

**Ginsenosides Rb3 and Rd reduce polyyps formation while reinstate the
dysbiotic gut microbiota and the intestinal microenvironment in
Apc^{Min/+} mice**

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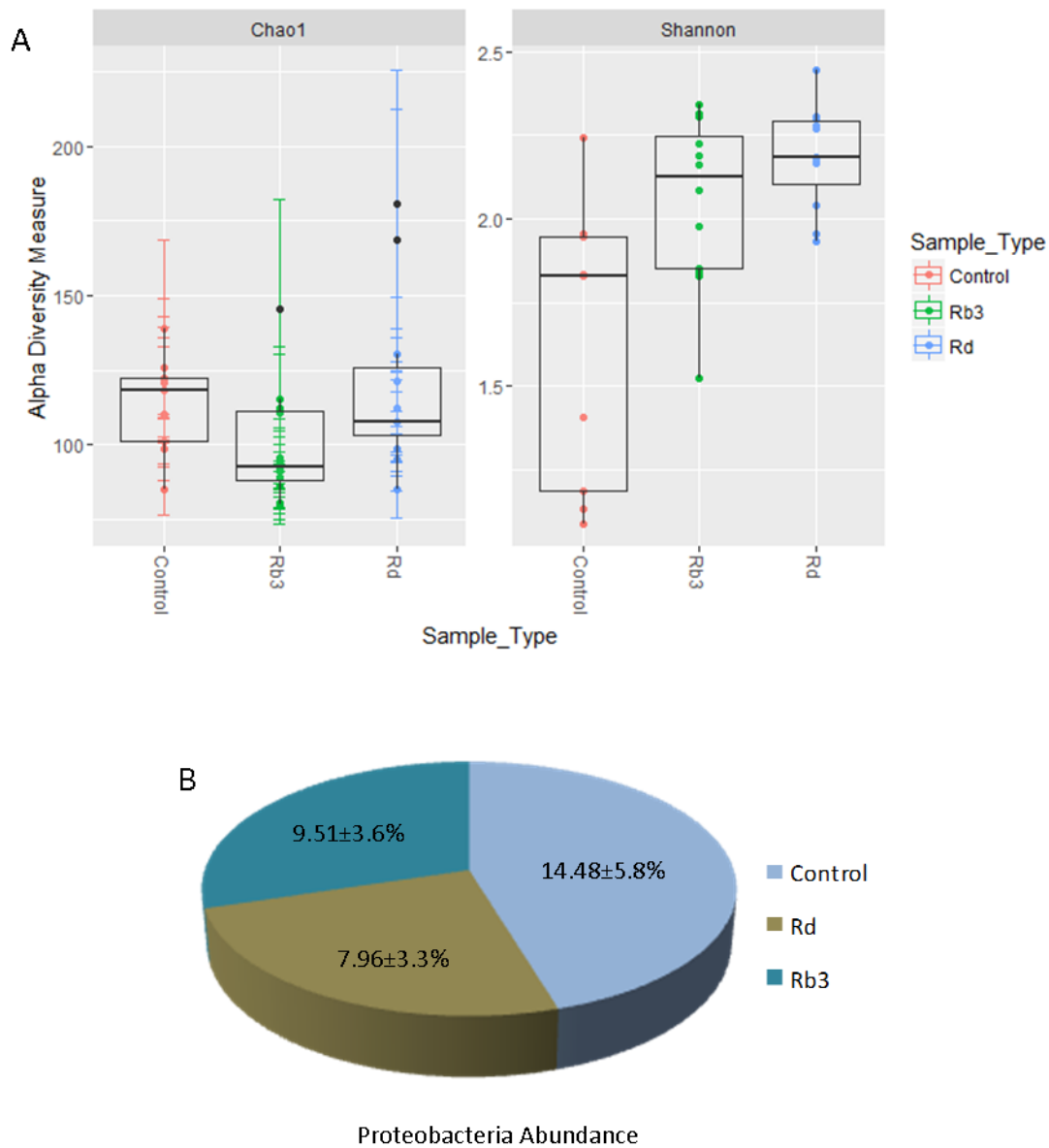


Figure S1. Alpha diversity analysis of phylum Proteobacteria. (A) The dataset was sub-group to Proteobacteria and OTUs diversity analyses were performed. (B) Average relative abundance of phylum Proteobacteria.

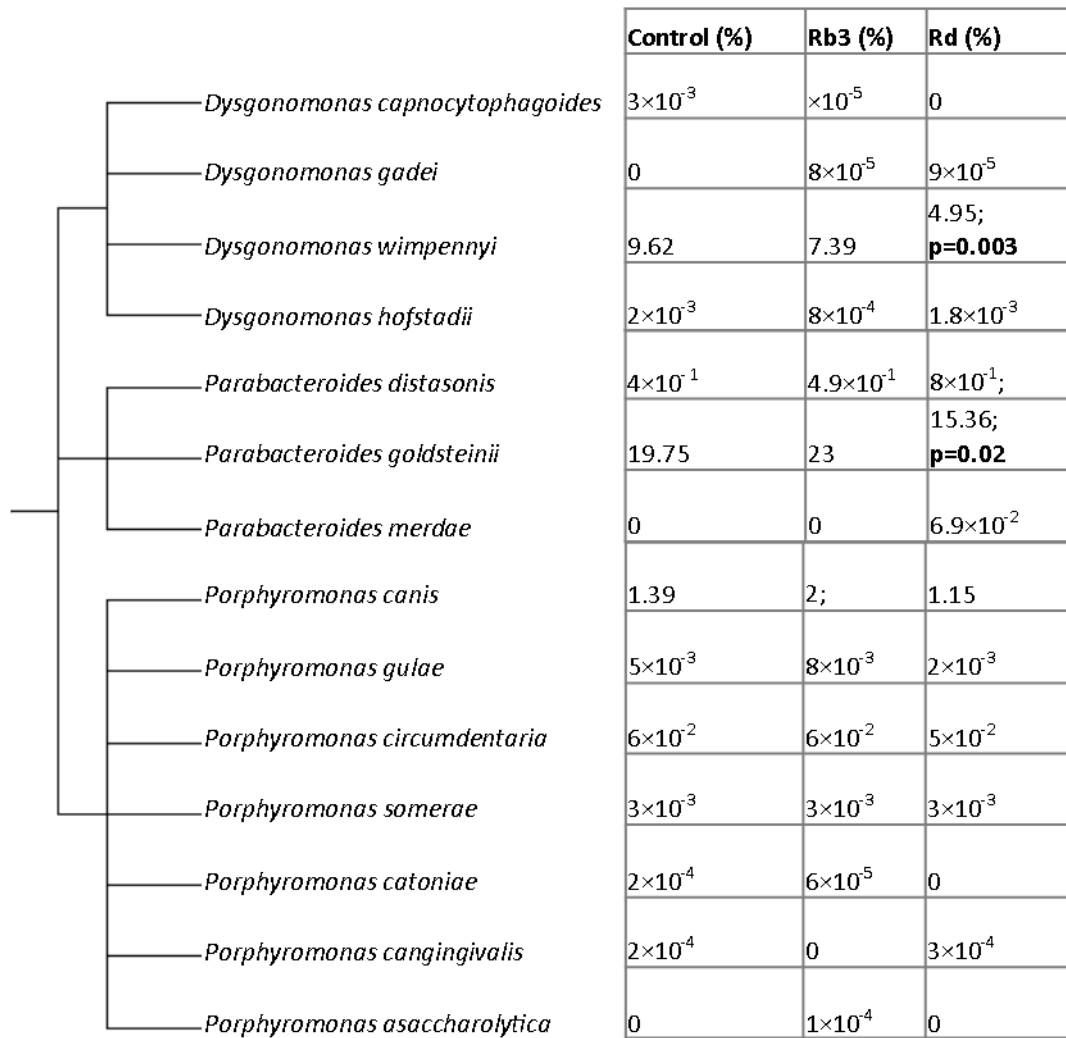


Figure S2. Phylogenetic tree of species detected in family Porphyromonadaceae. Values are showing average relative abundance of each species. P values are showing statistical change in the relative abundance. Tree was generated using NCBI phyloT.

	Control (%)	Rb3 (%)	Rd (%)
<i>Paraprevotella clara</i>	76×10^{-2}	12×10^{-1}	37×10^{-1} ; p=0.007
<i>Prevotella tanneriae</i>	1×10^{-4}	0	0
<i>Prevotella enoeca</i>	0	0	1×10^{-4}
<i>Prevotella amnii</i>	4×10^{-4}	1×10^{-3} ; p=0.04	8×10^{-4}
<i>Prevotella aurantiaca</i>	6×10^{-4}	4×10^{-4}	6×10^{-4}
<i>Prevotella loescheii</i>	3.6×10^{-1}	7×10^{-1}	9.1×10^{-1}
<i>Prevotella buccalis</i>	3×10^{-3}	5×10^{-3} ; p=0.047	5.3×10^{-3}
<i>Prevotella maculosa</i>	4.4×10^{-2}	6×10^{-2}	9.9×10^{-2}
<i>Prevotella timonensis</i>	1×10^{-4}	5×10^{-4}	3×10^{-4}
<i>Prevotella multisaccharivorax</i>	1×10^{-3}	1×10^{-3}	1.4×10^{-3}
<i>Prevotella paludivivens</i>	4×10^{-2}	1×10^{-2}	5.9×10^{-2} ; p=0.007
<i>Prevotella dentalis</i>	4×10^{-3}	6×10^{-3}	6.5×10^{-3}
<i>Prevotella marshii</i>	5×10^{-3}	3×10^{-3}	5×10^{-3}
<i>Prevotella dentasini</i>	20.5	17.93	23.8
<i>Prevotella pleuritidis</i>	1×10^{-3}	1×10^{-3}	1.8×10^{-3}
<i>Prevotella albensis</i>	3×10^{-2}	2.3×10^{-2}	3.3×10^{-2} ;
<i>Prevotella multiformis</i>	8×10^{-3}	7×10^{-3}	8×10^{-3}
<i>Prevotella micans</i>	1×10^{-3}	4×10^{-3}	3.7×10^{-3}
<i>Prevotella saccharolytica</i>	0	4×10^{-4}	0
<i>Prevotella shahii</i>	3×10^{-2}	3×10^{-2}	3.6×10^{-2}
<i>Prevotella corporis</i>	0	0	1×10^{-4}
<i>Prevotella baroniae</i>	0	0	1×10^{-4}

Figure S3. Phylogenetic tree of species detected in family Prevotellaceae. Values are showing average relative abundance of each species. p values are showing statistical change in the relative abundance. Tree was generated using NCBI PhyloT.

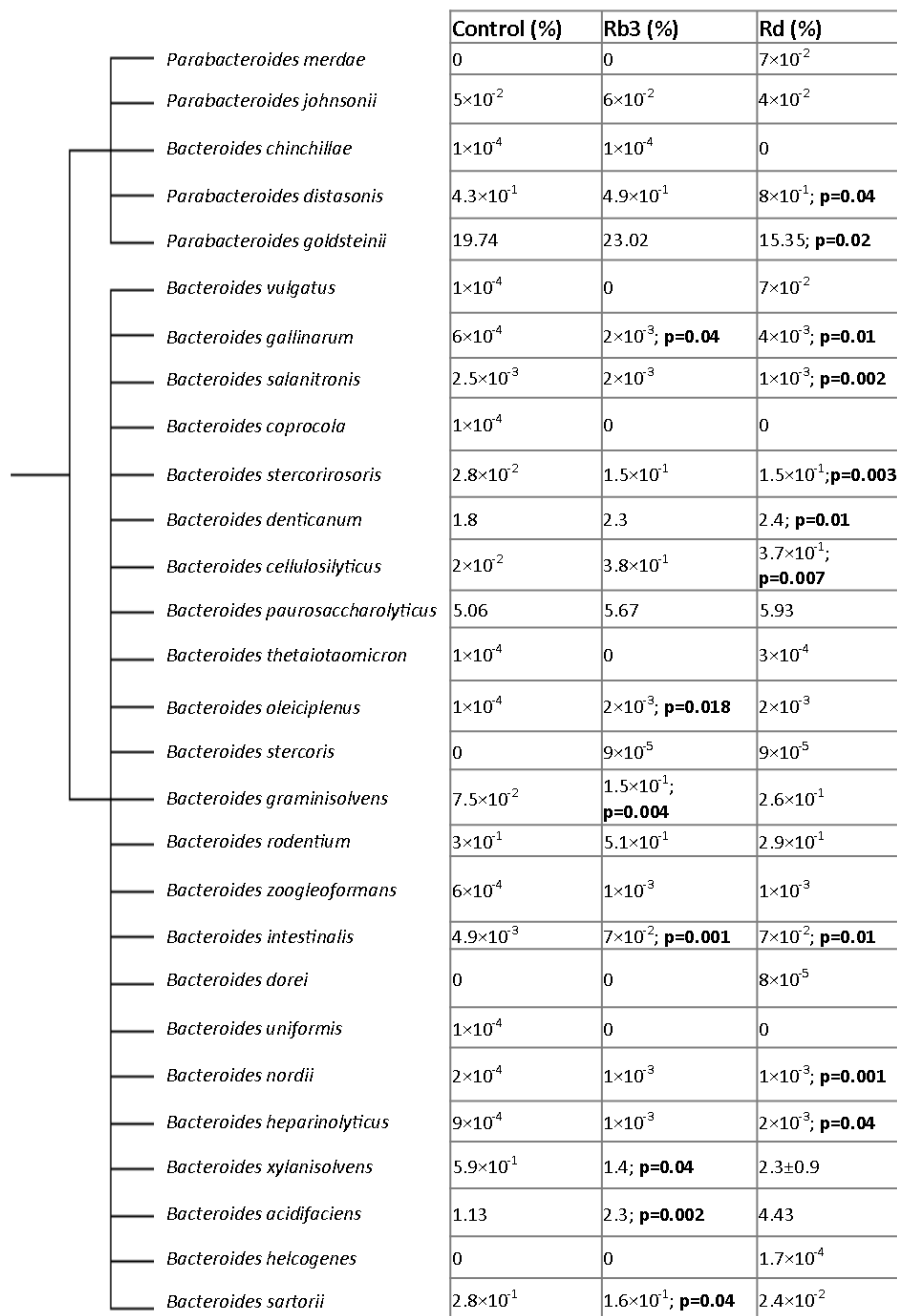


Figure S4. Phylogenetic tree of species detected in family Bacteroidaceae. Values are showing average relative abundance of each species. p values are showing statistical change in the relative abundance. Tree was generated using NCBI PhyloT.

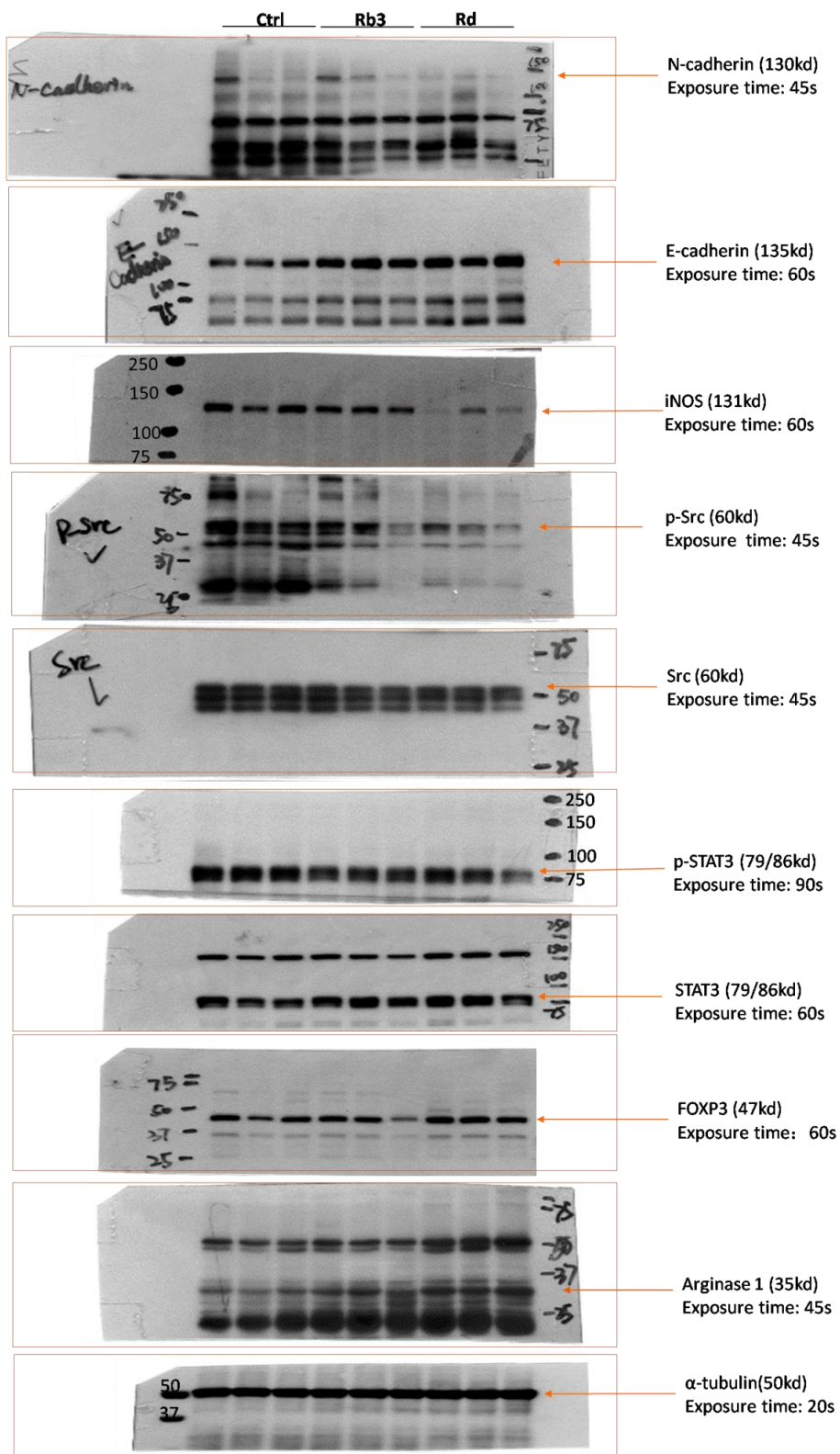


Figure S5. The full-length blots of the Western blots showed in Figure 2. Each lane represents sample obtained from individual mouse (n=3).

Table S1. List of unique species from three dominant phyla detected in the control group

Species	Phyla	Relative abundance (%)
<i>Myroides injenensis</i>	Bacteroidetes	1×10^{-4}
<i>Balneola vulgaris</i>	Bacteroidetes	8.49×10^{-5}
<i>Bacteroides coprocola</i>	Bacteroidetes	8.39×10^{-5}
<i>Bacteroides uniformis</i>	Bacteroidetes	7.67×10^{-5}
<i>Prevotella tannerae</i>	Bacteroidetes	7.14×10^{-5}
<i>Natronincola peptidivorans</i>	Firmicutes	4.8×10^{-4}
<i>Lactobacillus faeni</i>	Firmicutes	1×10^{-4}
<i>Bacillus okhensis</i>	Firmicutes	1×10^{-4}
<i>Paenibacillus donghaensis</i>	Firmicutes	9.7×10^{-5}
<i>Salinicoccus luteus</i>	Firmicutes	9.7×10^{-5}
<i>Thermobacillus xylanilyticus</i>	Firmicutes	9.7×10^{-5}
<i>Paenibacillus ourofinensis</i>	Firmicutes	8.49×10^{-5}
<i>Anoxybacillus tengchongensis</i>	Firmicutes	8.49×10^{-5}
<i>Salinicoccus iranensis</i>	Firmicutes	7.94×10^{-5}
<i>Coprothermobacter platensis</i>	Firmicutes	7.94×10^{-5}
<i>Jeotgalicoccus halotolerans</i>	Firmicutes	7.67×10^{-5}
<i>Jeotgalicoccus psychrophilus</i>	Firmicutes	7.67×10^{-5}
<i>Thauera selenatis</i>	Proteobacteria	1.9×10^{-4}
<i>Mesorhizobium huakuii</i>	Proteobacteria	1.7×10^{-4}
<i>Acinetobacter junii</i>	Proteobacteria	1.6×10^{-4}
<i>Acinetobacter gerneri</i>	Proteobacteria	1×10^{-4}
<i>Desulfovibrio longreachensis</i>	Proteobacteria	1×10^{-4}
<i>Phenylobacterium mobile</i>	Proteobacteria	9.71×10^{-5}
<i>Bradyrhizobium pachyrhizi</i>	Proteobacteria	9.71×10^{-5}
<i>Agrobacterium rubi</i>	Proteobacteria	9.71×10^{-5}
<i>Helicobacter winghamensis</i>	Proteobacteria	9.71×10^{-5}
<i>Lysobacter deserti</i>	Proteobacteria	8.49×10^{-5}
<i>Ralstonia detusculanense</i>	Proteobacteria	8.39×10^{-5}
<i>Halomonas gudaonensis</i>	Proteobacteria	8.39×10^{-5}
<i>Stenotrophomonas terrae</i>	Proteobacteria	8.39×10^{-5}
<i>Lautropia mirabilis</i>	Proteobacteria	8.16×10^{-5}
<i>Moritella japonica</i>	Proteobacteria	7.67×10^{-5}
<i>Vibrio littoralis</i>	Proteobacteria	7.67×10^{-5}
<i>Gluconobacter morbifer</i>	Proteobacteria	7.67×10^{-5}
<i>Brevundimonas olei</i>	Proteobacteria	7.3×10^{-5}

Table S2. List of unique species from three dominant phyla detected in the Rb3 group

Species	Phyla	Relative abundance (%)
<i>Lentibacillus kapialis</i>	Firmicutes	8×10^{-5}
<i>Virgibacillus byunsanensis</i>	Firmicutes	7×10^{-5}
<i>Bacillus pseudofirmus</i>	Firmicutes	8×10^{-5}
<i>Lactobacillus intestinalis</i>	Firmicutes	7×10^{-4}
<i>Lactobacillus panis</i>	Firmicutes	9×10^{-5}
<i>Lactobacillus oris</i>	Firmicutes	9×10^{-5}
<i>Ureibacillus thermophilus</i>	Firmicutes	1×10^{-4}
<i>Staphylococcus intermedius</i>	Firmicutes	7×10^{-5}
<i>Caloramator viterbiensis</i>	Firmicutes	8×10^{-5}
<i>Caloramator fervidus</i>	Firmicutes	5×10^{-5}
<i>Clostridium papyrosolvans</i>	Firmicutes	2×10^{-4}
<i>Fusibacter paucivorans</i>	Firmicutes	7×10^{-5}
<i>Helcococcus ovis</i>	Firmicutes	7×10^{-5}
<i>Mogibacterium timidum</i>	Firmicutes	1×10^{-4}
<i>Anaerofilum agile</i>	Firmicutes	1×10^{-4}
<i>Syntrophomonas bryantii</i>	Firmicutes	5×10^{-5}
<i>Porphyromonas asaccharolytica</i>	Bacteroidetes	1×10^{-4}
<i>Prevotella saccharolytica</i>	Bacteroidetes	3×10^{-4}
<i>Chryseobacterium culicis</i>	Bacteroidetes	2.7×10^{-4}
<i>Exiguobacterium taiwanense</i>	Bacteroidetes	7×10^{-5}
<i>Flavobacterium weaverense</i>	Bacteroidetes	8×10^{-5}
<i>Polaribacter filamentus</i>	Bacteroidetes	1×10^{-4}
<i>Tenacibaculum japonica</i>	Bacteroidetes	2×10^{-4}
<i>Lewinella marina</i>	Bacteroidetes	2×10^{-4}
<i>Ochrobactrum thiophenivorans</i>	Proteobacteria	7×10^{-5}
<i>Kaistia soli</i>	Proteobacteria	8×10^{-5}
<i>Novispirillum peregrinum</i>	Proteobacteria	4×10^{-4}
<i>Novosphingobium yangbajingensis</i>	Proteobacteria	1×10^{-4}
<i>Novosphingobium acidiphilum</i>	Proteobacteria	5×10^{-5}
<i>Sphingomonas roseiflava</i>	Proteobacteria	2.8×10^{-4}
<i>Ancylobacter rudongensis</i>	Proteobacteria	8×10^{-5}
<i>Burkholderia ubonensis</i>	Proteobacteria	7×10^{-5}
<i>Desulfitobacterium chlororespirans</i>	Proteobacteria	2.9×10^{-5}
<i>Desulfovermiculus halophilus</i>	Proteobacteria	9×10^{-5}
<i>Desulfovibrio gracilis</i>	Proteobacteria	7×10^{-5}
<i>Syntrophobacter wolinii</i>	Proteobacteria	8×10^{-5}
<i>Helicobacter canis</i>	Proteobacteria	8×10^{-5}

<i>Microbulbifer epialgicus</i>	Proteobacteria	9×10^{-5}
<i>Morganella psychrotolerans</i>	Proteobacteria	9×10^{-5}
<i>Serratia ureilytica</i>	Proteobacteria	9×10^{-5}
<i>Moritella yayanosii</i>	Proteobacteria	9×10^{-5}
<i>Chelonobacter oris</i>	Proteobacteria	9×10^{-5}

Table S3. List of unique species from three dominant phyla detected in the Rd group

Species	Phyla	Relative abundance (%)
<i>Bacteroides dorei</i>	Bacteroidetes	8×10^{-5}
<i>Bacteroides helcogenes</i>	Bacteroidetes	1×10^{-4}
<i>Parabacteroides merdae</i>	Bacteroidetes	6.9×10^{-2}
<i>Prevotella baroniae</i>	Bacteroidetes	9×10^{-5}
<i>Prevotella corporis</i>	Bacteroidetes	9×10^{-5}
<i>Prevotella enoea</i>	Bacteroidetes	8×10^{-5}
<i>Chryseobacterium oranimense</i>	Bacteroidetes	1.8×10^{-4}
<i>Maribacter goseongensis</i>	Bacteroidetes	1.7×10^{-4}
<i>Polaribacter dokdonensis</i>	Bacteroidetes	1.9×10^{-4}
<i>Salegentibacter holothuriorum</i>	Bacteroidetes	9×10^{-5}
<i>Alkalibacillus salilacus</i>	Firmicutes	9×10^{-5}
<i>Bacillus horneckiae</i>	Firmicutes	8×10^{-5}
<i>Enterococcus faecalis</i>	Firmicutes	3.2×10^{-4}
<i>Geobacillus thermoglucosidans</i>	Firmicutes	2.6×10^{-4}
<i>Lactobacillus thailandensis</i>	Firmicutes	1.6×10^{-4}
<i>Paenibacillus contaminans</i>	Firmicutes	8×10^{-5}
<i>Streptococcus pluranimalium</i>	Firmicutes	1.8×10^{-4}
<i>Streptococcus thoralensis</i>	Firmicutes	8×10^{-5}
<i>Weissella minor</i>	Firmicutes	8×10^{-5}
<i>Weissella thailandensis</i>	Firmicutes	8×10^{-5}
<i>Clostridium chromoreductans</i>	Firmicutes	8×10^{-5}
<i>Clostridium frigidicarnis</i>	Firmicutes	9×10^{-5}
<i>Moorella glycerini</i>	Firmicutes	2.4×10^{-4}
<i>Ruminococcus torques</i>	Firmicutes	8×10^{-5}
<i>Thermoanaerobacter sulfurignens</i>	Firmicutes	8×10^{-5}
<i>Erysipelothrix inopinata</i>	Firmicutes	3.5×10^{-4}
<i>Acidiphilium symbioticum</i>	Proteobacteria	9×10^{-5}
<i>Azospirillum halopraeferens</i>	Proteobacteria	9×10^{-5}
<i>Azospirillum rugosum</i>	Proteobacteria	8×10^{-5}
<i>Devosia terrae</i>	Proteobacteria	8×10^{-5}
<i>Methylobacterium jeotgali</i>	Proteobacteria	8×10^{-5}
<i>Sphingomonas insulae</i>	Proteobacteria	9×10^{-5}
<i>Sphingomonas pseudosanguinis</i>	Proteobacteria	8×10^{-5}
<i>Thalassospira xianhensis</i>	Proteobacteria	9×10^{-5}
<i>Cupriavidus pauculus</i>	Proteobacteria	1.6×10^{-5}
<i>Hydrogenophilus hirschii</i>	Proteobacteria	8×10^{-5}
<i>Variovorax boronicumulans</i>	Proteobacteria	8×10^{-5}
<i>Desulfosarcina ovata</i>	Proteobacteria	1.9×10^{-4}
<i>Desulfovibrio vulgaris</i>	Proteobacteria	8×10^{-5}

<i>Nitrospina gracilis</i>	Proteobacteria	9×10^{-5}
<i>Caminibacter profundus</i>	Proteobacteria	8×10^{-5}
<i>Allochromatium palmeri</i>	Proteobacteria	8×10^{-5}
<i>Amphritea atlantica</i>	Proteobacteria	9×10^{-5}
<i>Enterobacter aceae</i>	Proteobacteria	8×10^{-5}
<i>Halomonas fontilapidosi</i>	Proteobacteria	2.1×10^{-4}
<i>Moraxella caviae</i>	Proteobacteria	2.6×10^{-4}
<i>Pseudomonas panacis</i>	Proteobacteria	8×10^{-5}
<i>Psychrobacter phenylpyruvicus</i>	Proteobacteria	9×10^{-5}
<i>Stenotrophomonas retroflexus</i>	Proteobacteria	8×10^{-5}
<i>Thiothrix nivea</i>	Proteobacteria	2.7×10^{-4}
<i>Vibrio pommerensis</i>	Proteobacteria	8×10^{-5}

Table S4. List of metabolically important bacterial species that modulated with Rb3/Rd treatment

Species	Control (%)	Rb3 (%)	Rd (%)	Percent change in Rb3	Percent change in Rd
<i>Akkermansia muciniphila</i>	0.165	0.025	0.035	-84.84	-78.8
<i>Aminiphilus circumscriptus</i>	0.011	0.018	0.019	66.46	72.92
<i>Bacteroides acidifaciens</i>	1.132	2.343	4.437	106.98	292.031
<i>Bacteroides cellulosilyticus</i>	0.020	0.383	0.374	1789.92	1744.83
<i>Bacteroides graminisolvens</i>	0.075	0.154	0.266	104.53	253.18
<i>Bacteroides intestinalis</i>	0.005	0.070	0.071	1332.15	1355.35
<i>Bacteroides paurosaccharolyticus</i>	5.066	5.671	5.933	11.95	17.11
<i>Bacteroides rodentium</i>	0.301	0.519	0.298	72.55	-0.89
<i>Bacteroides sartorii</i>	0.282	0.169	0.024	-39.99	-91.59
<i>Bacteroides stercorisoris</i>	0.028	0.151	0.152	437.71	444.31
<i>Bacteroides xylanisolvens</i>	0.600	1.408	2.321	134.88	287.11
<i>Bifidobacterium choerinum</i>	0.033	0.118	0.055	252.87	63.96
<i>Blautia coccoides</i>	2.844	1.806	1.799	-36.5	-36.74
<i>Blautia hansenii</i>	0.707	0.528	0.769	-25.33	8.86
<i>Blautia hydrogenotrophica</i>	0.008	0.016	0.003	97.52	-64.53
<i>Blautia wexlerae</i>	0.911	0.676	0.914	-25.8	0.2564
<i>Butyricimonas synergistica</i>	1.042	0.654	0.384	-37.22	-63.096
<i>Butyricimonas virosa</i>	0.142	0.195	0.172	37.86	21.713
<i>Butyrivibrio proteoclasticus</i>	0.129	0.138	0.205	7.033	58.66
<i>Deferribacter autotrophicus</i>	0.003	0.003	0.177	1.24	5178.36
<i>Desulfonauticus autotrophicus</i>	0.032	0.035	0.052	9.51	63.62
<i>Desulfotomaculum indicum</i>	0.062	0.083	0.055	33.76	-11.98
<i>Desulfovibrio fairfieldensis</i>	0.159	0.117	0.156	-26.4	-1.88
<i>Desulfovibrio litoralis</i>	0.004	0.138	0.041	3269.7	897.27
<i>Desulfovibrio oryzae</i>	0.007	0.011	0.009	63.4	28.86
<i>Desulfovibrio piger</i>	1.266	1.773	1.561	40.03	23.28
<i>Desulfovibrio psychrotolerans</i>	0.202	0.245	0.246	21.02	21.51
<i>Desulfovibrio simplex</i>	0.011	0.015	0.056	35.36	402.6
<i>Desulfurispirillum alkaliphilum</i>	0.015	0.018	0.013	17.58	-12.33
<i>Desulfurispora thermophila</i>	0.064	0.118	0.013	82.98	-80
<i>Dysgonomonas wimpennyi</i>	9.620	7.391	4.951	-23.16	-48.53
<i>Eggerthella sinensis</i>	0.009	0.029	0.015	216.99	62.46
<i>Halanaerobium alcaliphilum</i>	0.041	0.056	0.068	34.81	65.64
<i>Lachnospira pectinoschiza</i>	0.698	0.641	0.540	-8.07	-22.57

<i>Lactobacillus antri</i>	0.002	0.048	0.012	2847.4	660.6
<i>Lactobacillus equi</i>	0.003	0.011	0.019	308.05	635.76
<i>Lactobacillus hayakitensis</i>	0.043	0.166	0.329	290.68	672.37
<i>Lactobacillus johnsonii</i>	0.124	0.115	0.149	-7.48	20.25
<i>Lactobacillus siliginis</i>	0.004	0.017	0.025	352.23	543.5
<i>Lactobacillus taiwanensis</i>	0.024	0.028	0.034	14.68	39.06
<i>Lactobacillus vaginalis</i>	0.001	0.022	0.004	2327.96	366.1
<i>Lentibacillus salinarum</i>	0.015	0.016	0.016	4.27	8.08
<i>Limnobacter litoralis</i>	0.145	0.317	0.551	118.92	281.27
<i>Moryella indoligenes</i>	0.092	0.031	0.036	-66.29	-61.44
<i>Oscillospira eae</i>	2.182	2.519	2.924	15.47	34.05
<i>Oscillospira guilliermondii</i>	0.852	0.759	0.779	-10.89	-8.54
<i>Parabacteroides distasonis</i>	0.438	0.491	0.805	12.12	83.58
<i>Parabacteroides goldsteinii</i>	19.748	23.024	15.356	16.58	-22.24
<i>Parabacteroides johnsonii</i>	0.052	0.062	0.044	19.39	-14.85
<i>Paraprevotella clara</i>	0.756	1.224	3.721	61.77	391.86
<i>Pedobacter kwangyangensis</i>	0.394	0.561	0.350	42.24	-11.27
<i>Peptoniphilus gorbachii</i>	0.018	0.039	0.005	123.58	-71.32
<i>Peptoniphilus methioninivorax</i>	0.018	0.043	0.055	133.46	203.48
<i>Porphyromonas circumdentaria</i>	0.063	0.062	0.055	-1.87	-12.99
<i>Prevotella albensis</i>	0.027	0.029	0.033	6.26	21.91
<i>Prevotella dentasini</i>	20.501	17.935	23.771	-12.52	15.94
<i>Prevotella loescheii</i>	0.361	0.770	0.914	113.49	153.29
<i>Prevotella maculosa</i>	0.044	0.063	0.100	44.927	128.53
<i>Prevotella paludivivens</i>	0.044	0.042	0.059	-2.69	35.74
<i>Prevotella shahii</i>	0.028	0.032	0.037	14.2	29.24
<i>Rhodococcus percolatus</i>	0.062	0.089	0.087	43.03	39.3
<i>Rikenella microfus</i>	0.860	1.424	0.463	65.57	-46.19
<i>Ruminococcus callidus</i>	0.005	0.016	0.006	246.42	42.04
<i>Ruminococcus flavefaciens</i>	0.032	0.054	0.038	70.98	20.75
<i>Ruminococcus gnavus</i>	0.099	0.260	0.090	163.02	-9.16
<i>Runella limosa</i>	0.019	0.028	0.024	47.92	23.55
<i>Sedimentibacter hydroxybenzoicus</i>	0.919	0.975	0.707	6.13	-23.05
<i>Sutterella sanguinis</i>	0.070	0.653	0.027	831.8	-61.8
<i>Thermodesulfatator atlanticus</i>	0.010	0.012	0.007	26.506	-25.64
<i>Thermodesulfobivrio thiophilus</i>	0.031	0.032	0.029	2.14	-7.85
<i>Thiohalorhabdus denitrificans</i>	0.025	0.025	0.037	1.473	48.56
<i>Tindallia magadiensis</i>	0.026	0.043	0.055	63.39	111.07

<i>Turicibacter sanguinis</i>	0.0002	0.04	0.0003	21099.03	38.43
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Table S5. List of cachexia associated bacterial species that reduced with Rb3/Rd treatment

Species	Control (%)	Rb3 (%)	Rd (%)	Percent change in Rb3	Percent change in Rd
<i>Butyricimonas synergistica</i>	1.0416	0.6539	0.3844	-37.22	-63.10
<i>Butyricimonas virosa</i>	0.1416	0.1952	0.1723	37.87	21.71
<i>Campylobacter canadensis</i>	0.0282	0.0272	0.0256	-3.37	-9.25
<i>Campylobacter faecalis</i>	0.0083	0.0040	0.0026	-51.42	-68.84
<i>Dysgonomonas capnocytophagoideis</i>	0.0003	0.0001	0	-71.03	-100.00
<i>Dysgonomonas hofstadii</i>	0.0002	0.0001	0.0002	-64.64	-27.63
<i>Dysgonomonas wimpennyi</i>	9.6202	7.3915	4.95	-23.17	-48.53
<i>Fusobacterium naviforme</i>	0.0014	0.0011	0.0021	-20.78	53.50
<i>Helicobacter acinonychis</i>	0.0001	0	0.0001	-100.00	13.38
<i>Helicobacter anseris</i>	0.0002	0.0006	0.0001	222.31	-56.75
<i>Helicobacter baculiformis</i>	0.0007	0.0006	0.0003	-16.18	-50.74
<i>Helicobacter brantae</i>	0.0011	0.0002	0.0003	-85.51	-77.04
<i>Helicobacter canadensis</i>	0.0001	0	0.0001	-100.00	-3.32
<i>Helicobacter cholecystus</i>	0.0001	0	0.0001	-100.00	3.70
<i>Helicobacter equorum</i>	0.0007	0.0003	0.0002	-62.08	-75.23
<i>Helicobacter ganmani</i>	8.3468	0.7313	0.5761	-91.24	-93.10
<i>Helicobacter mastomyrinus</i>	1.7704	2.5918	1.3424	46.39	-24.18
<i>Helicobacter rappini</i>	0.0366	0.0279	0.0212	-23.90	-42.06
<i>Helicobacter rodentium</i>	0.0153	0.0010	0.0003	-93.31	-97.76
<i>Helicobacter salomonis</i>	0.0002	0	0.0001	-100.00	-44.44
<i>Helicobacter suis</i>	0.0002	0	0.0003	-100.00	47.15
<i>Helicobacter suncus</i>	0.4553	0.3365	0.2098	-26.10	-53.93
<i>Helicobacter trogonum</i>	0.0025	0.0012	0.0008	-50.33	-68.86
<i>Helicobacter winthamensis</i>	0.0001	0	0	-100.00	-100.00
<i>Porphyromonas cangingivalis</i>	0.0003	0.0000	0.0003	-100.00	1.18
<i>Porphyromonas canis</i>	1.3956	2.0155	1.1550	44.42	-17.24
<i>Porphyromonas cansulci</i>	0.0003	0.0005	0.0001	72.90	-71.62
<i>Porphyromonas catoniae</i>	0.0002	0.0001	0	-76.17	-100.00
<i>Porphyromonas circumdentaria</i>	0.0633	0.0621	0.0551	-1.87	-13.00
<i>Porphyromonas gulae</i>	0.0052	0.0079	0.0017	51.67	-66.36
<i>Streptococcus bovis</i>	0.0041	0.0023	0.0043	-43.55	5.17

Table S6: List of primers used in qPCR

Target gene	Nucleotide sequence of primer (5' to 3')	
	Forward	Reverse
β -actin	TGTTACCAACTGGGACGACA	CTGGGTCATCTTTTCACGGT
iNOS	GTTCTCAGCCCAACAATACAAGA	GTGGACGGGTCGATGTCAC
CXCL 10	CCAAGTGCTGCCGTCATTTTC	GGCTCGCAGGGATGATTTCAA
Arginase 1	TGGCTTGCGAGACGTAGAC	GCTCAGGTGAATCGGCCTTTT
MR	GCTGAATCCCAGAAATTCCGC	ATCACAGGCATACAGGGTGAC
Trem 2	CTGGAACCGTCACCATCACTC	CGAAACTCGATGACTCCTCGG
Ym 1	TTATCCTGAGTGACCCTTCTAAG	TCATTACCCTGATAGGCATAGG
IL-1 β	GCTGAAAGCTCTCCACCTCA	GGCCACAGGTATTTTGTCTG
IL-6	CTTCCATCCAGTTGCCTTCTTG	AATTAAGCCTCCGACTTGTGAAG
IL-12	ACTCTGCGCCAGAAACCTC	CACCCTGTTGATGGTCACGAC
IL-17	TTTAACTCCCTTGGCGCAAAA	CTTTCCTCCGCATTGACAC
IL-23	GCACCTGCTTGACTCTGACA	ATCCTCTGGCTGGAGGAGTT
IL-4	GGTCTCAACCCCCAGCTAGT	GCCGATGATCTCTCTCAAGTGAT
IL-10	GCTCTTACTGACTGGCATGAG	CGCAGCTCTAGGAGCATGTG
TNF- α	CAAATGGCCTCCCTCTCAT	CTCCTCCACTTGGTGGTTTG
INF- γ	ATGAACGCTACACACTGCATC	CCATCCTTTTGCCAGTTCCTC
FOXP3	CCCATCCCCAGGAGTCTTG	ACCATGACTAGGGGCACTGTA