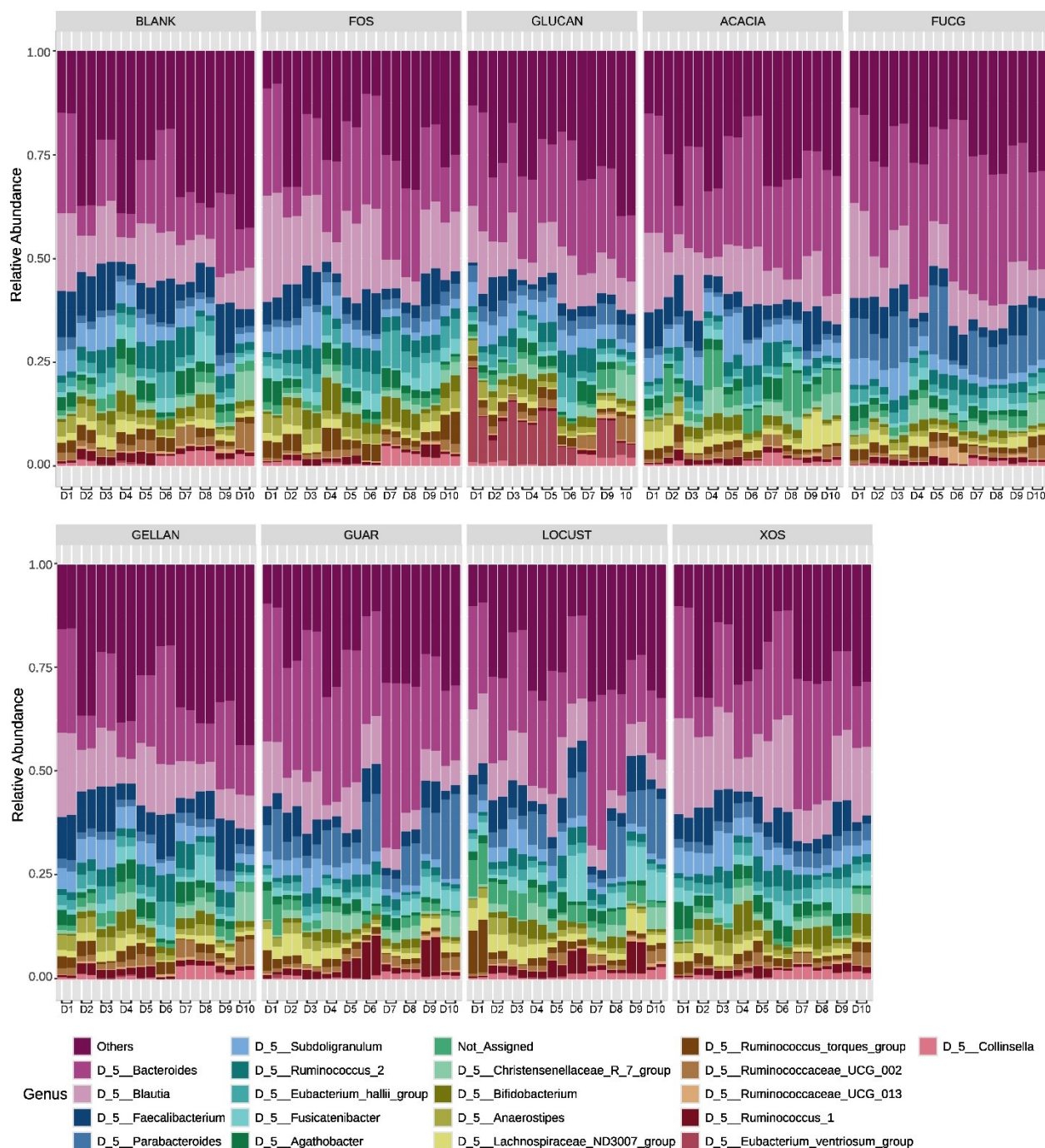
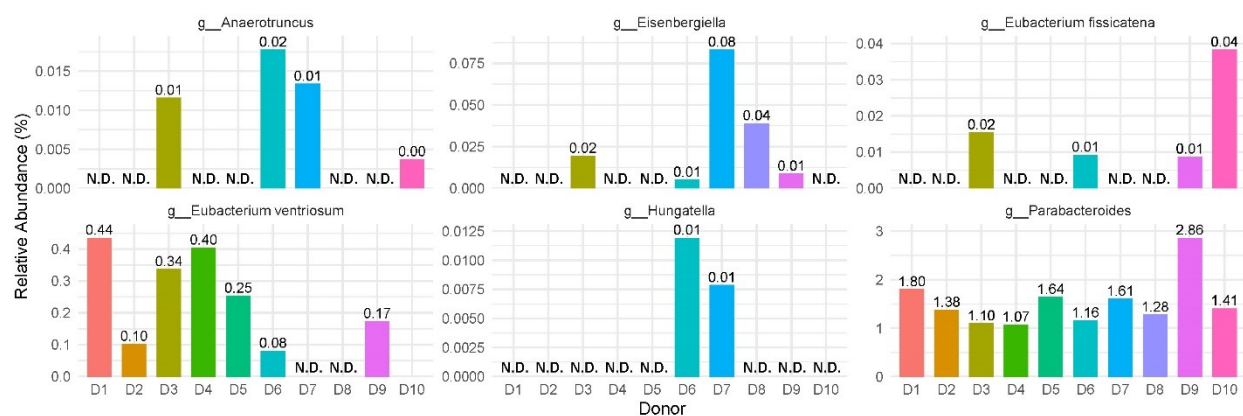
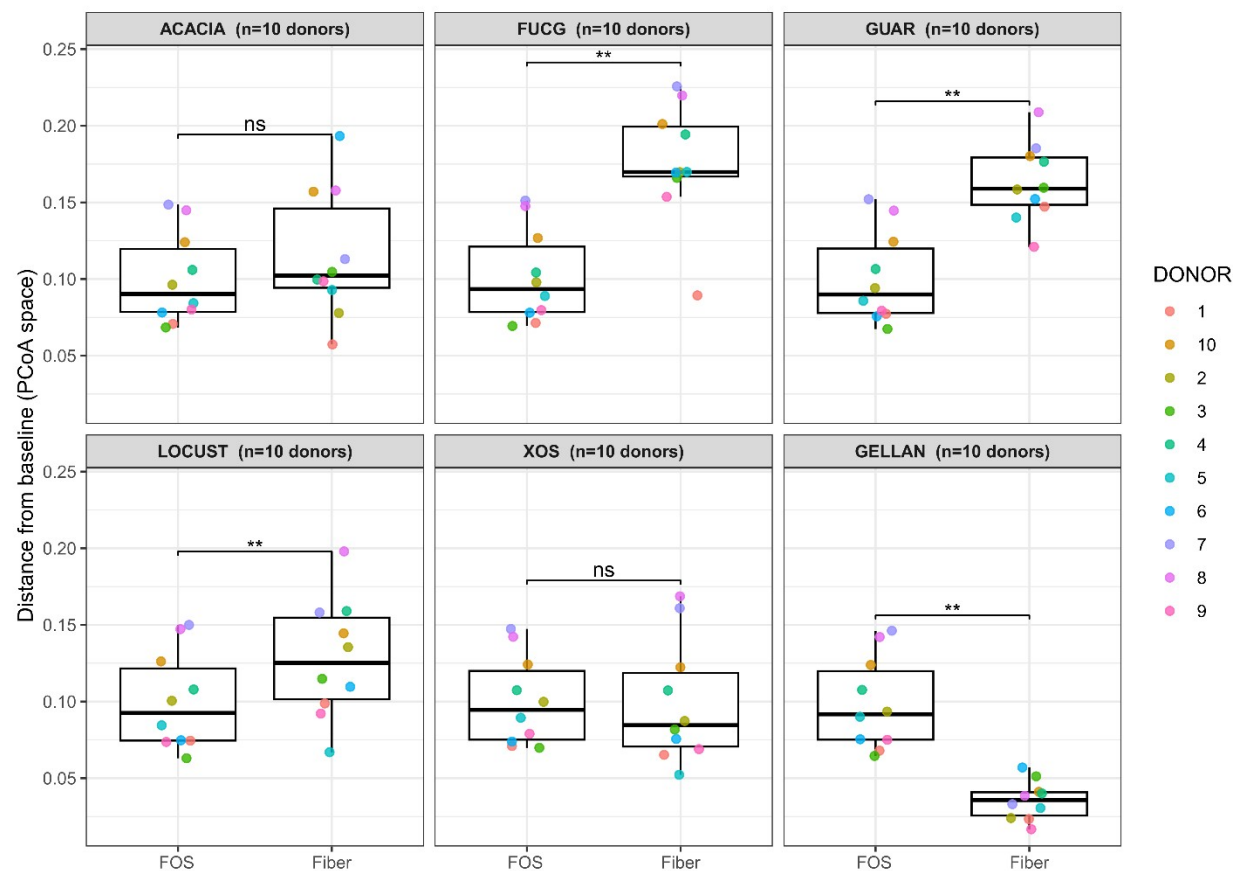




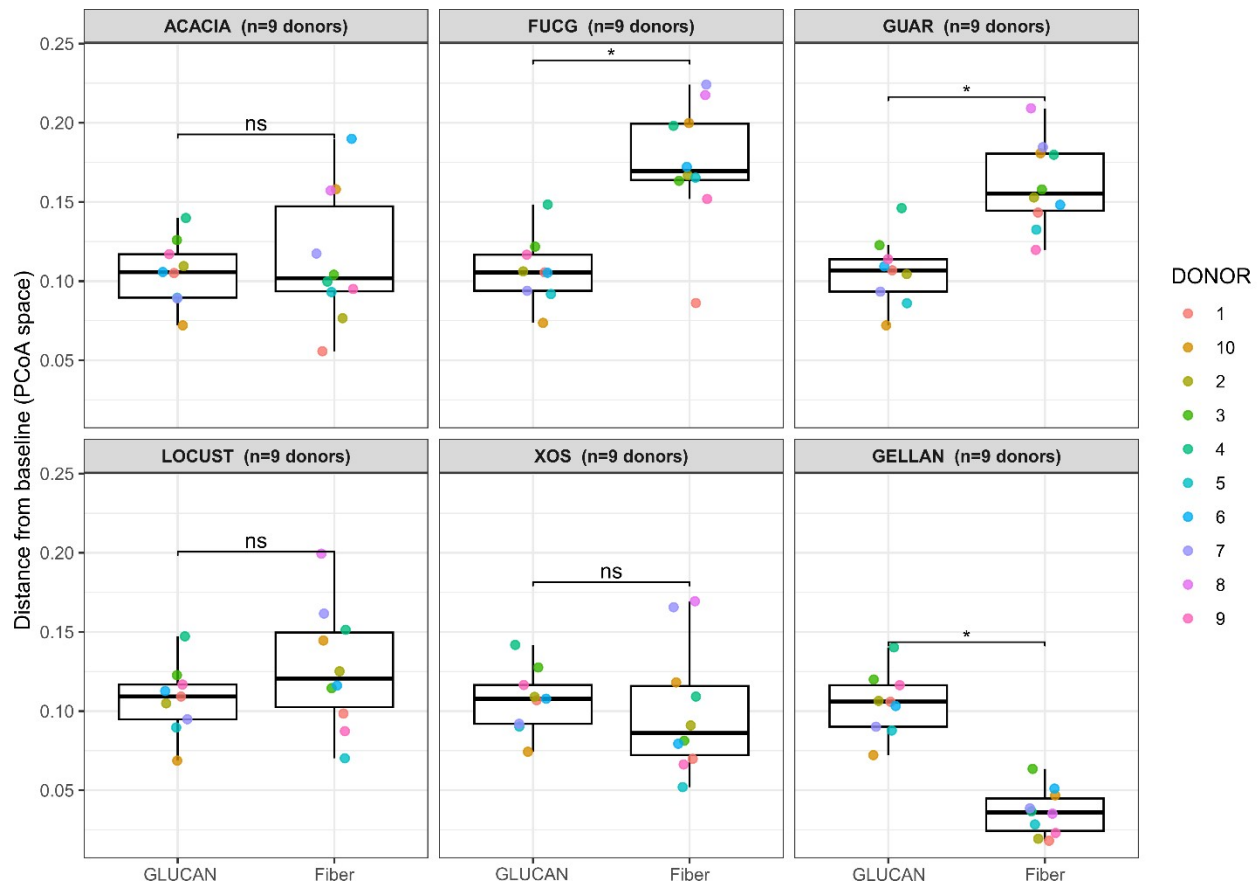
Supplementary Figure 1. Baseline and post-fermentation relative abundance profiles of fecal microbiota. Stacked bar plots showing relative abundances of microbial genera across all 10 donors for each fiber treatment and blank. Tested fibers included: ACACIA (acacia gum), FUCG (fucogalactan), GELLAN (gellan gum), GUAR (guar gum), LOCUST (locust bean gum), XOS (xylooligosaccharides), and the controls FOS (fructooligosaccharides), and GLUCAN (insoluble β -1,3-glucan from *Cookeina speciosa*).



Supplementary Figure 2. Detection of target taxa in baseline samples. Relative abundances of taxa identified by ANCOM-II in donor samples prior to fiber fermentation. Bars represent donors where the taxon was detected, with the exact relative abundance (%) indicated above each bar. "N.D." denotes cases where the taxon was not detected in that donor. Tested fibers included: ACACIA (acacia gum), FUCG (fucogalactan), GELLAN (gellan gum), GUAR (guar gum), LOCUST (locust bean gum), XOS (xylooligosaccharides), and the controls FOS (fructooligosaccharides), and GLUCAN (insoluble β -1,3-glucan from *Cookeina speciosa*).



Supplementary Figure 3. Distances from baseline in fiber-specific Weighted UniFrac PCoA spaces compared to FOS. Panels show the Euclidean distance between donor-specific centroids of BLANK samples and those after fermentation with the indicated fiber, calculated within the PCoA ordination generated for that fiber. Boxplots summarize the distribution of distances for BLANK→FOS and BLANK→ tested fiber. Tested fibers included: ACACIA (acacia gum), FUCG (fucogalactan), GELLAN (gellan gum), GUAR (guar gum), LOCUST (locust bean gum), and XOS (xylooligosaccharides). Statistical significance between control and fiber within each panel was assessed using paired Wilcoxon tests; ns = not significant, * $q < 0.05$, ** $q < 0.01$.



Supplementary Figure 4. Distances from baseline in fiber-specific Weighted UniFrac PCoA spaces compared to GLUCAN. Panels show the Euclidean distance between donor-specific centroids of BLANK samples and those after fermentation with the indicated fiber, calculated within the PCoA ordination generated for that fiber. Boxplots summarize the distribution of distances for BLANK→GLUCAN and BLANK→ tested fiber. Tested fibers included: ACACIA (acacia gum), FUCG (fucogalactan), GELLAN (gellan gum), GUAR (guar gum), LOCUST (locust bean gum) and XOS (xylooligosaccharides). Statistical significance between control and fiber within each panel was assessed using paired Wilcoxon tests; ns = not significant, * $q < 0.05$, ** $q < 0.01$.

Supplementary Table 1. Pairwise Kruskal-Wallis comparisons of Observed ASVs and Pielou's evenness between ACACIA, FUCG, GELLAN, GUAR, LOCUST, and XOS and the control groups (FOS, Blank, and GLUCAN).

Comparisons	Observed ASVs			Pielou's evenness		
	H	p value	q value	H	p value	q value
ACACIA vs. FOS (n=40)	0.703	0.402	0.971	0.749	0.387	0.559
FUCG vs. FOS (n=40)	1.482	0.223	0.957	4.007	0.045	0.116
GELLAN vs. FOS (n=40)	2.056	0.152	0.957	7.613	0.006	0.038
GUAR vs. FOS (n=40)	0.022	0.882	0.971	5.927	0.015	0.054
LOCUST vs. FOS (n=40)	0.001	0.978	0.998	0.293	0.589	0.776
XOS vs. FOS (n=40)	0.534	0.465	0.971	0.574	0.449	0.619
ACACIA vs. Blank (n=40)	0.022	0.882	0.971	3.285	0.070	0.141
FUCG vs. Blank (n=40)	0.001	0.978	0.998	16.027	0.000	0.001
GELLAN vs. Blank (n=40)	0.143	0.705	0.971	0.026	0.871	0.967
GUAR vs. Blank (n=40)	1.450	0.229	0.957	15.597	0.000	0.001
LOCUST vs. Blank (n=40)	1.113	0.291	0.957	7.171	0.007	0.039
XOS vs. Blank (n=40)	0.514	0.473	0.971	4.338	0.037	0.103
ACACIA vs. GLUCAN (n=37)	0.102	0.749	0.971	0.004	0.951	0.973
FUCG vs. GLUCAN (n=37)	0.335	0.562	0.971	6.094	0.014	0.052
GELLAN vs. GLUCAN (n=37)	0.864	0.353	0.957	1.638	0.201	0.338
GUAR vs. GLUCAN (n=37)	0.558	0.455	0.971	7.357	0.007	0.038
LOCUST vs. GLUCAN (n=37)	0.471	0.493	0.971	1.272	0.259	0.414
XOS vs. GLUCAN (n=37)	0.075	0.784	0.971	0.093	0.761	0.905

Significant FDR-P values ($q < 0.05$) are bolded and italicized.

Supplementary Table 2. Pairwise Permutational Multivariate Analyses of Variance (PERMANOVA) and Permutational Analysis of Multivariate Dispersions (PERMDISP) compared to the controls FOS, Blank and GLUCAN

Comparisons	PERMANOVA			PERMDISP		
	Pseudo-F	p value	q value	Pseudo-F	p value	q value
ACACIA vs. FOS (n=40)	3.272211	0.005	<i>0.007</i>	0.105	0.733	0.7330
FUCG vs. FOS (n=40)	15.005	0.001	<i>0.002</i>	1.452	0.193	0.204
GELLAN vs. FOS (n=40)	2.813	0.017	<i>0.026</i>	0.898	0.313	0.470
GUAR vs. FOS (n=40)	14.140	0.001	<i>0.002</i>	5.234	0.027	<i>0.041</i>
LOCUST vs. FOS (n=40)	5.184	0.001	<i>0.002</i>	1.602	0.210	0.260
XOS vs. FOS (n=40)	0.736	0.573	0.573	0.002	0.966	0.966
ACACIA vs. Blank (n=40)	5.918	0.001	<i>0.003</i>	2.394	0.118	0.272
FUCG vs. Blank (n=40)	20.701	0.001	<i>0.002</i>	5.981	0.015	<i>0.045</i>
GELLAN vs. Blank (n=40)	0.224	0.973	0.973	0.075	0.746	0.746
GUAR vs. Blank (n=40)	18.511	0.001	<i>0.002</i>	15.864	0.001	<i>0.003</i>
LOCUST vs. Blank (n=40)	8.952	0.001	<i>0.002</i>	1.208	0.260	0.260
XOS vs. Blank (n=40)	4.202	0.002	<i>0.006</i>	1.478	0.206	0.309
ACACIA vs. GLUCAN (n=37)	5.831	0.001	<i>0.001</i>	0.270	0.607	0.607
FUCG vs. GLUCAN (n=37)	14.556	0.001	<i>0.001</i>	0.079	0.764	0.764
GELLAN vs. GLUCAN (n=37)	4.332	0.001	<i>0.002</i>	3.654	0.055	0.083
GUAR vs. GLUCAN (n=37)	12.930	0.001	<i>0.002</i>	2.465	0.109	0.109
LOCUST vs. GLUCAN (n=37)	4.834	0.001	<i>0.002</i>	0.015	0.879	0.879
XOS vs. GLUCAN (n=37)	3.374	0.007	<i>0.007</i>	1.200	0.258	0.258

PERMANOVA and PERMDISP results are based on weighted UniFrac data. Significance values are based on 999 permutations and corrected for multiple testing using the Benjamini-Hochberg method ($q < 0.05$). Significant FDR-P values ($q < 0.05$) are bolded and italicized.