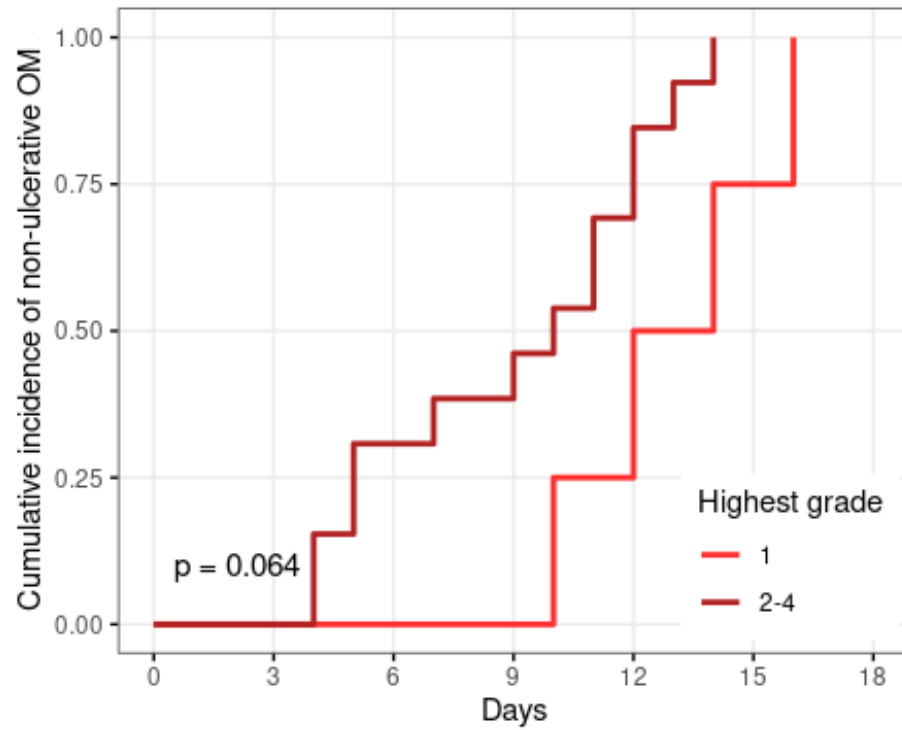


**SUPPLEMENTAL MATERIAL**



**Figure S1: Cumulative incidence curves of non-ulcerative OM with patients stratified by the highest OM grade during OM clinical course (1/2-4).** Statistical significance was evaluated by the log-rank test, with P-value indicated.

	<b>n = 30</b>
<b>Age in years (median, range)</b>	50 (19-73)
<b>Sex (male)</b>	16 (53%)
<b>Oral Mucositis Grades (WHO)</b>	
Grade 0	12 (40%)
Grade I	5 (17%)
Grade II	4 (13%)
Grade III	6 (20%)
Grade IV	3 (10%)
<b>Conditioning Intensity</b>	
Reduced Intensity	18 (60%)
<b>Total Body Irradiation</b>	11 (37%)
<b>Alkylating Agents</b>	
Busulfan	15 (50%)
Cyclophosphamide	10 (33%)
Melphalan	4 (13%)
Bendamustine	1 (3%)
Treosulfan	1 (3%)
<b>Graft Source</b>	
Bone Marrow	10 (33%)
Peripheal Blood	20 (67%)
<b>Underlying Disease</b>	
Acute Myeloid Leukemia	18 (60%)
Acute Lymbhoblastic Leukemia	7 (23%)
Non-hodgkin Lymphoma	5 (17%)
Myelodysplastic Syndrome	4 (13%)
Chronic Lymphocytic Leukemia	1 (3%)
Chronic Myeloid Leukemia	2 (3%)
Multiple Myeloma	3 (3%)
<b>Graft-versus-Host Disease Prophylaxis</b>	
Mycophenolate+Cyclosporin A	11 (37%)
Methotrexate+Cyscclorin A	10 (33%)
Mycophenolate+Cyclosporin A+Cyclophosphamide	9 (30%)

**Table S1: Clinical characteristics of study patients.**

Genus	log(FoldChange)	P-value	Adjusted P-value	Differentially abundant
D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Actinomycetales;D_4_Actinomycetaceae;D_5_Actinomyces	-0,59	0,46	1	No
D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Actinomycetales;D_4_Actinomycetaceae;D_5_F0332	0,79	0,00	0	No
D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Bifidobacteriales;D_4_Bifidobacteriaceae;D_5_Bifidobacterium	-0,85	0,00	0	No
D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Bifidobacteriales;D_4_Bifidobacteriaceae;	0,59	0,00	0	No
D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Micrococcales;D_4_Micrococcaceae;D_5_Rothia	-0,24	0,76	1	No
D_0_Bacteria;D_1_Actinobacteria;D_2_Coriobacterii;D_3_Coriobacteriales;D_4_Atopobiaceae;D_5_Atopobium	-0,29	0,74	1	No
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Porphyrionadaceae;D_5_Porphyrionas	-0,70	0,54	1	No
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Prevotellaceae;D_5_Alloprevotella	-0,07	0,95	1	No
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Prevotellaceae;D_5_Prevotella	0,85	0,28	1	No
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Prevotellaceae;D_5_Prevotella 2	-0,33	0,72	1	No
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Prevotellaceae;D_5_Prevotella 6	0,51	0,62	1	No
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Prevotellaceae;D_5_Prevotella 7	-0,02	0,98	1	No
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Tannerellaceae;D_5_Tannerella	1,19	0,00	0	No
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Flavobacteriales;D_4_Flavobacteriaceae;D_5_Capnocytophaga	1,00	0,33	1	No
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Flavobacteriales;D_4_Weeksellaceae;D_5_Bergeyella	0,56	0,60	1	No
D_0_Bacteria;D_1_Epsilonbacteraeota;D_2_Campylobacteria;D_3_Campylobacteriales;D_4_Campylobacteraceae;D_5_Campylobacter	0,38	0,60	1	No
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Family XI;D_5_Gemella	-0,31	0,75	1	No
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Carnobacteriaceae;D_5_Granulicatella	-0,95	0,37	1	No
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Lactobacillaceae;D_5_Lactobacillus	-0,17	0,85	1	No
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Streptococcaceae;D_5_Lactococcus	1,38	0,00	0	No
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Streptococcaceae;D_5_Streptococcus	-0,70	0,40	1	No
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Family XI;D_5_Parvimonas	-0,71	0,31	1	No
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Family XIII;D_5_Mogibacterium	0,96	0,00	0	No
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Family XIII;D_5_[Eubacterium] nodatum group	0,16	0,83	1	No
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Butyrvibrio 2	-0,21	0,77	1	No
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Catonella	0,33	0,66	1	No
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Lachnoanaerobaculum	1,09	0,21	1	No
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Oribacterium	0,55	0,42	1	No
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Stomatobaculum	0,46	0,57	1	No
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;	0,06	0,95	1	No
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Peptostreptococcaceae;D_5_Peptostreptococcus	0,14	0,81	1	No
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Ruminococcaceae UCG-014	-1,04	0,27	1	No
D_0_Bacteria;D_1_Firmicutes;D_2_Erysipelotrichia;D_3_Erysipelotrichales;D_4_Erysipelotrichaceae;D_5_Solobacterium	0,28	0,69	1	No
D_0_Bacteria;D_1_Firmicutes;D_2_Negativicutes;D_3_Selenomonadales;D_4_Veillonellaceae;D_5_Dialister	0,67	0,00	0	No
D_0_Bacteria;D_1_Firmicutes;D_2_Negativicutes;D_3_Selenomonadales;D_4_Veillonellaceae;D_5_Megasphaera	-0,29	0,78	1	No
D_0_Bacteria;D_1_Firmicutes;D_2_Negativicutes;D_3_Selenomonadales;D_4_Veillonellaceae;D_5_Selenomonas	0,16	0,84	1	No
D_0_Bacteria;D_1_Firmicutes;D_2_Negativicutes;D_3_Selenomonadales;D_4_Veillonellaceae;D_5_Selenomonas 3	0,71	0,37	1	No
D_0_Bacteria;D_1_Firmicutes;D_2_Negativicutes;D_3_Selenomonadales;D_4_Veillonellaceae;D_5_Veillonella	-0,26	0,71	1	No
D_0_Bacteria;D_1_Fusobacteria;D_2_Fusobacterii;D_3_Fusobacteriales;D_4_Fusobacteriaceae;D_5_Fusobacterium	0,19	0,83	1	No
D_0_Bacteria;D_1_Fusobacteria;D_2_Fusobacterii;D_3_Fusobacteriales;D_4_Leptotrichiaceae;D_5_Leptotrichia	0,25	0,76	1	No
D_0_Bacteria;D_1_Patescibacteria;D_2_Saccharimonadia;D_3_Saccharimonadales;D_4_Saccharimonadaceae;D_5_Candidatus Saccharimonas	1,76	0,00	0	No
D_0_Bacteria;D_1_Patescibacteria;D_2_Saccharimonadia;D_3_Saccharimonadales;D_4_Saccharimonadaceae;D_5_uncultured bacterium	-0,65	0,53	1	No
D_0_Bacteria;D_1_Patescibacteria;D_2_Saccharimonadia;D_3_Saccharimonadales;D_4_uncultured bacterium;D_5_uncultured bacterium	0,89	0,00	0	No
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Betaproteobacteriales;D_4_Burkholderiaceae;D_5_Lautropia	0,60	0,42	1	No
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Betaproteobacteriales;D_4_Neisseriaceae;D_5_Kingella	1,10	0,00	0	No
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Betaproteobacteriales;D_4_Neisseriaceae;D_5_Neisseria	-0,64	0,68	1	No
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Cardiobacteriales;D_4_Cardiobacteriaceae;D_5_Cardiobacterium	-0,48	0,40	1	No
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Pasteurellales;D_4_Pasteurellaceae;D_5_Haemophilus	-0,59	0,61	1	No
D_0_Bacteria;D_1_Spirochaetes;D_2_Spirochaetia;D_3_Spirochaetales;D_4_Spirochaetaceae;D_5_Treponema 2	-0,33	0,64	1	No

**Table S2: Differential abundance analysis between oral mucositis (OM) and OM-free patients at preconditioning.** The analysis was performed with ANCOM-BC at genus level. No genera passed the log(FoldChange) and adjusted P-value cutoffs to be considered as significantly differentially abundant between groups.

Genus	P-value	HR	HR (2.5 percentile)	HR (97.5 percentile)	% Group1	% Group0
D_0_Bacteria.D_1_Actinobacteria.D_2_Actinobacteria.D_3_Actinomycetales.D_4_Actinomycetales.D_5_Actinomyces	0,56	1,38	0,46	4,12	50	40
D_0_Bacteria.D_1_Actinobacteria.D_2_Actinobacteria.D_3_Micrococcales.D_4_Micrococaceae.D_5_Rothia	0,23	0,51	0,17	1,55	36	53
D_0_Bacteria.D_1_Actinobacteria.D_2_Coriobacterii.D_3_Coriobacteriales.D_4_Atopobiaceae.D_5_Atopobium	0,53	1,41	0,47	4,22	50	40
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Porphyrromonadaceae.D_5_Porphyrromonas	0,95	1,04	0,35	3,08	43	47
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Prevotellaceae.D_5_Alloprevotella	0,48	0,67	0,22	2,05	36	53
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Prevotellaceae.D_5_Prevotella	0,56	1,38	0,46	4,13	50	40
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Prevotellaceae.D_5_Prevotella.6	0,53	1,41	0,47	4,22	50	40
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Prevotellaceae.D_5_Prevotella.7	0,93	0,95	0,32	2,83	43	47
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Flavobacteriales.D_4_Flavobacteriaceae.D_5_Capnocytophaga	0,27	1,85	0,6	5,68	57	33
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Flavobacteriales.D_4_Weeksellaceae.D_5_Bergeyella	0,59	1,35	0,45	4,02	50	40
D_0_Bacteria.D_1_Epsilonbacteraeota.D_2_Campylobacteria.D_3_Campylobacteriales.D_4_Campylobacteraceae.D_5_Campylobacter	0,46	1,51	0,51	4,5	50	40
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Bacillales.D_4_Family.XI.D_5_Gemella	0,27	0,54	0,18	1,64	36	53
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Lactobacillales.D_4_Carnobacteriaceae.D_5_Granulicatella	0,08	0,36	0,11	1,17	29	60
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Lactobacillales.D_4_Lactobacillaceae.D_5_Lactobacillus	0,21	2,01	0,65	6,16	57	33
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Lactobacillales.D_4_Streptococcaceae.D_5_Streptococcus	0,21	0,49	0,16	1,52	36	53
D_0_Bacteria.D_1_Firmicutes.D_2_Clostridia.D_3_Clostridiales.D_4_Lachnospiraceae.D_5_Catonella	0,74	1,2	0,4	3,58	50	40
D_0_Bacteria.D_1_Firmicutes.D_2_Clostridia.D_3_Clostridiales.D_4_Lachnospiraceae.D_5_Lachnoanaerobaculum	0,61	1,32	0,44	3,95	50	40
D_0_Bacteria.D_1_Firmicutes.D_2_Clostridia.D_3_Clostridiales.D_4_Lachnospiraceae.D_5_Oribacterium	0,69	1,25	0,42	3,72	50	40
D_0_Bacteria.D_1_Firmicutes.D_2_Clostridia.D_3_Clostridiales.D_4_Lachnospiraceae.D_5_Stomatobaculum	0,74	1,2	0,4	3,58	50	40
D_0_Bacteria.D_1_Firmicutes.D_2_Erysipelotrichia.D_3_Erysipelotrichales.D_4_Erysipelotrichaceae.D_5_Solobacterium	0,89	0,93	0,31	2,77	43	47
D_0_Bacteria.D_1_Firmicutes.D_2_Negativicutes.D_3_Selenomonadales.D_4_Veillonellaceae.D_5_Megasphaera	0,39	0,62	0,2	1,88	36	53
D_0_Bacteria.D_1_Firmicutes.D_2_Negativicutes.D_3_Selenomonadales.D_4_Veillonellaceae.D_5_Selenomonas.3	0,50	1,46	0,49	4,36	50	40
D_0_Bacteria.D_1_Firmicutes.D_2_Negativicutes.D_3_Selenomonadales.D_4_Veillonellaceae.D_5_Veillonella	0,55	1,4	0,47	4,16	50	40
D_0_Bacteria.D_1_Fusobacteria.D_2_Fusobacterii.D_3_Fusobacteriales.D_4_Fusobacteriaceae.D_5_Fusobacterium	0,85	0,9	0,3	2,67	43	47
D_0_Bacteria.D_1_Fusobacteria.D_2_Fusobacterii.D_3_Fusobacteriales.D_4_Leptotrichiaceae.D_5_Leptotrichia	0,86	0,91	0,31	2,71	43	47
D_0_Bacteria.D_1_Patescibacteria.D_2_Saccharimonadia.D_3_Saccharimonadales.D_4_Saccharimonadaceae.D_5_uncultured.bacterium	0,41	0,63	0,21	1,93	36	53
D_0_Bacteria.D_1_Proteobacteria.D_2_Gammaproteobacteria.D_3_Betaproteobacteriales.D_4_Neisseriaceae.D_5_Neisseria	0,30	0,56	0,18	1,7	36	53
D_0_Bacteria.D_1_Proteobacteria.D_2_Gammaproteobacteria.D_3_Pasteurellales.D_4_Pasteurellaceae.D_5_Haemophilus	0,42	0,63	0,21	1,94	36	53

**Table S3: Association between genera relative abundance at preconditioning and oral mucositis (OM) risk.** Groups were stratified based on median genus relative abundance and association with the risk of OM was assessed by estimating the Cox proportional hazards between groups. HR, Hazard Ratio; % Group1, percentage of patients classified as having high genus relative abundance at preconditioning that developed OM; % Group0, percentage of patients classified as having low genus relative abundance at preconditioning that developed OM.

Genus	P-value	Spearman rho
D_0_Bacteria.D_1_Actinobacteria.D_2_Actinobacteria.D_3_Actinomycetales.D_4_Actinomycetaceae.D_5_Actinomyces	0,57	0,11
D_0_Bacteria.D_1_Actinobacteria.D_2_Actinobacteria.D_3_Micrococcales.D_4_Micrococcaceae.D_5_Rothia	0,11	-0,30
D_0_Bacteria.D_1_Actinobacteria.D_2_Coriobacteriia.D_3_Coriobacteriales.D_4_Atopobiaceae.D_5_Atopobium	0,86	-0,03
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Porphyrimonadaceae.D_5_Porphyrimonas	0,96	0,01
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Prevotellaceae.D_5_Alloprevotella	0,78	0,05
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Prevotellaceae.D_5_Prevotella	0,15	0,27
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Prevotellaceae.D_5_Prevotella.6	0,45	0,15
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Prevotellaceae.D_5_Prevotella.7	0,82	-0,04
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Flavobacteriales.D_4_Flavobacteriaceae.D_5_Capnocytophaga	0,37	0,17
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Flavobacteriales.D_4_Weeksellaceae.D_5_Bergeyella	0,46	0,14
D_0_Bacteria.D_1_Epsilonbacteraeota.D_2_Campylobacteria.D_3_Campylobacteriales.D_4_Campylobacteraceae.D_5_Campylobacter	0,95	-0,01
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Bacillales.D_4_Family.XI.D_5_Gemella	0,71	-0,07
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Lactobacillales.D_4_Carnobacteriaceae.D_5_Granulicatella	0,76	-0,06
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Lactobacillales.D_4_Lactobacillaceae.D_5_Lactobacillus	0,95	0,01
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Lactobacillales.D_4_Streptococcaceae.D_5_Streptococcus	0,06	-0,35
D_0_Bacteria.D_1_Firmicutes.D_2_Clostridia.D_3_Clostridiales.D_4_Lachnospiraceae.D_5_Catonella	0,64	0,09
D_0_Bacteria.D_1_Firmicutes.D_2_Clostridia.D_3_Clostridiales.D_4_Lachnospiraceae.D_5_Lachnoanaerobaculum	0,74	0,06
D_0_Bacteria.D_1_Firmicutes.D_2_Clostridia.D_3_Clostridiales.D_4_Lachnospiraceae.D_5_Oribacterium	0,61	0,10
D_0_Bacteria.D_1_Firmicutes.D_2_Clostridia.D_3_Clostridiales.D_4_Lachnospiraceae.D_5_Stomatobaculum	0,58	0,11
D_0_Bacteria.D_1_Firmicutes.D_2_Erysipelotrichia.D_3_Erysipelotrichales.D_4_Erysipelotrichaceae.D_5_Solobacterium	0,25	0,22
D_0_Bacteria.D_1_Firmicutes.D_2_Negativicutes.D_3_Selenomonadales.D_4_Veillonellaceae.D_5_Megasphaera	0,73	-0,07
D_0_Bacteria.D_1_Firmicutes.D_2_Negativicutes.D_3_Selenomonadales.D_4_Veillonellaceae.D_5_Selenomonas.3	0,90	-0,03
D_0_Bacteria.D_1_Firmicutes.D_2_Negativicutes.D_3_Selenomonadales.D_4_Veillonellaceae.D_5_Veillonella	0,79	0,05
D_0_Bacteria.D_1_Fusobacteria.D_2_Fusobacteriia.D_3_Fusobacteriales.D_4_Fusobacteriaceae.D_5_Fusobacterium	0,76	-0,06
D_0_Bacteria.D_1_Fusobacteria.D_2_Fusobacteriia.D_3_Fusobacteriales.D_4_Leptotrichiaceae.D_5_Leptotrichia	0,99	0,00
D_0_Bacteria.D_1_Patescibacteria.D_2_Saccharimonadia.D_3_Saccharimonadales.D_4_Saccharimonadaceae.D_5_uncultured.bacterium	0,94	0,02
D_0_Bacteria.D_1_Proteobacteria.D_2_Gammaproteobacteria.D_3_Betaproteobacteriales.D_4_Neisseriaceae.D_5_Neisseria	0,60	0,10
D_0_Bacteria.D_1_Proteobacteria.D_2_Gammaproteobacteria.D_3_Pasteurellales.D_4_Pasteurellaceae.D_5_Haemophilus	0,54	-0,12

**Table S4: Correlation between genera relative abundance at preconditioning and ulcerative oral mucositis (OM) grade.** All OM grades (0-4) are considered in this analysis. Spearman correlation was used.

Genus	P-value	Spearman rho
D_0_Bacteria.D_1_Actinobacteria.D_2_Actinobacteria.D_3_Actinomycetales.D_4_Actinomycetaceae.D_5_Actinomyces	0,69	0,12
D_0_Bacteria.D_1_Actinobacteria.D_2_Actinobacteria.D_3_Micrococcales.D_4_Micrococcaceae.D_5_Rothia	0,67	-0,13
D_0_Bacteria.D_1_Actinobacteria.D_2_Coriobacteriia.D_3_Coriobacteriales.D_4_Atopobiaceae.D_5_Atopobium	0,89	-0,04
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Porphyrromonadaceae.D_5_Porphyrromonas	0,03	0,61
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Prevotellaceae.D_5_Alloprevotella	0,07	0,51
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Prevotellaceae.D_5_Prevotella	0,59	0,17
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Prevotellaceae.D_5_Prevotella.6	0,66	-0,14
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Prevotellaceae.D_5_Prevotella.7	0,47	-0,22
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Flavobacteriales.D_4_Flavobacteriaceae.D_5_Capnocytophaga	0,46	0,22
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Flavobacteriales.D_4_Weeksellaceae.D_5_Bergeyella	0,22	0,37
D_0_Bacteria.D_1_Epsilonbacteraeota.D_2_Campylobacteria.D_3_Campylobacteriales.D_4_Campylobacteraceae.D_5_Campylobacter	0,37	-0,27
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Bacillales.D_4_Family.XI.D_5_Gemella	0,82	-0,07
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Lactobacillales.D_4_Carnobacteriaceae.D_5_Granulicatella	0,44	0,23
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Lactobacillales.D_4_Lactobacillaceae.D_5_Lactobacillus	0,31	-0,31
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Lactobacillales.D_4_Streptococcaceae.D_5_Streptococcus	0,52	-0,20
D_0_Bacteria.D_1_Firmicutes.D_2_Clostridia.D_3_Clostridiales.D_4_Lachnospiraceae.D_5_Catonella	0,65	-0,14
D_0_Bacteria.D_1_Firmicutes.D_2_Clostridia.D_3_Clostridiales.D_4_Lachnospiraceae.D_5_Lachnoanaerobaculum	0,40	-0,26
D_0_Bacteria.D_1_Firmicutes.D_2_Clostridia.D_3_Clostridiales.D_4_Lachnospiraceae.D_5_Oribacterium	0,47	0,22
D_0_Bacteria.D_1_Firmicutes.D_2_Clostridia.D_3_Clostridiales.D_4_Lachnospiraceae.D_5_Stomatobaculum	0,67	0,13
D_0_Bacteria.D_1_Firmicutes.D_2_Erysipelotrichia.D_3_Erysipelotrichales.D_4_Erysipelotrichaceae.D_5_Solobacterium	0,35	0,29
D_0_Bacteria.D_1_Firmicutes.D_2_Negativicutes.D_3_Selenomonadales.D_4_Veillonellaceae.D_5_Megasphaera	0,26	-0,34
D_0_Bacteria.D_1_Firmicutes.D_2_Negativicutes.D_3_Selenomonadales.D_4_Veillonellaceae.D_5_Selenomonas.3	0,20	-0,38
D_0_Bacteria.D_1_Firmicutes.D_2_Negativicutes.D_3_Selenomonadales.D_4_Veillonellaceae.D_5_Veillonella	0,21	-0,37
D_0_Bacteria.D_1_Fusobacteria.D_2_Fusobacteriia.D_3_Fusobacteriales.D_4_Fusobacteriaceae.D_5_Fusobacterium	0,67	0,13
D_0_Bacteria.D_1_Fusobacteria.D_2_Fusobacteriia.D_3_Fusobacteriales.D_4_Leptotrichiaceae.D_5_Leptotrichia	0,51	-0,20
D_0_Bacteria.D_1_Patescibacteria.D_2_Saccharimonadia.D_3_Saccharimonadales.D_4_Saccharimonadaceae.D_5_uncultured.bacterium	0,95	-0,02
D_0_Bacteria.D_1_Proteobacteria.D_2_Gammaproteobacteria.D_3_Betaproteobacteriales.D_4_Neisseriaceae.D_5_Neisseria	0,19	0,39
D_0_Bacteria.D_1_Proteobacteria.D_2_Gammaproteobacteria.D_3_Pasteurellales.D_4_Pasteurellaceae.D_5_Haemophilus	0,23	-0,35

**Table S5: Correlation between genera relative abundance at preconditioning and ulcerative oral mucositis (OM) grade.** Only ulcerative OM grades (2-4) are considered in this analysis. Spearman correlation was used.

Genus	P-value	HR	HR (2.5 percentile)	HR (97.5 percentile)
D_0_Bacteria.D_1_Actinobacteria.D_2_Actinobacteria.D_3_Actinomycetales.D_4_Actinomycetaceae.D_5_Actinomyces	0,42	1,59	0,51	5,01
D_0_Bacteria.D_1_Actinobacteria.D_2_Actinobacteria.D_3_Bifidobacteriales.D_4_Bifidobacteriaceae.	0,16	2,47	0,67	9,01
D_0_Bacteria.D_1_Actinobacteria.D_2_Actinobacteria.D_3_Micrococcales.D_4_Micrococcaceae.D_5_Rothia	0,94	1,04	0,33	3,34
D_0_Bacteria.D_1_Actinobacteria.D_2_Coriobacteriia.D_3_Coriobacteriales.D_4_Atopobiaceae.D_5_Atopobium	0,95	1,04	0,33	3,25
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Porphyrromonadaceae.D_5_Porphyrromonas	0,07	0,3	0,08	1,2
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Prevotellaceae.D_5_Alloprevotella	0,86	1,1	0,35	3,45
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Prevotellaceae.D_5_Prevotella	0,88	1,09	0,35	3,43
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Prevotellaceae.D_5_Prevotella.6	0,28	2,03	0,54	7,55
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Prevotellaceae.D_5_Prevotella.7	0,77	0,84	0,27	2,66
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Flavobacteriales.D_4_Flavobacteriaceae.D_5_Capnocytophaga	0,84	0,89	0,28	2,81
D_0_Bacteria.D_1_Epsilonbacteraeota.D_2_Campylobacteria.D_3_Campylobacteriales.D_4_Campylobacteraceae.D_5_Campylobacter	0,98	0,99	0,32	3,08
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Bacillales.D_4_Family.XI.D_5_Gemella	0,08	0,3	0,08	1,24
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Lactobacillales.D_4_Carnobacteriaceae.D_5_Granulicatella	0,96	1,03	0,33	3,23
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Lactobacillales.D_4_Lactobacillaceae.D_5_Lactobacillus	0,04	4,99	0,96	26,04
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Lactobacillales.D_4_Streptococcaceae.D_5_Streptococcus	0,15	0,4	0,11	1,42
D_0_Bacteria.D_1_Firmicutes.D_2_Clostridia.D_3_Clostridiales.D_4_Lachnospiraceae.D_5_Lachnoanaerobaculum	0,16	0,38	0,1	1,51
D_0_Bacteria.D_1_Firmicutes.D_2_Clostridia.D_3_Clostridiales.D_4_Lachnospiraceae.D_5_Oribacterium	0,91	1,07	0,34	3,35
D_0_Bacteria.D_1_Firmicutes.D_2_Negativicutes.D_3_Selenomonadales.D_4_Veillonellaceae.D_5_Selenomonas.3	0,16	2,47	0,67	9,01
D_0_Bacteria.D_1_Firmicutes.D_2_Negativicutes.D_3_Selenomonadales.D_4_Veillonellaceae.D_5_Veillonella	0,10	0,33	0,08	1,3
D_0_Bacteria.D_1_Fusobacteria.D_2_Fusobacteriia.D_3_Fusobacteriales.D_4_Fusobacteriaceae.D_5_Fusobacterium	0,39	0,6	0,19	1,92
D_0_Bacteria.D_1_Fusobacteria.D_2_Fusobacteriia.D_3_Fusobacteriales.D_4_Leptotrichiaceae.D_5_Leptotrichia	0,97	1,02	0,33	3,2

**Table S6: Association between genera relative abundance at oral mucositis (OM) onset and time to OM healing.** Groups were stratified based on median genus relative abundance and association with time to OM healing was assessed by estimating the Cox proportional hazards between groups. HR, Hazard Ratio.