

Supplementary data

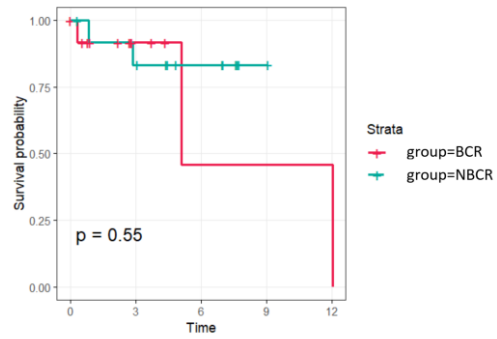


Figure S1. Kaplan–Meier survival analysis for biochemical recurrence (BCR) and with no biochemical recurrence (NBCR) .

Table S1. Clinical characteristics of patients analyzed in this study.

	NBCR (n=13)	BCR (n=13)	P value
Age	73	72	0.6084
PSA	13.5±4.5	14.9±6.6	0.8570
Gleason score			
Median	7	7	0.7213
Range	6-9	5-9	
Gleason grade			
Median	2	2	1.0000
range	1-4	1-4	
Risk stratification	Low risk = 4 Intermediate risk =7 High risk =2	Low risk=3 Intermediate risk=5 High risk =5	0.4137
Pathologic T stage	T1= 4 T2= 4	T1= 7 T2= 1	0.3591

BCR= Biochemical recurrence; NBCR= No biochemical recurrence.

Table S2. Averaged taxonomic composition for the biochemical recurrence group or no biochemical recurrence group.

Taxon rank	Taxon name	BCR	NBCR	p-value
Phylum	Proteobacteria	42.6	49.7	N.S.
	Actinobacteria	6.5	8.2	N.S.
	Bacteroidetes	26.0	19.1	N.S.
	Firmicutes	24.4	22.3	N.S.
	ETC(<1%)	0.5	0.7	
Class	Alphaproteobacteria	15.3	21.2	N.S.
	Bacteroidia	25.4	18.5	N.S.
	Bacilli	4.7	5.2	N.S.
	Actinobacteria c	6.5	8.1	N.S.
	Gammaproteobacteria	11.3	13.5	N.S.
	Betaproteobacteria	16.0	14.9	N.S.
	Clostridia	19.4	16.9	N.S.
	ETC(<1%)	1.4	1.6	
		7.4	6.6	N.S.
Order	Pseudomonadales	7.4	6.6	N.S.
	Bacteroidales	25.4	18.5	N.S.
	Enterobacteriales	1.2	1.5	N.S.
	Burkholderiales	15.5	14.5	N.S.
	Corynebacteriales	2.5	5.3	N.S.
	Clostridiales	19.4	16.9	N.S.
	Propionibacteriales	3.1	1.9	N.S.
	Rhizobiales	13.7	18.1	N.S.
	Bacillales	1.5	1.3	N.S.
	Xanthomonadales	2.2	5.0	N.S.
	Lactobacillales	3.2	3.9	N.S.
	Sphingomonadales	0.0	1.6	N.S.
	ETC(<1%)	4.8	5.0	
		21.7	15.7	N.S.
	Muribaculaceae	1.2	0.0	N.S.
	Staphylococcaceae	1.2	0.0	N.S.
	Comamonadaceae	14.9	12.6	N.S.
	Christensenellaceae	4.8	4.2	N.S.
Family	Xanthomonadaceae	2.2	5.0	N.S.
	Bacteroidaceae	1.9	1.9	N.S.
	Streptococcaceae	2.2	2.8	N.S.
	Prevotellaceae	1.6	0.0	N.S.
	Bradyrhizobiaceae	13.3	17.7	N.S.
	Propionibacteriaceae	3.1	1.9	N.S.
	Lachnospiraceae	1.8	1.6	N.S.
	Yersiniaceae	1.1	1.4	N.S.
	Corynebacteriaceae	1.6	1.6	N.S.
	Ruminococcaceae	12.7	11.0	N.S.
	Moraxellaceae	6.7	5.2	N.S.
	Lawsonella f	0.0	2.1	N.S.
	Sphingomonadaceae	0.0	1.4	N.S.
	Mycobacteriaceae	0.0	1.6	N.S.
	Pseudomonadaceae	0.0	1.4	N.S.
	ETC(<1%)	9.0	10.9	
		3.0	1.9	N.S.
	Cutibacterium	1.9	4.0	N.S.
	Stenotrophomonas	4.9	3.4	N.S.
	Oscillibacter	10.8	8.9	N.S.
	PAC000186 g	1.6	0.0	N.S.
	Prevotella	1.8	1.5	N.S.
	PAC001127 g	1.1	1.4	N.S.
	Serratia	1.9	1.9	N.S.
	Bacteroides	1.3	1.2	N.S.
	Christensenellaceae uc	1.2	0.0	N.S.
	PAC001063 g	2.2	2.7	N.S.
	Streptococcus	1.6	1.5	N.S.
	Corynebacterium	6.6	6.3	N.S.
	Pseudoflavonifractor	1.9	1.7	N.S.
	PAC001360 g	2.9	2.4	N.S.
	PAC001066 g	2.9	3.8	N.S.
Genus	Afipia	2.6	0.0	N.S.
	PAC001068 g	14.5	11.3	N.S.
	Pelomonas	6.3	4.6	N.S.
	Enhydrobacter	10.3	13.8	N.S.
	Bradyrhizobium	0.0	1.3	N.S.
	Pseudomonas	0.0	2.1	N.S.
	Lawsonella	0.0	1.6	N.S.
	Mycobacterium	0.0	1.4	N.S.
	Sphingomonas	0.0	1.1	N.S.
	JZUE g	0.0		
	ETC(<1%)	18.7	20.2	

Relative abundances less than 1 % were expressed as ETC. Wilcoxon rank-sum test was used to analyze the significance between the two groups. N.S. Not significant.