

Microbial organisms and taxonomic classification to ASVs					
	Phylum	Genus	Species	Log2FoldChange	p-value
Abundant in Patient Samples Without Eyedrops	Verrucomicrobiota	Akkermansia	muciniphila	4.483	4.78E-08
	Firmicutes	Eubacterium siraeum group	..	4.209	9.76E-11
	Verrucomicrobiota	Akkermansia	muciniphila	4.183	4.50E-08
	Proteobacteria	Gluconobacter	..	3.973	4.53E-10
	Actinobacteriota	Bifidobacterium	bifidum	3.678	6.55E-09
	Firmicutes	Roseburia	intestinalis	3.308	2.40E-07
	Firmicutes	Ruminococcus torques group	..	3.242	4.03E-06
	Actinobacteriota	Bifidobacterium	longum	3.159	1.12E-04
	Firmicutes	Lachnospiraceae	..	3.000	4.78E-06
	Firmicutes	Blautia	..	2.877	3.15E-06
	Firmicutes	Oscillospiraceae UCG-002	..	2.877	3.37E-06
	Firmicutes	Faecalibacterium	prausnitzii	2.871	1.15E-04
	Firmicutes	Lachnospiraceae NK4A136 group	..	2.868	3.40E-06
	Firmicutes	Lachnospiraceae NK4A136 group	..	2.868	3.94E-06
	Firmicutes	Oscillospiraceae UCG-002	..	2.838	8.13E-06
	Firmicutes	Oscillospiraceae NKA214 group	..	2.700	2.07E-05
	Firmicutes	Faecalibacterium	prausnitzii	2.692	0.0020
	Proteobacteria	Komagataeibacter	rhaeticus/xylinus	2.667	7.00E-06
	Firmicutes	Eubacterium xylanophilum group	..	2.643	2.09E-05
	Firmicutes	Blautia	Obeum/wexlerae	2.621	6.43E-05
	Firmicutes	Oscillospiraceae	..	2.561	2.33E-05
	Firmicutes	Eubacterium coprostanoligenes group	..	2.548	2.12E-05
	Firmicutes	Ruminococcaceae CAG-352	..	2.498	8.34E-05
	Firmicutes	Lachnospiraceae NK4A136 group	..	2.365	3.28E-05
	Firmicutes	Clostridia UCG-014	..	2.336	3.03E-04
	Firmicutes	Christensenellaceae R-7 group	..	2.336	1.94E-04
	Firmicutes	Eubacterium eligens group	..	2.322	1.96E-04
	Firmicutes	Intestimonas	..	2.321	1.15E-04
	Firmicutes	Colidextribacter	..	2.247	1.72E-04
	Firmicutes	Intestimonas	..	2.238	5.29E-04
	Firmicutes	Candidatus	arthromitus	2.233	1.92E-04
	Firmicutes	Roseburia	inulinivorans	2.165	0.0020
	Firmicutes	Agathobacter	..	2.028	0.015
	Firmicutes	Faecalibacterium	prausnitzii	1.992	0.0012
	Firmicutes	Lachnospira	..	1.982	2.80E-04
	Firmicutes	Eubacterium coprostanoligenes group	..	1.964	7.91E-04
	Firmicutes	Monoglobus	..	1.959	0.0036
	Firmicutes	Anaerovoracaceae Family XIII AD3011 group	..	1.906	0.0015
	Firmicutes	Oscillospiraceae UCG-002	..	1.906	0.0015
	Firmicutes	Christensenellaceae R-7 group	..	1.887	0.0017
	Firmicutes	Eubacterium eligens group	..	1.878	0.0052
	Firmicutes	Methanobrevibacter	..	1.872	0.0054
	Firmicutes	Eubacterium eligens group	..	1.868	0.0019
	Firmicutes	Lactobacillus	..	1.848	0.0020
	Firmicutes	Subdoligranulum	..	1.827	0.0022
Firmicutes	Anaerostipes	hadrus	1.808	0.0024	
Firmicutes	Oscillospiraceae UCG-002	..	1.772	0.016	

Abundant in Patient Samples Without Eyedrops

Firmicutes	Faecalibacterium	prausnitzii	1.731	0.010
Firmicutes	Clostridia vadin BB60 group	..	1.722	0.0030
Firmicutes	Oscillospiraceae UCG-002	..	1.717	0.017
Firmicutes	Incertae Sedis	..	1.678	0.0063
Firmicutes	Incertae Sedis	..	1.656	0.0052
Firmicutes	Ruminococcus	bicirculans	1.656	0.0071
Actinobacteriota	Bifidobacterium	..	1.655	0.0036
Patescibacteria	Candidatus Saccharimonas	..	1.610	0.0063
Firmicutes	Blautia	..	1.610	0.0045
Firmicutes	Ruminococcus	callidus	1.585	0.0075
Firmicutes	Ruminococcus	..	1.585	0.0054
Firmicutes	Negativibacillus	..	1.561	0.0086
Firmicutes	Lachnospiraceae NK4A136 group	..	1.536	0.0088
Firmicutes	Oscillospiraceae UCG-003	..	1.519	0.016
Firmicutes	Romboutsia	ilealis/timonensis	1.486	0.0074
Synergistota	Cloacibacillus	..	1.460	0.016
Firmicutes	Clostridia UCG-014	..	1.460	0.016
Firmicutes	Lachnoclostridium	..	1.460	0.016
Firmicutes	Lachnospiraceae NK4A136 group	..	1.442	0.036
Firmicutes	Lachnospira	pectinoschiza	1.404	0.030
Actinobacteriota	Enterorhabdus	..	1.403	0.019
Firmicutes	Anaerostipes	..	1.379	0.021
Firmicutes	Lachnospiraceae genus	..	1.351	0.018
Firmicutes	Lachnospiraceae A2	..	1.338	0.024
Firmicutes	Ruminococcaceae genus	..	1.321	0.021
Firmicutes	Oscillibacter	..	1.299	0.028
Firmicutes	Peptoniphilus	..	1.294	0.024
Firmicutes	Selenomonadales	..	1.293	0.027
Firmicutes	Agathobacter	..	1.283	0.042
Firmicutes	Eubacterium nodatum group	..	1.264	0.024
Firmicutes	Eubacterium coprostanoligenes group	..	1.263	0.024
Verrucomicrobiota	Akkermansia	..	1.233	0.026
Firmicutes	Roseburia	..	1.232	0.033
Firmicutes	Peptoniphilus	..	1.105	0.030
Firmicutes	Colidextribacter	..	1.104	0.045
Bacteroidota	Muribaculaceae	..	1.071	0.032
Firmicutes	Blautia	..	1.037	0.042
Firmicutes	Christensenellaceae genus	..	1.036	0.042
Actinobacteriota	Enterorhabdus	..	-1.279	0.044
Firmicutes	Agathobacter	..	-1.321	0.044
Firmicutes	Eubacterium coprostanoligenes group	..	-1.382	0.036
Firmicutes	Peptoniphilus	..	-1.382	0.024
Firmicutes	Blautia	..	-1.382	0.036
Actinobacteriota	Slackia	isoflavoniconvertens	-1.420	0.032
Proteobacteria	Methylobacterium	jeotgali	-1.439	0.022
Firmicutes	Roseburia	..	-1.440	0.025

Abundant in Control Subject Samples	Firmicutes	Anaerovoracaceae Family XIII AD3011 group	..	-1.513	0.024
	Bacteriodota	Muribaculaceae	..	-1.533	0.023
	Actinobacteriota	Corynebacterium	afermentans/coyleae	-1.549	0.016
	Actinobacteriota	Atopobium	parvulum	-1.550	0.024
	Patescibacteria	Endobacter	medicaginis	-1.567	0.021
	Firmicutes	Lachnospiraceae NK4A136 group	..	-1.600	0.016
	Firmicutes	Roseburia	hominis	-1.600	0.019
	Actinobacteriota	Rothia	..	-1.601	0.016
	Firmicutes	Tyzzera	..	-1.606	0.016
	Actinobacteriota	Eggerthella	lenta	-1.634	0.017
	Firmicutes	Oscillospiraceae UCG-002	..	-1.635	0.017
	Actinobacteriota	Lawsonella	..	-1.683	0.021
	Firmicutes	Agathobacter	..	-1.805	0.0080
	Actinobacteriota	Rothia	dentocariosa	-1.821	0.0038
	Proteobacteria	Sphingobium	yanoikuyae	-1.945	0.0036
	Actinobacteriota	Micrococcus	aloeverae/luteus/lylae/yunnanensis	-1.985	0.0032
	Firmicutes	Lachnospiraceae A2	..	-2.046	0.0042
	Actinobacteriota	Corynebacterium	fournieri/mucifaciens/ureicelerivora	-2.110	0.0020
	Fusobacteriota	Fusobacterium	periodonticum	-2.235	6.54E-04
	Proteobacteria	Novosphingobium	..	-2.288	3.89E-04
	Firmicutes	Eubacterium ruminantium group	..	-2.320	9.31E-04
	Firmicutes	Ruminococcus	bromii	-2.371	4.56E-04
	Firmicutes	Anaerococcus	..	-2.401	2.53E-04
	Actinobacteriota	Corynebacterium	kroppenstedtii	-2.569	6.74E-04
	Firmicutes	Eubacterium coprostanoligenes	..	-2.673	2.67E-04
	Actinobacteriota	Bifidobacterium	adolescentis/faecale/stercoris	-2.746	7.58E-05
	Firmicutes	Blautia	..	-2.783	5.82E-05
	Actinobacteriota	Cutibacterium	granulosum	-2.983	2.33E-05
	Proteobacteria	Bradyrhizobium	..	-3.164	2.81E-08
	Actinobacteriota	Corynebacterium	amycolatum/jeikeium/lactis/urealyticum/vitaeruminis	-3.930	4.50E-08
	Actinobacteriota	Corynebacterium	kroppenstedtii	-4.323	4.50E-08
	Actinobacteriota	Corynebacterium	kroppenstedtii	-4.376	3.58E-05
	Actinobacteriota	Cutibacterium	..	-4.517	2.84E-08
	Actinobacteriota	Lawsonella	..	-4.909	9.76E-11
	Actinobacteriota	Corynebacterium	aurimucosum/pseudogenitalium/tuberculostearicum	-4.933	6.62E-08
	Actinobacteriota	Corynebacterium	kroppenstedtii	-5.273	4.22E-10
	Actinobacteriota	Cutibacterium	acnes/avidum	-5.502	6.09E-13
	Actinobacteriota	Corynebacterium	kroppenstedtii	-5.568	1.68E-08
Actinobacteriota	Corynebacterium	bovis	-6.193	2.27E-12	
Actinobacteriota	Corynebacterium	..	-7.277	2.91E-13	
Actinobacteriota	Corynebacterium	..	-7.556	4.89E-20	
Actinobacteriota	Corynebacterium	kroppenstedtii	-7.566	4.94E-17	
Actinobacteriota	Corynebacterium	macginleyi	-8.585	4.94E-17	
Actinobacteriota	Corynebacterium	bovis	-8.716	4.94E-17	

Supplemental Table 2. Microbial organisms associated with relatively abundant amplicon sequence variants (ASVs) in control subjects compared to patient samples without eyedrops. The patient samples represent those coming from the eye without glaucoma and no

medication therapy. ASVs were classified taxonomically using QIIME2 q2-feature-classifier plugin by identifying k-mers that are diagnostic for particular taxonomic groups. In our analysis, we used a 99% SILVA reference set trained on the 16S region. The classified phyla, genus, and species are noted in the table. Log2foldchange is the effect size estimate representing the change in abundance of an ASV, with increased abundance in controls as positive values and increased abundance in treated patients as negative values. The p-values are generated using the Wald test and corrected for false discovery rate (FDR) using the Benjamini and Hochberg method. Corrected p-values < 0.05 were considered significant. Only significantly abundant organisms were included in the table and corrected p-values are shown.