Supplementary materials

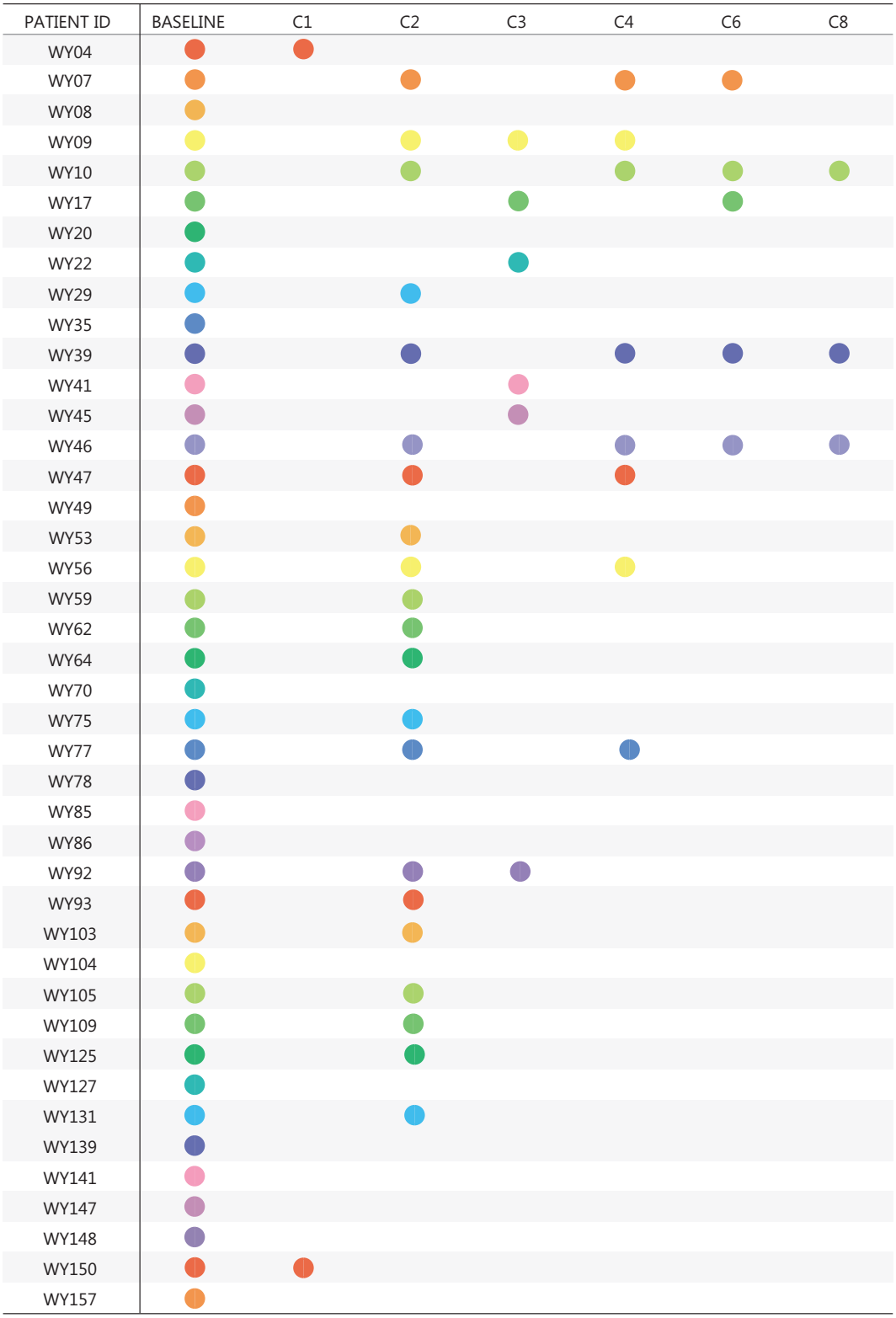


Figure S1 A summary of each patient's sample time points.

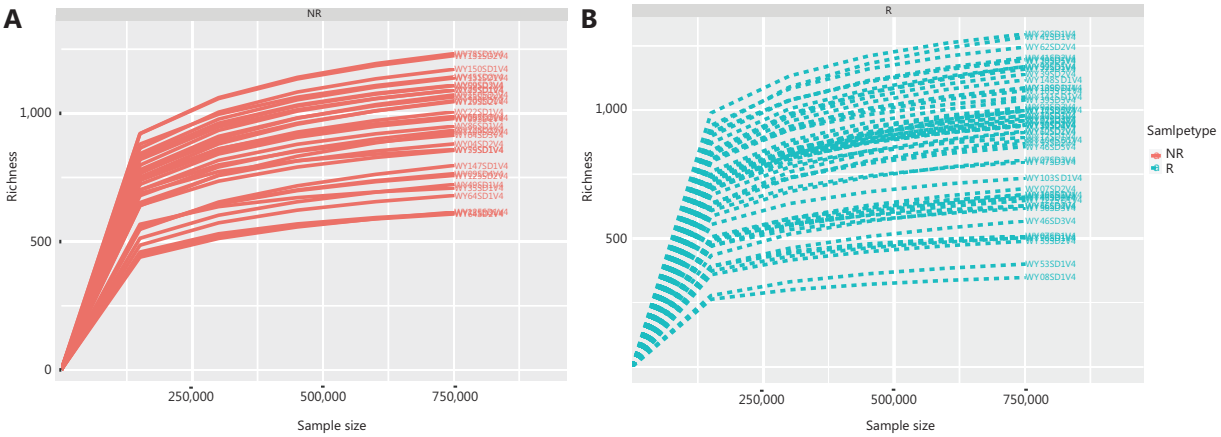
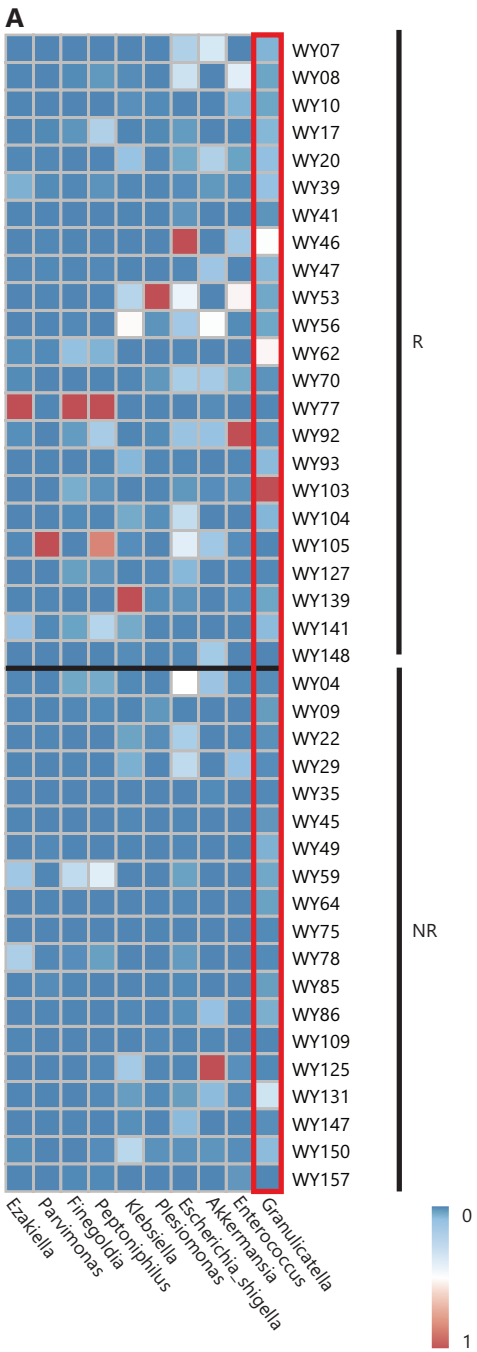


Figure S2 Rarefaction curves of fecal samples using 16S ribosomal RNA gene sequencing from the nonresponder (A) and responder groups (B).



B

Family level	Genus level
Carnobacteriaceae	Granulicatella
Enterococcaceae	Enterococcus
Akkermansiaceae	Akkermansia
Enterobacteriaceae	Escherichia_shigella
	Plesiomonas
	Klebsiella
Clostridiales family XI	Peptoniphilus
	Finegoldia
	Parvimonas
	Ezakiella

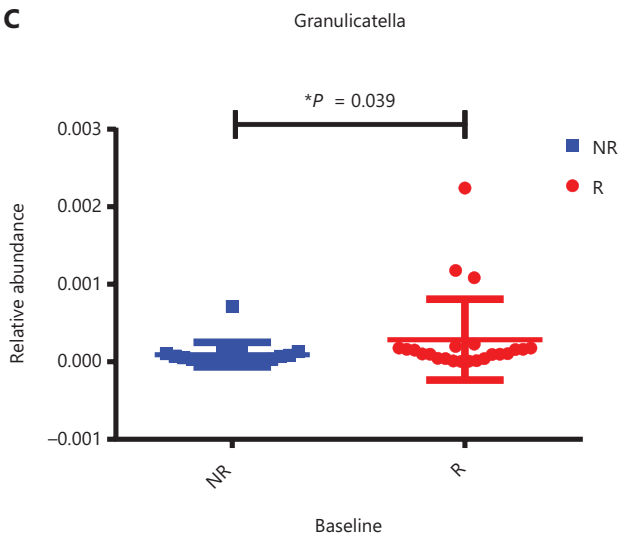


Figure S3 Comparison of 5 bacterial families with different abundances at the genus level. (A) Heat map of the dominant gut microbial genera belonging to the 5 bacterial families. (B) Description of the commensal microbiome summarized at the family and genus levels. (C) Comparison of the *Granulicatella* bacterial genus between responders (n = 23) and nonresponders (n = 19). Statistical analysis was performed using the Mann-Whitney test. *P < 0.05.

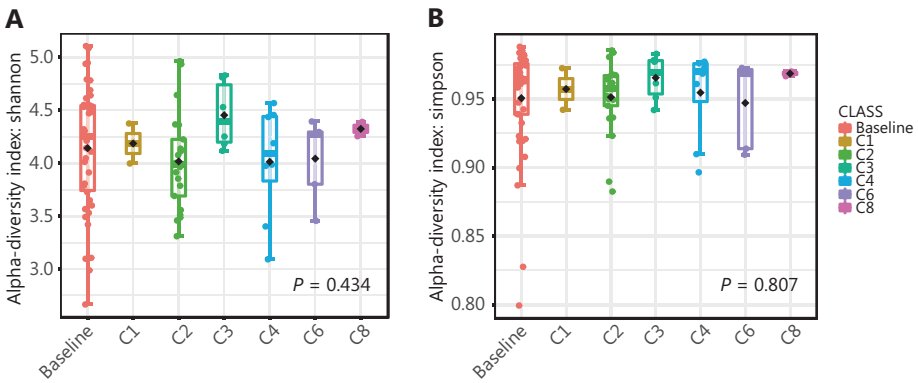


Figure S4 The diversity of the gut microbiome during anti-PD-1 treatment. Dynamics of the Shannon index (A) and Simpson index (B) in longitudinal stool samples. Statistical analysis was performed using the Kruskal-Wallis test. $P > 0.05$ for all tests.

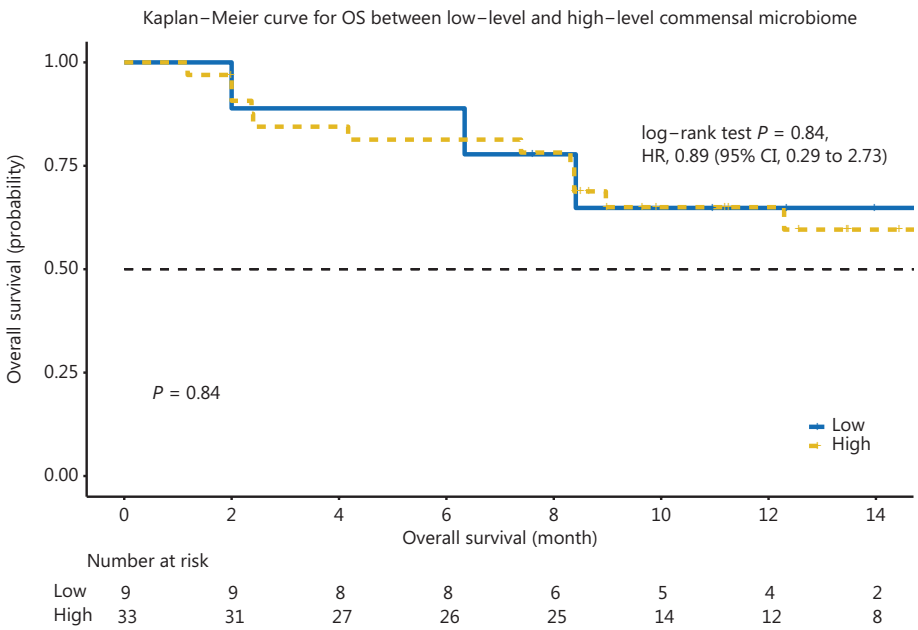


Figure S5 Kaplan-Meier plot of overall survival with log-rank tests in patients treated with immune checkpoint inhibitors, stratified by high versus low levels of the baseline commensal microbes.

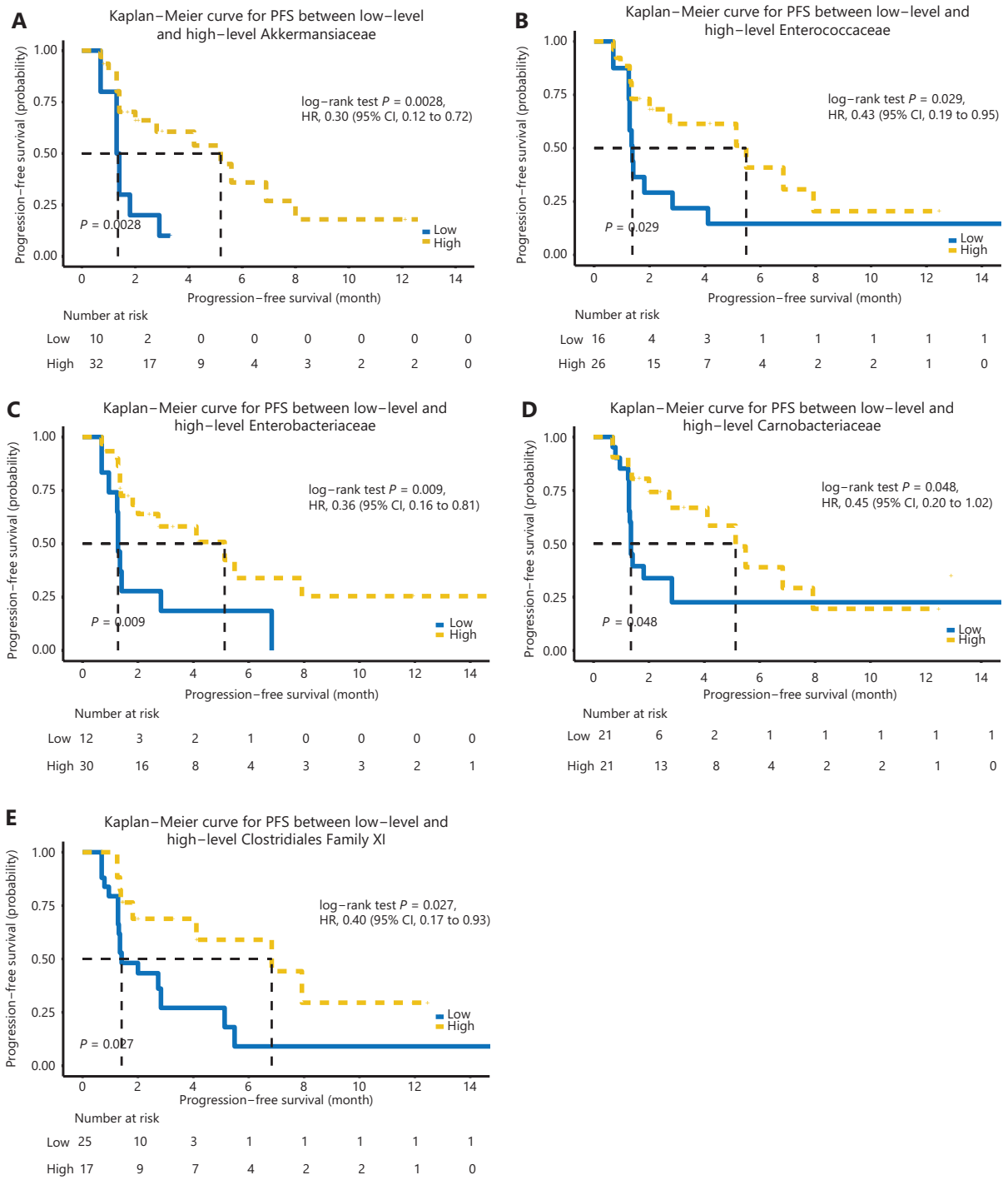


Figure S6 Kaplan-Meier plot of progression-free survival using log-rank tests in patients with high versus low levels of *Akkermansiaceae* (A), *Enterococcaceae* (B), *Enterobacteriaceae* (C), *Carnobacteriaceae* (D), and *Clostridiales Family XI* (E).