisseria	0.185 197	0.0134 81	0.02533 7	0.162 937	0.0153 88	0.02773 8	0.5 504 5	1
Veillonella	0.099 958	0.0023 83	0.01065 3	0.087 556	0.0031 91	0.01263 1	0.4 575 42	1
Haemophilus	0.082 472	0.0024 9	0.01088 9	0.063 993	0.0061 3	0.01750 7	0.3 906 09	1
Rothia	0.070 489	0.0045 1	0.01465 5	0.045 838	0.0012 33	0.00785 2	0.1 468 53	1
Leptotrichia	0.032 249	0.0004 58	0.00467 1	0.050 582	0.0022 25	0.01054 8	0.1 258 74	1
Porphyromonas	0.045 06	0.0016 3	0.00881 1	0.016 535	0.0002 26	0.00336 3	0.0 019 98	0.5 402 75
Fusobacterium	0.040 198	0.0010 48	0.00706 5	0.009 29	6.33E- 05	0.00177 8	0.0 009 99	0.5 402 75
Granulicatella	0.021 364	8.58E- 05	0.00202 2	0.025 828	0.0002 68	0.00366 2	0.2 887 11	1
Gemella	0.021 511	0.0002 07	0.00313 8	0.023 907	0.0003 02	0.00388 7	0.6 163 84	1
Abiotrophia	0.002 219	1.64E- 05	0.00088 3	0.039 505	0.0260 81	0.03611 2	0.2 397 6	1
Prevotella_7	0.021 581	0.0011 56	0.00742	0.015 325	0.0001 62	0.00284 8	0.5 414	1

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f__Saccharimonadaceae_Unclassified	0.012 265	9.31E- 05	0.00210 5	0.021 123	0.0004 91	0.00495 3	0.1 028 97	1
Peptostreptococcus	0.013 95	0.0001 03	0.00221 7	0.017 159	0.0002 3	0.00339 3	0.4 415 58	1
Atopobium	0.008 809	8.01E- 05	0.00195 3	0.022 282	0.0005 18	0.00509 1	0.0 129 87	1
Campylobacter	0.016 188	0.0001 14	0.00233 4	0.013 934	0.0002 49	0.00352 7	0.5 934 07	1
Actinomyces	0.007 413	2.67E- 05	0.00112 8	0.017 55	0.0004 3	0.00463 9	0.0 239 76	1
Capnocytophaga	0.009 598	8.35E- 05	0.00199 3	0.013 535	0.0001 42	0.00266 6	0.2 467 53	1
Parvimonas	0.010 179	0.0001 64	0.00279 5	0.012 424	0.0003 11	0.00394 2	0.6 763 24	1
f__Neisseriaceae_Unclassified	0.005 68	3.43E- 05	0.00127 9	0.009 825	0.0001	0.00223 6	0.1 547 84	1
[Eubacterium]_nodatum_group	0.007 185	2.97E- 05	0.00119	0.007 105	2.5E- 05	0.00111 8	1	1
f__Ambiguous_taxa_Unclassified	0.006 566	0.0001 64	0.00279 4	0.007 674	0.0003 3	0.00406 2	0.8 527 2	1
Aggregatibacter	0.009 104	0.0001 33	0.00251 5	0.004 63	4.53E- 05	0.00150 5	0.0 887 03	1
Oribacterium	0.005 114	1.16E- 05	0.00074 4	0.008 68	7.23E- 05	0.00190 1	0.2 554 57	1
Megasphaera	0.004 09	4.76E- 05	0.00150 5	0.007 67	9.3E- 05	0.00215 7	0.2 199 54	1
Dialister	0.003	1.06E-	0.00071	0.007	0.0001	0.00235	0.0	1

	547	05	1	419	11	4	864 05	
Prevotella	0.005 198	0.0001 17	0.00235 6	0.005 44	3.41E- 05	0.00130 5	1 256 95	1
Selenomonas_3	0.003 552	6.25E- 06	0.00054 5	0.006 78	0.0001 26	0.00251	0.1 256 95	1
Unclassified_Unclassi fied	0.003 509	1.07E- 05	0.00071 4	0.006 2	6.22E- 05	0.00176 3	0.2 529 69	1
Lachnoanaerobaculu m	0.004 233	7.3E- 06	0.00059	0.004 18	1.04E- 05	0.00072	1	1
Ruminococcaceae_U CG-014	0.002 814	1.29E- 05	0.00078 4	0.004 135	2.13E- 05	0.00103 3	0.5 991 29	1
Filifactor	0.002 933	6.72E- 06	0.00056 6	0.003 445	1.66E- 05	0.00091 1	0.7 858 56	1
Stomatobaculum	0.003 304	5.91E- 06	0.00053 1	0.002 79	1.73E- 05	0.00093 1	1	1
f_P5D1- 392_Unclassified	0.002 49	1.29E- 05	0.00078 5	0.003 025	1.42E- 05	0.00084 3	0.7 693 05	1
Moraxella	0.003 804	9.54E- 05	0.00213 2	0.001 535	2.12E- 05	0.00102 9	0.2 274 68	1
Lautropia	0.003 094	7.38E- 05	0.00187 5	0.002 235	7.27E- 06	0.00060 3	0.7 543 39	1
Actinobacillus	0.003 634	5.78E- 05	0.00165 9	0.001 619	3.53E- 05	0.00132 8	0.2 274 99	1
[Eubacterium]_brac hy_group	0.002 081	5.91E- 06	0.00053 1	0.003 125	4E-05	0.00141 4	0.5 394 68	1
Corynebacterium	0.003 171	0.0001 21	0.00240 4	0.001 88	1.87E- 05	0.00096 7	0.5 496 48	1
Prevotella_6	0.002 085	1.22E- 05	0.00076 3	0.002 775	1.77E- 05	0.00094	0.5 394	1

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Cardiobacterium	0.000543	2.87E-07	0.000117	0.00405	0.000143	0.002677	0.018657	1
Shuttleworthia	0.000886	2.32E-06	0.000332	0.003625	4.52E-05	0.001503	0.101294	1
Candidatus_Saccharimonas	0.001905	2.66E-06	0.000356	0.00202	4.11E-06	0.000453	1	1
Centipeda	0.00199	9.06E-06	0.000657	0.001875	1.14E-05	0.000756	1	1
Mogibacterium	0.001709	2.05E-06	0.000312	0.00188	3.83E-06	0.000438	1	1
f_Lachnospiraceae_Unclassified	0.000238	2.36E-07	0.000106	0.00312	4.16E-05	0.001442	0.013422	1
Selenomonas	0.001852	5.57E-06	0.000515	0.00143	1.53E-06	0.000277	1	1
candidate_division_SR1_bacterium_taxon_345	0.001405	2.86E-06	0.000369	0.001775	6.66E-06	0.000577	0.720179	1
Solobacterium	0.001114	8.33E-07	0.000199	0.00201	8.13E-06	0.000638	0.442101	1
f_Veillonellaceae_Unclassified	0.001381	4.62E-06	0.000469	0.001255	2.45E-06	0.00035	1	1
Johnsonella	0.001366	2.06E-06	0.000313	0.00091	9.23E-07	0.000215	1	1
Alloprevotella	0.001433	2.35E-05	0.001057	0.00075	1.36E-06	0.000261	1	1
Selenomonas_4	0.001085	2.01E-06	0.000309	0.00105	4.54E-06	0.000477	1	1
Tannerella	0.000785	5.12E-06	0.000494	0.0013	1.84E-06	0.000303	0.680029	1
Fretibacterium	0.001014	1.63E-06	0.000279	0.0009	1.7E-06	0.000292	1	1
Candidatus_Saccharibacteria_bacterium_UB2523	0.000609	1.12E-06	0.000231	0.000975	5.94E-06	0.000545	0.615984	1

Anaeroglobus	0.001009	1.63E-06	0.000278	0.000435	2.51E-07	0.000112	1	1
Phocaeicola	0.000219	3.06E-07	0.000121	0.001215	1.51E-05	0.000868	0.237893	1
[Eubacterium]_saphe num_group	0.000719	1.71E-06	0.000286	0.00065	1.51E-06	0.000274	1	1
F0058	0.000543	2.2E-06	0.000324	0.000795	8.39E-07	0.000205	0.615984	1
Eikenella	0.000576	5.33E-07	0.000159	0.000755	2.01E-06	0.000317	0.616073	1
Bifidobacterium	0.000148	9.26E-08	6.64E-05	0.001	1.46E-05	0.000854	0.237893	1
Comamonas	0.000129	4.71E-08	4.74E-05	0.000925	7.79E-06	0.000624	0.237893	1
Bergeyella	0.00049	6.91E-07	0.000181	0.0005	7.41E-07	0.000192	1	1
Olsenella	0.000476	3.09E-06	0.000384	0.000285	1.7E-07	9.21E-05	1	1
Lactobacillus	0.000276	1.28E-06	0.000247	0.0004	5.63E-07	0.000168	1	1
Treponema_2	0.000405	2.09E-06	0.000315	0.00019	3.15E-08	3.97E-05	1	1
Chryseobacterium	0.000557	6.51E-06	0.000557	0	0	0	1	1
Cryptobacterium	0.000181	1.85E-07	9.38E-05	0.00039	2.54E-07	0.000113	0.487805	1
Kingella	0.000405	7.57E-07	0.00019	7.5E-05	2.51E-08	3.55E-05	1	1
Erysipelotrichaceae_UCG-006	0.000224	9.49E-08	6.72E-05	0.000265	3.45E-07	0.000131	0.48793	1
Catonella	0.000267	2.7E-07	0.000113	0.00019	4.62E-08	4.81E-05	1	1
Alloscardovia	0.000	7.19E-	0.00018	0.000	3.46E-	0.00013	1	1

	214	07	5	235	07	1		
f_Family_XIII_Unclassified	0.000281	5.31E-07	0.000159	0.00016	7.52E-08	6.13E-05	1	1
Butyrivibrio_2	7.14E-05	3.41E-08	4.03E-05	0.000375	3.81E-07	0.000138	0.487805	1
Bacteroides	9.04E-05	4.78E-08	4.77E-05	0.000295	1.66E-07	9.1E-05	0.487805	1
Scardovia	0.00011	4.19E-08	4.47E-05	0.000265	1.69E-07	9.18E-05	0.48793	1
Faucicola	0.000271	1.44E-06	0.000262	6E-05	3.3E-08	4.06E-05	1	1
Mycoplasma	0.000314	2.07E-06	0.000314	5E-06	5E-10	5E-06	1	1
Pyramidobacter	0.000148	2.7E-07	0.000113	0.00014	1.78E-07	9.44E-05	1	1
Desulfovibrio	7.62E-05	5.79E-08	5.25E-05	0.000175	1.16E-07	7.6E-05	1	1
f_Corynebacteriaceae_Unclassified	0.00011	2.09E-08	3.15E-05	0.000115	7.93E-08	6.3E-05	1	1
Peptococcus	2.38E-05	4.9E-09	1.53E-05	0.000195	2.73E-07	0.000117	1	1
Desulfobulbus	7.14E-05	1.11E-08	2.3E-05	0.000145	8.16E-08	6.39E-05	1	1
Bulleidia	5.71E-05	6.57E-09	1.77E-05	0.00015	4.68E-08	4.84E-05	1	1
Mobiluncus	2.86E-05	5.14E-09	1.56E-05	0.000165	2.07E-07	0.000102	1	1
Pseudoramibacter	1.9E-05	1.62E-09	8.78E-06	0.000165	3.59E-07	0.000134	1	1
Propionivibrio	4.76E-06	4.76E-10	4.76E-06	0.000165	4.48E-07	0.00015	1	1
Flexilinea	2.86E-05	2.14E-09	1.01E-05	0.00015	1.43E-07	8.45E-05	1	1
Parascardovia	8.09E-05	6.86E-08	5.72E-05	6E-05	1.62E-08	2.85E-05	1	1
Erysipelotrichaceae_UCG-004	0	0	0	0.00014	3.64E-07	0.000135	1	1

[Eubacterium]_coprostanoligenes_group	3.33E-05	4.33E-09	1.44E-05	9E-05	5.57E-08	5.28E-05	1	1
Candidatus_Endomicrobium	0.000119	9.06E-08	6.57E-05	1E-05	9.47E-10	6.88E-06	1	1
W5053	6.67E-05	6.33E-09	1.74E-05	6E-05	1.62E-08	2.85E-05	1	1
Prevotella_2	7.62E-05	5.68E-08	5.2E-05	3E-05	3.26E-09	1.28E-05	1	1
Pelospora	2.38E-05	2.9E-09	1.18E-05	7.5E-05	2.2E-08	3.31E-05	1	1
f__Atopobiaceae_Unclassified	6.67E-05	1.93E-08	3.03E-05	2.5E-05	1.97E-09	9.93E-06	1	1
Howardella	4.76E-05	4.62E-09	1.48E-05	6.5E-05	8.7E-09	2.09E-05	1	1
Rikenellaceae_RC9_gut_group	7.62E-05	7.98E-08	6.16E-05	1.5E-05	1.34E-09	8.19E-06	1	1
Lactococcus	6.66E-05	9.33E-08	6.66E-05	0	0	0	1	1
Escherichia-Shigella	1.9E-05	1.62E-09	8.78E-06	3E-05	8.53E-09	2.06E-05	1	1
Peptoanaerobacter	3.33E-05	4.33E-09	1.44E-05	1.5E-05	2.39E-09	1.09E-05	1	1
f__Enterobacteriaceae_Unclassified	3.33E-05	2.33E-08	3.33E-05	0	0	0	1	1
f__Lentimicrobiaceae_Unclassified	1.9E-05	4.61E-09	1.48E-05	1E-05	9.47E-10	6.88E-06	1	1
f__Pasteurellaceae_Unclassified	2.38E-05	3.91E-09	1.36E-05	0	0	0	1	1
Propionibacterium	0	0	0	1.5E-05	1.34E-09	8.19E-06	1	1