

Supplementary Material

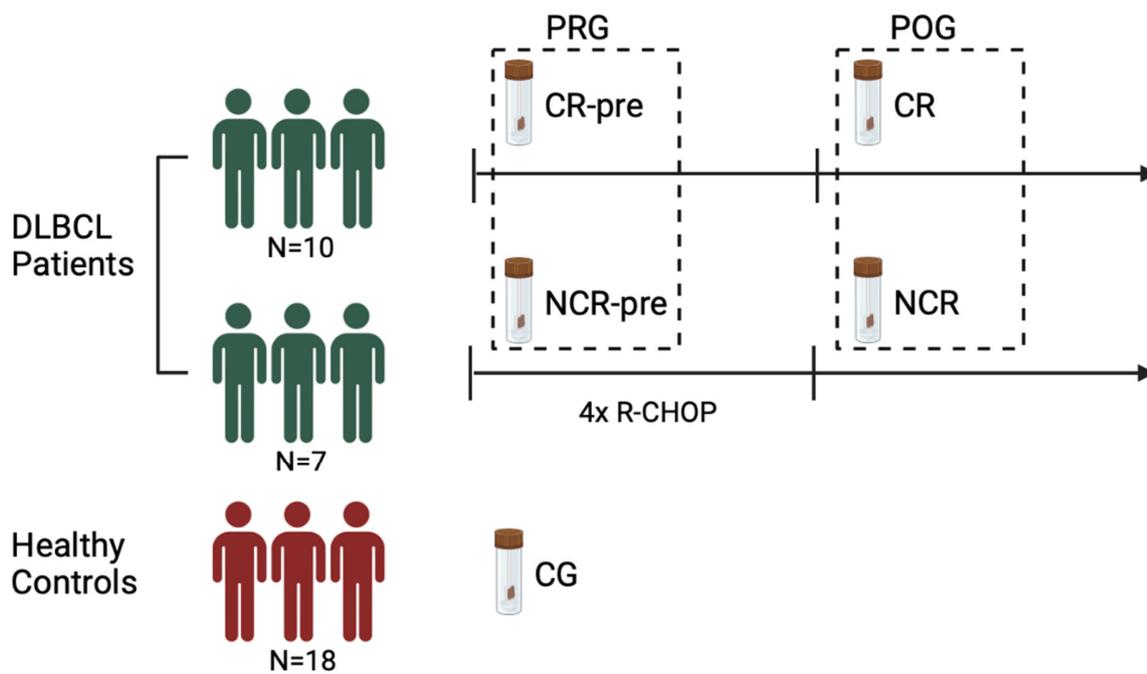
The Gut Microbiome Correlated to Chemotherapy Efficacy in Diffuse Large B-cell Lymphoma Patients

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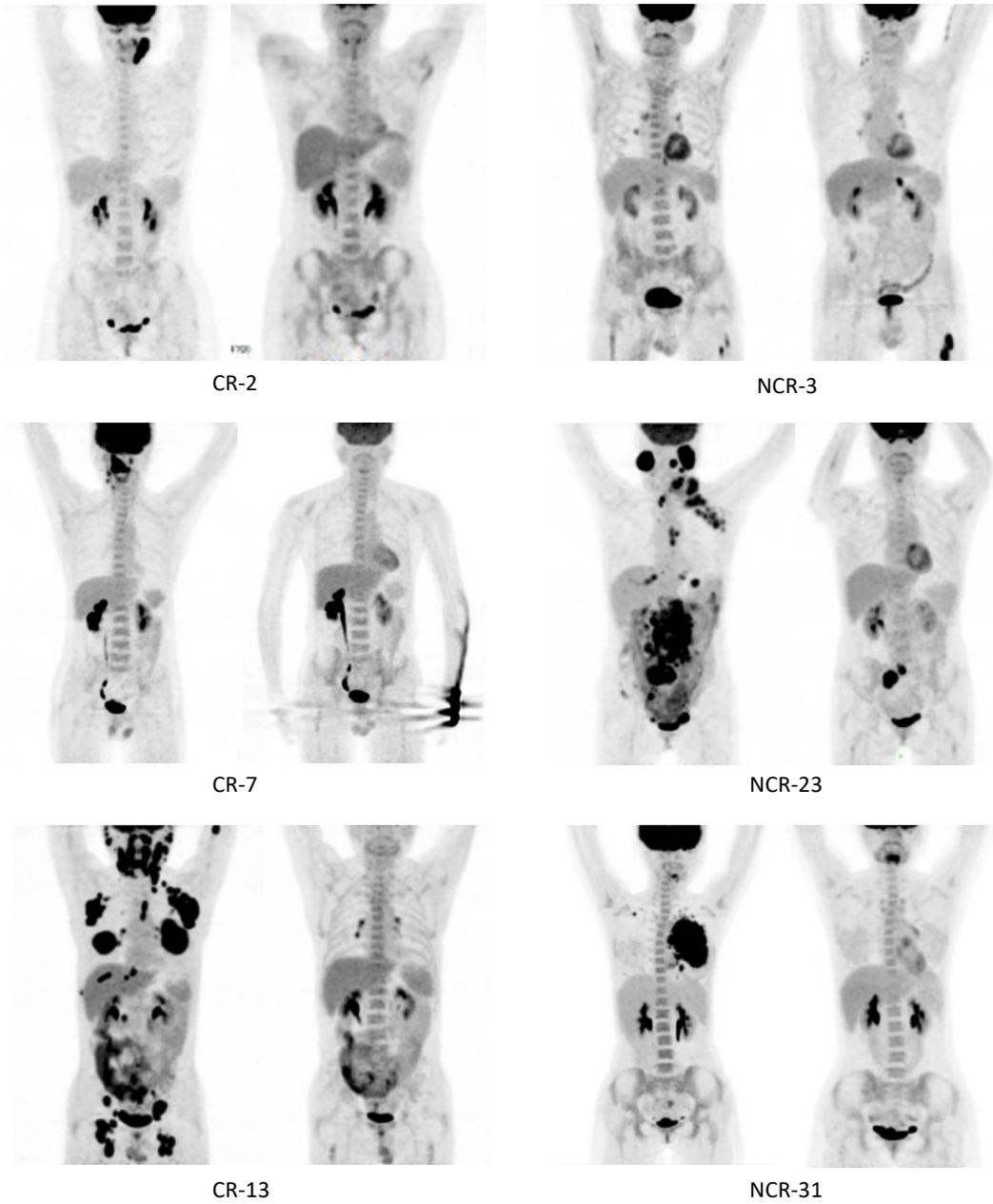
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1 Supplementary Figures and Tables

1.1 Supplementary Figures

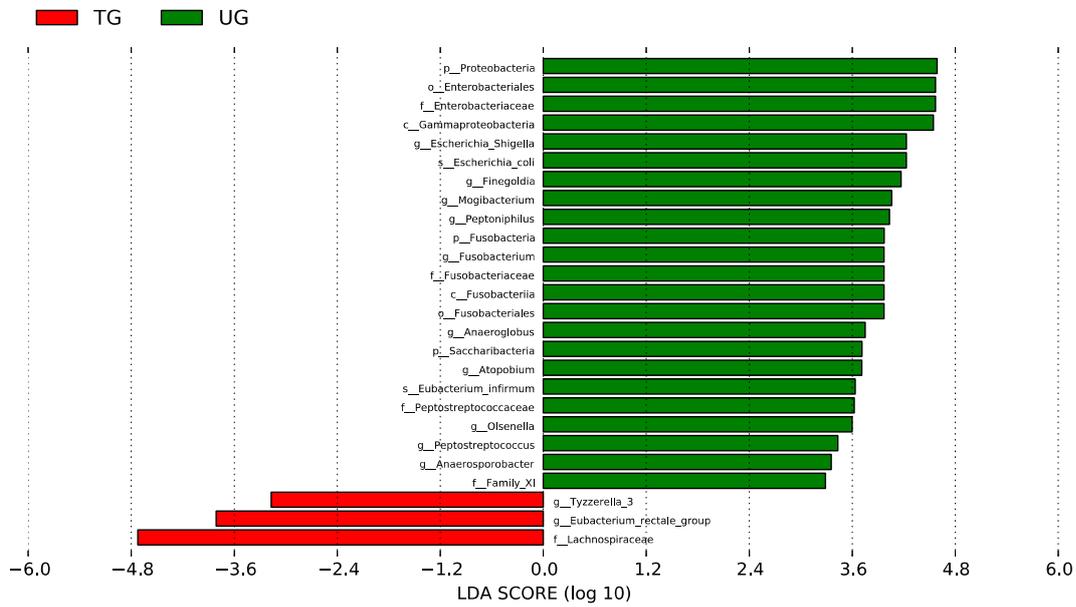


Supplementary Figure S1. Schematic outline of the study design.

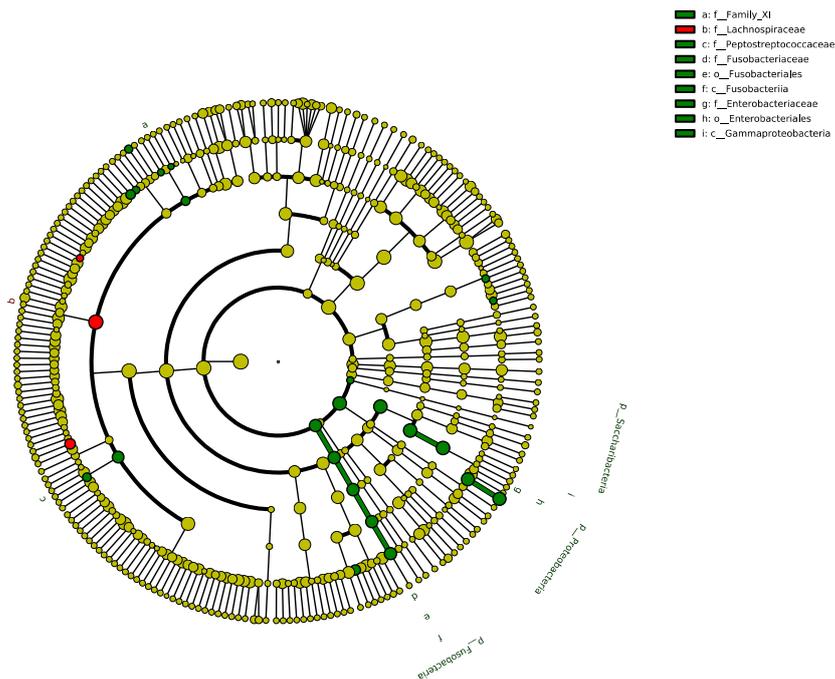


Supplementary Figure S2. PET/CT images of CR/NCR patients. For each patient, left: pre-treatment, right: post-treatment (4x R-CHOP)

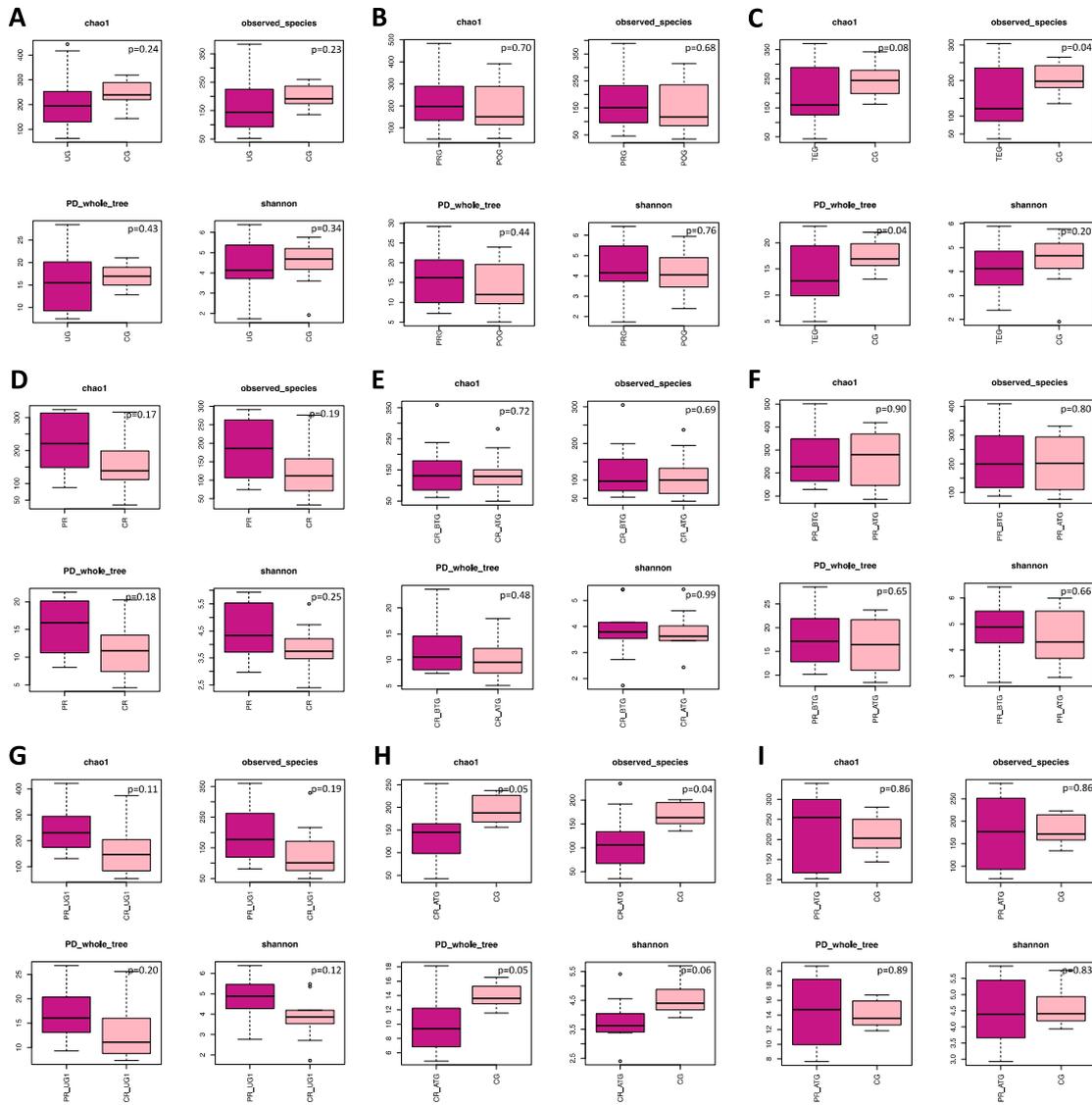
A.



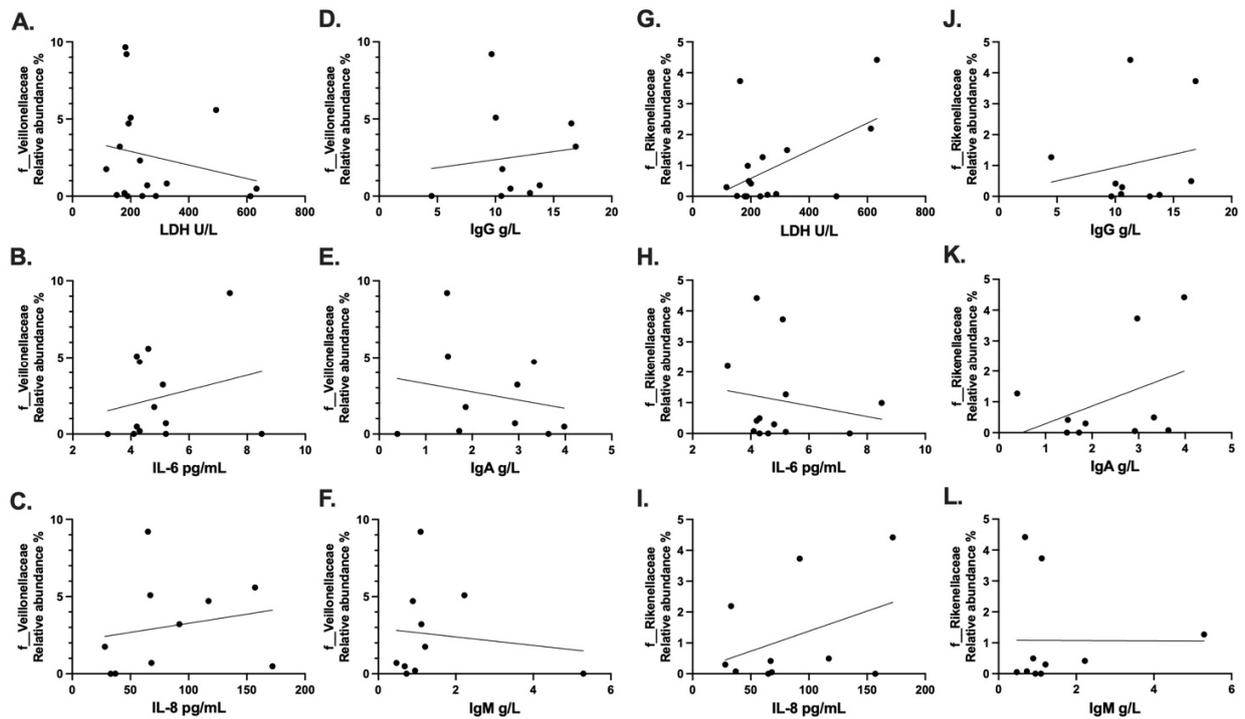
B.



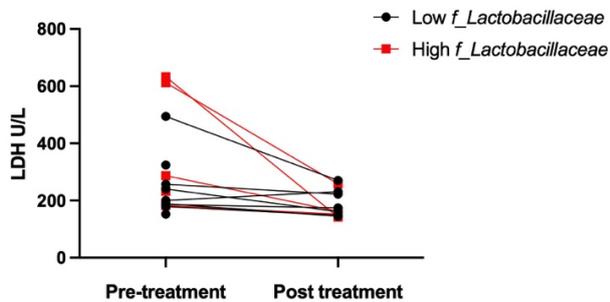
Supplementary Figure S3. GMB composition of untreated patients, and treated patients. (UG: untreated patients, TG: treated patients.) A: LEfSe analysis of taxa abundance, UG vs. TG. B: Cladogram, UG vs. TG.



Supplementary Figure S4. A-I: The α -diversity analysis of each pair of groups. The p-values by Turkey-group-test were indicated in the figures.



Supplementary Figure S5. A-F: The correlations of serum inflammation markers/immunology markers (LDH, IL-6, IL-8, IgG, IgA, IgM) and relative abundance of *Veillonellaceae*. G-L: The correlations of serum inflammation markers/immunology markers (LDH, IL-6, IL-8, IgG, IgA, IgM) and relative abundance of *Rikenellaceae*.



Supplementary Figure S6. The serum LDH level before and after treatment. Patients with high *Lactobacillaceae* abundance (post-treatment) was labeled red color.

1.2 Supplementary Tables

Supplementary Table S1. Virulence factors of *E.coli* in PRG vs. CG

Virulence factors	Gene	p value	Function
Adhesins	<i>fimH</i>	0.036	d-Mannose-specific adhesin
	<i>bfpA</i>	0.057	Type IV bundle-forming pili
	<i>focG</i>	0.086	Pilus tip molecule
	<i>fliC</i>	0.100	Flagellin variant
	<i>aidA</i>	0.317	Adhesin involved in diffuse adherence
	<i>papC</i>	0.346	Pilus assembly
	<i>fasA</i>	0.584	F6 fimbrial adhesin
	<i>papG</i>	0.681	Gal(1-4)Gal-specific pilus tip adhesin molecule
	<i>papA</i>	0.774	Major structural subunit of pilus
	<i>papEF</i>	0.895	Minor tip pilins
Capsule synthesis	<i>rfc</i>	0.348	O4 lipopolysaccharide synthesis
Toxins	<i>vat</i>	0.033	vacuolating toxin
	<i>astA</i>	0.052	Enteroaggregative E.coli toxin
	<i>hlyD</i>	0.057	Hemolysin
	<i>hlyA</i>	0.287	Hemolysin
	<i>east1</i>	0.348	Heat-stable enterotoxin
	<i>clbB/clbN</i>	0.348	Colibactin
	<i>cvaC</i>	0.401	Colicin V
	<i>sat</i>	0.695	Secreted autotransporter toxin
Siderophores	<i>fyuA</i>	0.032	yersiniabactin receptor
	<i>iroN</i>	0.057	Novel catecholate siderophore
Additional virulence genes	<i>malX</i>	0.005	Pathogenicity island marker
	<i>traT</i>	0.022	Serum survival
	<i>usp</i>	0.022	Uropathogen-specific protein
	<i>ompT</i>	0.339	Outer membrane protease
	<i>PAI</i>	0.844	Pathogenicity-associated island

Supplementary Table S2. Exopolysaccharides synthesis pathway in *Lactobacillus* in CR vs. NCR

EPS Pathway	Gene	p value	Function
Protease	<i>prtD</i>	0.103	Protease
	<i>pepN</i>	0.560	Peptidase
Regulation	<i>lytR/epsA</i>	0.711	Transcriptional regulation of EPS synthesis
Synthesis	<i>epsB</i>	0.175	Tyrosine kinase modulator
	<i>epsC</i>	0.257	Tyrosine kinase
	<i>epsD</i>	0.870	Phosphotyrosine phosphatase
	<i>epsE</i>	0.158	Priming glycosyltransferase
	<i>epsF</i>	0.036	Unknown
	<i>wzx</i>	0.168	Flippase
	<i>wzy</i>	0.087	Polysaccharide polymerase
Export	<i>epsG</i>	0.543	Putative membrane protein
	<i>dppA</i>	0.063	Transporter protein