

<b>Microbial organisms and taxonomic classification to ASVs</b>					
	<b>Phyla</b>	<b>Genus</b>	<b>Species</b>	<b>Log2FoldChange</b>	<b>p-value</b>
<b>Abundant in Patient Eye Samples with Eyedrops</b>	Proteobacteria	Komagataeibacter	rhaeticus/xylinus	4.363	1.77E-10
	Firmicutes	Eubacterium siraeum	..	4.238	1.87E-09
	Verrucomicrobiota	Akkermansia	muciniphila	4.228	5.11E-08
	Firmicutes	Eubacterium eligens	..	3.861	1.46E-08
	Actinobacteriota	Bifidobacterium	bifidum	3.765	6.45E-08
	Firmicutes	Ruminococcaceae CAG-352	..	3.364	8.78E-06
	Firmicutes	Blautia	..	3.320	1.78E-06
	Firmicutes	Oscillospiraceae NK4A214 group	..	3.306	1.25E-06
	Firmicutes	Lachnospiraceae NK4A136 group	..	3.240	8.78E-06
	Firmicutes	Gaecalibacterium	prausnitzii	3.042	2.47E-05
	Proteobacteria	Gluconobacter	oxydans	2.965	7.68E-06
	Firmicutes	Faecalibacterium	prausnitzii	2.953	0.0018
	Firmicutes	Lachnospiraceae genus	..	2.947	2.88E-05
	Actinobacteriota	Bifidobacterium	longum	2.918	0.0021
	Firmicutes	Lachnospiraceae NK4A136 group	..	2.847	2.38E-05
	Firmicutes	Ruminococcus torques group	..	2.827	4.39E-05
	Firmicutes	Roseburia	..	2.815	4.39E-05
	Firmicutes	Eubacterium coprostanoligenes group	..	2.811	8.69E-05
	Firmicutes	Ruminococcus torques group	..	2.764	5.40E-05
	Firmicutes	Roseburia	inulinivorans	2.763	6.11E-04
	Firmicutes	Oscillospiraceae genus	..	2.762	3.07E-05
	Firmicutes	Monoglobus	..	2.606	3.88E-04
	Firmicutes	Lachnospira	..	2.572	1.76E-04
	Firmicutes	Ruminococcus gnavus group	..	2.560	6.79E-04
	Firmicutes	Oscillospiraceae UCG-002	..	2.537	6.79E-04
	Firmicutes	Clostridia vadin BB60 group	..	2.534	3.55E-04
	Firmicutes	Lachnospiraceae NK4A136 group	..	2.499	6.79E-04
	Firmicutes	Lachnospiraceae genus	..	2.469	6.11E-04
	Verrucomicrobiota	Akkermansia	muciniphila	2.453	0.021
	Firmicutes	Ruminococcus	callidus	2.405	6.79E-04
	Firmicutes	Clostridia vadin BB60 group	..	2.379	6.79E-04
	Firmicutes	Negativibacillus	..	2.350	7.70E-04
	Firmicutes	Ruminococcus	bromii	2.342	0.0046
	Firmicutes	Oscillibacter	..	2.342	6.79E-04
	Firmicutes	Lachnospiraceae NK4A136 group	..	2.306	6.63E-04
	Firmicutes	Eubacterium coprostanoligenes	..	2.278	0.0011
	Firmicutes	Blautia	obeum/wexlerae	2.179	0.0089
	Firmicutes	Lachnospiraceae NK4A136 group	..	2.166	0.030
	Firmicutes	Anaerococcus	vaginalis	2.109	0.014
	Firmicutes	Lachnospiraceae NK4A136 group	..	2.091	0.015
	Firmicutes	Lachnoclostridium	..	2.077	0.014
	Firmicutes	Anaerostipes	hadrus	2.016	0.0044
	Firmicutes	Roseburia	intestinalis	1.963	0.014
	Actinobacteriota	Rothia	mucilaginososa	1.944	0.033
	Firmicutes	Eubacterium hallii group	..	1.908	0.021
Firmicutes	Flavonifractor	plautii	1.899	0.041	
Firmicutes	Butyricicoccus	..	1.886	0.0055	
Actinobacteriota	Enterorhabdus	..	1.846	0.015	
Firmicutes	Ezakiella	..	1.818	0.017	
Firmicutes	Faecalibacterium	prausnitzii	1.800	0.036	
Firmicutes	Intestinibacter	bartlettii	1.728	0.015	

Abundant in Control Subjects	Firmicutes	Ruminococcaceae genus	..	1.720	0.025
	Firmicutes	Peptoniphilus	coxii	1.700	0.019
	Firmicutes	Eubacterium coprostanoligenes	..	1.610	0.039
	Firmicutes	Blautia	..	1.561	0.037
	Firmicutes	Ruminococcaceae genus	..	1.560	0.037
	Firmicutes	Anaerostipes	..	1.511	0.048
	Proteobacteria	Bradyrhizobium	..	-1.741	0.046
	Actinobacteriota	Rothia	dentocariosa	-1.822	0.018
	Firmicutes	Blautia	coccoides/hansenii/mar asmi/producta	-1.906	0.020
	Proteobacteria	Sphingobium	yanoikuyae	-1.946	0.017
	Firmicutes	Lachnospiraceae genus	..	-1.960	0.020
	Firmicutes	Lachnospiraceae A2 group	..	-1.973	0.025
	Firmicutes	Clostridium sensu stricto 1	perfringens/thermophilu s	-1.986	0.014
	Actinobacteriota	Micrococcus	aloverae/luteus/lylae/y unnanensis	-1.987	0.015
	Actinobacteriota	Lawsonella	..	-2.063	0.021
	Actinobacteriota	Corynebacterium	fournieri/mucifaciens/ur eicelerivorans	-2.111	0.010
	Proteobacteria	Novosphingobium	..	-2.290	0.0018
	Firmicutes	Eubacterium ruminantium group	..	-2.321	0.0044
	Firmicutes	Anaerococcus	..	-2.401	0.0012
	Actinobacteriota	Corynebacterium	kroppenstedtii	-2.569	0.0032
	Actinobacteriota	Bifidobacterium	adolescentis/faecale/ster coris	-2.747	3.80E-04
	Actinobacteriota	Lawsonella	..	-3.487	1.10E-04
	Actinobacteriota	Cutibacterium	granulosum	-3.791	2.75E-07
	Actinobacteriota	Corynebacterium	kroppenstedtii	-4.238	9.32E-04
	Actinobacteriota	Corynebacterium	kroppenstedtii	-4.324	2.28E-07
	Actinobacteriota	Cutibacterium	..	-4.518	1.29E-07
	Actinobacteriota	Corynebacterium	aurimucosum/pseudoge nitalium/tuberculosteari cum	-5.142	3.10E-08
	Actinobacteriota	Corynebacterium	kroppenstedtii	-5.269	1.92E-09
	Actinobacteriota	Cutibacterium	acnes/avidum	-5.720	2.54E-13
	Actinobacteriota	Corynebacterium	bovis	-6.193	1.06E-11
	Actinobacteriota	Corynebacterium	kroppenstedtii	-6.468	3.09E-11
	Actinobacteriota	Corynebacterium	..	-7.277	1.15E-12
Actinobacteriota	Corynebacterium	..	-7.556	7.82E-20	
Actinobacteriota	Corynebacterium	kroppenstedtii	-7.566	2.02E-16	
Actinobacteriota	Corynebacterium	macginleyi	-9.671	8.55E-23	
Actinobacteriota	Corynebacterium	bovis	-9.839	2.21E-21	

**Supplemental Table 1. Microbial organisms associated with relatively abundant amplicon sequence variants (ASVs) in control subjects compared to eyedrop treated patients.** Eyedrop treated patients represent eye samples obtained in the patient eyes with a diagnosis of glaucoma receiving topical 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 eyedrop treated patient eye samples as positive values and increased abundance in control subjects 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.