

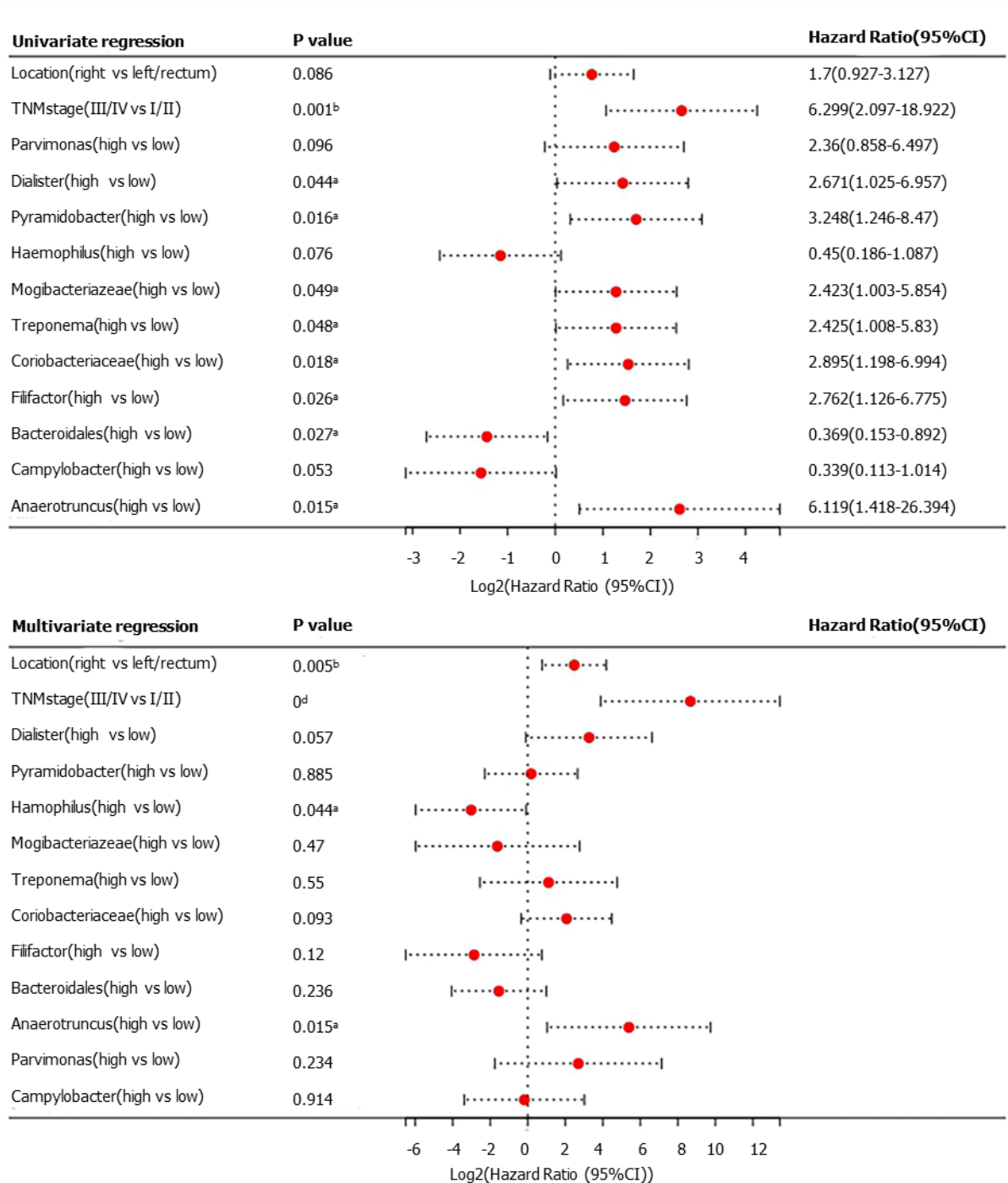
Univariate regression	P value	Hazard Ratio(95%CI)
Location(right vs left/rectum)	0.086	1.703(0.927-3.127)
TNMstage(III/IV vs I/II)	0.001 <sup>b</sup>	6.299(2.097-18.922)
Fusobacterium(high vs low)	0.067	0.424(0.169-1.063)
Pyramidobacter(high vs low)	0.036 <sup>a</sup>	2.61(1.065-6.392)
TG5(high vs low)	0.037 <sup>a</sup>	3.697(1.082-12.626)
Pseudoramibacter_Eubacterium (high vs low)	0.025 <sup>a</sup>	3.001(1.15-7.833)
Mogibacteriaceae	0.083	2.336(0.896-6.086)
Bacteroidales(high vs low)	0.03 <sup>a</sup>	3.067(1.113-8.448)
Anaerotruncus(high vs low)	0.017 <sup>a</sup>	2.992(1.22-7.337)

-2.5 -2.0 -1.5 -1.0 -0.5 0.0 0.5 1.0 1.5 2.0 2.5 3.0 3.5 4.0  
Log2(Hazard Ratio (95%CI))

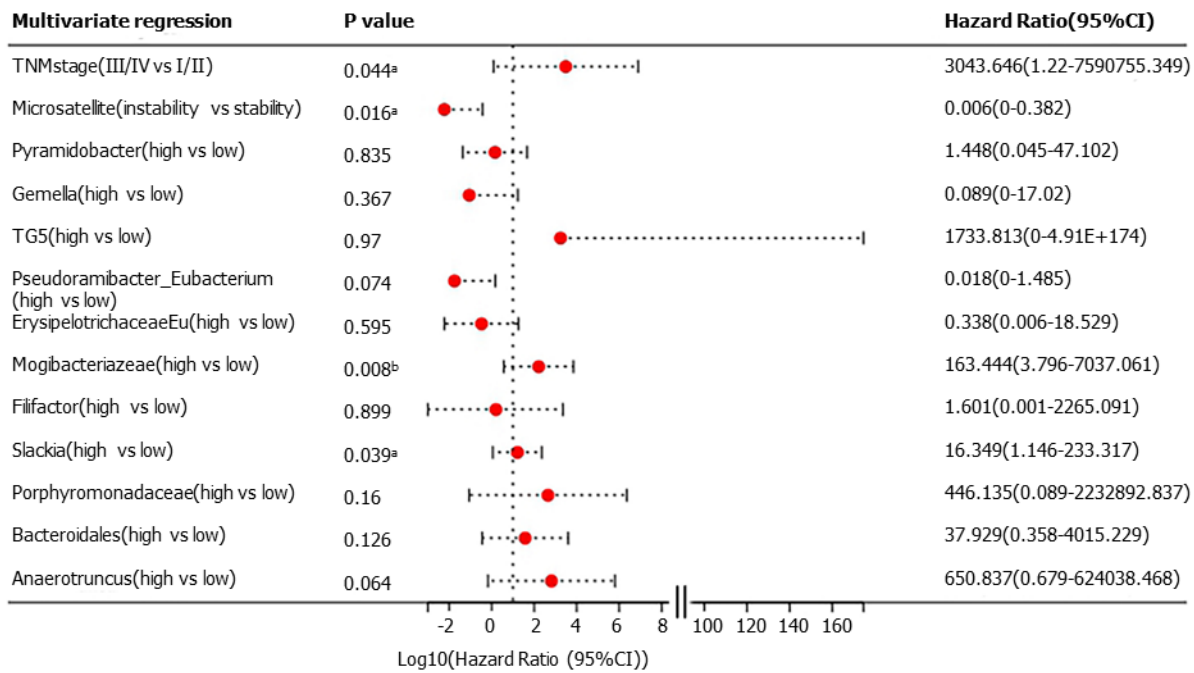
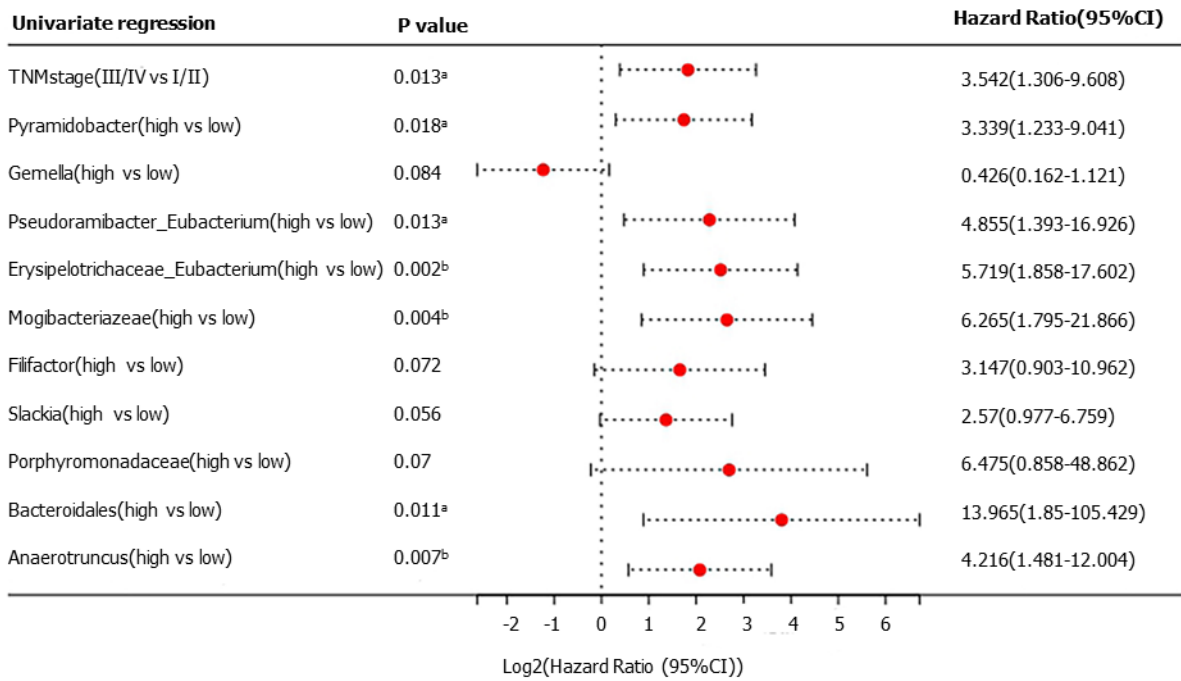
Multivariate regression	P value	Hazard Ratio(95%CI)
Location(right vs left/rectum)	0.042 <sup>a</sup>	2.625(1.036-6.65)
TNMstage(III/IV vs I/II)	0.002 <sup>b</sup>	93.487(5.414-1614.442)
Fusobacterium(high vs low)	0.616	0.713(0.19-2.678)
Parvimonas(high vs low)	0.169	0.357(0.082-1.549)
Pyramidobacter(high vs low)	0.277	2.197(0.531-9.089)
TG5(high vs low)	0.596	0.531(0.051-5.524)
Bacteroidales(high vs low)	0.569	1.654(0.293-9.329)
Anaerotruncus(high vs low)	0.587	1.629(0.279-9.5)
Pseudoramibacter_Eubacterium (high vs low)	0.314	0.384(0.06-2.473)
Mogibacteriaceae(high vs low)	0.093	9.573(0.686-133.504)

-4.0 -2.0 0.0 2.0 4.0 6.0 8.0 10.0  
Log2(Hazard Ratio (95%CI))

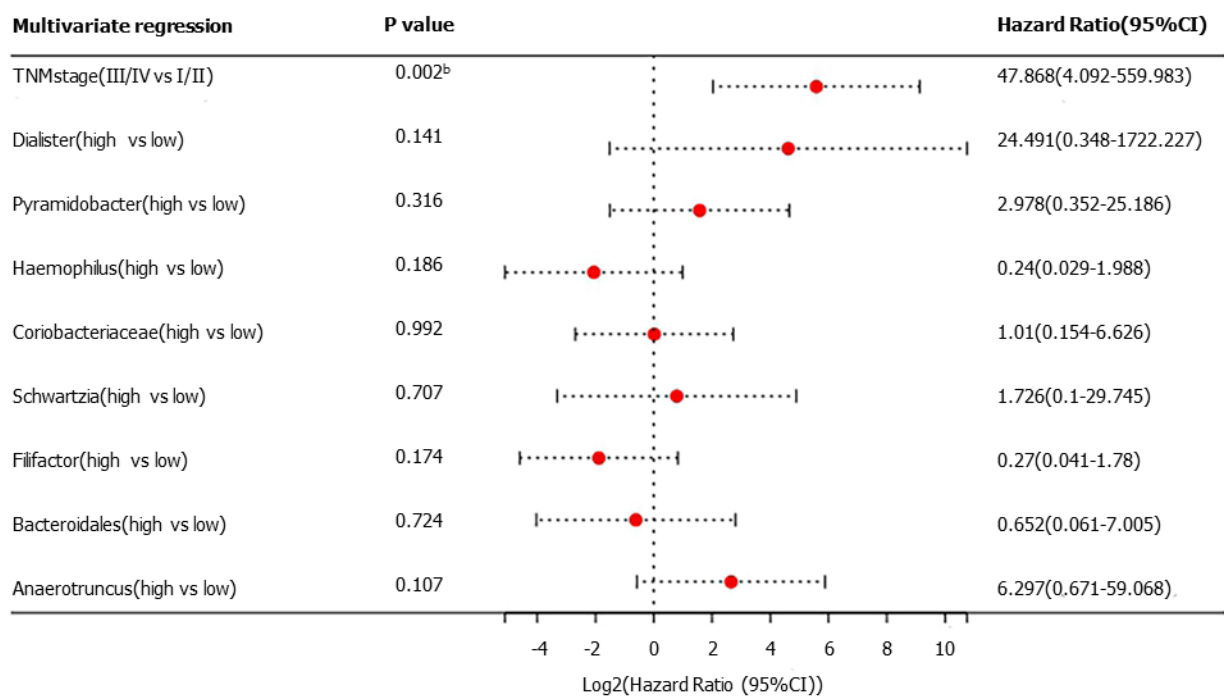
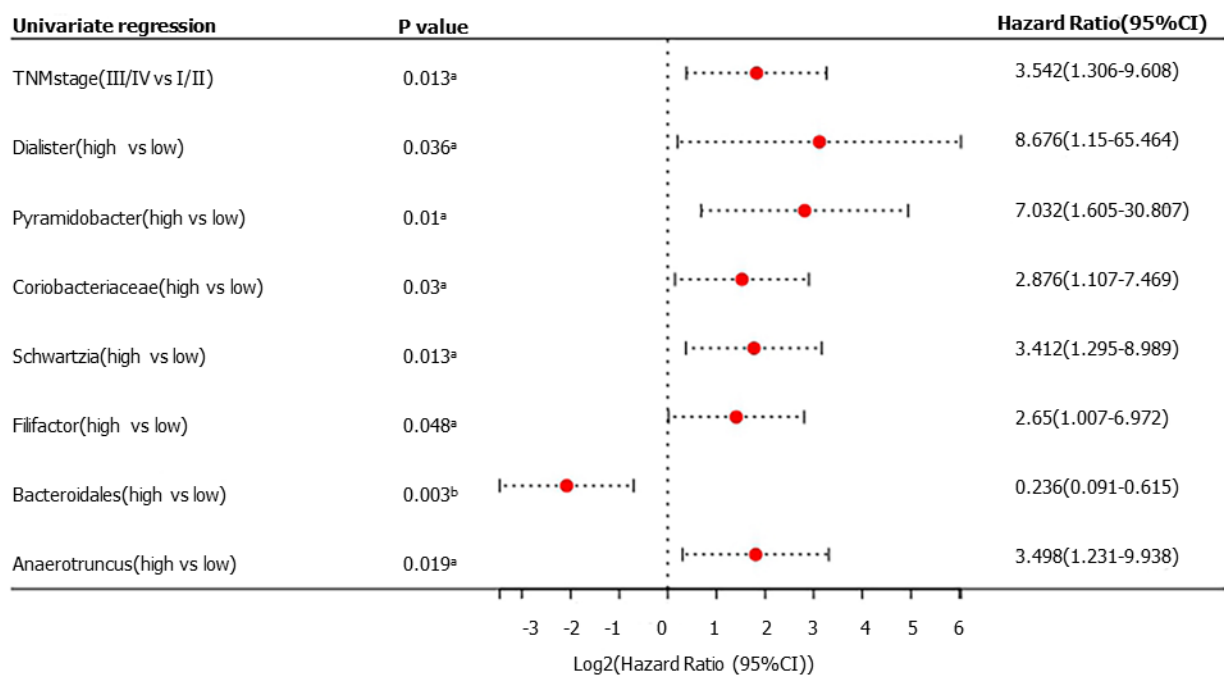
**Supplementary Figure 1 Univariate and multivariate Cox regression overall survival analyses of bacterial genera/families at on-tumor site.** <sup>a</sup> $P < 0.05$ ; <sup>b</sup> $P < 0.01$ ; <sup>c</sup> $P < 0.001$ ; <sup>d</sup> $P < 0.0001$ .



**Supplementary Figure 2 Univariate and multivariate Cox regression overall survival analyses of bacterial genera/families at adjacent-tumor site.** <sup>a</sup> $P < 0.05$ ; <sup>b</sup> $P < 0.01$ ; <sup>c</sup> $P < 0.001$ ; <sup>d</sup> $P < 0.0001$ .



**Supplementary Figure 3 Univariate and multivariate Cox regression disease-free survival analyses of bacterial genera/families at on-tumor site.** <sup>a</sup> $P < 0.05$ ; <sup>b</sup> $P < 0.01$ ; <sup>c</sup> $P < 0.001$ ; <sup>d</sup> $P < 0.0001$ .



**Supplementary Figure 4 Univariate and multivariate Cox regression disease-free survival analyses of bacterial genera/families at adjacent-tumor site.** <sup>a</sup> $P < 0.05$ ; <sup>b</sup> $P < 0.01$ ; <sup>c</sup> $P < 0.001$ ; <sup>d</sup> $P < 0.0001$ .

**Supplementary Table 1 List of reads information analyzed in this study**

<b>Reads ID</b>	<b>Sample type</b>
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H10	health
H11	health
H12	health
H13	health
H14	health
H15	health
H16	health
H17	health
H18	health
H19	health
H2	health
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H22	health
H23	health
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H25	health
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H4	health
H5	health
H6	health
H7	health
H8	health
H9	health
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N14	nn
N17	nn
N18	nn
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TR37	tr
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TR46	tr
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TR53	tr
TR57	tr
TR59	tr
TR61	tr
TR7	tr
TR9	tr

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Reads ID refer to the tags of reads submitted to the NCBI database.

**Supplementary Table 2 LefSe analysis of bacterial taxa at on-tumor (T), adjacent-tumor (P), and off-tumor (N) sites of patients with (*r*) and without (*n*) colorectal cancer recurrence**

	<i>P</i> values	FDR	health	nn	nr	pn	pr	tn	tr	LDAScore
Fusobacterium	7.48E-05	0.002621	91426	320360	292720	261560	691990	591990	819200	5.56
Faecalibacterium	0.00293	0.017579	485120	230780	97828	139820	166160	116810	92099	5.29
Peptostreptococcus	7.39E-05	0.002621	7382.2	95234	93355	74995	194510	279440	233320	5.13
Streptococcus	0.018685	0.063858	41500	71664	131670	124210	89411	274670	279500	5.08
Parvimonas	0.000417	0.007205	23956	74331	59167	73169	153580	242930	201070	5.04
Burkholderiales	3.39E-05	0.001832	26068	164130	115450	83040	239260	58966	44853	5.03
Pseudomonas	0.0063	0.030137	112920	59477	150510	139110	73233	19661	46713	4.82
Mitsuokella	0.001131	0.010608	119420	537.74	968.53	778.54	806.83	415.16	472.73	4.77
Caulobacteraceae_1	0.000175	0.004303	47559	81563	85578	62261	143020	33092	26585	4.77
Pseudomonadales	0.001163	0.010608	1598.6	584.92	115310	1073.2	994.49	1562.6	295.81	4.76
Burkholderiaceae_1	0.005619	0.027585	110770	28469	22311	80836	40984	6877.4	6308.6	4.72
Dialister	0.031319	0.09555	38677	28400	43902	25493	71721	67753	121010	4.68
Methylobacterium	0.000743	0.009973	19077	32176	98469	26244	95749	8301.6	3894.3	4.67
Campylobacter	7.20E-06	0.000847	2294.3	9118.6	5800.3	15943	15766	96613	59743	4.67
Comamonadaceae_1	0.000762	0.009973	75249	40776	103180	48921	80980	20515	15915	4.64
Pyramidobacter	0.004695	0.024377	5351.6	1258.7	10093	773.4	82082	4074	73229	4.61
Oxalobacteraceae_1	0.001143	0.010608	16276	63248	64030	70613	95065	36722	26643	4.6
Selenomonas	0.013469	0.05051	951.34	2563	4613	4836.5	32021	32702	75664	4.57
Haemophilus	0.022854	0.074349	83918	37876	13768	34266	28478	22620	51188	4.55
Bradyrhizobium	1.91E-08	1.03E-05	7278.6	42220	58603	43737	70508	10703	9714	4.5

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Intrasporangiaceae_1	0.001426	0.011127	1458.2	2420.6	51081	1379	2106.5	1087.8	781.32	4.4
Gemella	0.001195	0.010608	1178.1	18578	13164	27412	20067	31258	43237	4.32
Staphylococcus	0.000232	0.005226	4378.4	19076	18980	14426	36256	14609	2451.4	4.23
Bradyrhizobiaceae_1	0.009886	0.041808	4645.3	11476	34909	11705	27006	3779	1683.9	4.22
TG5	0.011162	0.045662	2428.4	1638.1	4810.8	3296	30459	10648	34200	4.21
Eubacterium	0.006307	0.030137	10618	40272	14340	31861	19463	19269	28281	4.17
Agrobacterium	0.008499	0.037617	9111.9	12457	28173	11379	27857	7295.3	997.4	4.13
Burkholderia	0.000836	0.009973	27825	7073.6	6842.8	12348	11745	3028.5	1698	4.12
Sphingomonadaceae_1	0.008252	0.037328	26680	2475.1	4233.4	2763.6	3445.3	1463.8	1137.8	4.11
Corynebacterium	0.002357	0.015332	11691	28367	23394	30842	27691	24790	5284.2	4.11
Eggerthella	3.38E-05	0.001832	2350.7	28087	16056	21360	14606	18880	15636	4.11
Bacillus	0.008293	0.037328	3095	2695.1	26135	2471.1	3662.5	1350.7	1116.7	4.1
Brevundimonas	0.000467	0.007205	13173	12384	22928	10819	27683	3908.9	3432.5	4.08
Mogibacteriaceae_1	0.002338	0.015332	3590.7	8180.7	8328.3	7022.9	22026	16185	25375	4.04
Ralstonia	0.003105	0.018227	6371.4	16236	15479	9903.2	25338	6282.8	4116.7	4.03
Rhodococcus	0.000958	0.010147	19585	6879.1	13956	3565.9	9398.2	2930.1	925.93	3.97
Leptotrichia	0.005422	0.02686	1314.2	8360.7	2518.4	11948	18338	15656	9086.1	3.93
Treponema	1.56E-06	0.000422	98.067	583.9	5862.1	6735.7	2166	1206.3	16180	3.91
Comamonadaceae	0.003149	0.018287	2996	9644.2	19059	16765	13153	6873.3	14703	3.9
Methylobacteriaceae_1	0.001579	0.011595	15320	1240.4	1551.1	1553.6	1949.5	677.47	429.01	3.87
Xanthomonadaceae_1	0.001288	0.010608	5088.8	13218	16773	19018	11038	8513.8	8174.6	3.84
Propionibacterium	4.76E-05	0.002183	5747.7	9602.3	8647.8	12199	16058	7270.1	2427.7	3.83
Coriobacteriaceae_1	0.022921	0.074349	4042.6	8770.3	5146	7055.8	13457	10260	17244	3.82

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Gemellaceae_1	0.003323	0.019087	2307.8	7895.1	7100	11116	9568.5	15456	15577	3.82
Sphingomonadaceae	0.001272	0.010608	14991	8977.3	14325	11121	15737	3652.7	2928.3	3.81
Schwartzia	0.006155	0.029945	143.85	430.47	2427.4	1228.4	11723	2853.1	12721	3.8
Neisseriaceae_1	0.004415	0.023363	3864.6	9490.1	5781.9	14163	9352.8	5133.2	2523.3	3.76
Streptophyta	0.000902	0.009973	3237.8	6775.9	1839	1447	12055	664.57	1079.6	3.76
Pseudonocardia	0.000108	0.003074	11685	779.31	485.33	57.922	392.03	634.67	283.61	3.76
Rheinheimera	0.013373	0.050499	11700	3449.7	12424	4428.9	8568.4	3181	1183.8	3.75
Magnetospirillum	0.003535	0.020092	255.99	9923.5	9728.4	7185.3	11504	5023.7	3810.2	3.75
Phyllobacterium	0.004351	0.02326	2404.8	4617.7	11687	4411.7	10545	2483.7	633.34	3.74
Streptomyces	0.002036	0.013915	742.14	592.92	10619	553.53	695.71	410.31	287.29	3.71
Peptoniphilus	0.022645	0.074349	3858.8	3644.8	5047.7	3615.3	3621.8	13023	4646.7	3.67
Actinomycetales	0.001321	0.010649	6885.1	6154.7	12872	7920.9	12915	4395.6	4408.1	3.63
Rhizobiaceae	0.008771	0.038195	8732.2	5685.1	8910.6	4522.5	7540.5	2267.8	782.26	3.61
Skermanella	0.000597	0.008953	264.44	6179.7	6346.7	6129.7	8465.3	3831	2588	3.61
Anaerotruncus	0.030809	0.094528	964.65	3478.9	734.32	1376.2	8643.5	1508.5	3008.1	3.6
Rothia	0.004209	0.02274	8360.8	817.68	681.09	962.89	1149.1	492.15	923.06	3.59
Dethiosulfatibacter	0.000276	0.005725	728.4	2167.7	2009.9	2466.3	5402.8	7929.2	5727.7	3.56
Moraxellaceae_1	0.000252	0.005446	4845	3018.5	8760.1	2914.1	4031.4	2279.7	1511.2	3.56
Sphingobium	0.001297	0.010608	7401.1	757.25	1454.4	2764.9	1558.9	383.68	245.52	3.55
Rhizobiales_1	0.001589	0.011595	6989.3	3949.9	6705.9	4396	8351.3	2194.8	1457.5	3.54
Pseudoramibacter_Eubacteriu m	0.003089	0.018227	119.81	4767.2	6892.2	3418.3	3692.9	2367	6748.9	3.53
Actinobacillus	0.010507	0.043311	6909.2	1271.5	422.83	793.24	541.16	558.82	446.65	3.51

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Filifactor	0.014786	0.054031	136.35	208.78	2434.9	1762.5	937.09	464.03	6161.7	3.48
Hyphomicrobiaceae_1	0.000131	0.003532	699.51	3157.2	4231.5	4705.7	6805.2	2277.3	1318	3.48
Phenylobacterium	0.00164	0.011654	2146.7	4201.8	5176.4	4571.5	7693.4	3117.7	1956.3	3.46
Paracoccus	4.85E-05	0.002183	4063.1	7119.7	6835.7	8046.9	8200.5	3158	2479.1	3.46
Deinococcus	0.022993	0.074349	1063	6673.6	6114	3707.8	5144.1	4692.2	1184.1	3.45
Rhizobiales	0.000857	0.009973	2669.8	3613.6	6317.5	3336.9	6142.3	1761.2	1147.9	3.41
Sinobacteraceae_1	0.00529	0.026449	511.64	5252.8	762.55	2926.4	1723.6	484.31	511.55	3.38
Slackia	0.010171	0.042576	131.24	3063.7	339.15	1450	3944.8	2461.5	4637	3.35
Microbacteriaceae	0.001212	0.010608	1849.8	2238.7	2893.3	4834.7	2658.8	1218.9	545.12	3.33
Chromatiaceae_1	0.017449	0.061186	3178.2	920.01	4364.8	1179.2	2438.6	447.82	150.21	3.32
Lactobacillales_1	0.000801	0.009973	86.024	2825.6	996.36	2811.9	523.05	3793.1	672.08	3.27
Intrasporangiaceae	0.00144	0.011127	1929	1484.4	3735.8	725.01	1939.9	788.12	157.89	3.25
Microbispora	0.0004	0.007204	1127.9	1039.5	3839	1825.2	1414	490.73	266.48	3.25
Mycoplana	0.000858	0.009973	2128.5	1485.1	2394.1	2067.5	3913.5	652.3	479.61	3.24
Aurantimonadaceae_1	1.16E-05	0.001043	1110.7	1404.7	1974.2	3774	2618.2	620.22	323.84	3.24
Rhodobacter	0.013224	0.05029	1498	1398.2	1782.7	1032.9	3703.9	389.64	323.26	3.23
Porphyromonadaceae	0.012475	0.049427	2590.3	3854.8	1549.1	2882.7	3660.2	2152.4	4804.1	3.21
Bacillaceae_1	0.000451	0.007205	86.552	517.4	3333.5	842.34	586.02	544.23	421.93	3.21
Bosea	2.42E-06	0.000435	599.2	2763.8	3395.7	3260	3834.9	1292.9	877.01	3.21
Betaproteobacteria	0.00115	0.010608	1401.6	4323.6	3593.8	4058.8	3079.1	2877.3	1346.4	3.17
Fimbriimonas	0.006366	0.030155	12.606	2402.9	1010.2	1263.9	2874.3	894.32	837.36	3.16
Burkholderiaceae	0.001054	0.010608	2401.6	2820.2	2062.1	3185.2	3541.9	967.94	711.69	3.15
Bradyrhizobiaceae	7.84E-06	0.000847	867.2	1675.2	2920.3	1688	3193.4	496.84	558	3.13

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Kocuria	0.00991	0.041808	1302.3	939.32	2962.3	1289.9	2145	597.69	302.31	3.12
Tissierellaceae	0.014388	0.053217	4357.3	2921.9	1834.6	2767.7	2670.9	3193.2	3195.8	3.1
Alphaproteobacteria	0.001504	0.011441	2264.6	2311.6	3938.8	2667.2	2856.1	1672.3	1419.8	3.1
Acetobacteraceae_1	0.0128	0.049726	2827.2	1140.9	2159.9	3058.5	1446.7	2011.2	608.42	3.09
Bacteroidales_1	0.032035	0.097184	1983.3	2615.1	2488.2	2340.3	3074.4	1662.2	4083.4	3.08
Oxalobacteraceae	0.000757	0.009973	1824.9	2182.5	2724.5	2024.8	3090.5	983.13	668.16	3.08
Alteromonadales	0.012998	0.050041	2302.5	1637.9	2330.7	1964.1	2153.4	3336	1061.8	3.06
Rhodospirillaceae_1	0.01707	0.060643	1087	2402.8	3319.9	2658.5	2880.5	1482.8	1073.1	3.05
Geodermatophilaceae	0.011591	0.047061	878.16	610.15	824.53	1269.8	2510.1	244.18	565.84	3.05
Azospirillum	0.002423	0.015573	225.67	1593.1	2378.8	1540.6	2078.1	687.51	601.85	3.03
Phyllobacteriaceae_1	0.002123	0.014328	2019.6	1323.9	2018.4	919.56	2268.4	387.65	106.24	3.03
Caulobacteraceae	8.05E-05	0.002621	896.9	1176.9	1571.8	959.56	2451.6	429.94	301.41	3.03

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Reads ID refer to the tags of reads submitted to the NCBI database.



**Supplementary Table 3 The list of abundance cut-off values of different bacterial genera in K-M survival analyses**

	On-tumor (T) site_OS					Adjacent-tumor (P) site_OS					On-tumor (T) site_DFS					Adjacent-tumor (P) site_DFS				
	H R	Lo we r	Up per	P	CUT- OFF	H R	Lo we r	Up per	P	CUT- OFF	HR	Low er	Up per	P	CUT- OFF	H R	Lo we r	Up per	P	CUT- OFF
Fusobacterium	2.53	1.0	6.3	0.04	0.046	0.5	0.2	1.2	0.15	0.0057	2.3	0.88	6.0	0.08	0.092	0.4	0.1	1.3	0.15	0.0057
					2009	5	1	8		64488			7		467	4	7	2		645
Parvimonas	0.37	0.1	1.0	0.04	0.005	2.5	0.9	6.9	0.06	0.0005	0.44	0.12	1.5	0.18	0.010	2.1	0.7	6.3	0.14	0.0005
					09812	5	2	6		84			3		404	1	6			84
Dialister	1.62	0.6	4.0	0.3	0.009	2.8	1.1	7.4	0.02	0.0008	1.48	0.55	3.9	0.43	0.004	4.0	1.3	12.	8.00	0.0005
					33424	8		6		12			4		02	0	2	47	E-03	99
Pyramidobacter	2.81	1.1	6.8	0.02	7.66E-05	3.4	1.3	9.1	6.50	5.77E-03	3.64	1.34	9.8	6.60	6.78E-05	7.6	1.7	33.	1.50	2.54E-05
						4	4		E-03	05			5	E-03	-05	6	3	3	E-03	05
Selenomonas	2.01	0.7	5.1	0.14	0.000	1.5	0.6	3.9	0.34	9.92E-05	0.39	0.09	1.7	0.2	0.000	0.5	0.2	1.5	0.27	0.0003
					14696	5	2	9		05			1		624	5	2	6		66
Haemophilus	1.57	0.5	3.9	0.41	0.000	0.3	0.1	0.9	0.02	0.0002	2.11	0.68	6.5	0.19	0.000	0.2	0.0	1.0	0.04	0.0006
					28584	3	6			2749			5		2858	2	8	2		468

	7										9									
Gemella	0.	0.2	1.4	0.2	2.40E	1.	0.6	4.0	0.29	0.0005	0.28	0.11	0.7	5.20	2.49E	2.	0.7	8.9	0.13	2.74E-
	5	2			-05	6	5	3		57			3	E-03	-05	5	3	6		05
	5					2										5				
TG5	3.	1.1	13.	0.02	4.80E	1.	0.6	3.8	0.35	0.0001	3.4E	0.00	Na	4.30	2.10E	3.	0.7	14.	0.09	2.05E-
	9	6	56		-05	5	2	9		48	+08	E+00	N	E-03	-05	2	5	39		05
	7					5										9				
Pseudoramibacter _Eubacterium	3.	1.2	8.4	0.01	2.76E	0.	0.2	1.5	0.3	1.44E-	5.25	1.5	18.	3.70	1.67E	0.	0.2	1.8	0.45	1.44E-
	2	3	1		-05	6	5	5		05			29	E-03	-05	6	6	1		05
	2					2										9				
Erysipelotrichace a_Eubacterium	1.	0.6	3.8	0.28	0.000	0.	0.2	1.3	0.2	0.0003	5.72	1.86	17.	6.00	0.000	1.	0.7	4.8	0.19	0.0012
	6	7	7		64387	5	4	7		99			6	E-04	608	8	2	6		42
	1					7										7				
Mogibacteriazeae	2.	0.9	6.5	0.05	0.000	2.	1	5.8	0.04	0.0008	6.27	1.8	21.	1.00	0.000	2.	0.9	6.2	0.07	0.0005
	5	6	2		82838	4		5		61			87	E-03	916	3	1	7		39
						2										8				
Treponema	0.	0.2	1.4	0.23	7.49E	2.	1.1	6.3	0.02	6.86E-	3.07	0.88	10.	0.06	2.86E	0.	0.0	1.5	0.14	5.77E-
	5	3	4		-05	6		5		05			69		-05	3	8	1		05
	7					4										4				
Coriobacteriaceae	1.	0.6	3.8	0.36	0.000	2.	1.2	6.9	0.01	0.0005	2.23	0.64	7.7	0.2	0.000	2.	1.1	7.4	0.02	0.0005
	5	1	3		936	8		9		55			6		196	8	1	7		55
	3					9										8				

Schwartzia	0.61	0.2	1.8	0.37	5.00E-05	1.4	0.8	4.6	0.13	1.53E-05	1.58	0.61	4.1	0.34	2.63E-05	3.7	1.4	9.8	4.10	1.53E-05	
			3			9		7								5		2	9	E-03	05
						4															
Dethiosulfatibacter	0.49	0.1	1.1	0.08	1.89E-05	1.8	0.7	4.5	0.18	0.000144	0.57	0.21	1.5	0.26	1.89E-05	3.8	0.6	13.12	0.13	0	
			3			8		5					4					8	12		
						4															
Filifactor	1.96	0.7	5.4	0.18	6.07E-06	2.9	1.2	7.3	0.01	7.01E-06	3.41	0.98	11.87	0.04	6.07E-06	2.8	1.1	7.6	0.02	6.86E-06	
						9		2													
						8															
Slackia	1.56	0.6	3.7	0.32	3.34E-05	0.4	0.2	1.1	0.1	8.98E-06	3.25	1.2	8.8	0.01	3.71E-05	1.9	0.7	5.1	0.17	5.08E-05	
			4			4		8										4	4		
						9															
Porphyromonadaceae	0.5	0.2	1.2	0.12	1.71E-05	0.4	0.1	1.4	0.18	3.51E-05	7.1	0.94	53.56	0.03	1.24E-05	0.7	0.2	1.8	0.47	1.44E-05	
			3			4		6										7	7	2	
						8															
Bacteroidales	3.29	1.1	9.0	0.01	0.000156	0.3	0.1	0.7	8.70E-03	0.000129	15.0	2	114	4.50E-04	0.000149	0	0.0	0.5	2.90E-04	0.000129	
			5			3		4										2	8	2	
						3															
Peptostreptococcus	0.52	0.1	1.4	0.2	0.012839	1.7	0.7	4.1	0.23	0.005434	0.55	0.18	1.6	0.29	0.012839	0	0.0	1.0	5.00E-02	0.003355888	
			3			7		1					9					3	9	8	
						1															
Streptococcus	0.48	0.1	1.0	0.06	0.001623	0.5	0.2	1.3	0.19	0.001928	0.46	0.18	1.2	0.11	0.001623	1.9	0.7	5.0	0.18	0.004758	
			4			5		3					2					3	7		

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	3					6										3				
Campylobacter	0.	0.2	1.9	0.43	0.005	0.	0.1	1.1	0.07	0.0004	0.48	0.16	1.4	0.2	0.002	2.	0.8	7.6	0.1	0.0001
	6	1	2		09	3	3	4		68			9		781	5	1	6		71
	4					8														
Anaerotruncus	3.	1.3	7.9	6.60	6.69E	6.	1.4	26.	5.60	0	4.59	1.61	13.	1.70	5.09E	3.	1.3	10.	7.20	2.40E-
	2	2	5	E-03	-05	1	2	4	E-03				08	E-03	-05	7	3	77	E-03	05
	4					2										9				

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**Supplementary Table 4 Univariate disease-free survival Cox regression analyses of clinicopathological features**

	B	Standard error	Wald	Freedom	Significance	Exp(B)	Exp(B) 95%CI	
							Lower	Upper
Gender	-.665	.533	1.555	1	.212	.515	.181	1.462
Age	.008	.026	.109	1	.742	1.008	.959	1.060
Location	.311	.300	1.072	1	.300	1.365	.758	2.458
Differentiation	-.017	.289	.003	1	.954	.983	.558	1.733
Stage	1.265	.509	6.172	1	.013 <sup>a</sup>	3.542	1.306	9.608
Smoking	.302	.508	.353	1	.552	1.352	.500	3.657
Drinking	-.689	.487	2.003	1	.157	.502	.193	1.303
Microsatellite	-.211	.548	.149	1	.700	.809	.277	2.369

<sup>a</sup> $P < 0.05$ ; <sup>b</sup> $P < 0.01$ ; <sup>c</sup> $P < 0.001$ ; <sup>d</sup> $P < 0.0001$ .

**Supplementary Table 5 Univariate overall survival Cox regression analyses of clinicopathological features**

	B	Standard error	Wald	Freedom	Significance	Exp(B)	Exp(B) 95%CI	
							Lower	Upper
Gender	-.840	.517	2.640	1	.104	.432	.157	1.189
Age	.023	.023	1.013	1	.314	1.024	.978	1.071
Location	.532	.310	2.948	1	.086	1.703	.927	3.127
Differentiation	.299	.267	1.251	1	.263	1.349	.799	2.278
Stage	1.840	.561	10.756	1	.001 <sup>b</sup>	6.299	2.097	18.922
Smoking	.084	.457	.034	1	.854	1.087	.444	2.660
Drinking	-.340	.457	.554	1	.457	.712	.291	1.742
Microsatellite	-.220	.500	.193	1	.660	.803	.301	2.139

<sup>a</sup> $P < 0.05$ ; <sup>b</sup> $P < 0.01$ ; <sup>c</sup> $P < 0.001$ ; <sup>d</sup> $P < 0.0001$ .