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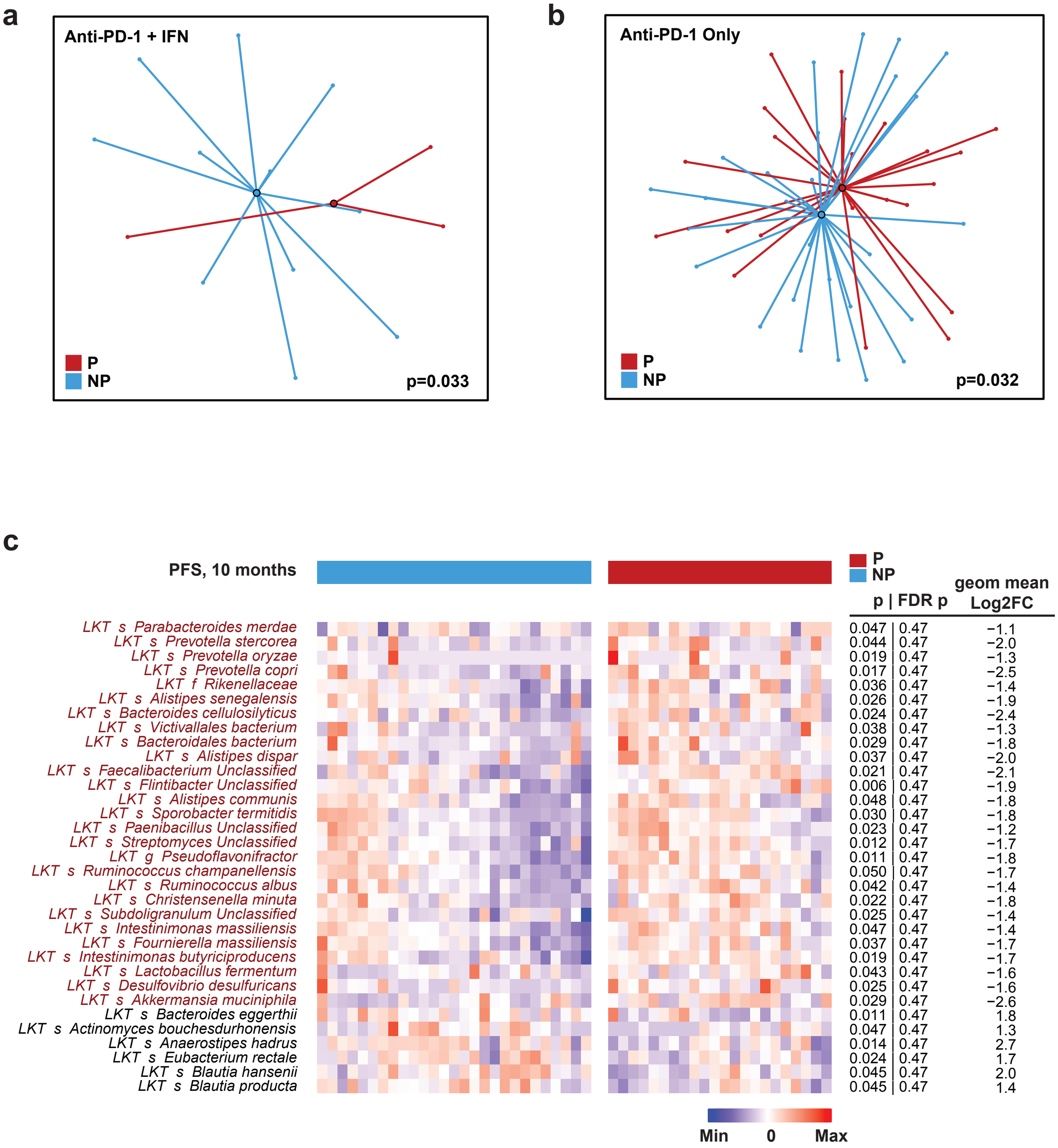
Supplementary information

Intestinal microbiota signatures of clinical response and immune-related adverse events in melanoma patients treated with anti-PD-1

SUPPLEMENTARY INFORMATION

Intestinal Microbiota Signatures of Clinical Response and Immune-related Adverse Events in Melanoma Patients treated with anti-PD-1

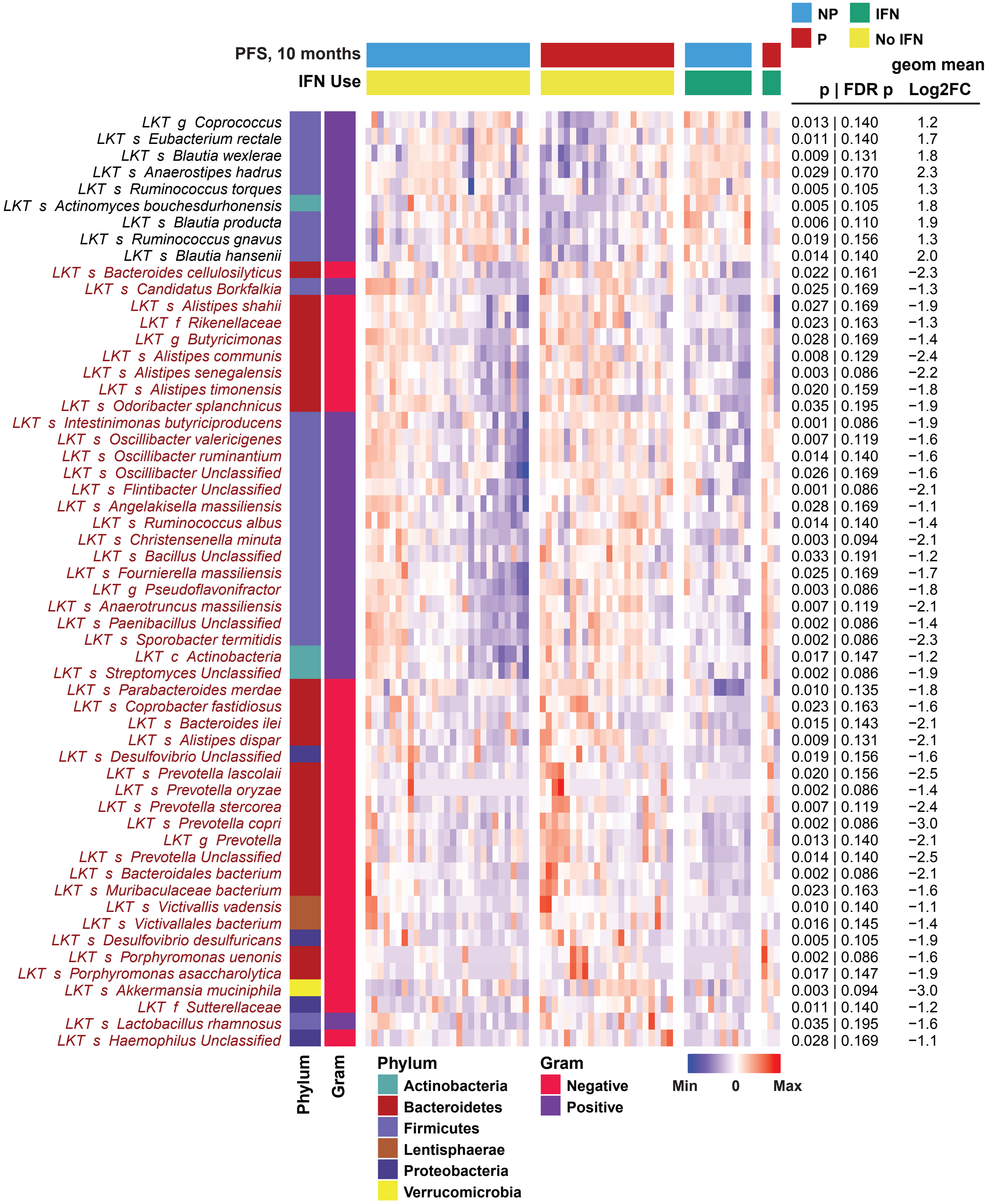
Supplementary Fig. 1 │ Analysis of microbiome composition in progressor vs non-progressor patients treated with anti-PD-1 alone or anti-PD-1 + pegIFN



Supplementary Fig. 1 │ Analysis of microbiome composition in progressor vs non-progressor patients treated with anti-PD-1 alone or anti-PD-1 + pegIFN.

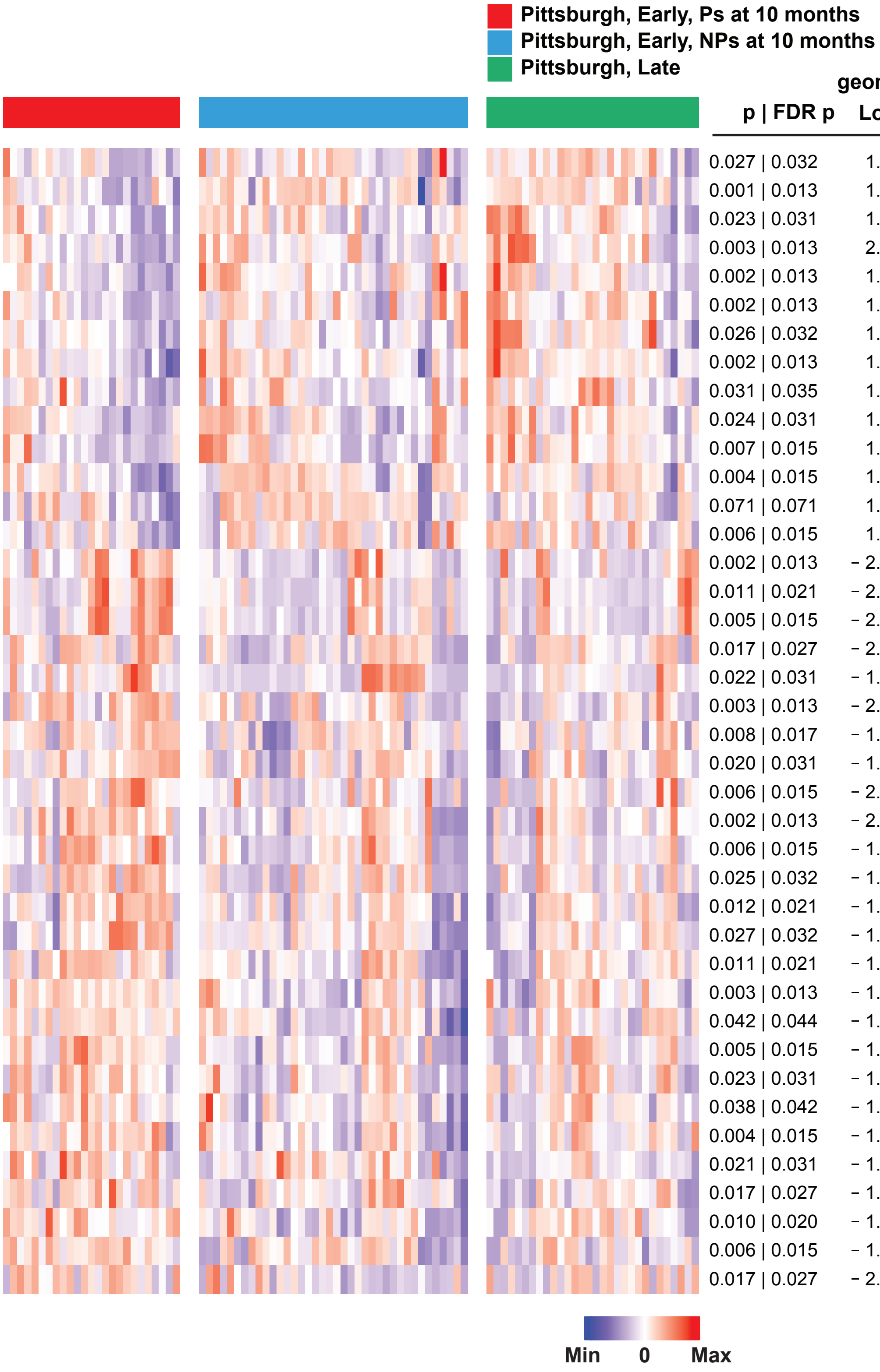
a and b. t-UMAP plots depicting differences of gut microbial taxa between non-progressor (NP) and progressor (P) patients at time of maximal difference from start of therapy (10 months) in metastatic melanoma patients treated with pembrolizumab/pegIFN **(a)** or anti-PD-1 alone **(b)**. Empty circles represent centroids, with lines connecting them to corresponding samples from each group. Two-tailed p values were calculated using PERMANOVA. **c.** Heatmap of hierarchically clustered differentially abundant taxa ($p<0.05$, FC>2) from anti-PD-1 alone cohort. Each column represents an independent melanoma patient, while each row represents differentially abundant bacteria. Statistical significance was calculated using two-tailed Mann-Whitney U test.

Supplementary Fig. 2 │ Comparative analysis of microbiome composition in progressor vs non-progressor patients treated with anti-PD-1 alone or anti-PD-1 + pegIFN



Supplementary Fig. 2 │ Comparative analysis of microbiome composition in progressor vs non-progressor patients treated with anti-PD-1 alone or anti-PD-1 + pegIFN. Metagenomic shotgun sequencing of fecal microbiota samples identifies differentially abundant taxa in progresor (P) vs. non-progressor (NP) patients at 10 months from start of therapy. Heatmap shows differentially abundant taxa (FDR < 0.2 and FC > 2). Columns denote patients grouped by progression status and single or dual therapy and clustered within each group; rows denote bacterial taxa enriched (black) or depleted (red) in NPs versus Ps, clustered based on microbiota composition. Statistical significance was calculated by two-tailed Mann-Whitney U test.

Supplementary Fig. 3 │Comparative analysis of microbiome composition in progressor vs non-progressor patients from early and late Pittsburgh cohorts

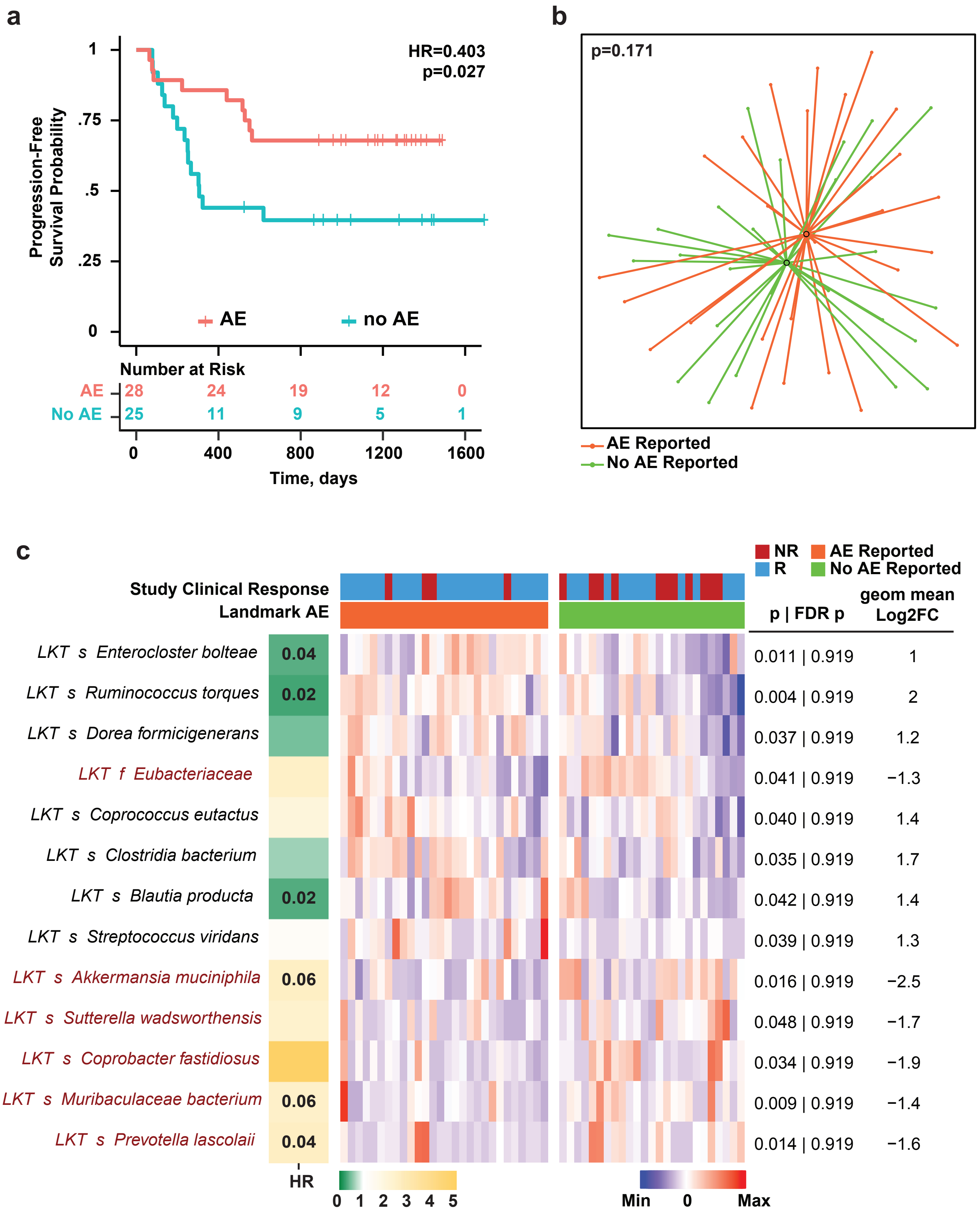


Cohorts	p | FDR p	geom mean Log2FC
LKT s Actinomyces Unclassified	0.027 | 0.032	1.2
LKT s Ruminococcus torques	0.001 | 0.013	1.5
LKT s Faecalimonas umbilicata	0.023 | 0.031	1.3
LKT s Blautia hansenii	0.003 | 0.013	2.3
LKT s Blautia producta	0.002 | 0.013	1.8
LKT s Ruminococcus gnavus	0.002 | 0.013	1.5
LKT s Coprococcus Unclassified	0.026 | 0.032	1.4
LKT s Lachnospiraceae bacterium	0.002 | 0.013	1.1
LKT s Tyzzerella nexilis	0.031 | 0.035	1.3
LKT g Anaerostipes	0.024 | 0.031	1.3
LKT s Anaerostipes caccae	0.007 | 0.015	1.6
LKT s Blautia wexlerae	0.004 | 0.015	1.8
LKT s Anaerostipes hadrus	0.071 | 0.071	1.8
LKT s Eubacterium rectale	0.006 | 0.015	1.7
LKT s Prevotella copri	0.002 | 0.013	− 2.6
LKT s Prevotella Unclassified	0.011 | 0.021	− 2.4
LKT g Prevotella	0.005 | 0.015	− 2.1
LKT s Alistipes communis	0.017 | 0.027	− 2.0
LKT s Candidatus Borkfalkia	0.022 | 0.031	− 1.4
LKT s Bacteroides cellulosilyticus	0.003 | 0.013	− 2.6
LKT s Parabacteroides merdae	0.008 | 0.017	− 1.7
LKT s Bacteroides caccae	0.020 | 0.031	− 1.7
LKT s Alistipes dispar	0.006 | 0.015	− 2.0
LKT s Alistipes senegalensis	0.002 | 0.013	− 2.0
LKT s Alistipes timonensis	0.006 | 0.015	− 1.8
LKT s Odoribacter splanchnicus	0.025 | 0.032	− 1.8
LKT s Alistipes shahii	0.012 | 0.021	− 1.9
LKT f Rikenellaceae	0.027 | 0.032	− 1.1
LKT s Oscillibacter ruminantium	0.011 | 0.021	− 1.4
LKT s Intestinimonas butyriciproducens	0.003 | 0.013	− 1.6
LKT s Oscillibacter Unclassified	0.042 | 0.044	− 1.4
LKT s Streptomyces Unclassified	0.005 | 0.015	− 1.5
LKT s Anaerotruncus massiliensis	0.023 | 0.031	− 1.6
LKT s Fournierella massiliensis	0.038 | 0.042	− 1.4
LKT g Pseudoflavonifractor	0.004 | 0.015	− 1.4
LKT f Eubacteriaceae	0.021 | 0.031	− 1.4
LKT s Eubacterium siraeum	0.017 | 0.027	− 1.7
LKT s Flintibacter Unclassified	0.010 | 0.020	− 1.6
LKT s Faecalibacterium Unclassified	0.006 | 0.015	− 1.9
LKT s Akkermansia muciniphila	0.017 | 0.027	− 2.2

Supplementary Fig. 3 │Comparative analysis of microbiome composition in progressor vs non-progressor patients from early and late Pittsburgh cohorts.

Metagenomic shotgun sequencing of fecal microbiota samples identifies differentially abundant taxa in progressor (P) vs. non-progressor (NP) patients. Heatmap shows the top 40 differentially abundant taxa identified. Columns denote patients grouped by progression status at 10 months and time of feces collection, and clustered within each group; rows denote bacterial taxa enriched (black font) or depleted (red font) in NPs versus Ps, clustered based on microbiota composition. Statistical significance was calculated by two-tailed Mann-Whitney U test. Microbiota composition of non-progressor patients in the Pittsburgh cohort whose stool samples were collected 4 to 41 months after initiation of the therapy was enriched for similar bacterial taxa as observed in the initial microbiome of patients who did not progress at 10 months.

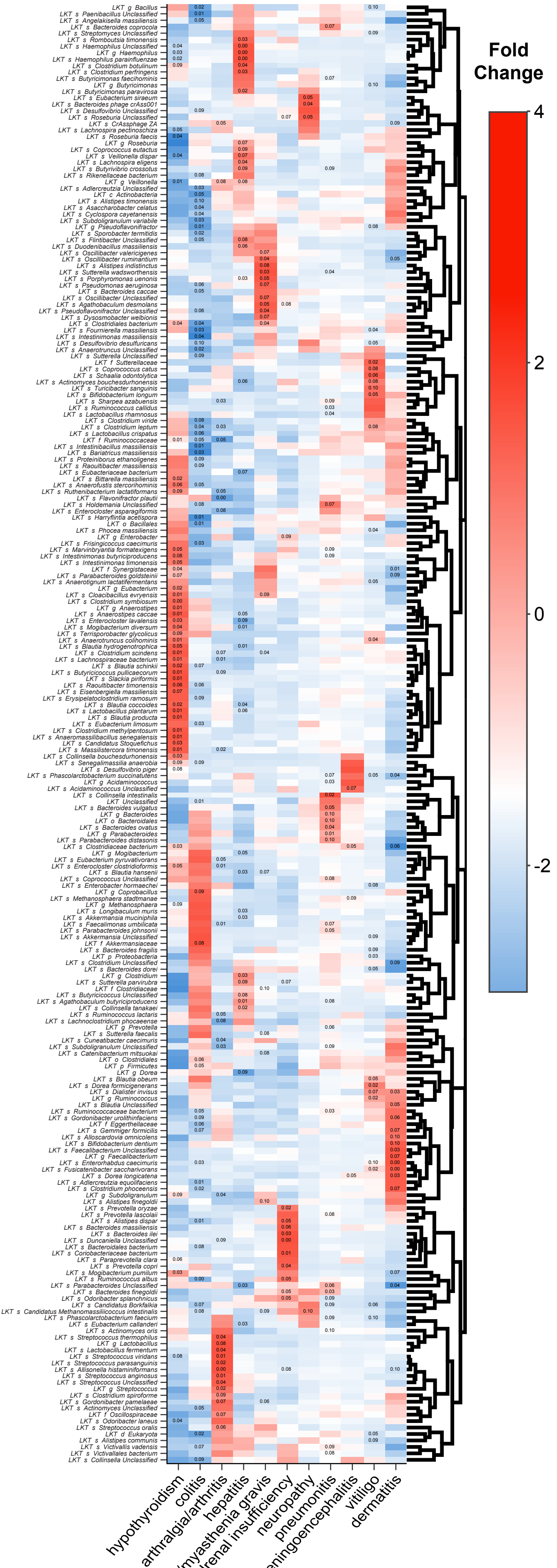
Supplementary Fig. 4 | Relation of immune-related adverse effects to progression free survival and microbiome composition



Supplementary Fig. 4 │ Relation of immune-related adverse effects to progression free survival and microbiome composition.

Landmark analysis using patients who survived for at least 10 months after initiation of therapy. An immune-related adverse effect (irAE) was considered to be present only if was developed before the landmark date. **a**. Kaplan-Meier plot and Cox regression analysis of progression-free survival (PFS) for patients with and without irAE at landmark. Hazard Ratio (HR) and score (logrank) test two-tailed p-value from Cox proportional hazards regression analysis. **b.** tUMAP plot depicting compositional differences between melanoma patients (landmark time 10 months) who developed grade 1-4 irAEs or not. Two-tailed p value was calculated using PERMANOVA. **c**. Heatmap of differentially abundant taxa ($p<0.05$ and FC >2) in patients (landmark time 10 months) who developed grade 1-4 irAEs or not. irAE severity was graded with CTCAE v5.0. The column on the left shows HR and Storey's q-value (if < 0.1) for each last known taxon (LKT). Columns in the heatmap depict patients grouped by reported or non-reported irAE and clustered within corresponding groups based on gut microbiome composition. Rows depict bacterial taxa enriched (black) or depleted (red) in melanoma patients with irAEs (grade 1-4) and clustered based on gut microbiota composition. Statistical significance was calculated by two-tailed Mann-Whitney U test.

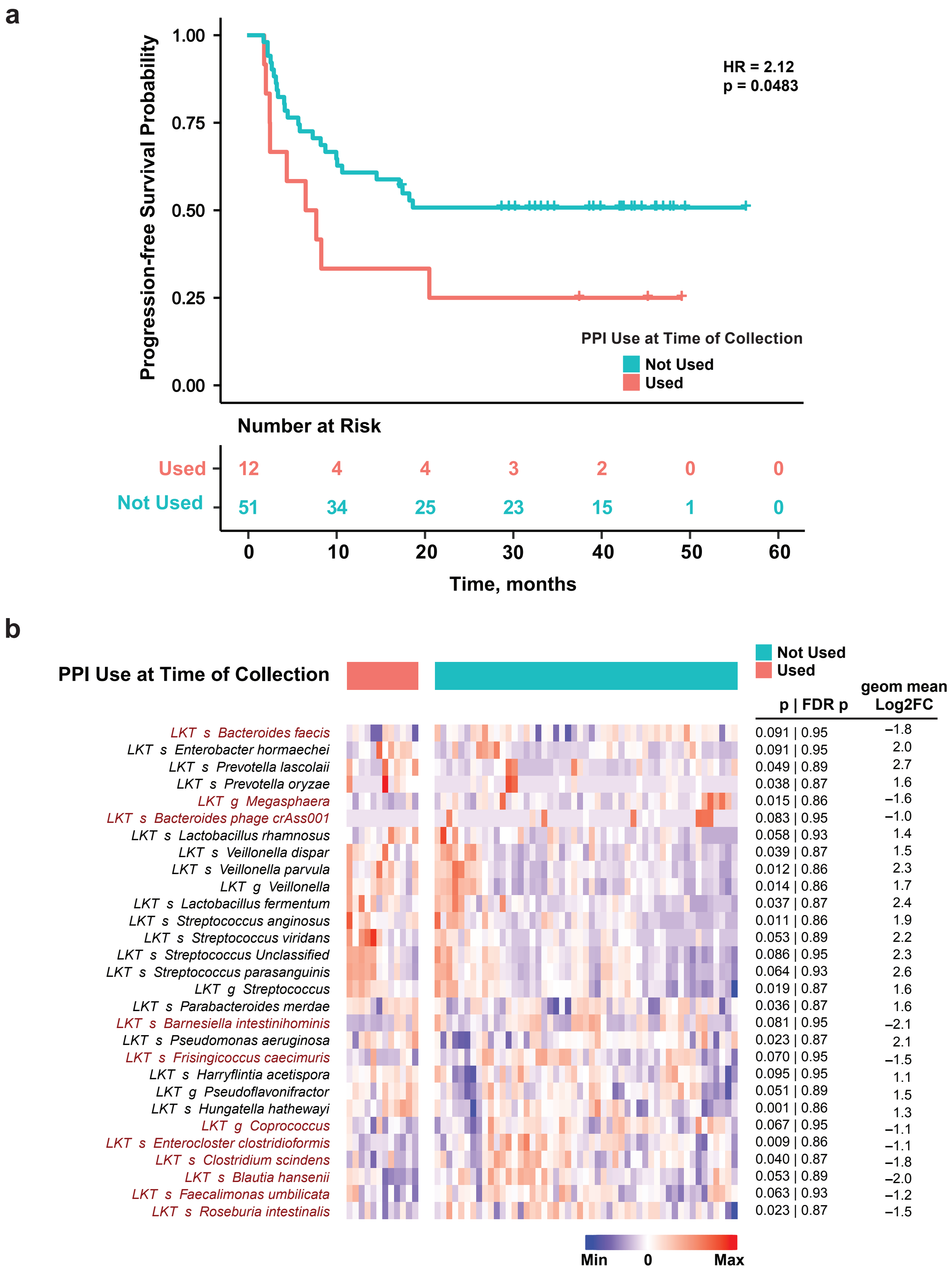
Supplementary Fig. 5 │ Complete list of taxa associated with various immune-related adverse effects in melanoma patients treated with anti-PD-1 immunotherapy in Pittsburgh cohort



Supplementary Fig. 5 │ Complete list of taxa associated with various immune-related adverse effects in melanoma patients treated with anti-PD-1 immunotherapy in Pittsburgh cohort.

Heatmap depicts metagenomic compositional differences between patients with distinct irAEs using scaled fold differences (high – red; low – blue) in abundances of specific bacteria between patients with the indicated type of irAE (x axis) as compared to patients with other irAEs. Values in individual cells represent unadjusted p values calculated using two-tailed Mann-Whitney U test with p values <0.1 displayed within cells.

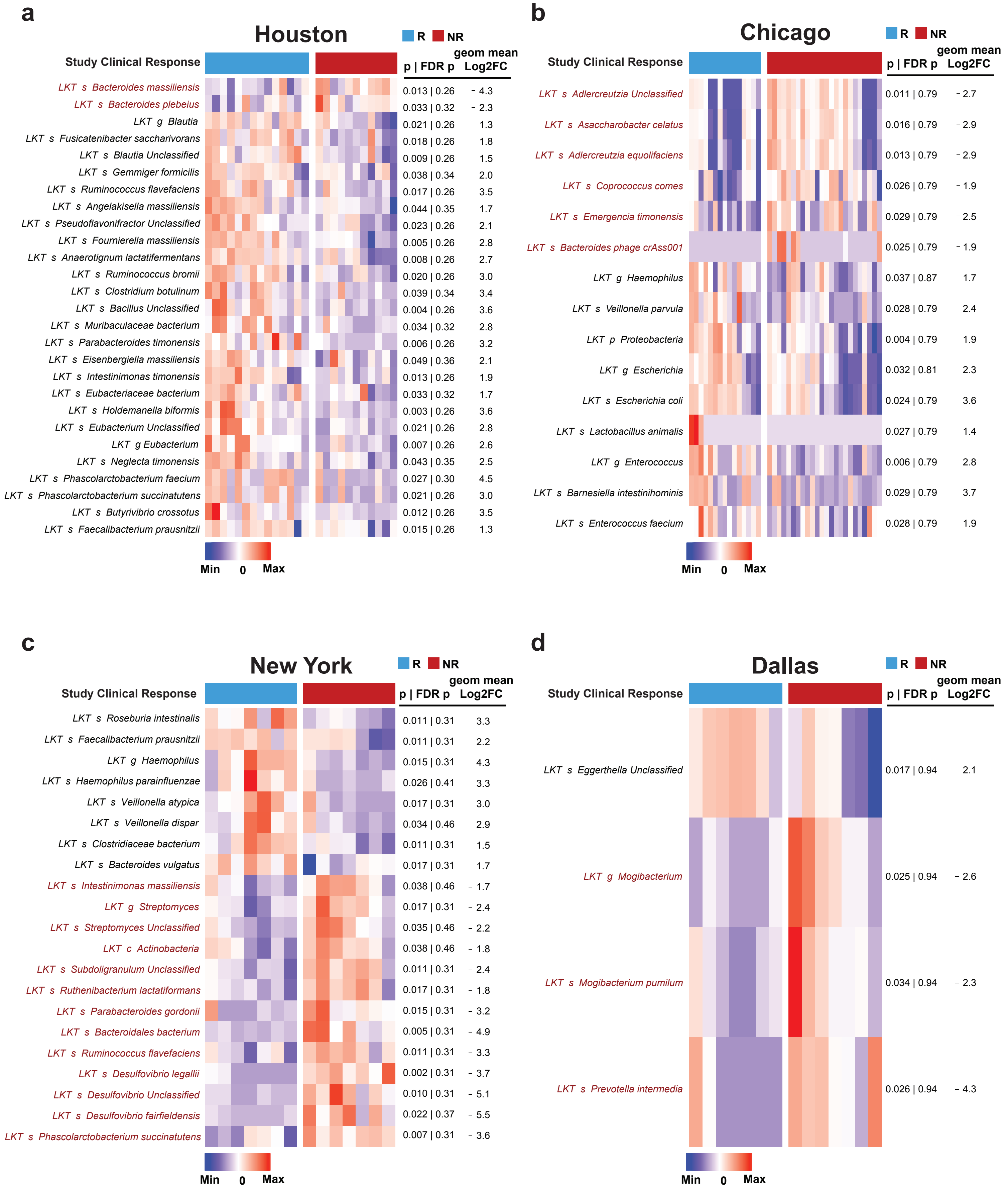
Supplementary Fig. 6 | Proton pump inhibitor exposure is associated with differential abundance of select taxa and shorter progression free survival in Pittsburgh cohort



Supplementary Fig. 6 │ Proton pump inhibitor exposure is associated with differential abundance of select taxa and shorter progression free survival in Pittsburgh cohort.

a. Effect of proton pump inhibitor (PPI) exposure at the time of stool collection upon progression free survival using Cox proportional hazard model in samples from Pittsburgh. The number of people at risk in either group is shown below each panel. Hazard Ratio (HR) and score (logrank) test two-tailed p-value from Cox proportional hazards regression analysis. **b.** Heatmap shows hierarchically clustered differentially abundant taxa ($p<0.1$, $FC>2$) between patients with PPI exposure as compared to patients without PPI exposure. Each column represents an independent melanoma patient, while each row represents differentially abundant bacteria. Statistical significance was calculated by two-tailed Mann-Whitney U test.

Supplementary Fig. 7 | Heatmaps of differentially abundant taxa analyzed using the same bioinformatic pipeline in four previously published cohorts of melanoma patients treated with anti-PD-1 immunotherapy

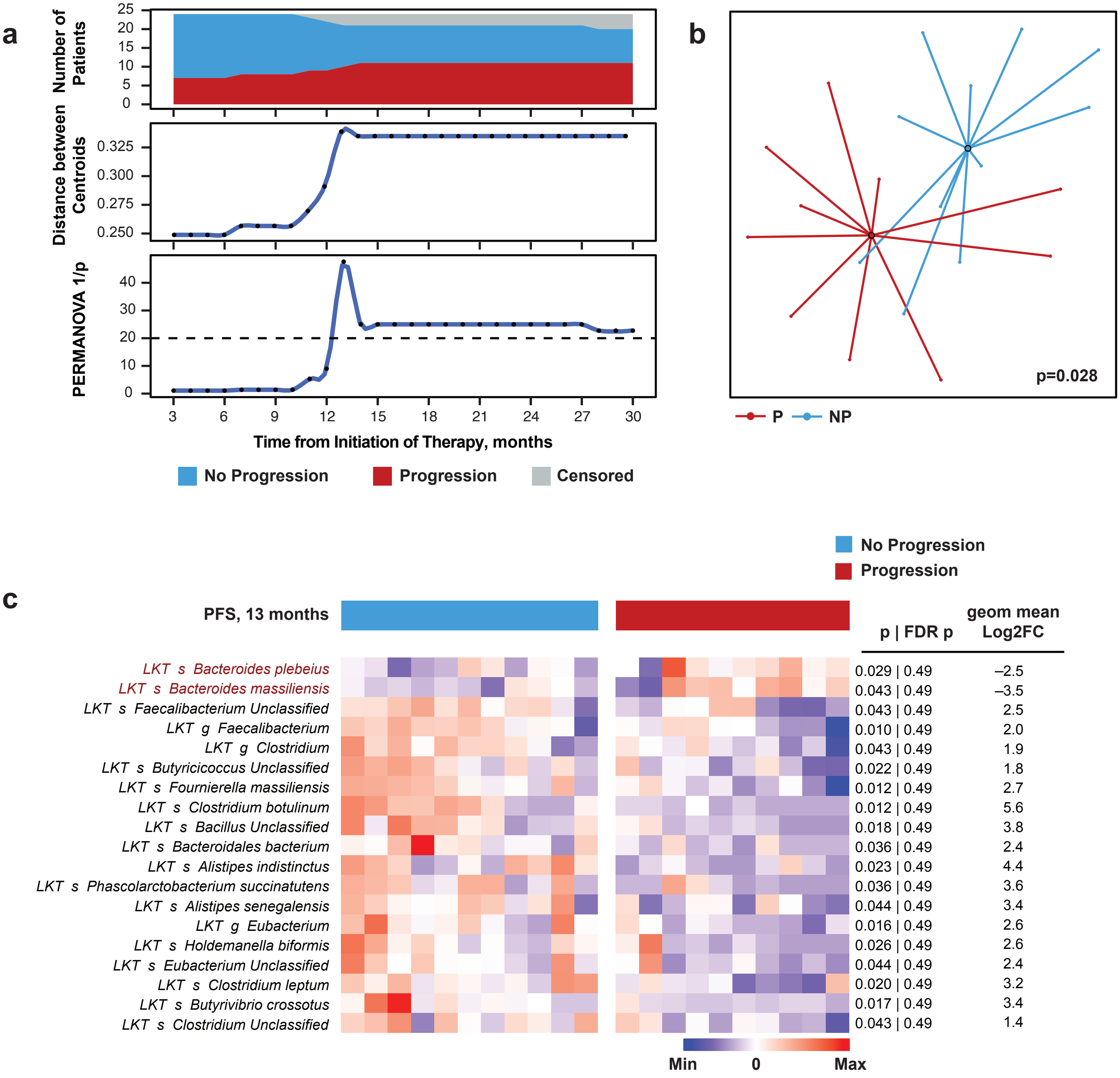


Supplementary Fig. 7 │ Heatmaps of differentially abundant taxa analyzed using the same bioinformatic pipeline in four previously published cohorts of melanoma patients treated with anti-PD-1 immunotherapy.

a-d. Each heatmap depicts differentially abundant taxa identified by metagenomic shotgun sequencing ($p<0.05$, $FC>2$) from four independent melanoma cohorts (**a** – Houston; **b** – Chicago; **c** – New York; **d** – Dallas). Columns denote patients grouped by response status. Response to therapy in the published cohorts was determined as described in each study (**Supplementary Table S3**). Rows denote bacterial taxa enriched (black) or depleted (red) in responder (R) vs non-responder (NR) patients clustered based on microbiota composition.

Statistical significance was calculated by two-tailed Mann-Whitney U test.

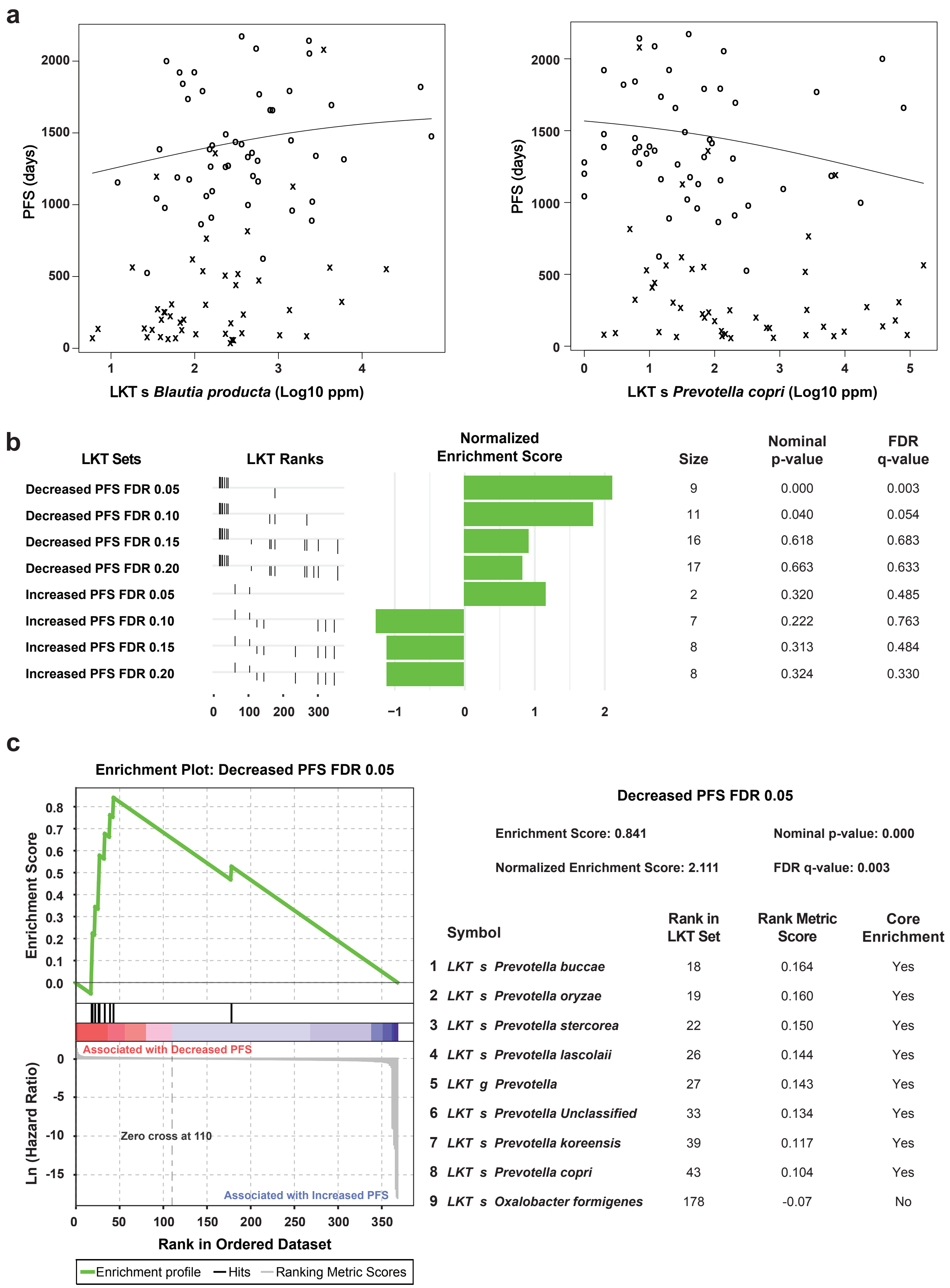
Supplementary Fig. 8 | Compositional differences in the gut microbiome of anti-PD-1 treated melanoma patients from Houston are associated with progression free survival.



Supplementary Fig. 8 │ Compositional differences in the gut microbiome of anti-PD-1 treated melanoma patients from Houston cohort are associated with progression free survival.

a. Evaluation of effects of initial (pre-treatment up to 3 months on treatment) fecal microbiome composition (metagenomic shotgun sequencing) upon investigator-assessed response to anti-PD-1 therapy. Top panel depicts number of patients on follow-up at each timepoint in relation to response status. Middle panel shows the distance in composition of the initial microbiome between progressor (P) and non-progressor (NP) patients identified at each treatment visit. Distances between the P and NP group centroids was calculated at each timepoint as the Euclidean distance between the two centroids in all component dimensions of Bray-Curtis distance principal component analysis. Bottom panel shows the significance (two-tailed p-value) of the difference at each time point using PERMANOVA 1/p of Bray-Curtis distance. **b.** t-UMAP plot depicting fecal microbiota compositional differences between NPs and Ps at time of maximal difference from start of therapy (13 months). Empty circles represent centroids with lines connecting them to corresponding samples from each group. Two-tailed p-values were calculated using PERMANOVA. **c.** Metagenomic shotgun sequencing of fecal microbiota samples identifies differentially abundant taxa in Ps vs. NPs at 13 months from start of therapy. Heatmap shows differentially abundant taxa identified by metagenomic shotgun sequencing ($p<0.05$ and FC >2). Columns denote patients grouped by progression status and clustered within NP/P groups; rows denote bacterial taxa enriched (black) or depleted (red) in NPs versus Ps clustered based on microbiota composition. Statistical significance was calculated by two-tailed Mann-Whitney U test.

Supplementary Fig. 9 │ Correlation of microbial abundance with progression free survival and in-silico validation of significant microbes in an independent cohort



LKT Sets	Size	Nominal p-value	FDR q-value
Decreased PFS FDR 0.05	9	0.000	0.003
Decreased PFS FDR 0.10	11	0.040	0.054
Decreased PFS FDR 0.15	16	0.618	0.683
Decreased PFS FDR 0.20	17	0.663	0.633
Increased PFS FDR 0.05	2	0.320	0.485
Increased PFS FDR 0.10	7	0.222	0.763
Increased PFS FDR 0.15	8	0.313	0.484
Increased PFS FDR 0.20	8	0.324	0.330

Decreased PFS FDR 0.05

Enrichment Score: 0.841

Nominal p-value: 0.000

Normalized Enrichment Score: 2.111

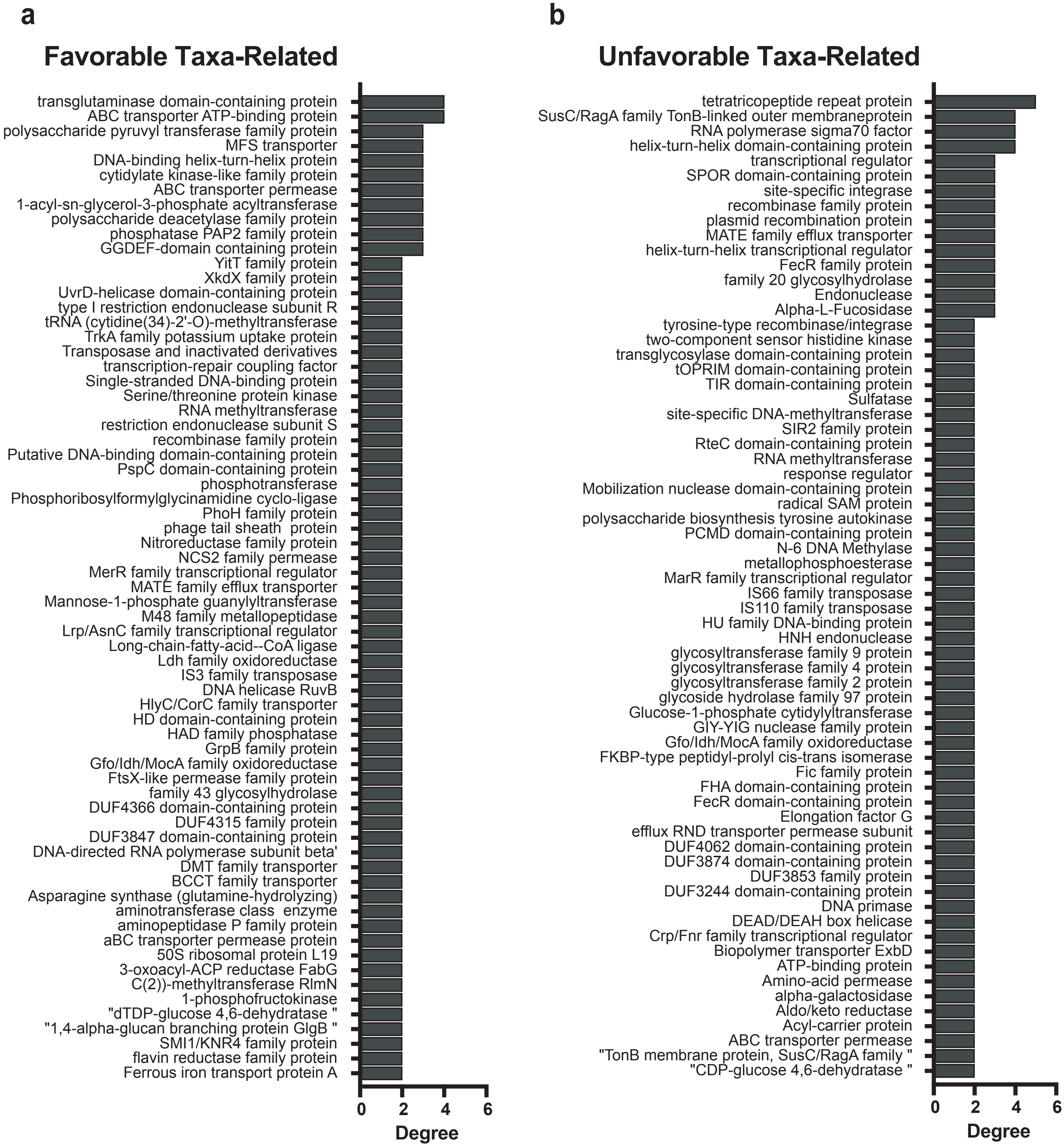
FDR q-value: 0.003

	Symbol	Rank in LKT Set	Rank Metric Score	Core Enrichment
1	*LKT s Prevotella buccae*	18	0.164	Yes
2	*LKT s Prevotella oryzae*	19	0.160	Yes
3	*LKT s Prevotella stercorea*	22	0.150	Yes
4	*LKT s Prevotella lascolaii*	26	0.144	Yes
5	*LKT g Prevotella*	27	0.143	Yes
6	*LKT s Prevotella Unclassified*	33	0.134	Yes
7	*LKT s Prevotella koreensis*	39	0.117	Yes
8	*LKT s Prevotella copri*	43	0.104	Yes
9	*LKT s Oxalobacter formigenes*	178	-0.07	No

Supplementary Fig. 9 │ Correlation of microbial abundance with progression free survival and in-silico validation of significant microbes in an independent cohort.

a. Scatterplot of microbial abundance vs progression free survival (PFS) for two representative microbes from the Pittsburgh cohort. The spline represents a smooth, nonparametric estimate of the median PFS as a function of last known taxon (LKT) abundance, calculated using the sm-survival algorithm. **x** indicates PFS; **o** indicates time of last observation for patients who did not progress. **b.** and **c.** Gene set enrichment analysis (GSEA) to check whether the significant taxa at different FDR cutoffs ("LKT sets") at different FDR cutoffs (0.05, 0.10, 0.15, 0.20) from one cohort (Pittsburgh) are enriched ($q<0.05$) in an independent cohort (Houston) pre-ranked as per beta from CV Cox Regression (Supplementary Table 10). Only unfavorable LKTs (microbes associated with shorter PFS) from one cohort were enriched in the independent cohort; and increasing FDR cutoff for favorable LKTs only introduced noise without increasing significance. **c.** Enrichment plot and list of LKTs from the leading edge for the most significant LKT set from (**b**).

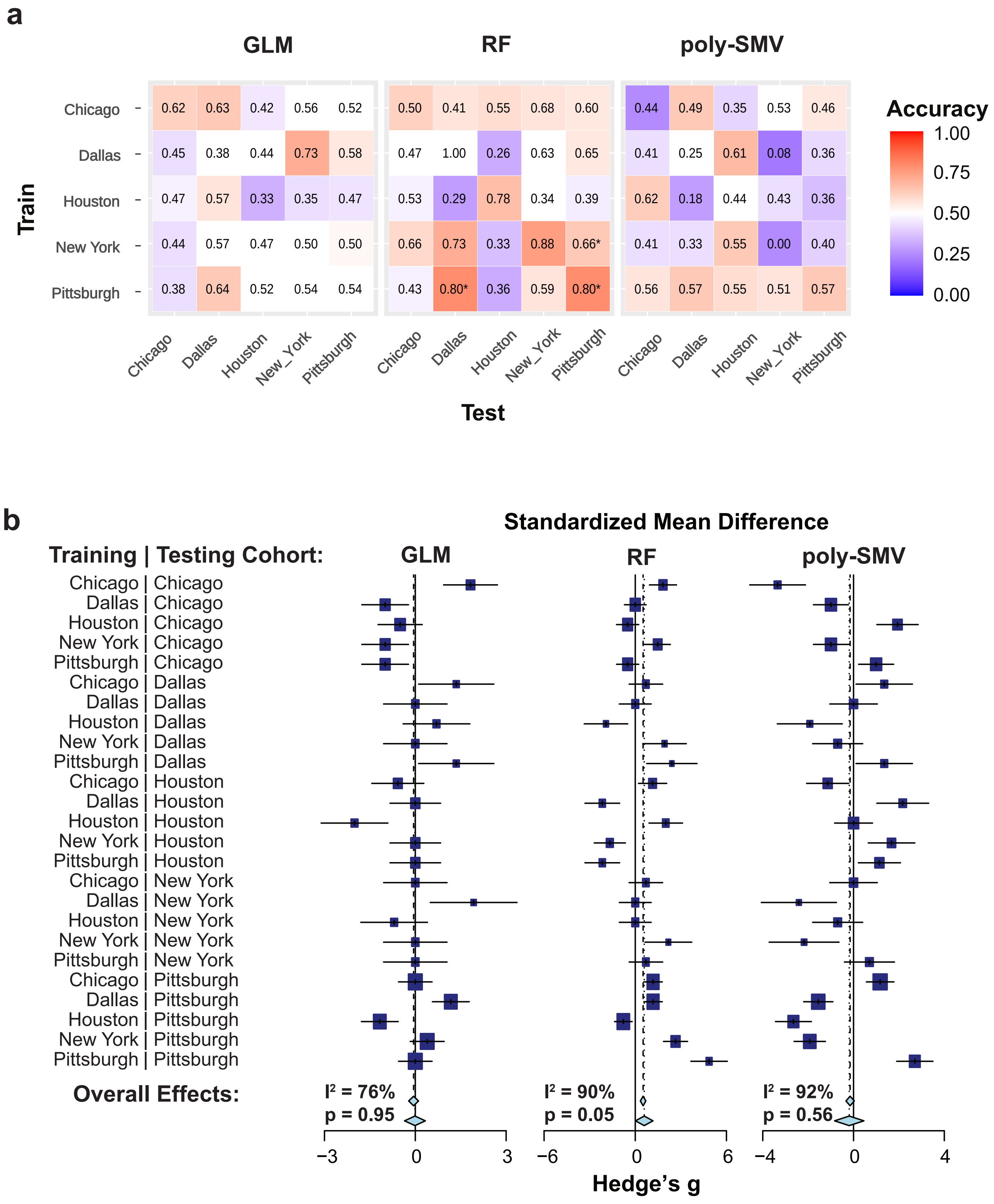
Supplementary Fig. 10 │ Microbial genes differentially enriched in responder and non-responder patients by fecal microbiome meta-analysis of five independent cohorts of anti-PD-1 treated melanoma patients



Supplementary Fig. 10 │ Microbial genes differentially enriched in responder and non-responder patients by fecal microbiome meta-analysis of five independent cohorts of anti-PD-1 treated melanoma patients.

After removing study-related batch effects using ComBat R package, the resultant batch-corrected dataset was further analyzed using linear discriminant analysis effect size (LEfSe).

Supplementary Fig. 11 │ Machine learning models trained on one cohort and tested on another show limited predictive ability



GLM

Train \ Test	Chicago	Dallas	Houston	New_York	Pittsburgh
Chicago	0.62	0.63	0.42	0.56	0.52
Dallas	0.45	0.38	0.44	0.73	0.58
Houston	0.47	0.57	0.33	0.35	0.47
New York	0.44	0.57	0.47	0.50	0.50
Pittsburgh	0.38	0.64	0.52	0.54	0.54

RF

Train \ Test	Chicago	Dallas	Houston	New_York	Pittsburgh
Chicago	0.50	0.41	0.55	0.68	0.60
Dallas	0.47	1.00	0.26	0.63	0.65
Houston	0.53	0.29	0.78	0.34	0.39
New York	0.66	0.73	0.33	0.88	0.66*
Pittsburgh	0.43	0.80*	0.36	0.59	0.80*

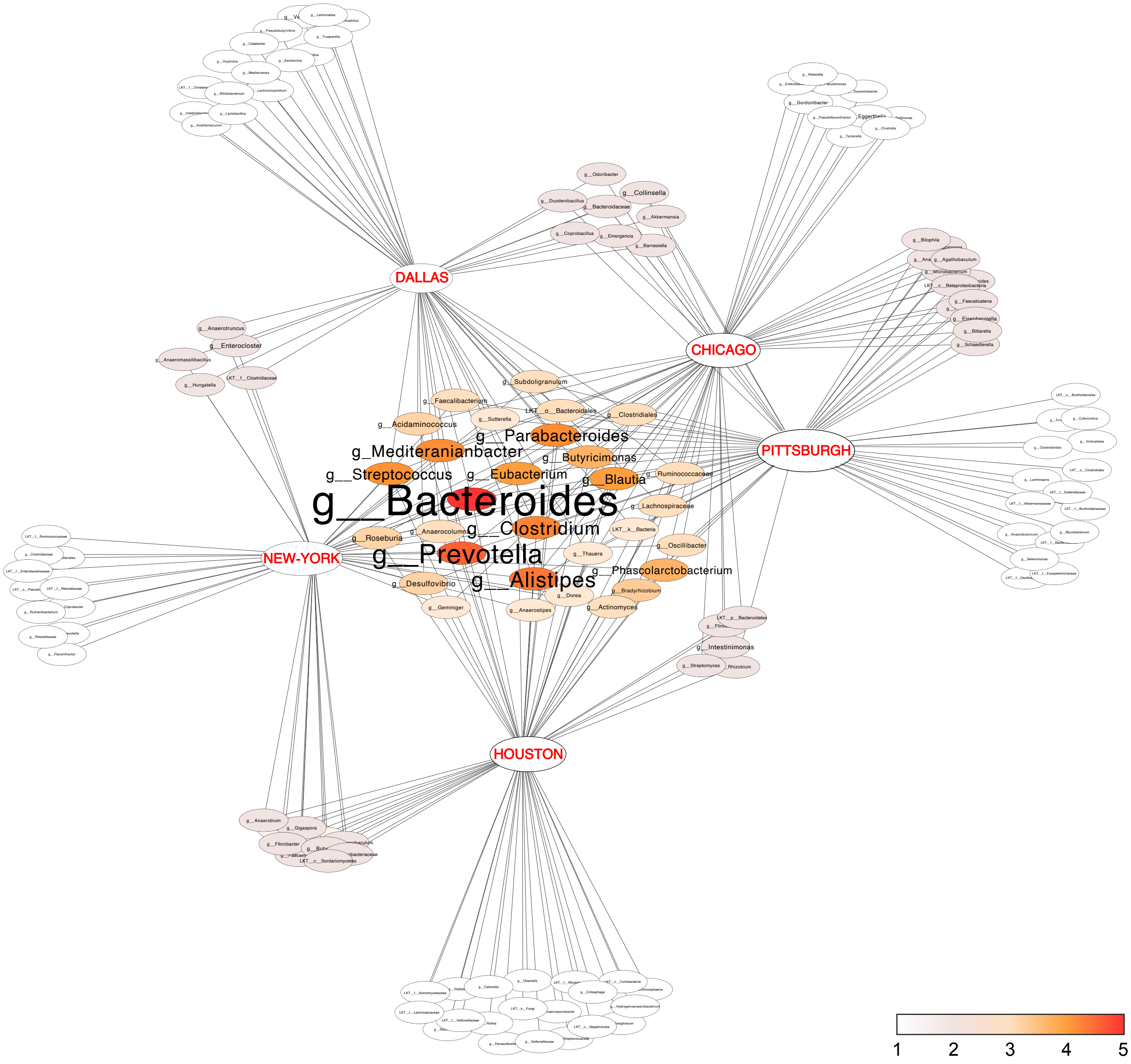
poly-SMV

Train \ Test	Chicago	Dallas	Houston	New_York	Pittsburgh
Chicago	0.44	0.49	0.35	0.53	0.46
Dallas	0.41	0.25	0.61	0.08	0.36
Houston	0.62	0.18	0.44	0.43	0.36
New York	0.41	0.33	0.55	0.00	0.40
Pittsburgh	0.56	0.57	0.55	0.51	0.57

Supplementary Fig. 11 │ Machine learning models trained on one cohort and tested on another show limited predictive ability.

a. Heatmap showing all 25 combinations of train and test cohorts for each machine learning method [generalized linear model (GLM), random forest (RF), polynomial support vector machine (poly-SMV)]. Accuracies are shown by color scale, and area under the curve (AUC) by numbers with an asterisk if the result is significant ($p < 0.05$) (p[accuracy] > no information rate] via the one-tailed binomial test). In cases where the train and test cohort are the same, accuracy given is that of the 30% test set rather than the full cohort to avoid testing on the training set. **b.** Forest plots based on results from **(a)**. Each machine learning method gets a separate forest plot with the cohorts shown on different lines. Hedge's g (squares, standardized mean difference, size proportional to sample size) and associated 95% confidence intervals (bars) are shown along with the dotted vertical line of no effect. To control for unobserved heterogeneity, we separately evaluated Hedge's g using random effect model on metagenomic data and performed I^2 test for heterogeneity as shown.

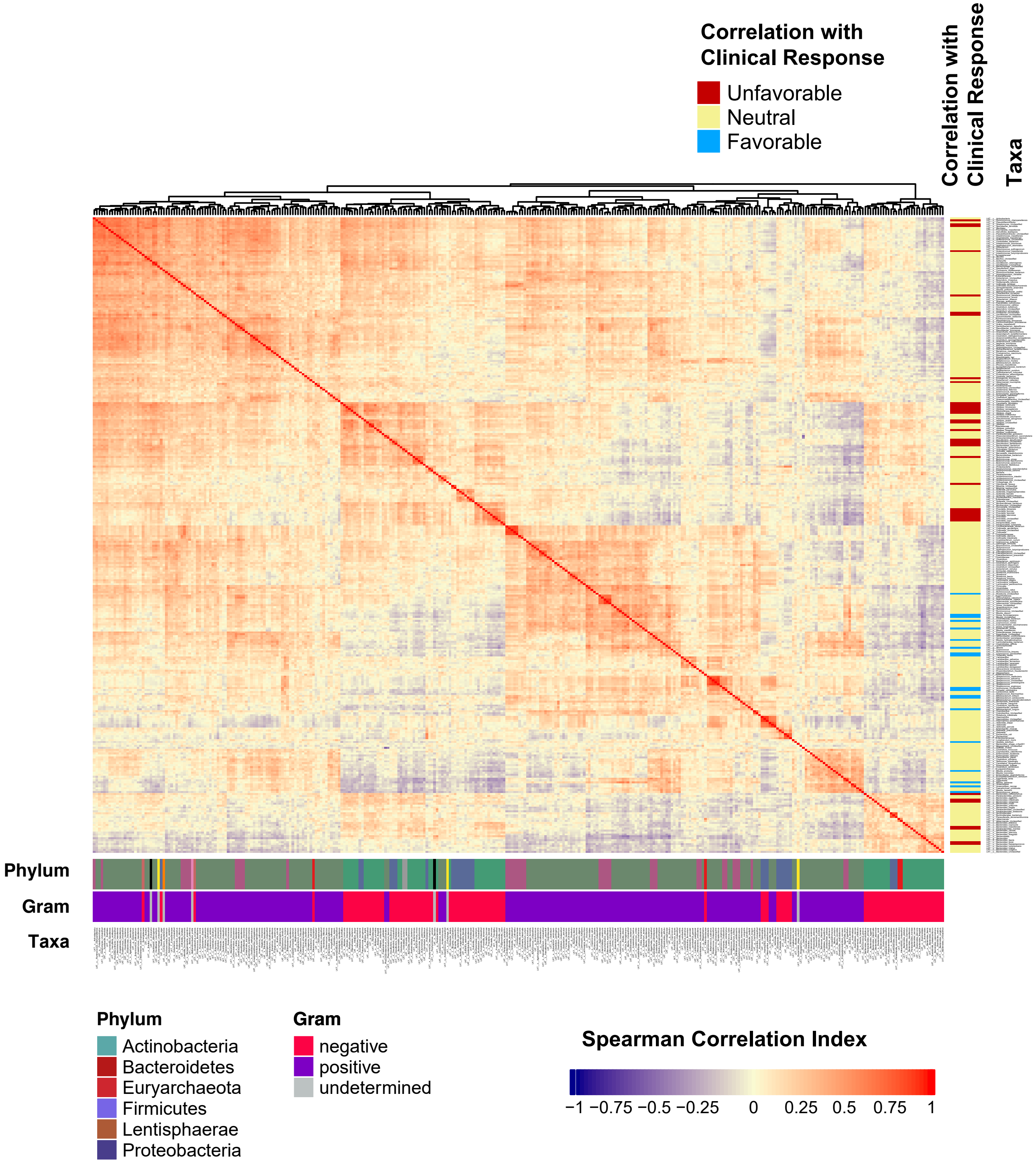
Supplementary Fig. 12 │ Network of shared organisms important for response prediction based on leave one-out analysis.



Supplementary Fig. 12 | Network of shared organisms important for response prediction based on leave one-out analysis.

The organisms shown are among the top 20 organisms in model importance in at least one of the five cohorts in the random forest leave one-out analysis. Size of the organism label (and color of the node) is based on how many of the five cohorts had that organism among its top 20.

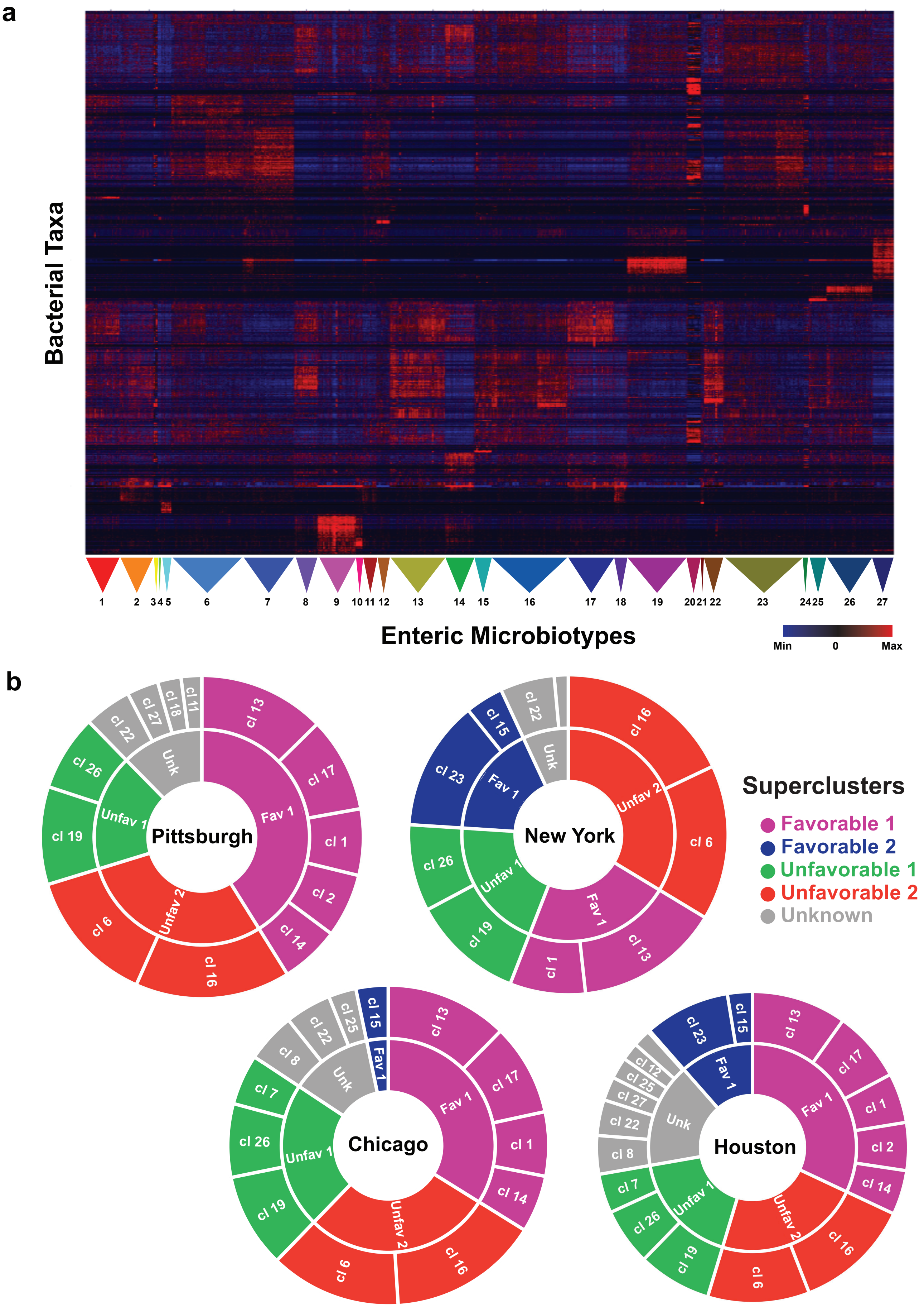
Supplementary Fig. 13 │ Correlogram of taxa abundance to each other using metagenomic data from five melanoma cohorts



Supplementary Fig. 13 │ Correlogram of taxa abundance to each other using metagenomic data from five melanoma cohorts.

Pairwise correlations between the COMBAT batch-corrected relative abundances of the top 330 most variant taxa across samples were calculated using Spearman's rank correlation coefficient. Taxa whose largest Spearman ρ with any other taxon was < 0.3 are not shown. Bar on right represents taxa significantly associated (blue – beneficial; red - detrimental) with response or non-response to anti-PD-1 therapy, while bars on the bottom represent phylum and Gram stain characteristics of each taxa. To be considered significantly associated with response or non-response to anti-PD-1 therapy, a taxon had to present a raw p-value of at least 0.1 as calculated by the Mann-Whitney-Wilxocon U-test and an absolute log2 fold-change of at least 0.5 between responder and non-responder patients on the same COMBAT batch-corrected relative abundances as used for the correlogram.

Supplementary Fig. 14 | Enteric microbiotypes identified in the American Gut Project database and their distribution within the four cohorts of PD-1-treated melanoma patients



Supplementary Fig. 14 │ Enteric microbiotypes identified in the American Gut Project database and their distribution within the four cohorts of PD-1-treated melanoma patients.

a. The heatmap shows the distribution of differentially abundant taxa in different clusters/ microbiotypes from American Gut Project (AGP) fecal microbiota dataset identified using PhenoGraph R package. **b.** Nested pie charts show relative distribution of microbiotypes and favorable or unfavorable superclusters within four cohorts of PD-1-treated melanoma patients.

Supplementary Table 1. Patient characteristics (Pittsburgh cohorts)

Characteristics	Total (n = 94)	Early Sample Cohort (n = 63)	Late Sample Cohort (n = 31)
Age (Years):			
Median, range	70 (32-90)	67 (32-90)	74 (41-89)
Sex:			
Male	66 (70%)	42 (67%)	24 (77%)
Race:			
Caucasian	94 (100%)	63 (100%)	31 (100%)
Body Mass Index:			
Males: Median, range	29 (19-43)	28 (19-43)	29 (20-42)
Females: Median, range	30 (18-42)	32 (18-42)	29 (25-42)
Melanoma Stage IV Grouping:			
M1a	29 (31%)	18 (29%)	11 (36%)
M1b	20 (21%)	14 (22%)	6 (19%)
M1c	34 (36%)	24 (38%)	10 (32%)
M1d	1 (12%)	7 (11%)	4 (13%)
Lactate Dehydrogenase:			
Median, range (U/ml)	202 (136-1108)	202 (141-603)	202 (136-1108)
Ratio to high normal (171u/ml)	1.18 (0.80-6.48)	1.18 (0.82-3.53)	1.18 (0.80-6.48)
Neutrophil Lymphocyte Ratio:			
Median, range	2.73(1.06-17.29)	2.74 (1.29-17.29)	2.69 (1.06-11.29)
Prior therapy:			
None	78 (83%)	60 (95%)	18 (58%)
Anti-CTLA-4	13 (14%)	3 (5%)	10 (32%)
High Dose IL-2	3 (3%)	0	3 (10%)
BRAF/MEK Inhibitors	4 (4%)	1 (2%)	3 (10%)
Melanoma Vaccine	1 (1%)	0	1 (3%)
Immunotherapy type:			
Nivolumab	23 (25%)	18 (29%)	5 (16%)
Pembrolizumab	48 (51%)	29 (46%)	19 (61%)
Pembrolizumab/PEG-Interferon	21 (22%)	14 (22%)	7 (23%)
Anti-PD-1 (investigational)	2 (2%)	2 (3%)	0
Immune-related Adverse Events			
None	37 (39%)	24 (38%)	13 (42%)
Any	57 (61%)	39 (62%)	18 (58%)
Highest Grade Event			
Grade 1-2	32 (34%)	23 (37%)	9 (29%)
Grade 3-4	25 (27%)	16 (25%)	9 (29%)

Supplementary Table 2. Cox regression models on overall survival and progression free survival (Pittsburgh early sample cohort)

Factors	Overall Survival		Factors	Progression Free Survival	
	Univariate HR, 95% CI, p-value	**Multivariate HR, 95% CI, p-value**		**Univariate HR, 95% CI, p-value**	**Multivariate HR, 95% CI, p-value**
Sex (M vs F)	1.31 (0.578 – 2.99), P=0.513		Sex (M vs F)	1.36 (0.649 – 2.85), P=0.413	
Age in years (≥76.51 vs <76.51)	1.71 (0.799 – 3.65), P=0.162		Age in years (≥56.02 vs <56.02)	0.55 (0.238 – 1.27), P=0.154	
BMI (≥26.4 vs <26.4)	0.388 (0.184 – 0.82), P=0.010	0.424 (0.198 – 0.909), P=0.028	BMI (≥26.4 vs <26.4)	0.552 (0.278 – 1.09), P=0.084	
Lines of treatment (≥1 vs 0)	1.79 (0.423 – 7.56), P=0.423		Lines of treatment (≥1 vs 0)	1.25 (0.299 – 5.22), P=0.759	
PPI usage (yes vs no)	2.07 (0.907 – 4.71), P=0.078		PPI usage	2.12 (0.988 – 4.56), P=0.048	2.197 (1.01 – 4.80), P=0.0483
LDH ratio (≥1.69 vs <1.69)	2.24 (0.946 – 5.28), P=0.060		LDH ratio (≥1.368 vs <1.368)	1.43 (0.706 – 2.89), P=0.318	
Neutrophil to lymphocyte ratio (≥3.75 vs <3.75)	2.4 (1.11 – 5.19), P=0.022	2.227 (1.025 – 4.841), P=0.043	Neutrophil to lymphocyte ratio (≥3.75 vs <3.75)	2.53 (1.23 – 5.17), P=0.009	2.443 (1.19 – 5.01), P=0.015

Abbreviations:
HR = Hazard Ratio
95% CI = 95% Confidence Interval
p-value = Score (logrank) test two-tailed p-value
M = Male
F = Female
BMI = Body Mass Index
PPI = Proton Pump Inhibitors
LDH = Lactate Dehydrogenase

Supplementary Table 3. Characteristics of melanoma patient cohorts from previously published studies

Study	Region	Patient Characteristics (response breakdwon)	Analytic Pipeline	Database Corrections	Duration of Follow-up	Definition of response
Peters et al., 2019	New York	14 metastatic melanoma patients on anti-PD1 therapy (7 non-progressors, 7 progressors) • Fecal samples analyzed by 16S and shotgun metagenomic + metatranscriptomic sequencing	• 16S sequencing: QIIME 2, Greengenes database • Shotgun sequencing: MetaPhlAn2, HUMAnN2	Taxa unidentified at the genus or species level removed	Start of therapy to progression, death, or loss to follow up (10-25 months)	PD or death from any cause vs non progression during follow-up period
Frankel et al., 2017	Dallas	14 non-resectable or metastatic melanoma patients on anti-PD1 therapy (7 non-progressors, 7 progressors) • Fecal samples analyzed by shotgun metagenomic sequencing	• MetaPhlAn, HUMAnN and FMAP		Not reported	Response by RECIST v1.1 (CR/PR/SD vs. PD, evaluated at 3-6 month intervals)
Matson et al., 2018	Chicago	38 metastatic melanoma patients on anti-PD1 therapy +4 patients on anti-CTLA-4 therapy (16 responders, 26 non-responders) • Fecal samples from 42 patients analyzed by 16S sequencing • Fecal samples from 39 patients analyzed by shotgun metagenomic sequencing (15 responders, 24 non-responders)	• 16S sequencing: QIIME, NCBI database • Shotgun sequencing: MetaPhlAn2	Composite analysis-Species identified in 16S, qPCR, and shotgun were retained	Not reported	Response by RECIST v1.1 (CR/PR any time during the study vs. no response)
Gopalakrishnan et al., 2018	Houston	43 metastatic melanoma patients on anti-PD1 therapy (30 responders, 13 non-responders) • Fecal samples from 43 patients analyzed by 16S sequencing • Fecal samples from 25 patients analyzed by shotgun metagenomic sequencing (14 responders, 11 non-responders)	• 16S sequencing: QIIME, Greengenes, RDP, and Silva databases • Shotgun sequencing: MetaOMineR	16S restricted to family level	Not reported	Response by RECIST v1.1 (CR/PR or SD>6 months vs. PD or SD<6 months)

CR=complete response, PR=partial response, PD=progressive disease, SD=stable disease, FMAP=Functional Mapping and Analysis Pipeline, RECIST=Response Evaluation Criteria In Solid Tumors-version 1.1., QIIME=Quantitative Insights Into Microbial Ecology, MetaPhlAn: Metagenomic Phylogenetic Analysis, HUMAnN=HMP Unified Metabolic Analysis Network, NCBI= National Center for Biotechnology Information, RDP=Ribosomal Database Project, MetaOMineR=Mining Metaomics Data.

Supplementary Table 4. Taxa associated with improved progression free survival (Pittsburgh early sample cohort)

LKT	Cutpoint	Biomarker<Cutpoint n (%)	Biomarker>=Cutpoint n (%)	HR	95% CI	Storey q-value
LKT__s__Blautia_coccoides	6	10 (16%)	53 (84%)	0.223	(0.104 - 0.477)	0.012
LKT__s__Ruminococcus_torques	3664	32 (51%)	31 (49%)	0.271	(0.128 - 0.573)	0.020
LKT__s__Blautia_producta	86	20 (32%)	43 (68%)	0.324	(0.163 - 0.644)	0.020
LKT__s__Absiella_dolichum	4	32 (51%)	31 (49%)	0.329	(0.16 - 0.679)	0.020
LKT__s__Anaerostipes_hadrus	3690	29 (46%)	34 (54%)	0.358	(0.178 - 0.719)	0.021
LKT__s__Clostridium_scindens	32	15 (24%)	48 (76%)	0.356	(0.175 - 0.723)	0.027
LKT__s__Enterocloster_clostridioformis	495	13 (21%)	50 (79%)	0.345	(0.165 - 0.719)	0.030
LKT__s__Collinsella_intestinalis	40	50 (79%)	13 (21%)	0.163	(0.039 - 0.682)	0.038
LKT__s__Enterocloster_bolteae	289	17 (27%)	46 (73%)	0.345	(0.173 - 0.692)	0.038
LKT__s__Lachnospiraceae_bacterium	8746	23 (37%)	40 (63%)	0.372	(0.189 - 0.733)	0.038
LKT__s__Blautia_wexlerae	581	13 (21%)	50 (79%)	0.379	(0.18 - 0.797)	0.038
LKT__f__Lachnospiraceae	7515	11 (17%)	52 (83%)	0.268	(0.124 - 0.575)	0.038
LKT__s__Ruminococcus_gnavus	693	14 (22%)	49 (78%)	0.405	(0.195 - 0.839)	0.045
LKT__s__Bifidobacterium_bifidum	8	20 (32%)	43 (68%)	0.352	(0.179 - 0.693)	0.045
LKT__s__Enterorhabdus_caecimuris	39	52 (83%)	11 (17%)	0.0975	(0.0133 - 0.714)	0.050
LKT__g__Coprococcus	49	26 (41%)	37 (59%)	0.393	(0.199 - 0.776)	0.057
LKT__s__Eisenbergiella_massiliensis	220	34 (54%)	29 (46%)	0.357	(0.17 - 0.75)	0.060
LKT__s__Mogibacterium_diversum	9	35 (56%)	28 (44%)	0.456	(0.221 - 0.938)	0.060
LKT__s__Anaerostipes_caccae	6	23 (37%)	40 (63%)	0.459	(0.233 - 0.904)	0.061
LKT__f__Erysipelotrichaceae	188	11 (17%)	52 (83%)	0.3	(0.138 - 0.652)	0.078
LKT__s__Adlercreutzia_equolifaciens	1547	52 (83%)	11 (17%)	0.206	(0.0491 - 0.861)	0.085
LKT__g__Anaerostipes	305	52 (83%)	11 (17%)	0.341	(0.104 - 1.12)	0.095
LKT__s__Blautia_hydrogenotrophica	45	15 (24%)	48 (76%)	0.398	(0.196 - 0.809)	0.096
LKT__s__Clostridium_methylpentosum	149	40 (63%)	23 (37%)	0.415	(0.188 - 0.92)	0.098

Abbreviations:
LKT = Last Known Taxon
HR = Hazard Ratio
95% CI = 95% Confidence Interval
n = number of patients

Supplementary Table 5. Taxa associated with decreased progression free survival (Pittsburgh early sample cohort)

LKT	Cutpoint	Biomarker<Cutpoint n (%)	Biomarker>=Cutpoint n (%)	HR	95% CI	Storey q-value
LKT__g__Prevotella	521	52 (83%)	11 (17%)	5.1	(2.4 - 10.8)	0.001
LKT__s__Prevotella_copri	431	47 (75%)	16 (25%)	4.37	(2.16 - 8.81)	0.001
LKT__k__Bacteria	8711	52 (83%)	11 (17%)	4.87	(2.26 - 10.5)	0.002
LKT__s__Prevotella_Unclassified	565	51 (81%)	12 (19%)	3.81	(1.83 - 7.94)	0.011
LKT__s__Prevotella_buccae	59	53 (84%)	10 (16%)	3.88	(1.77 - 8.48)	0.012
LKT__s__Prevotella_koreensis	6	52 (83%)	11 (17%)	4.14	(1.93 - 8.89)	0.013
LKT__s__Prevotella_oryzae	3	53 (84%)	10 (16%)	3.83	(1.75 - 8.37)	0.020
LKT__s__Parabacteroides_merdae	11165	52 (83%)	11 (17%)	3.61	(1.66 - 7.85)	0.020
LKT__s__Streptomyces_Unclassified	59	31 (49%)	32 (51%)	3.39	(1.61 - 7.13)	0.020
LKT__s__Veillonella_parvula	7	36 (57%)	27 (43%)	3.12	(1.55 - 6.27)	0.020
LKT__s__Sporobacter_termitidis	39	38 (60%)	25 (40%)	3.05	(1.53 - 6.08)	0.020
LKT__s__Lactobacillus_fermentum	28	45 (71%)	18 (29%)	3.01	(1.51 - 5.99)	0.020
LKT__s__Alistipes_senegalensis	299	38 (60%)	25 (40%)	2.98	(1.5 - 5.91)	0.020
LKT__g__Pseudoflavonifractor	124	37 (59%)	26 (41%)	2.97	(1.49 - 5.91)	0.020
LKT__s__Bacteroidales_bacterium	15	46 (73%)	17 (27%)	3.01	(1.49 - 6.09)	0.021
LKT__s__Flintibacter_Unclassified	150	48 (76%)	15 (24%)	2.92	(1.43 - 5.96)	0.021
LKT__s__Fournierella_massiliensis	752	50 (79%)	13 (21%)	3.06	(1.48 - 6.33)	0.023
LKT__s__Intestinimonas_butyriciproducens	280	28 (44%)	35 (56%)	3.63	(1.68 - 7.84)	0.023
LKT__g__Haemophilus	3	28 (44%)	35 (56%)	3.24	(1.51 - 6.98)	0.023
LKT__s__Ruminococcus_flavefaciens	962	21 (33%)	42 (67%)	3.99	(1.54 - 10.3)	0.027
LKT__g__Veillonella	91	49 (78%)	14 (22%)	3.07	(1.5 - 6.28)	0.027
LKT__s__Acinetobacter_baumannii	98	38 (60%)	25 (40%)	2.64	(1.34 - 5.19)	0.027
LKT__s__Clostridium_perfringens	218	52 (83%)	11 (17%)	3.25	(1.53 - 6.91)	0.030
LKT__s__Bacteroides_caccae	10876	48 (76%)	15 (24%)	2.48	(1.23 - 5.03)	0.030
LKT__s__Christensenella_minuta	21	29 (46%)	34 (54%)	2.78	(1.32 - 5.86)	0.030
LKT__s__Prevotella_stercorea	75	51 (81%)	12 (19%)	3.24	(1.53 - 6.86)	0.032
LKT__c__Actinobacteria	157	38 (60%)	25 (40%)	2.64	(1.33 - 5.22)	0.033
LKT__s__Prevotella_lascolaii	5	39 (62%)	24 (38%)	2.51	(1.27 - 4.93)	0.035
LKT__s__Eubacterium_pyruvativorans	3	16 (25%)	47 (75%)	5.17	(1.57 - 17)	0.037
LKT__p__Proteobacteria	628	46 (73%)	17 (27%)	3.11	(1.56 - 6.21)	0.037
LKT__s__Oscillibacter_valericigenes	241	50 (79%)	13 (21%)	2.88	(1.39 - 5.99)	0.037
LKT__s__Porphyromonas_uenonis	1	33 (52%)	30 (48%)	2.7	(1.34 - 5.42)	0.037
LKT__s__Alistipes_dispar	44	35 (56%)	28 (44%)	2.63	(1.32 - 5.25)	0.037
LKT__Unclassified	51400	33 (52%)	30 (48%)	2.66	(1.32 - 5.35)	0.038
LKT__s__Oxalobacter_formigenes	7	49 (78%)	14 (22%)	2.55	(1.23 - 5.28)	0.038
LKT__g__Klebsiella	115	50 (79%)	13 (21%)	2.87	(1.38 - 5.94)	0.050
LKT__s__Odoribacter_splanchnicus	2436	44 (70%)	19 (30%)	2.37	(1.19 - 4.72)	0.050
LKT__s__Cuneatibacter_caecimuris	155	53 (84%)	10 (16%)	3.31	(1.53 - 7.16)	0.051
LKT__s__Streptococcus_mutans	413	53 (84%)	10 (16%)	3.31	(1.53 - 7.16)	0.051
LKT__s__Paenibacillus_Unclassified	52	40 (63%)	23 (37%)	2.21	(1.12 - 4.36)	0.051
LKT__s__Anaerotruncus_massiliensis	916	51 (81%)	12 (19%)	2.3	(1.06 - 4.95)	0.052
LKT__s__Lactobacillus_gasseri	57	49 (78%)	14 (22%)	2.38	(1.16 - 4.9)	0.053
LKT__g__Acidaminococcus	10	31 (49%)	32 (51%)	2.36	(1.16 - 4.78)	0.053
LKT__s__Bacteroides_ilei	16	39 (62%)	24 (38%)	2.35	(1.19 - 4.63)	0.053
LKT__g__Lactobacillus	25	20 (32%)	43 (68%)	2.57	(1.06 - 6.22)	0.056
LKT__s__Odoribacter_laneus	18	46 (73%)	17 (27%)	2.34	(1.16 - 4.68)	0.056
LKT__f__Sutterellaceae	5	34 (54%)	29 (46%)	2.33	(1.17 - 4.64)	0.057
LKT__s__Agathobaculum_desmolans	270	53 (84%)	10 (16%)	3.1	(1.43 - 6.74)	0.060
LKT__s__Haemophilus_Unclassified	1	20 (32%)	43 (68%)	2.48	(1.08 - 5.7)	0.060
LKT__s__Agathobaculum_butyriciproducens	473	53 (84%)	10 (16%)	2.29	(1.03 - 5.1)	0.060
LKT__s__Akkermansia_muciniphila	5080	43 (68%)	20 (32%)	2.49	(1.25 - 4.95)	0.061
LKT__s__Acidaminococcus_fermentans	4	24 (38%)	39 (62%)	2.29	(1.07 - 4.92)	0.063
LKT__s__Oscillibacter_ruminantium	267	42 (67%)	21 (33%)	2.94	(1.49 - 5.82)	0.063
LKT__s__Haemophilus_parainfluenzae	2	30 (48%)	33 (52%)	2.44	(1.18 - 5.02)	0.063
LKT__s__Alistipes_timonensis	120	49 (78%)	14 (22%)	2.41	(1.14 - 5.09)	0.063
LKT__s__Muribaculaceae_bacterium	34	51 (81%)	12 (19%)	2.37	(1.09 - 5.12)	0.063

LKT__s__Bacteroides_coprocola	29	30 (48%)	33 (52%)	1.99	(0.993 - 3.97)	0.063
LKT__d__Eukaryota	80	30 (48%)	33 (52%)	2.21	(1.09 - 4.48)	0.064
LKT__s__Pseudoflavonifractor_Unclassified	373	38 (60%)	25 (40%)	2.17	(1.1 - 4.26)	0.066
LKT__s__Bacteroides_cellulosilyticus	225	16 (25%)	47 (75%)	2.58	(0.997 - 6.68)	0.075
LKT__s__Veillonella_dispar	19	47 (75%)	16 (25%)	2.09	(1.03 - 4.23)	0.075
LKT__s__Bacteriophage_Unclassified	5	14 (22%)	49 (78%)	4.19	(1.28 - 13.7)	0.078
LKT__s__Subdoligranulum_Unclassified	2806	50 (79%)	13 (21%)	3.22	(1.54 - 6.7)	0.078
LKT__s__Victivallales_bacterium	3	33 (52%)	30 (48%)	2.43	(1.21 - 4.88)	0.078
LKT__s__Muribaculum_Unclassified	1	14 (22%)	49 (78%)	2.99	(1.05 - 8.53)	0.081
LKT__s__Bacillus_Unclassified	26	31 (49%)	32 (51%)	2.41	(1.19 - 4.91)	0.086
LKT__s__Angelakisella_massiliensis	101	14 (22%)	49 (78%)	4.13	(1.26 - 13.6)	0.096
LKT__s__Duncaniella_Unclassified	1	31 (49%)	32 (51%)	1.96	(0.978 - 3.93)	0.096
LKT__s__Porphyromonas_asaccharolytica	3	44 (70%)	19 (30%)	1.85	(0.922 - 3.72)	0.100

Abbreviations:
LKT = Last Known Taxon
HR = Hazard Ratio
95% CI = 95% Confidence Interval
n = number of patients

Supplemental Table 6. Cox regression models for immune related adverse effects (Pittsburgh early sample cohort, landmark analysis, time 10 months)

irAE	Samples in irAE group (n in no irAE = 25)	Overall Survival	Progression Free Survival
		Univariate HR, 95% CI, p-value	Univariate HR, 95% CI, p-value
Grade 1-4 vs no irAE reported	28	0.464 (0.180 - 1.20), P=0.104	0.403 (0.175 - 0.926), P=0.027
Grade 1-2 only[#] vs no irAE-reported	18	0.530 (0.184 - 1.53), P=0.232	0.317 (0.114 - 0.877), P=0.020
Grade 3-4 only[#] vs no irAE-reported	7	0.565 (0.125 - 2.55), P=0.452	0.623 (0.180 - 2.160), P=0.452
Grade 3-4 all vs no irAE-reported	10	0.365 (0.080 - 1.65), P=0.173	0.601 (0.199 - 1.820), P=0.361

Patients alive at the landmark time (10 months) were analyzed. An irAE was considered to be present if developed before the landmark time.

[#] Patients who developed the other grade irAE before landmark time are excluded.

Abbreviations:
HR = Hazard Ratio
95% CI = 95% Confidence Interval
p-value = Score (logrank) test two-tailed p-value

Supplementary Table 7. Linear discrimination analysis scores of differentially abundant taxa from five separate anti-PD-1-treated melanoma patient cohorts

Taxa	Abundance	Class	LDA score	p-value
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Mycobacteriaceae; g__Unclassified	1.440	Non_Responder	2.072	0.015
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Mycobacteriaceae; g__Unclassified; LKT__f__Mycobacteriaceae	1.440	Non_Responder	2.072	0.015
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides; LKT__s__Bacteroides_cellulosilyticus	4.273	Non_Responder	3.716	0.013
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides; LKT__s__Bacteroides_fragilis	4.216	Non_Responder	3.425	0.040
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides; LKT__s__Bacteroides_intestinalis	4.274	Non_Responder	3.422	0.031
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Odoribacteraceae	4.095	Non_Responder	3.265	0.014
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Odoribacteraceae; g__Butyricimonas	3.400	Non_Responder	2.566	0.044
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Odoribacteraceae; g__Butyricimonas; LKT__s__Butyricimonas_virosa	3.054	Non_Responder	2.263	0.047
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Odoribacteraceae; g__Odoribacter	3.964	Non_Responder	3.183	0.015
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Odoribacteraceae; g__Odoribacter; LKT__g__Odoribacter	2.963	Non_Responder	2.374	0.047
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Odoribacteraceae; g__Odoribacter; LKT__s__Odoribacter_laneus	3.132	Non_Responder	2.722	0.009
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Odoribacteraceae; g__Odoribacter; LKT__s__Odoribacter_splanchnicus	3.822	Non_Responder	3.069	0.048
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae	4.454	Non_Responder	3.822	0.003
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella	4.397	Non_Responder	3.781	0.002
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; LKT__g__Prevotella	2.899	Non_Responder	2.443	0.031
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; LKT__s__Prevotella_copri	4.044	Non_Responder	3.457	0.000
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; LKT__s__Prevotella_lascolaii	2.876	Non_Responder	2.361	0.001
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; LKT__s__Prevotella_ruminicola	2.561	Non_Responder	2.084	0.003
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; LKT__s__Prevotella_stercorea	3.270	Non_Responder	2.764	0.000
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; LKT__s__Prevotella_Unclassified	3.927	Non_Responder	3.404	0.000
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotellamassilia	2.593	Non_Responder	2.172	0.000
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotellamassilia; LKT__s__Prevotellamassilia_timonensis	2.593	Non_Responder	2.172	0.000
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae	4.794	Non_Responder	4.031	0.043
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Alistipes	4.791	Non_Responder	4.038	0.037
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Alistipes; LKT__g__Alistipes	3.208	Non_Responder	2.382	0.021
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Alistipes; LKT__s__Alistipes_obesi	3.572	Non_Responder	2.942	0.019
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Alistipes; LKT__s__Alistipes_senegalensis	3.659	Non_Responder	2.980	0.034
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Alistipes; LKT__s__Alistipes_timonensis	3.183	Non_Responder	2.554	0.005
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Alistipes; LKT__s__Alistipes_Unclassified	4.123	Non_Responder	3.441	0.028
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae; g__Rummeliibacillus	0.745	Non_Responder	2.025	0.027
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae; g__Rummeliibacillus; LKT__s__Rummeliibacillus_pycnus	0.745	Non_Responder	2.025	0.027
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; LKT__s__Lactobacillus_animalis	2.534	Non_Responder	2.362	0.001
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Oscillospiraceae; g__Unclassified	3.448	Non_Responder	2.193	0.038
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Oscillospiraceae; g__Unclassified; LKT__f__Oscillospiraceae	3.448	Non_Responder	2.193	0.038
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Ruminococcaceae; g__Unclassified	3.537	Non_Responder	2.571	0.027
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Ruminococcaceae; g__Unclassified; LKT__f__Ruminococcaceae	3.537	Non_Responder	2.571	0.027
k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfovibrionales; f__Desulfovibrionaceae; g__Desulfovibrio	3.285	Non_Responder	2.511	0.038
k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfovibrionales; f__Desulfovibrionaceae; g__Desulfovibrio; LKT__s__Desulfovibrio_fairfieldensis	2.730	Non_Responder	2.181	0.034
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Aeromonadales; f__Aeromonadaceae; g__Aeromonas; LKT__s__Aeromonas_veronii	1.304	Non_Responder	2.022	0.047
k__Bacteria; p__Verrucomicrobia	4.217	Non_Responder	3.302	0.005
k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae	4.217	Non_Responder	3.302	0.005
k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae; o__Verrucomicrobiales	4.217	Non_Responder	3.302	0.005
k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae; o__Verrucomicrobiales; f__Akkermansiaceae	4.217	Non_Responder	3.302	0.005
k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae; o__Verrucomicrobiales; f__Akkermansiaceae; g__Akkermansia	4.217	Non_Responder	3.302	0.005
k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae; o__Verrucomicrobiales; f__Akkermansiaceae; g__Akkermansia; LKT__g__Akkermansia	3.263	Non_Responder	2.719	0.045
k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae; o__Verrucomicrobiales; f__Akkermansiaceae; g__Akkermansia; LKT__s__Akkermansia_muciniphila	4.166	Non_Responder	3.269	0.005
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales	2.739	Responder	2.038	0.008
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae	2.739	Responder	2.038	0.008
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Unclassified	0.195	Responder	2.654	0.000
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Unclassified; LKT__f__Actinomycetaceae	0.195	Responder	2.654	0.000
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Bifidobacteriales; f__Bifidobacteriaceae; g__Bifidobacterium; LKT__s__Bifidobacterium_pseudocatenulatum	3.033	Responder	2.585	0.030
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Promicromonosporaceae	0.991	Responder	2.093	0.001
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Promicromonosporaceae; g__Xylanimonas	0.991	Responder	2.093	0.001
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Promicromonosporaceae; g__Xylanimonas; LKT__s__Xylanimonas_cellulosilytica	0.991	Responder	2.093	0.001
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Sanguibacteraceae	0.883	Responder	2.147	0.002
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Sanguibacteraceae; g__Sanguibacter	0.883	Responder	2.147	0.002
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Sanguibacteraceae; g__Sanguibacter; LKT__s__Sanguibacter_keddieii	0.883	Responder	2.147	0.002
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; LKT__s__Prevotella_buccae	2.996	Responder	2.529	0.028
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; LKT__s__Prevotella_denticola	2.619	Responder	2.118	0.007
k__Bacteria; p__Firmicutes	5.647	Responder	4.557	0.001
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; LKT__s__Lactobacillus_acidophilus	0.803	Responder	2.008	0.022
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; LKT__g__Streptococcus	2.569	Responder	2.006	0.037
k__Bacteria; p__Firmicutes; c__Clostridia	5.602	Responder	4.530	0.002
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales	5.602	Responder	4.530	0.002
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae; g__Butyricicoccus	3.548	Responder	2.533	0.049
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae; g__Clostridium; LKT__g__Clostridium	3.593	Responder	2.623	0.027
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae; g__Clostridium; LKT__s__Clostridium_cadaveris	1.053	Responder	2.132	0.034
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae; g__Clostridium; LKT__s__Clostridium_kluyveri	1.084	Responder	2.072	0.020
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae; g__Clostridium; LKT__s__Clostridium_Unclassified	4.326	Responder	3.321	0.041
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae; g__Missing	2.925	Responder	2.003	0.001
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae; g__Missing; LKT__s__Clostridiaceae_bacterium	2.925	Responder	2.003	0.001
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Eubacteriaceae; g__Eubacterium; LKT__s__Eubacterium_ventriosum	3.155	Responder	2.087	0.036
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae	5.240	Responder	4.295	0.001
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Anaerostipes	3.493	Responder	2.726	0.013
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Anaerostipes; LKT__s__Anaerostipes_hadrus	3.429	Responder	2.715	0.039
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Blautia	4.667	Responder	3.738	0.008
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Blautia; LKT__g__Blautia	3.708	Responder	2.821	0.006
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Blautia; LKT__s__Blautia_hansenii	3.670	Responder	2.856	0.005
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Blautia; LKT__s__Blautia_massiliensis	2.950	Responder	2.287	0.020
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Blautia; LKT__s__Blautia_obeum	3.960	Responder	2.775	0.042
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Blautia; LKT__s__Blautia_producta	3.231	Responder	2.508	0.009
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Blautia; LKT__s__Blautia_Unclassified	4.072	Responder	3.123	0.004
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Blautia; LKT__s__Blautia_wexlerae	3.361	Responder	2.587	0.007
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Blautia; LKT__s__Ruminococcus_gnavus	3.751	Responder	3.091	0.007
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Butyrivibrio	3.581	Responder	2.994	0.032
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Butyrivibrio; LKT__s__Butyrivibrio_crossotus	3.343	Responder	2.947	0.000
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Butyrivibrio; LKT__s__Butyrivibrio_fibrisolvens	1.542	Responder	2.169	0.010
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Butyrivibrio; LKT__s__Butyrivibrio_proteoclasticus	1.696	Responder	2.017	0.005
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Coprococcus; LKT__s__Coprococcus_Unclassified	2.835	Responder	2.087	0.000
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Dorea; LKT__s__Dorea_formicigenerans	3.411	Responder	2.650	0.003
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Dorea; LKT__s__Dorea_Unclassified	3.048	Responder	2.116	0.008
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Lachnoclostridium	3.988	Responder	2.893	0.037
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Lachnoclostridium; LKT__s__Lachnoclostridium_phytofermentans	1.310	Responder	2.170	0.013
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Missing	4.655	Responder	3.843	0.001
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Missing; LKT__s__Eubacterium_rectale	4.455	Responder	3.717	0.001
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Missing; LKT__s__Lachnospiraceae_bacterium	4.222	Responder	3.244	0.040
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Roseburia	4.424	Responder	3.374	0.009
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Roseburia; LKT__g__Roseburia	3.209	Responder	2.484	0.000
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Roseburia; LKT__s__Roseburia_faecis	3.269	Responder	2.466	0.028
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Roseburia; LKT__s__Roseburia_hominis	3.657	Responder	2.780	0.022
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Roseburia; LKT__s__Roseburia_Unclassified	3.777	Responder	3.017	0.001
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Sellimonas	3.358	Responder	2.799	0.007
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Sellimonas; LKT__s__Sellimonas_intestinalis	3.358	Responder	2.799	0.007

k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptococcaceae; g__Desulfotomaculum; LKT__s__Desulfotomaculum_Unclassified	1.572	Responder	2.011	0.002
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae; g__Clostridioides	3.197	Responder	2.055	0.003
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae; g__Clostridioides; LKT__s__Clostridioides_difficile	3.197	Responder	2.055	0.003
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Ruminococcaceae	5.130	Responder	4.033	0.046
k__Bacteria; p__Firmicutes; c__Erysipelotrichia	3.928	Responder	3.014	0.044
k__Bacteria; p__Firmicutes; c__Erysipelotrichia; o__Erysipelotrichales	3.928	Responder	3.014	0.044
k__Bacteria; p__Firmicutes; c__Erysipelotrichia; o__Erysipelotrichales; f__Erysipelotrichaceae	3.928	Responder	3.014	0.044
k__Bacteria; p__Firmicutes; c__Erysipelotrichia; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Catenibacterium	2.577	Responder	2.147	0.035
k__Bacteria; p__Firmicutes; c__Erysipelotrichia; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Catenibacterium; LKT__g__Catenibacterium	2.577	Responder	2.147	0.035
k__Bacteria; p__Firmicutes; c__Erysipelotrichia; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Coprobacillus; LKT__g__Coprobacillus	2.975	Responder	2.320	0.012
k__Bacteria; p__Firmicutes; c__Erysipelotrichia; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Coprobacillus; LKT__s__Coprobacillus_Unclassified	3.071	Responder	2.438	0.007
k__Bacteria; p__Firmicutes; c__Erysipelotrichia; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Turicibacter; LKT__g__Turicibacter	1.309	Responder	2.452	0.002
k__Bacteria; p__Firmicutes; c__Negativicutes; o__Selenomonadales; f__Selenomonadaceae; g__Megamonas	2.980	Responder	2.620	0.034
k__Bacteria; p__Firmicutes; c__Negativicutes; o__Selenomonadales; f__Selenomonadaceae; g__Megamonas; LKT__g__Megamonas	2.182	Responder	2.007	0.028
k__Bacteria; p__Firmicutes; c__Negativicutes; o__Selenomonadales; f__Selenomonadaceae; g__Megamonas; LKT__s__Megamonas_rupellensis	2.487	Responder	2.171	0.004
k__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales	3.597	Responder	2.936	0.049
k__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales; f__Veillonellaceae	3.597	Responder	2.936	0.049
k__Bacteria; p__Firmicutes; c__Tissierellia; o__Tissierellales; f__Peptoniphilaceae; g__Anaerococcus; LKT__g__Anaerococcus	1.305	Responder	2.145	0.008
k__Bacteria; p__Firmicutes; c__Tissierellia; o__Tissierellales; f__Peptoniphilaceae; g__Anaerococcus; LKT__s__Anaerococcus_vaginalis	0.475	Responder	2.339	0.011
k__Bacteria; p__Firmicutes; c__Tissierellia; o__Tissierellales; f__Peptoniphilaceae; g__Finegoldia	0.925	Responder	2.274	0.011
k__Bacteria; p__Firmicutes; c__Tissierellia; o__Tissierellales; f__Peptoniphilaceae; g__Finegoldia; LKT__s__Finegoldia_magna	0.925	Responder	2.274	0.011
k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium; LKT__s__Fusobacterium_varium	1.730	Responder	2.181	0.001
k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Comamonadaceae; g__Variovorax; LKT__g__Variovorax	0.141	Responder	3.018	0.002
k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Oxalobacteraceae; g__Janthinobacterium; LKT__s__Janthinobacterium_Unclassified	0.852	Responder	2.383	0.048

Linear discrimination analysis (LDA) scores computed for differentially abundant taxa calculated on batch-corrected metagenomic data obtained from five combined melanoma patient cohorts. Taxa with $p \leq 0.05$ for the Kruskal-Wallis H statistic and LDA score > 2 are listed.

Supplementary Table 8. Continuous variable Cox regression models (Pittsburgh full cohort)

Taxa Associated with Decreased PFS	beta	HR (95% CI for HR)	Storey q-value
LKT__s__Absiella_dolichum	-0.280	0.75543 (0.633-0.902)	0.04
LKT__s__Ruminococcus_gnavus	-0.224	0.79927 (0.692-0.923)	0.05
LKT__s__Mogibacterium_diversum	-0.204	0.81523 (0.712-0.934)	0.06
LKT__s__Blautia_coccoides	-0.217	0.80514 (0.694-0.934)	0.07
LKT__s__Blautia_producta	-0.191	0.82575 (0.721-0.946)	0.08
LKT__g__Blautia	-0.266	0.76658 (0.632-0.93)	0.08
LKT__s__Lachnospiraceae_bacterium	-0.265	0.76697 (0.633-0.93)	0.08
LKT__f__Lachnospiraceae	-0.431	0.64976 (0.469-0.9)	0.11

Taxa Associated with Increased PFS	beta	HR (95% CI for HR)	Storey q-value
LKT__s__Prevotella_oryzae	0.199	1.2204 (1.11-1.34)	0.01
LKT__s__Prevotella_lascolaii	0.131	1.1401 (1.06-1.22)	0.01
LKT__g__Prevotella	0.188	1.2063 (1.09-1.33)	0.01
LKT__s__Prevotella_koreensis	0.202	1.2236 (1.1-1.36)	0.01
LKT__s__Oxalobacter_formigenes	0.242	1.2741 (1.12-1.45)	0.01
LKT__s__Prevotella_stercorea	0.123	1.1304 (1.05-1.21)	0.03
LKT__s__Prevotella_Unclassified	0.125	1.1333 (1.05-1.22)	0.03
LKT__s__Prevotella_copri	0.102	1.107 (1.04-1.18)	0.04
LKT__s__Prevotella_buccae	0.120	1.1274 (1.05-1.21)	0.04
LKT__s__Bacteroides_caccae	0.150	1.1614 (1.05-1.29)	0.07
LKT__k__Bacteria	0.733	2.0817 (1.24-3.5)	0.08
LKT__s__Lactobacillus_paracasei	0.115	1.122 (1.03-1.22)	0.11
LKT__s__Acinetobacter_baumannii	0.177	1.1931 (1.04-1.36)	0.11
LKT__s__Acidaminococcus_fermentans	0.154	1.1659 (1.04-1.31)	0.11
LKT__s__Lactobacillus_rhamnosus	0.122	1.1296 (1.02-1.25)	0.14
LKT__s__Bacillus_Unclassified	0.199	1.2196 (1.04-1.43)	0.14
LKT__s__Faecalibacterium_Unclassified	0.130	1.1385 (1.02-1.27)	0.19

Abbreviations:

LKT = Last Known Taxon
PFS = Progression Free Survival
HR = Hazard Ratio
95% CI = 95% Confidence Interval

Supplementary Table 9. Differentially abundant taxa between different clusters from American Gut Project dataset identified using PhenoGraph R package

Taxa	Microbiotype_classification	LDA score (log10)	p-value
k__Bacteria.p__Actinobacteria	Beneficial I	3.819243502	3.29E-39
k__Bacteria.p__Actinobacteria.c__Bifidobacteriales	Beneficial I	3.691189427	4.16E-12
k__Bacteria.p__Actinobacteria.c__Bifidobacteriales.o__Bifidobacteriaceae	Beneficial I	3.691189427	4.16E-12
k__Bacteria.p__Actinobacteria.c__Bifidobacteriales.o__Bifidobacteriaceae.f__Bifidobacterium	Beneficial I	3.689824886	9.05E-11
k__Bacteria.p__Actinobacteria.c__Bifidobacteriales.o__Bifidobacteriaceae.f__Bifidobacterium.g__Bifidobacterium	Beneficial I	3.689824886	9.05E-11
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae	Beneficial I	4.70242304	4.08E-77
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides	Beneficial I	4.70242304	4.08E-77
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_acidifaciens	Beneficial I	4.159304822	1.37E-52
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_caccae	Beneficial I	3.729009039	1.18E-08
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_cellulosilyticus	Beneficial I	3.444473356	9.19E-21
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_dorei	Beneficial I	4.172780832	2.61E-26
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_fragilis	Beneficial I	3.89098049	3.35E-69
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_thetaiotaomicron	Beneficial I	3.75555452	5.81E-12
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Porphyromonadaceae	Beneficial I	3.92601832	3.30E-27
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Porphyromonadaceae.g__Dysgonomonas	Beneficial I	3.273404782	0.00250048
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Porphyromonadaceae.g__Dysgonomonas.s__Dysgonomonas_capnocytophagoides	Beneficial I	3.095098402	0.00324438
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Porphyromonadaceae.g__Parabacteroides	Beneficial I	3.812451692	4.35E-27
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Alistipes.s__Alistipes_finegoldii	Beneficial I	3.142527774	1.45E-28
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Alistipes.s__Alistipes_onderdonkii	Beneficial I	3.53230735	3.59E-24
k__Bacteria.p__Firmicutes.c__Bacilli	Beneficial I	3.936260536	1.66E-128
k__Bacteria.p__Firmicutes.c__Bacilli.o__Bacillales	Beneficial I	3.600549386	2.92E-101
k__Bacteria.p__Firmicutes.c__Bacilli.o__Bacillales.f__Bacillaceae	Beneficial I	3.184482887	7.92E-11
k__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales	Beneficial I	3.659730468	2.31E-79
k__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae	Beneficial I	3.048689172	0.00031837
k__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae	Beneficial I	3.274214595	1.13E-56
k__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Streptococcus	Beneficial I	3.191879415	5.09E-53
k__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Streptococcus.s__Streptococcus_salivarius	Beneficial I	3.016356545	2.35E-40
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Clostridiaceae	Beneficial I	3.390281462	2.50E-26
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Clostridiaceae.g__Hungatella	Beneficial I	3.225546866	2.00E-52
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Clostridiaceae.g__Hungatella.s__Clostridium_hathewayi	Beneficial I	3.225546866	2.00E-52
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Eubacteriaceae.g__Eubacterium.s__Eubacterium_coprostanoligenes	Beneficial I	3.748185827	1.43E-14
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Flavonifractor	Beneficial I	3.3827463	0
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Flavonifractor.g__Flavonifractor	Beneficial I	3.3827463	0
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Flavonifractor.g__Flavonifractor.s__Flavonifractor_plautii	Beneficial I	3.3827463	0
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae	Beneficial I	4.415557092	1.19E-84
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Anaerostipes	Beneficial I	3.419739044	3.42E-91
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Anaerostipes.s__Anaerostipes_caccae	Beneficial I	3.419739044	3.42E-91
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Blautia	Beneficial I	4.193999479	9.72E-135
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Blautia.s__Blautia_faecis	Beneficial I	3.173490081	5.57E-23
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Blautia.s__Blautia_wexlerae	Beneficial I	3.70130596	1.14E-29
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Blautia.s__Ruminococcus_gnavus	Beneficial I	3.470677739	7.34E-43
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Blautia.s__Ruminococcus_torques	Beneficial I	3.59456387	3.96E-139
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Eisenbergiella	Beneficial I	3.055902552	2.71E-14
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Eisenbergiella.s__Eisenbergiella_tayi	Beneficial I	3.055902552	2.71E-14
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Lachnospiraceae	Beneficial I	3.42241278	6.63E-214
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Lachnospiraceae.s__Clostridium_bolteae	Beneficial I	3.357974994	628523404e-311
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Peptostreptococcaceae	Beneficial I	3.058639056	6.80E-30
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Ruminococcaceae.g__Ruminiclostridium.s__Clostridium_leptum	Beneficial I	3.488811176	4.94E-44
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Ruminococcaceae.g__Subdoligranulum	Beneficial I	3.392874087	2.99E-158
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Ruminococcaceae.g__Subdoligranulum.s__Subdoligranulum_variabile	Beneficial I	3.392874087	2.99E-158
k__Bacteria.p__Firmicutes.c__Erysipelotrichia	Beneficial I	3.759608225	1.45E-104
k__Bacteria.p__Firmicutes.c__Erysipelotrichia.o__Erysipelotrichales	Beneficial I	3.759608225	1.45E-104
k__Bacteria.p__Firmicutes.c__Erysipelotrichia.o__Erysipelotrichales.f__Erysipelotrichaceae	Beneficial I	3.759608225	1.45E-104
k__Bacteria.p__Firmicutes.c__Erysipelotrichia.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Erysipelatoclostridium	Beneficial I	3.508658417	0
k__Bacteria.p__Firmicutes.c__Erysipelotrichia.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Erysipelatoclostridium.s__Clostridium_innocuum	Beneficial I	3.083136193	2.85E-173
k__Bacteria.p__Firmicutes.c__Negativicutes.o__Selenomonadales.f__Veillonellaceae.g__Dialister.s__Dialister_invisus	Beneficial I	3.321573457	5.68E-21
k__Bacteria.p__Firmicutes.c__Negativicutes.o__Selenomonadales.f__Veillonellaceae.g__Veillonella	Beneficial I	3.034274048	1.59E-09
k__Bacteria.p__Proteobacteria	Beneficial I	3.276964498	1.02E-18
k__Bacteria.p__Verrucomicrobia	Beneficial I	4.028224626	1.54E-18
k__Bacteria.p__Verrucomicrobia.c__Verrucomicrobiae	Beneficial I	4.028224626	1.54E-18
k__Bacteria.p__Verrucomicrobia.c__Verrucomicrobiae.o__Verrucomicrobiales	Beneficial I	4.028224626	1.54E-18
k__Bacteria.p__Verrucomicrobia.c__Verrucomicrobiae.o__Verrucomicrobiales.f__Akkermansiaceae	Beneficial I	4.027924965	2.13E-18
k__Bacteria.p__Verrucomicrobia.c__Verrucomicrobiae.o__Verrucomicrobiales.f__Akkermansiaceae.g__Akkermansia	Beneficial I	4.027924965	2.13E-18
k__Bacteria.p__Verrucomicrobia.c__Verrucomicrobiae.o__Verrucomicrobiales.f__Akkermansiaceae.g__Akkermansia.s__Akkermansia_muciniphila	Beneficial I	4.027924965	2.13E-18
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_eggerthii	Beneficial II	3.85217923	1.83E-54
k__Bacteria.p__Firmicutes	Beneficial II	4.594075446	2.06E-26
k__Bacteria.p__Firmicutes.c__Clostridia	Beneficial II	4.651187617	2.53E-34
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales	Beneficial II	4.651130026	2.51E-34
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Eubacteriaceae	Beneficial II	3.613304876	1.66E-17
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Eubacteriaceae.g__Eubacterium	Beneficial II	3.613304876	1.66E-17
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Eubacteriaceae.g__Eubacterium.s__Eubacterium_eligens	Beneficial II	3.789677137	1.16E-21
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Coprococcus	Beneficial II	3.704215745	1.09E-132
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Coprococcus.s__Coprococcus_eutactus	Beneficial II	3.708042675	3.16E-177
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Roseburia	Beneficial II	3.80135345	6.00E-39
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Roseburia.s__Roseburia_intestinalis	Beneficial II	3.797825264	7.46E-49
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Ruminococcaceae	Beneficial II	4.505907877	1.73E-80
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Ruminococcaceae.g__Faecalibacterium	Beneficial II	4.243499214	2.09E-98
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Ruminococcaceae.g__Faecalibacterium.s__Faecalibacterium_prausnitzii	Beneficial II	4.243499214	2.09E-98
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Ruminococcaceae.g__Ruminococcus	Beneficial II	3.663369746	4.23E-101
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Ruminococcaceae.g__Ruminococcus.s__Ruminococcus_bromii	Beneficial II	3.515374817	2.34E-52
k__Bacteria.p__Bacteroidetes	Detrimental I	4.570155149	7.96E-20
k__Bacteria.p__Bacteroidetes.c__Bacteroidia	Detrimental I	4.579688261	1.08E-20
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales	Detrimental I	4.579688261	1.08E-20
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_coprocola	Detrimental I	3.410770739	4.05E-45
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_coprophilus	Detrimental I	3.409526889	2.01E-46
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_plebeius	Detrimental I	4.15454528	1.26E-165
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae	Detrimental I	4.873942135	2.91E-298
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Paraprevotella	Detrimental I	3.429306761	1.68E-98

k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Paraprevotella.s__Paraprevotella_clara	Detrimental I	3.395656211	4.63E-88
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotella	Detrimental I	4.858163337	3.10E-259
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotella.s__Prevotella_copri	Detrimental I	4.804878001	2.23E-265
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotella.s__Prevotella_stercorea	Detrimental I	3.046336967	2.61E-06
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Butyrivibrio	Detrimental I	3.231967398	2.83E-77
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Butyrivibrio.s__Butyrivibrio_crossotus	Detrimental I	3.229243637	2.61E-72
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Roseburia.s__Roseburia_inulinivorans	Detrimental I	3.793236902	3.47E-35
k__Bacteria.p__Firmicutes.c__Negativicutes.o__Selenomonadales.f__Veillonellaceae	Detrimental I	3.608581791	2.90E-32
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_intestinalis	Detrimental II	3.184865466	4.37E-19
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_massiliensis	Detrimental II	4.006943092	4.97E-43
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_stercoris	Detrimental II	3.860989438	1.28E-57
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_uniformis	Detrimental II	3.987259424	4.54E-60
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Porphyromonadaceae.g__Barnesiella	Detrimental II	3.078344295	3.92E-62
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Porphyromonadaceae.g__Parabacteroides.s__Parabacteroides_goldsteinii	Detrimental II	3.30898263	8.92E-22
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae	Detrimental II	3.912723817	9.98E-49
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Alistipes	Detrimental II	3.912723817	9.98E-49
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Alistipes.s__Alistipes_putredinis	Detrimental II	3.327553199	1.92E-62
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Ruminococcaceae.g__Ruminiclostridium	Detrimental II	3.628399675	1.42E-48
k__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Ruminococcaceae.g__Ruminiclostridium.s__Eubacterium_siraeum_V10Sc8a	Detrimental II	3.665277663	6.88E-107

LDA scores and p-values were calculated using the LEFse package.

Abbreviation:
LDA = Linear discrimination analysis

Supplementary Table 10. Continuous variable Cox regression models for Pittsburgh (full cohort) and Houston.

	PITTSBURGH				HOUSTON			
LKT	beta	HR (95% CI for HR)	p.value	Storey FDR	beta	HR (95% CI for HR)	p.value	Same HR dir
LKT__s__Lactobacillus_paragasseri	-0.00909	0.99095 (0.894-1.1)	0.86	0.56	1.25	3.4759 (0.955-12.7)	0.06	0
LKT__s__Megasphaera_Unclassified	-0.208	0.81256 (0.664-0.995)	0.04	0.21	1.23	3.4179 (1.22-9.57)	0.02	0
LKT__s__Lactobacillus_plantarum	0.0149	1.015 (0.916-1.13)	0.78	0.54	0.729	2.0725 (1.2-3.59)	0.01	1
LKT__s__Lactobacillus_salivarius	0.065	1.0672 (0.973-1.17)	0.17	0.29	0.488	1.6294 (1.05-2.53)	0.03	1
LKT__s__Enterobacter_roggenkampii	-0.0329	0.96761 (0.844-1.11)	0.64	0.49	0.412	1.5103 (1.02-2.23)	0.04	0
LKT__s__Actinomyces_oris	-0.114	0.89262 (0.793-1)	0.06	0.21	0.303	1.3535 (0.808-2.27)	0.25	0
LKT__s__Bacteroides_plebeius	0.0992	1.1043 (0.988-1.23)	0.08	0.23	0.293	1.3407 (1.06-1.7)	0.01	1
LKT__s__Enterocloster_clostridioformis	-0.169	0.84424 (0.699-1.02)	0.08	0.23	0.256	1.2921 (0.977-1.71)	0.07	0
LKT__s__Desulfovibrio_piger	0.0172	1.0174 (0.932-1.11)	0.70	0.51	0.214	1.2392 (0.933-1.65)	0.14	1
LKT__g__Escherichia	0.0202	1.0204 (0.899-1.16)	0.75	0.53	0.187	1.2062 (0.964-1.51)	0.10	1
LKT__g__Megasphaera	-0.0743	0.92837 (0.824-1.05)	0.22	0.32	0.183	1.2005 (0.896-1.61)	0.22	0
LKT__s__Sutterella_parvirubra	0.0474	1.0485 (0.911-1.21)	0.51	0.47	0.178	1.1946 (1-1.43)	0.05	1
LKT__s__Eubacterium_maltosivorans	0.033	1.0335 (0.924-1.16)	0.57	0.48	0.178	1.1951 (0.909-1.57)	0.20	1
LKT__s__Enterocloster_lavalensis	-0.0737	0.92899 (0.806-1.07)	0.31	0.37	0.175	1.1911 (0.91-1.56)	0.20	0
LKT__s__Desulfovibrio_fairfieldensis	0.033	1.0336 (0.944-1.13)	0.47	0.45	0.172	1.1874 (1.02-1.38)	0.03	1
LKT__s__Bifidobacterium_dentium	-0.0104	0.98961 (0.9-1.09)	0.83	0.55	0.171	1.1864 (0.776-1.81)	0.43	0
LKT__f__Enterobacteriaceae	0.0244	1.0247 (0.891-1.18)	0.73	0.52	0.17	1.1852 (0.941-1.49)	0.15	1
LKT__s__Sutterella_faecalis	0.113	1.1199 (1.01-1.24)	0.04	0.21	0.166	1.1812 (0.962-1.45)	0.11	1
LKT__s__Prevotella_buccae	0.12	1.1274 (1.05-1.21)	1.50E-03	0.04	0.164	1.1781 (0.988-1.41)	0.07	1
LKT__s__Prevotella_oryzae	0.199	1.2204 (1.11-1.34)	5.50E-05	0.01	0.16	1.1731 (0.993-1.39)	0.06	1
LKT__s__Bacteroides_massiliensis	0.0811	1.0845 (1-1.17)	0.04	0.21	0.159	1.1719 (0.988-1.39)	0.07	1
LKT__s__Enterocloster_bolteae	-0.127	0.88085 (0.717-1.08)	0.23	0.32	0.157	1.1695 (0.842-1.63)	0.35	0
LKT__s__Prevotella_stercorea	0.123	1.1304 (1.05-1.21)	8.11E-04	0.03	0.15	1.1617 (1.01-1.34)	0.04	1
LKT__s__Duodenibacillus_massiliensis	0.0288	1.0292 (0.926-1.14)	0.59	0.48	0.149	1.1605 (0.975-1.38)	0.09	1
LKT__s__Lactobacillus_gasseri	0.0499	1.0512 (0.969-1.14)	0.23	0.32	0.148	1.1592 (0.886-1.52)	0.28	1
LKT__s__Sutterella_megalosphaeroides	0.0747	1.0776 (0.959-1.21)	0.21	0.32	0.146	1.1577 (0.971-1.38)	0.10	1
LKT__s__Prevotella_lascolaii	0.131	1.1401 (1.06-1.22)	2.73E-04	0.01	0.144	1.1545 (1-1.33)	0.04	1
LKT__g__Prevotella	0.188	1.2063 (1.09-1.33)	1.62E-04	0.01	0.143	1.1538 (0.981-1.36)	0.08	1
LKT__s__Acidaminococcus_intestini	0.0214	1.0216 (0.949-1.1)	0.57	0.48	0.143	1.154 (0.968-1.38)	0.11	1
LKT__p__Proteobacteria	0.099	1.1041 (0.927-1.31)	0.27	0.35	0.142	1.1528 (0.814-1.63)	0.42	1
LKT__g__Roseburia	0.0472	1.0484 (0.885-1.24)	0.59	0.48	0.14	1.1507 (0.808-1.64)	0.44	1
LKT__s__Eisenbergiella_tayi	-0.0703	0.93209 (0.817-1.06)	0.30	0.37	0.136	1.1452 (0.844-1.55)	0.38	0
LKT__s__Prevotella_Unclassified	0.125	1.1333 (1.05-1.22)	8.51E-04	0.03	0.134	1.1437 (1.01-1.3)	0.04	1
LKT__s__Bacteroides_Unclassified	-0.000593	0.99941 (0.865-1.16)	0.99	0.60	0.134	1.1436 (0.789-1.66)	0.48	0
LKT__s__Candidatus_Stoquefichus	-0.0279	0.97248 (0.861-1.1)	0.65	0.49	0.13	1.1384 (0.802-1.62)	0.47	0
LKT__s__Streptococcus_parasanguinis	-0.00183	0.99817 (0.906-1.1)	0.97	0.59	0.129	1.1377 (0.877-1.48)	0.33	0
LKT__s__Asaccharobacter_celatus	-0.0399	0.96093 (0.877-1.05)	0.39	0.41	0.128	1.137 (0.879-1.47)	0.33	0
LKT__s__Prevotella_koreensis	0.202	1.2236 (1.1-1.36)	2.89E-04	0.01	0.117	1.1247 (0.917-1.38)	0.26	1
LKT__s__Desulfovibrio_Unclassified	0.0725	1.0752 (0.985-1.17)	0.11	0.25	0.117	1.1239 (0.996-1.27)	0.06	1
LKT__s__Akkermansia_Unclassified	0.00208	1.0021 (0.912-1.1)	0.97	0.59	0.117	1.1239 (0.937-1.35)	0.21	1
LKT__s__Tyzzerella_nexilis	-0.117	0.88979 (0.787-1.01)	0.06	0.22	0.114	1.121 (0.898-1.4)	0.31	0
LKT__s__Paraprevotella_clara	0.0289	1.0293 (0.952-1.11)	0.47	0.45	0.113	1.1194 (0.98-1.28)	0.10	1
LKT__s__Streptococcus_vestibularis	0.032	1.0325 (0.943-1.13)	0.49	0.46	0.113	1.1201 (0.827-1.52)	0.46	1
LKT__s__Prevotella_copri	0.102	1.107 (1.04-1.18)	1.49E-03	0.04	0.104	1.1091 (1.01-1.21)	0.02	1
LKT__s__Raoultibacter_timonensis	-0.0111	0.98892 (0.911-1.07)	0.79	0.54	0.103	1.1083 (0.835-1.47)	0.48	0
LKT__s__Enterocloster_asparagiformis	-0.0437	0.95726 (0.821-1.12)	0.58	0.48	0.101	1.1066 (0.81-1.51)	0.53	0
LKT__g__Klebsiella	0.0149	1.015 (0.919-1.12)	0.77	0.53	0.0999	1.1051 (0.92-1.33)	0.29	1
LKT__s__Collinsella_bouchesdurhonensis	-0.0568	0.94481 (0.848-1.05)	0.31	0.37	0.098	1.1029 (0.832-1.46)	0.50	0
LKT__s__Cuneatibacter_caecimuris	0.194	1.2144 (1.03-1.44)	0.02	0.21	0.097	1.1018 (0.818-1.48)	0.52	1
LKT__g__Coprococcus	-0.135	0.87358 (0.74-1.03)	0.11	0.25	0.0951	1.0998 (0.762-1.59)	0.61	0
LKT__f__Eggerthellaceae	-0.0607	0.94115 (0.802-1.11)	0.46	0.45	0.095	1.0997 (0.799-1.51)	0.56	0
LKT__s__Desulfovibrio_desulfuricans	0.0721	1.0748 (0.988-1.17)	0.10	0.23	0.0945	1.0991 (0.91-1.33)	0.33	1
LKT__s__Paraprevotella_xylaniphila	0.0323	1.0328 (0.936-1.14)	0.52	0.47	0.0931	1.0976 (0.937-1.29)	0.25	1
LKT__s__Enterocloster_aldensis	-0.0676	0.93461 (0.796-1.1)	0.41	0.42	0.0914	1.0957 (0.879-1.37)	0.42	0
LKT__g__Streptococcus	-0.0152	0.98496 (0.857-1.13)	0.83	0.55	0.0906	1.0949 (0.808-1.48)	0.56	0
LKT__s__Escherichia_coli	0.00358	1.0036 (0.932-1.08)	0.93	0.58	0.0901	1.0942 (0.966-1.24)	0.16	1
LKT__s__Enterorhabdus_caecimuris	-0.112	0.89402 (0.787-1.02)	0.08	0.23	0.0868	1.0907 (0.507-2.35)	0.82	0
LKT__s__Bacteroides_stercoris	0.0327	1.0332 (0.942-1.13)	0.49	0.46	0.0853	1.0891 (0.885-1.34)	0.42	1
LKT__s__Adlercreutzia_Unclassified	-0.0375	0.9632 (0.888-1.04)	0.37	0.40	0.0852	1.0889 (0.841-1.41)	0.52	0
LKT__g__Akkermansia	-0.0224	0.97789 (0.882-1.08)	0.67	0.49	0.0834	1.087 (0.923-1.28)	0.32	0
LKT__g__Subdoligranulum	0.00922	1.0093 (0.863-1.18)	0.91	0.57	0.0797	1.0829 (0.752-1.56)	0.67	1
LKT__s__Eggerthella_lenta	-0.0948	0.90953 (0.826-1)	0.05	0.21	0.0741	1.0769 (0.76-1.53)	0.68	0
LKT__f__Akkermansiaceae	-0.0659	0.93623 (0.829-1.06)	0.29	0.37	0.0733	1.076 (0.914-1.27)	0.38	0
LKT__s__Absiella_dolichum	-0.28	0.75543 (0.633-0.902)	1.94E-03	0.04	0.0697	1.0722 (0.779-1.48)	0.67	0
LKT__s__Bacteroides_thetaiotaomicron	0.0874	1.0913 (0.968-1.23)	0.15	0.29	0.0672	1.0696 (0.819-1.4)	0.62	1
LKT__s__Clostridium_symbiosum	-0.103	0.90234 (0.755-1.08)	0.26	0.34	0.0666	1.0688 (0.841-1.36)	0.59	0
LKT__s__Streptococcus_mutans	0.0456	1.0467 (0.953-1.15)	0.34	0.39	0.0646	1.0667 (0.695-1.64)	0.77	1
LKT__s__Butyricimonas_virosa	0.0621	1.0641 (0.976-1.16)	0.16	0.29	0.0645	1.0666 (0.911-1.25)	0.42	1
LKT__s__Dialister_invisus	0.016	1.0161 (0.946-1.09)	0.66	0.49	0.064	1.0661 (0.949-1.2)	0.28	1
LKT__g__Acidaminococcus	0.0613	1.0633 (0.98-1.15)	0.14	0.28	0.0637	1.0658 (0.941-1.21)	0.32	1
LKT__s__Adlercreutzia_equolifaciens	-0.0569	0.94466 (0.873-1.02)	0.16	0.29	0.0629	1.0649 (0.844-1.34)	0.60	0
LKT__s__Acidaminococcus_Unclassified	0.0528	1.0542 (0.975-1.14)	0.18	0.31	0.061	1.0629 (0.914-1.24)	0.43	1
LKT__s__Akkermansia_muciniphila	0.0628	1.0648 (0.988-1.15)	0.10	0.24	0.0593	1.0611 (0.934-1.21)	0.36	1
LKT__s__Butyricimonas_faecihominis	0.0202	1.0205 (0.935-1.11)	0.65	0.49	0.0552	1.0567 (0.883-1.26)	0.55	1
LKT__s__Collinsella_intestinalis	-0.113	0.89343 (0.799-0.999)	0.05	0.21	0.0539	1.0553 (0.866-1.29)	0.59	0
LKT__g__Eggerthella	-0.0895	0.91442 (0.809-1.03)	0.15	0.29	0.0523	1.0537 (0.801-1.39)	0.71	0
LKT__s__Bacteroides_coprocola	0.0882	1.0922 (1.01-1.18)	0.03	0.21	0.0497	1.051 (0.888-1.24)	0.56	1
LKT__s__Romboutsia_timonensis	0.0273	1.0277 (0.944-1.12)	0.53	0.47	0.0465	1.0476 (0.852-1.29)	0.66	1
LKT__s__Faecalimonas_umbilicata	-0.11	0.89558 (0.798-1)	0.06	0.21	0.0463	1.0474 (0.755-1.45)	0.78	0
LKT__s__Veillonella_parvula	0.0742	1.077 (0.981-1.18)	0.12	0.26	0.0455	1.0466 (0.709-1.54)	0.82	1
LKT__g__Oscillibacter	0.0214	1.0216 (0.861-1.21)	0.81	0.55	0.0455	1.0466 (0.825-1.33)	0.71	1
LKT__s__Gordonibacter_pamelaeae	-0.0422	0.95868 (0.876-1.05)	0.36	0.40	0.0389	1.0397 (0.813-1.33)	0.76	0
LKT__s__Bacteroides_eggerthii	0.0112	1.0113 (0.923-1.11)	0.81	0.55	0.0375	1.0382 (0.894-1.21)	0.62	1

LKT__s__Sellimonas_intestinalis	-0.0722	0.93032 (0.841-1.03)	0.16	0.29	0.035	1.0356 (0.78-1.37)	0.81	0
LKT__s__Actinomyces_bouchesdurhonensis	-0.122	0.88487 (0.768-1.02)	0.09	0.23	0.0339	1.0345 (0.58-1.84)	0.91	0
LKT__s__Sutterella_wadsworthensis	0.0434	1.0444 (0.963-1.13)	0.30	0.37	0.0334	1.034 (0.916-1.17)	0.59	1
LKT__s__Anaerotruncus_colihominis	-0.0602	0.94159 (0.766-1.16)	0.57	0.48	0.033	1.0335 (0.633-1.69)	0.90	0
LKT__s__Lactobacillus_fermentum	0.0236	1.0239 (0.942-1.11)	0.58	0.48	0.0316	1.0321 (0.833-1.28)	0.77	1
LKT__g__Enterobacter	0.00121	1.0012 (0.911-1.1)	0.98	0.59	0.0306	1.0311 (0.701-1.52)	0.88	1
LKT__s__Catenibacterium_mitsuokai	-0.148	0.86265 (0.734-1.01)	0.07	0.23	0.0305	1.0309 (0.819-1.3)	0.80	0
LKT__s__Hungatella_hathewayi	0.0224	1.0226 (0.819-1.28)	0.84	0.56	0.0301	1.0306 (0.74-1.43)	0.86	1
LKT__s__Emergencia_timonensis	0.00573	1.0057 (0.921-1.1)	0.90	0.57	0.0262	1.0266 (0.845-1.25)	0.79	1
LKT__s__Parabacteroides_merdae	0.13	1.1385 (1.02-1.28)	0.03	0.21	0.0247	1.0251 (0.858-1.22)	0.78	1
LKT__s__Erysipelatoclostridium_ramosum	-0.105	0.89994 (0.809-1)	0.05	0.21	0.0238	1.0241 (0.758-1.38)	0.88	0
LKT__s__Burkholderiales_bacterium	-0.00671	0.99332 (0.911-1.08)	0.88	0.56	0.0214	1.0216 (0.89-1.17)	0.76	0
LKT__g__Veillonella	0.101	1.106 (0.978-1.25)	0.11	0.25	0.0175	1.0176 (0.738-1.4)	0.92	1
LKT__s__Dorea_formicigenerans	-0.135	0.87345 (0.754-1.01)	0.07	0.22	0.0167	1.0168 (0.685-1.51)	0.93	0
LKT__s__Bilophila_wadsworthia	0.0514	1.0527 (0.968-1.15)	0.23	0.32	0.0166	1.0167 (0.893-1.16)	0.80	1
LKT__s__CrAssphage_ZA	0.0197	1.0199 (0.943-1.1)	0.62	0.49	0.0162	1.0164 (0.923-1.12)	0.74	1
LKT__s__Haemophilus_parainfluenzae	0.0814	1.0848 (0.975-1.21)	0.14	0.27	0.012	1.0121 (0.823-1.24)	0.91	1
LKT__s__Victivallis_vadensis	0.088	1.092 (0.987-1.21)	0.09	0.23	0.0108	1.0109 (0.796-1.28)	0.93	1
LKT__s__Butyricimonas_paravirosa	0.0585	1.0603 (0.957-1.17)	0.26	0.34	0.0105	1.0106 (0.782-1.31)	0.94	1
LKT__s__Faecalitalea_cylindroides	0.065	1.0672 (0.972-1.17)	0.17	0.30	0.00824	1.0083 (0.763-1.33)	0.95	1
LKT__s__Roseburia_inulinivorans	-0.0421	0.95874 (0.84-1.09)	0.53	0.47	0.00774	1.0078 (0.789-1.29)	0.95	0
LKT__s__Oscillibacter_Unclassified	0.0981	1.1031 (0.971-1.25)	0.13	0.27	0.00726	1.0073 (0.782-1.3)	0.96	1
LKT__s__Ruminococcus_gnavus	-0.224	0.79927 (0.692-0.923)	2.36E-03	0.05	0.00665	1.0067 (0.611-1.66)	0.98	0
LKT__s__Anaerobutyricum_hallii	-0.0191	0.98106 (0.896-1.07)	0.68	0.50	0.00422	1.0042 (0.828-1.22)	0.97	0
LKT__g__Bacteroides	0.0994	1.1045 (0.885-1.38)	0.38	0.41	0.00362	1.0036 (0.488-2.06)	0.99	1
LKT__s__Parasutterella_excrementihominis	-0.00475	0.99526 (0.925-1.07)	0.90	0.57	0.000783	1.0008 (0.89-1.13)	0.99	0
LKT__g__Collinsella	-0.00159	0.99841 (0.888-1.12)	0.98	0.59	0.000769	1.0008 (0.812-1.23)	0.99	0
LKT__s__Acinetobacter_baumannii	0.177	1.1931 (1.04-1.36)	0.01	0.11	-0.000585	0.99942 (0.871-1.15)	0.99	0
LKT__s__Collinsella_Unclassified	0.00286	1.0029 (0.915-1.1)	0.95	0.59	-0.00129	0.99871 (0.837-1.19)	0.99	0
LKT__s__Alistipes_dispar	0.0789	1.0821 (1-1.17)	0.04	0.21	-0.00176	0.99824 (0.849-1.17)	0.98	0
LKT__s__Enterobacter_cloacae	-0.0322	0.96834 (0.873-1.07)	0.54	0.48	-0.00219	0.99782 (0.658-1.51)	0.99	1
LKT__s__Collinsella_stercoris	-0.103	0.90169 (0.807-1.01)	0.07	0.22	-0.00414	0.99587 (0.775-1.28)	0.97	1
LKT__s__Alistipes_putredinis	0.0274	1.0278 (0.946-1.12)	0.51	0.47	-0.00434	0.99567 (0.883-1.12)	0.94	0
LKT__s__Haemophilus_Unclassified	0.112	1.1187 (0.996-1.26)	0.06	0.21	-0.00537	0.99464 (0.78-1.27)	0.97	0
LKT__s__Eggerthella_Unclassified	-0.0665	0.93562 (0.847-1.03)	0.19	0.31	-0.00574	0.99428 (0.73-1.35)	0.97	1
LKT__s__Bacteroides_intestinalis	0.00716	1.0072 (0.92-1.1)	0.88	0.56	-0.00703	0.99299 (0.837-1.18)	0.94	0
LKT__s__Klebsiella_pneumoniae	-0.0338	0.9668 (0.89-1.05)	0.43	0.43	-0.00751	0.99252 (0.81-1.22)	0.94	1
LKT__s__Bilophila_Unclassified	0.0253	1.0256 (0.934-1.13)	0.60	0.48	-0.00789	0.99214 (0.854-1.15)	0.92	0
LKT__s__Lachnospira_eligens	0.0666	1.0688 (0.929-1.23)	0.35	0.40	-0.00796	0.99208 (0.802-1.23)	0.94	0
LKT__s__Streptococcus_Unclassified	-0.00988	0.99017 (0.896-1.09)	0.85	0.56	-0.0103	0.98971 (0.752-1.3)	0.94	1
LKT__g__Haemophilus	0.113	1.1199 (1-1.25)	0.05	0.21	-0.0113	0.98876 (0.814-1.2)	0.91	0
LKT__g__Butyricimonas	0.0926	1.0971 (0.984-1.22)	0.10	0.23	-0.0113	0.98877 (0.796-1.23)	0.92	0
LKT__o__Burkholderiales	0.0134	1.0135 (0.907-1.13)	0.81	0.55	-0.012	0.98803 (0.845-1.16)	0.88	0
LKT__s__Mogibacterium_diversum	-0.204	0.81523 (0.712-0.934)	3.18E-03	0.06	-0.0126	0.98747 (0.716-1.36)	0.94	1
LKT__s__Alistipes_shahii	0.035	1.0357 (0.95-1.13)	0.43	0.43	-0.0127	0.98735 (0.845-1.15)	0.87	0
LKT__s__Eubacterium_ventriosum	-0.0355	0.96517 (0.859-1.08)	0.55	0.48	-0.0131	0.98697 (0.817-1.19)	0.89	1
LKT__s__Odoribacter_splanchnicus	0.0833	1.0868 (0.998-1.18)	0.06	0.21	-0.0176	0.98257 (0.846-1.14)	0.82	0
LKT__s__Ruminococcus_callidus	0.0462	1.0473 (0.97-1.13)	0.24	0.33	-0.019	0.98115 (0.822-1.17)	0.83	0
LKT__s__Cyclospora_cayetanensis	0.0554	1.0569 (0.887-1.26)	0.54	0.47	-0.0236	0.9767 (0.753-1.27)	0.86	0
LKT__s__Lachnospira_pectinoschiza	0.0368	1.0375 (0.957-1.12)	0.37	0.40	-0.024	0.97624 (0.853-1.12)	0.73	0
LKT__g__Anaerostipes	-0.13	0.87828 (0.779-0.99)	0.03	0.21	-0.0244	0.97592 (0.724-1.31)	0.87	1
LKT__s__Bacteroides_cellulosilyticus	0.0794	1.0827 (0.998-1.17)	0.06	0.21	-0.0252	0.97513 (0.856-1.11)	0.71	0
LKT__s__Roseburia_Unclassified	0.0191	1.0193 (0.901-1.15)	0.76	0.53	-0.0252	0.9751 (0.699-1.36)	0.88	0
LKT__s__Bacteroides_nordii	0.0367	1.0374 (0.947-1.14)	0.43	0.43	-0.0265	0.97381 (0.818-1.16)	0.77	0
LKT__s__Streptococcus_salivarius	-0.0308	0.96963 (0.894-1.05)	0.46	0.45	-0.0273	0.97308 (0.761-1.24)	0.83	1
LKT__s__Klebsiella_variicola	0.018	1.0181 (0.9-1.15)	0.78	0.54	-0.028	0.97238 (0.741-1.28)	0.84	0
LKT__f__Coriobacteriaceae	-0.0318	0.96869 (0.857-1.09)	0.61	0.49	-0.0281	0.9723 (0.828-1.14)	0.73	1
LKT__s__Enterococcus_faecium	-0.0231	0.97718 (0.844-1.13)	0.76	0.53	-0.0281	0.97227 (0.766-1.23)	0.82	1
LKT__s__Roseburia_faecis	0.0131	1.0132 (0.93-1.1)	0.76	0.53	-0.0282	0.97219 (0.84-1.12)	0.70	0
LKT__s__Alloscardovia_omnicolens	-0.0423	0.95858 (0.845-1.09)	0.51	0.47	-0.0291	0.97133 (0.447-2.11)	0.94	1
LKT__s__Anaerotruncus_Unclassified	0.00612	1.0061 (0.895-1.13)	0.92	0.58	-0.0315	0.96904 (0.729-1.29)	0.83	0
LKT__s__Bacteroides_dorei	0.122	1.1301 (1.01-1.26)	0.03	0.21	-0.0322	0.96836 (0.755-1.24)	0.80	0
LKT__s__Odoribacter_laneus	0.0686	1.071 (0.99-1.16)	0.09	0.23	-0.0322	0.96827 (0.8-1.17)	0.74	0
LKT__s__Blautia_coccoides	-0.217	0.80514 (0.694-0.934)	4.16E-03	0.07	-0.0341	0.9665 (0.75-1.25)	0.79	1
LKT__s__Anaeromassilibacillus_Unclassified	-0.0453	0.95574 (0.861-1.06)	0.40	0.41	-0.0349	0.9657 (0.788-1.18)	0.74	1
LKT__g__Lactobacillus	0.0621	1.0641 (0.951-1.19)	0.28	0.36	-0.0353	0.96536 (0.752-1.24)	0.78	0
LKT__s__Dorea_longicatena	-0.0806	0.92257 (0.821-1.04)	0.18	0.30	-0.0363	0.96435 (0.734-1.27)	0.80	1
LKT__s__Ruminococcus_torques	-0.117	0.88972 (0.796-0.995)	0.04	0.21	-0.0385	0.96223 (0.714-1.3)	0.80	1
LKT__s__Collinsella_aerofaciens	0.00824	1.0083 (0.943-1.08)	0.81	0.55	-0.0394	0.96135 (0.814-1.13)	0.64	0
LKT__s__Barnesiella_intestinihominis	0.0213	1.0215 (0.947-1.1)	0.58	0.48	-0.0408	0.96 (0.856-1.08)	0.49	0
LKT__s__Longibaculum_muris	0.0161	1.0162 (0.931-1.11)	0.72	0.51	-0.0409	0.95991 (0.777-1.19)	0.71	0
LKT__s__Coriobacteriaceae_bacterium	-0.0215	0.97872 (0.892-1.07)	0.65	0.49	-0.0437	0.95729 (0.756-1.21)	0.72	1
LKT__s__Intestinibacter_bartlettii	-0.0391	0.96163 (0.884-1.05)	0.37	0.40	-0.0439	0.95707 (0.791-1.16)	0.65	1
LKT__s__Anaeromassilibacillus_senegalensis	-0.00662	0.9934 (0.907-1.09)	0.89	0.57	-0.0439	0.95706 (0.76-1.21)	0.71	1
LKT__s__Alistipes_communis	0.063	1.0651 (0.977-1.16)	0.15	0.29	-0.0457	0.95537 (0.827-1.1)	0.53	0
LKT__s__Bacteroides_ovatus	0.0714	1.074 (0.969-1.19)	0.17	0.30	-0.0457	0.9553 (0.787-1.16)	0.64	0
LKT__s__Roseburia_hominis	0.0311	1.0315 (0.912-1.17)	0.62	0.49	-0.0471	0.95395 (0.773-1.18)	0.66	0
LKT__s__Ruminococcus_lactaris	-0.0306	0.96982 (0.85-1.11)	0.65	0.49	-0.048	0.9531 (0.758-1.2)	0.68	1
LKT__s__Coprobacillus_cateniformis	-0.00198	0.99802 (0.894-1.11)	0.97	0.59	-0.048	0.95316 (0.741-1.23)	0.71	1
LKT__s__Veillonella_dispar	0.0883	1.0923 (0.975-1.22)	0.13	0.27	-0.0495	0.95169 (0.696-1.3)	0.76	0
LKT__s__Bacteroides_caccae	0.15	1.1614 (1.05-1.29)	4.19E-03	0.07	-0.053	0.94837 (0.797-1.13)	0.55	0
LKT__s__Agathobaculum_butyriciproducens	0.113	1.12 (0.97-1.29)	0.12	0.26	-0.0535	0.94792 (0.738-1.22)	0.68	0
LKT__g__Parabacteroides	0.0892	1.0933 (0.923-1.3)	0.30	0.37	-0.0535	0.94788 (0.787-1.14)	0.57	0
LKT__s__Senegalimassilia_anaerobia	-0.0257	0.97459 (0.883-1.08)	0.61	0.49	-0.0546	0.94685 (0.578-1.55)	0.83	1
LKT__s__Acidaminococcus_fermentans	0.154	1.1659 (1.04-1.31)	0.01	0.11	-0.0559	0.94561 (0.697-1.28)	0.72	0
LKT__s__Parabacteroides_johnsonii	0.00692	1.0069 (0.921-1.1)	0.88	0.56	-0.0572	0.94441 (0.814-1.1)	0.45	0
LKT__s__Actinomyces_Unclassified	-0.118	0.88901 (0.783-1.01)	0.07	0.22	-0.0587	0.94301 (0.602-1.48)	0.80	1
LKT__s__Gemmiger_formicilis	0.00776	1.0078 (0.927-1.1)	0.86	0.56	-0.0591	0.94259 (0.815-1.09)	0.43	0
LKT__s__Collinsella_tanakaei	-0.0724	0.93018 (0.831-1.04)	0.21	0.32	-0.0595	0.94225 (0.667-1.33)	0.74	1
LKT__s__Bacteroides_salyersiae	0.0706	1.0731 (0.975-1.18)	0.15	0.28	-0.061	0.94086 (0.782-1.13)	0.52	0

LKT__f__Rikenellaceae	0.096	1.1007 (0.939-1.29)	0.24	0.32	-0.0613	0.94059 (0.781-1.13)	0.52	0
LKT__s__Bacteriophage_Unclassified	0.0563	1.0579 (0.958-1.17)	0.27	0.35	-0.0633	0.93864 (0.775-1.14)	0.52	0
LKT__s__Bacteroides_ilei	0.0798	1.0831 (0.998-1.18)	0.06	0.21	-0.0643	0.93768 (0.766-1.15)	0.53	0
LKT__s__Clostridiaceae_bacterium	-0.0443	0.95667 (0.793-1.15)	0.64	0.49	-0.0643	0.93774 (0.662-1.33)	0.72	1
LKT__s__Bacteroides_finegoldii	0.069	1.0714 (0.969-1.18)	0.18	0.30	-0.0698	0.93259 (0.773-1.13)	0.47	0
LKT__s__Oxalobacter_formigenes	0.242	1.2741 (1.12-1.45)	2.05E-04	0.01	-0.0701	0.93226 (0.726-1.2)	0.58	0
LKT__s__Clostridiales_bacterium	0.0872	1.0911 (0.886-1.34)	0.41	0.42	-0.0707	0.93175 (0.644-1.35)	0.71	0
LKT__s__Eubacterium_siraeum	0.063	1.065 (0.964-1.18)	0.22	0.32	-0.0714	0.93112 (0.797-1.09)	0.37	0
LKT__s__Schaalia_odontolytica	-0.124	0.88369 (0.789-0.99)	0.03	0.21	-0.0722	0.93033 (0.572-1.51)	0.77	1
LKT__s__Candidatus_Borkfalkia	0.047	1.0481 (0.96-1.14)	0.30	0.37	-0.0725	0.93005 (0.801-1.08)	0.34	0
LKT__s__Bacteroidaceae_bacterium	0.0762	1.0792 (0.987-1.18)	0.10	0.23	-0.0728	0.92981 (0.806-1.07)	0.32	0
LKT__s__Clostridia_bacterium	-0.0303	0.97012 (0.878-1.07)	0.55	0.48	-0.0728	0.92983 (0.727-1.19)	0.56	1
LKT__s__Streptococcus_thermophilus	-0.0525	0.94888 (0.873-1.03)	0.22	0.32	-0.0737	0.92894 (0.736-1.17)	0.53	1
LKT__s__Parabacteroides_distasonis	0.0137	1.0138 (0.934-1.1)	0.74	0.52	-0.0742	0.92848 (0.807-1.07)	0.30	0
LKT__s__Porphyromonas_asaccharolytica	0.094	1.0986 (0.994-1.21)	0.07	0.22	-0.0757	0.92708 (0.701-1.23)	0.60	0
LKT__s__Alistipes_finegoldii	0.0259	1.0262 (0.937-1.12)	0.58	0.48	-0.0763	0.92652 (0.826-1.04)	0.19	0
LKT__s__Streptococcus_oralis	0.00302	1.003 (0.873-1.15)	0.97	0.59	-0.0764	0.92645 (0.554-1.55)	0.77	0
LKT__s__Bifidobacterium_gallinarum	-0.0253	0.97499 (0.847-1.12)	0.73	0.52	-0.0781	0.92491 (0.267-3.2)	0.90	1
LKT__s__Sutterella_Unclassified	-0.00912	0.99092 (0.895-1.1)	0.86	0.56	-0.0787	0.92431 (0.765-1.12)	0.42	1
LKT__s__Ruminococcus_bromii	0.0598	1.0617 (0.963-1.17)	0.23	0.32	-0.0794	0.92371 (0.774-1.1)	0.38	0
LKT__s__Bacteroides_faecis	0.098	1.103 (0.989-1.23)	0.08	0.23	-0.0802	0.92294 (0.604-1.41)	0.71	0
LKT__s__Sporobacter_termitidis	0.0878	1.0918 (0.98-1.22)	0.11	0.25	-0.0828	0.92052 (0.731-1.16)	0.48	0
LKT__s__Parabacteroides_goldsteinii	0.0239	1.0242 (0.942-1.11)	0.58	0.48	-0.0828	0.9205 (0.767-1.1)	0.37	0
LKT__s__Holdemania_Unclassified	-0.00541	0.99461 (0.885-1.12)	0.93	0.58	-0.0853	0.91822 (0.738-1.14)	0.44	1
LKT__s__Holdemania_filiformis	0.028	1.0284 (0.904-1.17)	0.67	0.49	-0.0854	0.9181 (0.771-1.09)	0.34	0
LKT__s__Clostridium_phoceensis	0.0339	1.0344 (0.893-1.2)	0.65	0.49	-0.0891	0.91476 (0.756-1.11)	0.36	0
LKT__s__Bittarella_massiliensis	-0.074	0.92868 (0.795-1.08)	0.35	0.40	-0.0894	0.91445 (0.673-1.24)	0.57	1
LKT__s__Clostridium_perfringens	0.0173	1.0174 (0.926-1.12)	0.72	0.51	-0.09	0.91396 (0.743-1.12)	0.39	0
LKT__s__Blautia_massiliensis	-0.0147	0.98539 (0.906-1.07)	0.73	0.52	-0.0908	0.91322 (0.624-1.34)	0.64	1
LKT__f__Sutterellaceae	0.0432	1.0442 (0.945-1.15)	0.40	0.41	-0.0917	0.91237 (0.746-1.12)	0.37	0
LKT__s__Blautia_hansenii	-0.0817	0.92151 (0.832-1.02)	0.12	0.26	-0.0922	0.91192 (0.698-1.19)	0.50	1
LKT__s__Eubacterium_rectale	-0.079	0.92403 (0.828-1.03)	0.16	0.29	-0.0959	0.90859 (0.686-1.2)	0.50	1
LKT__s__Streptococcus_viridans	-0.0714	0.9311 (0.798-1.09)	0.36	0.40	-0.0985	0.9062 (0.456-1.8)	0.78	1
LKT__s__Alistipes_onderdonkii	0.0157	1.0158 (0.942-1.1)	0.69	0.50	-0.0993	0.9055 (0.808-1.02)	0.09	0
LKT__s__Blautia_hydrogenotrophica	-0.109	0.89695 (0.805-1)	0.05	0.21	-0.0995	0.90525 (0.695-1.18)	0.46	1
LKT__s__Fusicatenibacter_Unclassified	-0.0511	0.95022 (0.846-1.07)	0.39	0.41	-0.0995	0.90527 (0.686-1.2)	0.48	1
LKT__s__Subdoligranulum_variabile	0.0693	1.0717 (0.943-1.22)	0.29	0.37	-0.101	0.90369 (0.725-1.13)	0.37	0
LKT__s__Anaerotruncus_massiliensis	0.0436	1.0446 (0.949-1.15)	0.37	0.40	-0.102	0.90323 (0.738-1.11)	0.33	0
LKT__s__Butyricicoccus_pullicaecorum	0.0384	1.0391 (0.92-1.17)	0.54	0.47	-0.102	0.90318 (0.715-1.14)	0.39	0
LKT__s__Phascolarctobacterium_faecium	0.0197	1.0199 (0.953-1.09)	0.57	0.48	-0.102	0.9032 (0.802-1.02)	0.09	0
LKT__s__Turicibacter_sanguinis	0.0514	1.0527 (0.967-1.15)	0.24	0.32	-0.103	0.90237 (0.688-1.18)	0.46	0
LKT__s__Alistipes_timonensis	0.102	1.1076 (0.988-1.24)	0.08	0.23	-0.104	0.90094 (0.758-1.07)	0.24	0
LKT__s__Flintibacter_Unclassified	0.0817	1.0851 (0.959-1.23)	0.20	0.32	-0.104	0.90131 (0.694-1.17)	0.44	0
LKT__s__Bifidobacterium_adolescentis	-0.0488	0.95233 (0.884-1.03)	0.20	0.32	-0.104	0.90127 (0.748-1.09)	0.27	1
LKT__o__Bacillales	0.0221	1.0223 (0.855-1.22)	0.81	0.55	-0.104	0.90165 (0.685-1.19)	0.46	0
LKT__s__Bacteroides_vulgatus	0.0984	1.1034 (0.967-1.26)	0.14	0.28	-0.106	0.89962 (0.66-1.23)	0.50	0
LKT__s__Allisonella_histaminiformans	0.0921	1.0965 (0.946-1.27)	0.22	0.32	-0.107	0.89827 (0.646-1.25)	0.52	0
LKT__f__Clostridiaceae	0.148	1.1592 (0.876-1.53)	0.30	0.37	-0.107	0.89878 (0.61-1.32)	0.59	0
LKT__s__Subdoligranulum_Unclassified	0.104	1.1091 (0.946-1.3)	0.20	0.32	-0.113	0.89306 (0.629-1.27)	0.53	0
LKT__s__Bifidobacterium_longum	-0.0262	0.97417 (0.902-1.05)	0.51	0.47	-0.113	0.89311 (0.763-1.05)	0.16	1
LKT__g__Alistipes	0.0348	1.0354 (0.889-1.21)	0.65	0.49	-0.113	0.89338 (0.755-1.06)	0.19	0
LKT__s__Victivallales_bacterium	0.0828	1.0863 (0.997-1.18)	0.06	0.21	-0.115	0.89151 (0.631-1.26)	0.52	0
LKT__s__Coprobacter_fastidiosus	0.0532	1.0546 (0.962-1.16)	0.26	0.34	-0.115	0.89135 (0.756-1.05)	0.17	0
LKT__s__Enterobacter_hormaechei	0.0461	1.0472 (0.956-1.15)	0.32	0.38	-0.115	0.89125 (0.641-1.24)	0.49	0
LKT__s__Anaerostipes_caccae	-0.119	0.88746 (0.791-0.995)	0.04	0.21	-0.116	0.89054 (0.628-1.26)	0.52	1
LKT__s__Faecalibacterium_prausnitzii	0.0824	1.0859 (0.948-1.24)	0.23	0.32	-0.116	0.8905 (0.714-1.11)	0.30	0
LKT__s__Coprococcus_comes	-0.0709	0.9316 (0.821-1.06)	0.27	0.35	-0.12	0.88666 (0.707-1.11)	0.30	1
LKT__f__Oscillospiraceae	-0.0146	0.98555 (0.817-1.19)	0.88	0.56	-0.12	0.88678 (0.697-1.13)	0.33	1
LKT__s__Oscillibacter_valericigenes	0.104	1.1097 (0.965-1.28)	0.14	0.28	-0.121	0.8856 (0.725-1.08)	0.23	0
LKT__s__Firmicutes_bacterium	-0.107	0.89816 (0.784-1.03)	0.12	0.26	-0.122	0.88505 (0.662-1.18)	0.41	1
LKT__s__Intestinimonas_massiliensis	0.116	1.1225 (0.941-1.34)	0.20	0.32	-0.122	0.88496 (0.645-1.21)	0.45	0
LKT__s__Lactobacillus_crispatus	-0.0547	0.94676 (0.845-1.06)	0.35	0.39	-0.122	0.88481 (0.66-1.19)	0.41	1
LKT__s__Rikenellaceae_bacterium	0.0387	1.0395 (0.93-1.16)	0.50	0.46	-0.122	0.88491 (0.734-1.07)	0.20	0
LKT__s__Ruminococcus_champanellensis	0.0744	1.0773 (0.963-1.21)	0.19	0.32	-0.124	0.88322 (0.702-1.11)	0.29	0
LKT__f__Lachnospiraceae	-0.431	0.64976 (0.469-0.9)	0.01	0.11	-0.125	0.88212 (0.402-1.94)	0.75	1
LKT__s__Bacteroides_xylanisolvens	0.00351	1.0035 (0.903-1.12)	0.95	0.59	-0.125	0.88292 (0.675-1.15)	0.36	0
LKT__g__Ruminococcus	-0.000565	0.99943 (0.842-1.19)	1.00	0.60	-0.125	0.88256 (0.582-1.34)	0.56	1
LKT__g__Pseudoflavonifractor	0.137	1.1471 (0.996-1.32)	0.06	0.21	-0.126	0.88157 (0.695-1.12)	0.30	0
LKT__s__Clostridium_disporicum	0.0182	1.0184 (0.941-1.1)	0.65	0.49	-0.127	0.88092 (0.722-1.08)	0.21	0
LKT__s__Ruthenibacterium_lactatiformans	0.0845	1.0882 (0.97-1.22)	0.15	0.29	-0.13	0.87801 (0.63-1.22)	0.44	0
LKT__f__Synergistaceae	0.0173	1.0174 (0.89-1.16)	0.80	0.55	-0.13	0.87845 (0.624-1.24)	0.46	0
LKT__s__Ruminococcus_Unclassified	-0.0155	0.98459 (0.863-1.12)	0.82	0.55	-0.13	0.8782 (0.656-1.17)	0.38	1
LKT__s__Arabia_massiliensis	-0.00498	0.99503 (0.885-1.12)	0.93	0.58	-0.132	0.87627 (0.481-1.6)	0.67	1
LKT__s__Alistipes_senegalensis	0.105	1.1106 (1.01-1.23)	0.04	0.21	-0.134	0.87422 (0.746-1.02)	0.10	0
LKT__s__Eubacterium_callanderi	-0.0314	0.96907 (0.881-1.07)	0.52	0.47	-0.134	0.87466 (0.653-1.17)	0.37	1
LKT__f__Erysipelotrichaceae	-0.209	0.81155 (0.668-0.986)	0.04	0.21	-0.135	0.87388 (0.55-1.39)	0.57	1
LKT__s__Ruminococcus_flavefaciens	0.0887	1.0928 (0.97-1.23)	0.14	0.28	-0.137	0.87223 (0.731-1.04)	0.13	0
LKT__s__Agathobaculum_desmolans	0.109	1.1154 (0.949-1.31)	0.19	0.31	-0.138	0.87107 (0.606-1.25)	0.46	0
LKT__s__Clostridium_innocuum	-0.0587	0.94302 (0.845-1.05)	0.30	0.37	-0.14	0.86942 (0.578-1.31)	0.50	1
LKT__s__Roseburia_intestinalis	-0.0619	0.93996 (0.83-1.06)	0.33	0.38	-0.141	0.8683 (0.662-1.14)	0.31	1
LKT__s__Streptomyces_Unclassified	0.147	1.1586 (1.02-1.32)	0.03	0.21	-0.143	0.86698 (0.666-1.13)	0.29	0
LKT__s__Oscillibacter_ruminantium	0.0753	1.0782 (0.948-1.23)	0.25	0.34	-0.144	0.8656 (0.694-1.08)	0.20	0
LKT__s__Dysosmobacter_welbionis	0.087	1.0908 (0.923-1.29)	0.31	0.37	-0.145	0.86486 (0.612-1.22)	0.41	0
LKT__s__Frisingicoccus_caecimuris	-0.0258	0.97453 (0.874-1.09)	0.64	0.49	-0.145	0.86493 (0.66-1.13)	0.29	1
LKT__g__Faecalibacterium	0.14	1.1503 (0.979-1.35)	0.09	0.23	-0.149	0.86127 (0.693-1.07)	0.18	0
LKT__s__Anaerostipes_hadrus	-0.0505	0.95073 (0.88-1.03)	0.20	0.32	-0.149	0.86157 (0.711-1.04)	0.13	1
LKT__s__Methanobrevibacter_smithii	-0.0157	0.98444 (0.912-1.06)	0.69	0.50	-0.149	0.86167 (0.575-1.29)	0.47	1
LKT__s__Intestinimonas_butyriciproducens	0.0734	1.0762 (0.955-1.21)	0.23	0.32	-0.15	0.86113 (0.676-1.1)	0.23	0
LKT__s__Muribaculaceae_bacterium	0.0887	1.0927 (0.985-1.21)	0.09	0.23	-0.153	0.8578 (0.69-1.07)	0.17	0
LKT__s__Eubacteriaceae_bacterium	-0.0969	0.90768 (0.809-1.02)	0.10	0.23	-0.153	0.85849 (0.64-1.15)	0.31	1

LKT__s__Parabacteroides_Unclassified	0.041	1.0418 (0.943-1.15)	0.42	0.43	-0.153	0.85784 (0.734-1)	0.05	0
LKT__s__Lactobacillus_rhamnosus	0.122	1.1296 (1.02-1.25)	0.01	0.14	-0.154	0.85766 (0.605-1.22)	0.39	0
LKT__s__Coprococcus_catus	-0.0375	0.96323 (0.848-1.09)	0.57	0.48	-0.155	0.85617 (0.574-1.28)	0.45	1
LKT__s__Duncaniella_Unclassified	0.0901	1.0942 (0.974-1.23)	0.13	0.27	-0.156	0.85552 (0.663-1.1)	0.23	0
LKT__s__Cloacibacillus_evryensis	0.00244	1.0024 (0.889-1.13)	0.97	0.59	-0.158	0.85376 (0.457-1.59)	0.62	0
LKT__s__Phascolarctobacterium_succinatutens	0.00356	1.0036 (0.917-1.1)	0.94	0.58	-0.159	0.85275 (0.712-1.02)	0.08	0
LKT__s__Ruminococcaceae_bacterium	-0.0572	0.94441 (0.79-1.13)	0.53	0.47	-0.16	0.85249 (0.647-1.12)	0.26	1
LKT__k__Bacteria	0.733	2.0817 (1.24-3.5)	0.01	0.08	-0.163	0.84973 (0.288-2.5)	0.77	0
LKT__g__Coprobacillus	-0.0276	0.97276 (0.865-1.09)	0.64	0.49	-0.164	0.84901 (0.687-1.05)	0.13	1
LKT__s__Neglecta_timonensis	-0.0723	0.93028 (0.846-1.02)	0.14	0.27	-0.166	0.84702 (0.686-1.05)	0.12	1
LKT__s__Gordonibacter_urolithinfaciens	-0.0675	0.93474 (0.854-1.02)	0.14	0.28	-0.168	0.84501 (0.607-1.18)	0.32	1
LKT__s__Clostridium_spiroforme	-0.011	0.98907 (0.903-1.08)	0.81	0.55	-0.168	0.84497 (0.677-1.05)	0.14	1
LKT__s__Blautia_wexlerae	-0.108	0.89784 (0.814-0.99)	0.03	0.21	-0.171	0.84255 (0.627-1.13)	0.26	1
LKT__g__Butyricicoccus	-0.0368	0.96383 (0.822-1.13)	0.65	0.49	-0.175	0.83986 (0.629-1.12)	0.24	1
LKT__s__Phocea_massiliensis	-0.0318	0.96867 (0.819-1.15)	0.71	0.51	-0.176	0.83882 (0.629-1.12)	0.23	1
LKT__s__Eubacterium_ramulus	-0.0289	0.97152 (0.876-1.08)	0.58	0.48	-0.177	0.83779 (0.677-1.04)	0.10	1
LKT__s__Anaerofustis_stercorihominis	-0.0541	0.94736 (0.829-1.08)	0.43	0.43	-0.178	0.83713 (0.639-1.1)	0.20	1
LKT__s__Flavonifractor_plautii	0.00229	1.0023 (0.826-1.22)	0.98	0.59	-0.178	0.83727 (0.555-1.26)	0.40	0
LKT__s__Marvinbryantia_formatexigens	0.0512	1.0525 (0.912-1.21)	0.48	0.46	-0.179	0.83573 (0.624-1.12)	0.23	0
LKT__s__Eisenbergiella_massiliensis	-0.102	0.90267 (0.811-1)	0.06	0.21	-0.18	0.83494 (0.643-1.08)	0.18	1
LKT__s__Lachnospira_multipara	-0.037	0.96365 (0.854-1.09)	0.55	0.48	-0.183	0.83253 (0.593-1.17)	0.29	1
LKT__s__Alistipes_Unclassified	0.0352	1.0359 (0.953-1.13)	0.41	0.42	-0.184	0.83178 (0.685-1.01)	0.06	0
LKT__s__Lactococcus_lactis	-0.005	0.99501 (0.885-1.12)	0.93	0.58	-0.185	0.83129 (0.566-1.22)	0.35	1
LKT__s__Terrisporobacter_glycolicus	0.0495	1.0508 (0.939-1.18)	0.39	0.41	-0.186	0.83062 (0.534-1.29)	0.41	0
LKT__f__Eubacteriaceae	0.0904	1.0946 (0.964-1.24)	0.16	0.29	-0.187	0.82928 (0.659-1.04)	0.11	0
LKT__s__Clostridium_viride	-0.0628	0.93916 (0.82-1.08)	0.37	0.40	-0.187	0.8293 (0.6-1.15)	0.26	1
LKT__s__Bifidobacterium_bifidum	-0.0209	0.97932 (0.889-1.08)	0.67	0.49	-0.187	0.82955 (0.625-1.1)	0.20	1
LKT__s__Faecalibacterium_Unclassified	0.13	1.1385 (1.02-1.27)	0.02	0.19	-0.193	0.82434 (0.666-1.02)	0.08	0
LKT__s__Clostridium_botulinum	0.0627	1.0647 (0.963-1.18)	0.22	0.32	-0.195	0.82269 (0.674-1)	0.06	0
LKT__s__Pseudomonas_aeruginosa	0.0209	1.0211 (0.943-1.11)	0.61	0.49	-0.195	0.82309 (0.708-0.956)	0.01	0
LKT__s__Alistipes_indistinctus	0.0241	1.0244 (0.949-1.11)	0.54	0.47	-0.196	0.82226 (0.672-1.01)	0.06	0
LKT__s__Raoultibacter_massiliensis	-0.0196	0.98055 (0.895-1.07)	0.67	0.49	-0.197	0.82134 (0.462-1.46)	0.50	1
LKT__s__Slackia_piriformis	-0.0189	0.98132 (0.907-1.06)	0.64	0.49	-0.198	0.82037 (0.438-1.54)	0.54	1
LKT__s__Angelakisella_massiliensis	0.17	1.1858 (1.01-1.39)	0.04	0.21	-0.199	0.81951 (0.614-1.09)	0.18	0
LKT__s__Harryflintia_acetispora	0.0335	1.0341 (0.909-1.18)	0.61	0.49	-0.2	0.81844 (0.629-1.06)	0.14	0
LKT__g__Clostridium	0.218	1.2431 (0.999-1.55)	0.05	0.21	-0.202	0.81712 (0.642-1.04)	0.10	0
LKT__s__Clostridium_methylpentosum	-0.0961	0.90841 (0.815-1.01)	0.08	0.23	-0.208	0.81232 (0.592-1.11)	0.20	1
LKT__s__Clostridium_leptum	-0.0922	0.91188 (0.819-1.01)	0.09	0.23	-0.21	0.81021 (0.643-1.02)	0.07	1
LKT__s__Lachnoclostridium_phocaeense	0.0484	1.0496 (0.916-1.2)	0.49	0.46	-0.21	0.81039 (0.616-1.07)	0.13	0
LKT__s__Lachnospiraceae_bacterium	-0.265	0.76697 (0.633-0.93)	0.01	0.08	-0.211	0.81 (0.505-1.3)	0.38	1
LKT__s__Bacillus_Unclassified	0.199	1.2196 (1.04-1.43)	0.02	0.14	-0.214	0.80735 (0.638-1.02)	0.08	0
LKT__s__Fusicatenibacter_saccharivorans	-0.0467	0.95438 (0.862-1.06)	0.37	0.40	-0.214	0.807 (0.592-1.1)	0.18	1
LKT__s__Anaerotignum_lactatifermentans	0.0637	1.0658 (0.933-1.22)	0.35	0.39	-0.217	0.80476 (0.631-1.03)	0.08	0
LKT__c__Actinobacteria	0.138	1.1477 (0.965-1.37)	0.12	0.26	-0.218	0.80384 (0.602-1.07)	0.14	0
LKT__s__Coprococcus_eutactus	0.0723	1.0749 (0.937-1.23)	0.30	0.37	-0.218	0.80388 (0.593-1.09)	0.16	0
LKT__s__Bacteroides_fragilis	0.0459	1.047 (0.923-1.19)	0.47	0.45	-0.219	0.80333 (0.559-1.15)	0.24	0
LKT__s__Coprobacillus_Unclassified	-0.0478	0.95328 (0.866-1.05)	0.33	0.38	-0.22	0.80224 (0.597-1.08)	0.14	1
LKT__s__Sharpea_azabuensis	-0.0143	0.98576 (0.866-1.12)	0.83	0.55	-0.222	0.80095 (0.592-1.08)	0.15	1
LKT__s__Intestinimonas_timonensis	0.0575	1.0592 (0.911-1.23)	0.45	0.45	-0.223	0.79984 (0.625-1.02)	0.08	0
LKT__s__Porphyromonas_uenonis	0.11	1.1162 (0.99-1.26)	0.07	0.23	-0.225	0.7987 (0.531-1.2)	0.28	0
LKT__s__Bacteroides_uniformis	0.0819	1.0854 (0.965-1.22)	0.17	0.30	-0.226	0.79771 (0.624-1.02)	0.07	0
LKT__s__Fournierella_massiliensis	0.115	1.1213 (1-1.25)	0.04	0.21	-0.235	0.7902 (0.637-0.98)	0.03	0
LKT__s__Erysipelotrichaceae_bacterium	-0.0000221	0.99998 (0.894-1.12)	1.00	0.60	-0.236	0.78947 (0.578-1.08)	0.14	1
LKT__s__Holdemanella_biformis	0.0322	1.0328 (0.925-1.15)	0.57	0.48	-0.24	0.78645 (0.585-1.06)	0.11	0
LKT__s__Bariatricus_massiliensis	-0.0258	0.97454 (0.852-1.11)	0.71	0.51	-0.24	0.78672 (0.565-1.1)	0.16	1
LKT__s__Eubacterium_Unclassified	0.0117	1.0117 (0.905-1.13)	0.84	0.55	-0.24	0.78695 (0.582-1.06)	0.12	0
LKT__p__Firmicutes	-0.115	0.89103 (0.631-1.26)	0.51	0.47	-0.242	0.78513 (0.44-1.4)	0.41	1
LKT__s__Clostridium_sporosphaeroides	-0.0108	0.98922 (0.904-1.08)	0.81	0.55	-0.242	0.78492 (0.588-1.05)	0.10	1
LKT__s__Blautia_obeum	-0.114	0.89209 (0.782-1.02)	0.09	0.23	-0.246	0.78225 (0.51-1.2)	0.26	1
LKT__s__Bacteroidales_bacterium	0.0827	1.0862 (0.999-1.18)	0.05	0.21	-0.255	0.77506 (0.559-1.07)	0.13	0
LKT__s__Pseudoflavonifractor_Unclassified	0.0841	1.0877 (0.939-1.26)	0.26	0.34	-0.255	0.77512 (0.567-1.06)	0.11	0
LKT__s__Blautia_producta	-0.191	0.82575 (0.721-0.946)	0.01	0.08	-0.256	0.77424 (0.543-1.1)	0.16	1
LKT__o__Bacteroidales	0.229	1.2573 (1-1.57)	0.05	0.21	-0.26	0.77104 (0.21-2.83)	0.70	0
LKT__s__Muribaculum_Unclassified	0.108	1.1137 (1-1.24)	0.04	0.21	-0.266	0.76639 (0.534-1.1)	0.15	0
LKT__s__Eubacterium_limosum	-0.0749	0.92781 (0.817-1.05)	0.25	0.33	-0.271	0.76256 (0.492-1.18)	0.23	1
LKT__s__Paenibacillus_Unclassified	0.142	1.1524 (0.97-1.37)	0.11	0.25	-0.283	0.75356 (0.532-1.07)	0.11	0
LKT__s__Blautia_schinkii	-0.0316	0.96891 (0.84-1.12)	0.67	0.49	-0.283	0.75338 (0.523-1.08)	0.13	1
LKT__s__Clostridium_scindens	-0.122	0.88513 (0.792-0.989)	0.03	0.21	-0.29	0.74854 (0.46-1.22)	0.24	1
LKT__g__Bacillus	0.101	1.1063 (0.948-1.29)	0.20	0.32	-0.291	0.74774 (0.552-1.01)	0.06	0
LKT__s__Butyrivibrio_Unclassified	0.0699	1.0724 (0.914-1.26)	0.39	0.41	-0.297	0.74329 (0.558-0.989)	0.04	0
LKT__s__Dorea_Unclassified	-0.0969	0.90765 (0.793-1.04)	0.16	0.29	-0.299	0.74143 (0.536-1.03)	0.07	1
LKT__g__Dorea	-0.0857	0.91785 (0.797-1.06)	0.24	0.32	-0.302	0.739 (0.416-1.31)	0.30	1
LKT__s__Proteiniborus_ethanoligenes	0.0283	1.0287 (0.93-1.14)	0.58	0.48	-0.305	0.73703 (0.212-2.56)	0.63	0
LKT__s__Clostridium_Unclassified	0.0912	1.0955 (0.862-1.39)	0.46	0.45	-0.308	0.73481 (0.508-1.06)	0.10	0
LKT__s__Blautia_Unclassified	-0.106	0.89925 (0.798-1.01)	0.08	0.23	-0.31	0.73324 (0.502-1.07)	0.11	1
LKT__s__Intestinibacillus_massiliensis	0.0642	1.0663 (0.935-1.22)	0.34	0.39	-0.311	0.73239 (0.53-1.01)	0.06	0
LKT__g__Eubacterium	0.044	1.0449 (0.909-1.2)	0.54	0.47	-0.316	0.72895 (0.535-0.993)	0.04	0
LKT__s__Christensenella_minuta	0.101	1.1065 (0.995-1.23)	0.06	0.21	-0.32	0.72646 (0.504-1.05)	0.09	0
LKT__s__Bifidobacterium_animalis	0.0484	1.0496 (0.951-1.16)	0.34	0.39	-0.34	0.71169 (0.311-1.63)	0.42	0
LKT__s__Ruminococcus_albus	0.0664	1.0686 (0.935-1.22)	0.33	0.39	-0.376	0.68659 (0.493-0.957)	0.03	0
LKT__s__Eubacterium_pyruvativorans	0.0323	1.0328 (0.897-1.19)	0.65	0.49	-0.376	0.6869 (0.424-1.11)	0.13	0
LKT__s__Streptococcus_anginosus	0.00948	1.0095 (0.911-1.12)	0.86	0.56	-0.376	0.6868 (0.265-1.78)	0.44	0
LKT__s__Coprococcus_Unclassified	-0.136	0.87293 (0.773-0.986)	0.03	0.21	-0.379	0.6846 (0.45-1.04)	0.08	1
LKT__s__Butyricicoccus_Unclassified	0.0847	1.0884 (0.946-1.25)	0.24	0.32	-0.385	0.68079 (0.473-0.981)	0.04	0
LKT__Unclassified	0.266	1.305 (0.86-1.98)	0.21	0.32	-0.386	0.68006 (0.315-1.47)	0.33	0
LKT__s__Candidatus_Methanomassiliicoccus_intestinalis	-0.0432	0.95771 (0.83-1.11)	0.56	0.48	-0.386	0.67979 (0.253-1.82)	0.44	1
LKT__g__Blautia	-0.266	0.76658 (0.632-0.93)	0.01	0.08	-0.388	0.67846 (0.452-1.02)	0.06	1
LKT__d__Eukaryota	0.153	1.165 (0.978-1.39)	0.09	0.23	-0.401	0.66941 (0.485-0.924)	0.01	0
LKT__s__Massilistercora_timonensis	0.0332	1.0338 (0.915-1.17)	0.59	0.48	-0.408	0.66489 (0.476-0.928)	0.02	0
LKT__s__Butyrivibrio_crossotus	0.0954	1.1001 (0.971-1.25)	0.13	0.27	-0.444	0.64124 (0.41-1)	0.05	0

LKT__f__Ruminococcaceae	0.208	1.2312 (0.894-1.7)	0.20	0.32	-0.467	0.62715 (0.336-1.17)	0.14	0
LKT__s__Bifidobacterium_pseudocatenulatum	0.00439	1.0044 (0.917-1.1)	0.93	0.58	-0.483	0.61685 (0.371-1.02)	0.06	0
LKT__s__Eubacterium_ruminantium	0.0578	1.0595 (0.943-1.19)	0.33	0.39	-0.487	0.6146 (0.379-0.997)	0.05	0
LKT__s__Clostridioides_difficile	-0.067	0.9352 (0.769-1.14)	0.50	0.47	-0.502	0.60531 (0.344-1.07)	0.08	1
LKT__o__Clostridiales	-0.137	0.87171 (0.631-1.2)	0.41	0.42	-0.548	0.5783 (0.143-2.34)	0.44	1
LKT__s__Denitrobacterium_detoxificans	-0.00796	0.99207 (0.905-1.09)	0.87	0.56	-0.61	0.54333 (0.165-1.79)	0.32	1
LKT__s__Lactobacillus_paracasei	0.115	1.122 (1.03-1.22)	0.01	0.11	-0.813	0.44365 (0.137-1.44)	0.18	0
LKT__s__Enorma_phocaeensis	-0.0342	0.96642 (0.847-1.1)	0.61	0.49	-0.866	0.42048 (0.127-1.39)	0.16	1
LKT__s__Lactobacillus_vaginalis	0.0286	1.029 (0.924-1.15)	0.60	0.49	-1.1	0.33424 (0.067-1.67)	0.18	0
LKT__s__Bacteroides_phage_crAss001	-0.18	0.83541 (0.679-1.03)	0.09	0.23	-8.93	0.0001329 (0-Inf)	1.00	1
LKT__s__Methanosphaera_stadtmanae	0.0669	1.0692 (0.958-1.19)	0.23	0.32	-9.05	0.00011742 (0-Inf)	1.00	0
LKT__g__Methanosphaera	0.0738	1.0766 (0.931-1.24)	0.32	0.38	-11.1	1.5416e-05 (0-Inf)	1.00	0
LKT__s__Propionibacterium_freudenreichii	-0.045	0.95603 (0.856-1.07)	0.43	0.43	-11.6	9.4816e-06 (0-Inf)	1.00	1
LKT__s__Mogibacterium_pumilum	-0.147	0.86325 (0.736-1.01)	0.07	0.22	-16.8	4.8415e-08 (0-Inf)	1.00	1
LKT__s__Cryptobacterium_curtum	0.0391	1.0399 (0.945-1.14)	0.43	0.43	-17.8	1.7907e-08 (0-Inf)	1.00	0
LKT__g__Mogibacterium	-0.0295	0.97089 (0.842-1.12)	0.69	0.50	-18	1.5033e-08 (0-Inf)	1.00	1

Abbreviations:

LKT = Last Known Taxon
HR = Hazard Ratio
95% CI = 95% Confidence Interval
p-value = Wald test two-tailed p-value
Same HR direction in two cohorts: 0=No; 1=Yes