

Taxa (genus level)	<i>Acidaminococcus</i>	-0.30	-0.20	0.09	-0.04	-0.08	-0.10
	<i>Agathobacter</i>	0.27	0.16	0.49	0.30	0.07	0.08
	<i>Agathobaculum</i>	0.09	-0.01	-0.06	-0.17	0.21	0.08
	<i>Akkermansia</i>	-0.07	0.11	0.07	-0.31	0.16	0.01
	<i>Alistipes</i>	-0.20	0.04	0.17	-0.06	0.16	0.00
	<i>Anaeromassilibacillus</i>	-0.27	0.09	-0.10	-0.01	0.01	-0.10
	<i>Bacteroides</i>	0.02	0.33	0.26	-0.33	-0.03	-0.04
	<i>Bifidobacterium</i>	-0.02	-0.21	-0.07	0.09	0.05	-0.07
	<i>Butyricicoccus</i>	-0.02	0.10	0.04	-0.02	-0.23	0.12
	<i>Butyricimonas</i>	-0.39	-0.02	0.06	0.04	0.16	0.09
	<i>Clostridium_IV</i>	0.02	-0.20	0.05	-0.00	0.15	-0.21
	<i>Clostridium_sensu_stricto</i>	0.48	-0.04	0.00	0.03	-0.00	-0.01
	<i>Clostridium_XIVa</i>	0.18	-0.12	0.08	-0.07	-0.29	0.13
	<i>Clostridium_XVIII</i>	0.06	0.27	-0.06	-0.14	-0.13	-0.18
	<i>Coprobacter</i>	0.02	-0.21	0.14	0.17	-0.06	0.15
	<i>Coprococcus</i>	0.19	0.07	-0.12	0.04	0.27	0.21
	<i>Dialister</i>	-0.13	-0.12	0.05	0.35	0.25	0.22
	<i>Dorea</i>	-0.02	-0.06	0.06	0.07	0.24	-0.02
	<i>Dysosmobacter</i>	-0.31	-0.12	-0.20	0.06	-0.32	-0.20
	<i>Eggerthella</i>	-0.08	0.01	-0.16	-0.03	-0.13	-0.21
	<i>Enterocloster</i>	0.00	-0.14	0.02	-0.03	-0.33	-0.06
	<i>Enterococcus</i>	0.15	0.10	-0.36	-0.04	-0.00	0.01
	<i>Faecalibacillus</i>	0.27	0.03	0.04	0.06	0.29	0.19
	<i>Flavonifractor</i>	0.00	-0.07	-0.02	-0.10	-0.34	-0.16
	<i>Frisingicoccus</i>	-0.16	-0.25	0.05	-0.02	0.07	0.00
	<i>Fusobacterium</i>	0.34	0.14	0.06	-0.15	-0.21	-0.03
	<i>Intestinimonas</i>	0.10	-0.05	-0.02	-0.13	-0.20	0.08
	<i>Lachnospira</i>	0.21	-0.11	0.05	0.03	0.24	0.12
	<i>Lactaseibacillus</i>	-0.19	0.07	-0.06	-0.09	-0.03	-0.20
	<i>Lactobacillus</i>	-0.16	-0.06	-0.11	-0.27	-0.19	-0.26
	<i>Ligilactobacillus</i>	-0.08	-0.07	0.05	-0.13	-0.38	-0.04
	<i>Limosilactobacillus</i>	-0.07	-0.11	0.04	-0.21	-0.15	-0.29
	<i>Mediterraneibacter</i>	-0.13	-0.41	0.17	0.23	0.02	0.16
	<i>Megasphaera</i>	-0.12	-0.06	-0.42	0.04	-0.28	0.10
	<i>Negativibacillus</i>	0.34	-0.21	-0.09	0.07	-0.27	-0.13
	<i>Neglecta</i>	-0.46	0.08	-0.09	0.19	0.07	-0.01
	<i>Odoribacter</i>	-0.12	-0.26	0.15	0.10	0.09	0.20
	<i>Olsenella</i>	-0.22	-0.14	-0.00	-0.05	0.03	0.02
	<i>Oscillibacter</i>	0.23	0.08	-0.12	0.04	0.29	0.10
	<i>Paraprevotella</i>	-0.50	-0.36	-0.03	0.09	0.09	-0.21
	<i>Parasutterella</i>	0.07	-0.22	-0.06	-0.03	-0.07	-0.15
	<i>Phascolarctobacterium</i>	0.06	0.18	-0.05	-0.19	0.03	-0.26
	<i>Prevotella</i>	-0.26	-0.32	-0.06	0.12	-0.04	-0.03
	<i>Prevotellamassilia</i>	0.00	-0.09	-0.27	-0.01	-0.07	0.08
	<i>Romboutsia</i>	0.24	0.17	0.29	0.17	0.09	0.07
	<i>Roseburia</i>	0.17	0.09	0.08	-0.12	0.35	0.01
	<i>Ruminococcus</i>	-0.25	-0.06	-0.05	-0.03	0.28	0.05
	<i>Ruminococcus2</i>	-0.04	0.02	0.36	0.14	-0.36	-0.07
	<i>Ruthenibacterium</i>	-0.04	-0.04	0.21	-0.15	-0.25	-0.03
	<i>Streptococcus</i>	-0.44	-0.06	-0.26	-0.39	-0.34	-0.61
	<i>Turicibacter</i>	0.08	-0.04	0.13	0.05	0.38	0.02
	<i>Veillonella</i>	0.14	0.12	-0.19	-0.24	-0.18	-0.16

50s_Male 60s_Male 70s_Male
50s_Female 60s_Female 70s_Female
Age group and sex

Supplementary Figure S1. The values of ALDEx2 effect size obtained by comparing the gastritis disease-affected and disease-free Japanese control groups. The comparisons were performed considering age and sex. Negative values of effect size indicate taxa that are more abundant in the disease-affected group than in the control group, and positive values indicate taxa that are less abundant. The values of effect size less than -0.2 are indicated with pink, and the values greater than 0.2 are indicated with light blue.

Taxa (genus level)		50s_Male	50s_Female	60s_Male	60s_Female
	<i>Agathobacter</i>	-0.07	0.27	0.11	0.26
	<i>Agathobaculum</i>	-0.24	-0.15	-0.16	0.01
	<i>Anaeromassilibacillus</i>	0.37	-0.30	0.10	-0.21
	<i>Anaerostipes</i>	-0.07	-0.11	0.23	0.07
	<i>Anaerotruncus</i>	-0.32	-0.20	0.06	0.01
	<i>Bacteroides</i>	-0.30	-0.00	0.11	-0.18
	<i>Blautia</i>	-0.24	-0.38	0.13	-0.04
	<i>Butyricimonas</i>	0.01	0.42	-0.12	-0.03
	<i>Clostridium_sensu_stricto</i>	-0.33	0.10	-0.07	-0.05
	<i>Clostridium_XIVa</i>	-0.48	-0.25	-0.10	-0.26
	<i>Clostridium_XIVb</i>	0.14	0.11	-0.17	0.26
	<i>Coprobacter</i>	0.63	-0.03	-0.03	0.32
	<i>Coprococcus</i>	0.05	0.12	-0.26	0.27
	<i>Dialister</i>	0.02	0.31	-0.02	-0.07
	<i>Dorea</i>	-0.27	0.05	0.07	0.10
	<i>Dysosmobacter</i>	0.04	-0.32	0.19	-0.11
	<i>Eggerthella</i>	-0.09	-0.09	0.15	-0.44
	<i>Eisenbergiella</i>	0.06	-0.32	0.05	0.10
	<i>Enterocloster</i>	-0.29	-0.15	0.16	-0.13
	<i>Faecalibacillus</i>	0.21	0.20	0.04	0.08
	<i>Faecalibacterium</i>	0.06	0.12	-0.03	0.24
	<i>Faecalimonas</i>	0.06	-0.27	0.06	-0.24
	<i>Flavonifractor</i>	-0.31	-0.45	-0.11	-0.38
	<i>Fournierella</i>	0.08	-0.23	0.06	-0.10
	<i>Fusobacterium</i>	0.06	-0.02	0.09	-0.34
	<i>Holdemania</i>	-0.10	-0.24	0.16	-0.04
	<i>Hungatella</i>	-0.04	-0.23	-0.04	-0.11
	<i>Intestinibacter</i>	-0.54	-0.38	0.03	-0.18
	<i>Lawsonibacter</i>	0.19	-0.21	0.22	0.12
	<i>Ligilactobacillus</i>	0.06	-0.09	-0.26	-0.03
	<i>Massilimicrobiota</i>	0.18	-0.22	0.08	0.14
	<i>Mediterraneibacter</i>	-0.26	0.06	0.13	0.23
	<i>Megamonas</i>	0.46	-0.08	0.05	0.08
	<i>Neglecta</i>	-0.01	-0.17	-0.23	-0.14
	<i>Odoribacter</i>	0.19	0.25	0.05	0.03
	<i>Oscillibacter</i>	0.02	0.27	-0.07	0.44
	<i>Parabacteroides</i>	-0.22	-0.02	0.18	-0.00
	<i>Paraprevotella</i>	0.30	0.07	-0.12	0.17
	<i>Prevotella</i>	0.18	0.03	0.23	0.30
	<i>Romboutsia</i>	0.22	0.08	0.12	-0.10
	<i>Roseburia</i>	0.10	0.35	-0.01	0.36
	<i>Ruminococcus</i>	-0.10	0.30	0.06	0.06
	<i>Ruthenibacterium</i>	-0.13	0.09	0.15	-0.26
	<i>Sellimonas</i>	-0.11	-0.31	0.07	0.09
	<i>Streptococcus</i>	0.27	-0.09	-0.14	-0.13
	<i>Terrisporobacter</i>	-0.22	0.00	-0.09	-0.04
	<i>Turicibacter</i>	-0.11	-0.00	-0.02	-0.25
	<i>Veillonella</i>	-0.23	-0.07	-0.11	0.11
		50s_Male	50s_Female	60s_Male	60s_Female
		Age group and sex			

Supplementary Figure S2. The values of ALDEx2 effect size obtained by comparing the kidney disease-affected and disease-free Japanese control groups. The comparisons were performed considering age and sex. Negative values of effect size indicate taxa that are more abundant in the disease-affected group than in the control group, and positive values indicate taxa that are less abundant. The values of effect size less than -0.2 are indicated with pink, and the values greater than 0.2 are indicated with light blue.

Taxa (genus level)	<i>Acidaminococcus</i>	0.35	0.03	0.01	0.03	-0.13	0.01	-0.18	0.01
	<i>Agathobacter</i>	0.05	0.32	-0.17	-0.00	0.00	0.10	0.15	0.06
	<i>Agathobaculum</i>	0.44	-0.05	-0.04	0.11	0.22	0.14	0.22	0.20
	<i>Alistipes</i>	0.49	0.05	-0.07	0.04	-0.05	0.24	0.08	0.18
	<i>Allisonella</i>	0.21	0.00	-0.05	0.03	0.01	0.05	-0.01	0.04
	<i>Amedibacterium</i>	-0.24	-0.08	0.04	-0.01	-0.03	-0.05	-0.09	-0.01
	<i>Anaerobutyricum</i>	0.07	0.18	-0.07	0.04	-0.07	-0.01	0.40	0.14
	<i>Anaeromassilibacillus</i>	-0.14	-0.10	-0.09	0.02	0.10	0.20	-0.28	-0.02
	<i>Anaerostipes</i>	-0.20	0.23	-0.13	0.35	0.43	-0.14	-0.17	0.25
	<i>Barnesiella</i>	0.07	0.06	0.09	0.11	0.10	0.28	0.02	0.10
	<i>Bifidobacterium</i>	0.06	0.14	-0.06	0.04	0.01	0.01	-0.36	-0.08
	<i>Butyricoccus</i>	-0.23	-0.06	0.02	0.01	-0.02	0.04	-0.23	0.11
	<i>Butyricimonas</i>	0.32	0.23	0.04	-0.09	-0.04	0.18	-0.02	0.28
	<i>Clostridium_IV</i>	0.07	0.20	-0.14	0.12	-0.02	0.14	-0.12	0.02
	<i>Clostridium_sensu_stricto</i>	0.11	0.02	-0.06	0.05	0.00	-0.17	0.39	0.20
	<i>Clostridium_XIVa</i>	-0.21	-0.12	0.01	-0.21	-0.05	-0.03	-0.24	-0.12
	<i>Clostridium_XIVb</i>	-0.21	0.09	0.09	0.08	0.03	0.14	0.11	0.03
	<i>Clostridium_XVIII</i>	0.03	-0.03	0.16	0.04	-0.13	-0.17	-0.23	-0.25
	<i>Collinsella</i>	0.49	0.10	-0.08	0.16	-0.14	0.27	0.36	0.16
	<i>Coprobacillus</i>	-0.22	-0.17	-0.01	0.05	0.03	0.03	0.08	-0.17
	<i>Coprobacter</i>	0.27	0.19	0.10	0.08	-0.18	0.43	0.29	0.04
	<i>Coprococcus</i>	0.15	0.14	0.14	-0.03	0.21	0.11	0.28	0.27
	<i>Dialister</i>	0.32	0.13	0.06	0.02	-0.23	-0.13	0.14	0.14
	<i>Dorea</i>	0.12	0.24	-0.05	0.24	-0.04	-0.01	0.29	0.22
	<i>Duodenibacillus</i>	-0.33	-0.11	-0.11	-0.07	-0.05	0.10	-0.01	0.03
	<i>Dysosmobacter</i>	0.37	0.08	-0.12	-0.04	-0.18	0.11	-0.03	-0.14
	<i>Eggerthella</i>	-0.13	0.10	0.04	0.04	-0.06	-0.15	-0.39	-0.12
	<i>Enterocloster</i>	-0.35	-0.24	-0.09	-0.14	0.06	-0.17	-0.07	-0.38
	<i>Enterococcus</i>	-0.17	-0.25	0.02	-0.10	-0.05	-0.27	-0.10	-0.14
	<i>Erysipelatoclostridium</i>	-0.29	-0.20	-0.04	-0.21	0.01	-0.31	-0.50	-0.21
	<i>Faecalibacillus</i>	0.46	0.19	0.01	0.07	0.39	0.11	0.28	0.42
	<i>Faecalibacterium</i>	0.38	0.25	0.14	0.07	0.11	0.07	0.02	0.14
	<i>Flavonifractor</i>	-0.10	-0.05	-0.08	-0.10	-0.12	-0.11	-0.49	-0.44
	<i>Frisingicoccus</i>	-0.02	-0.06	-0.07	0.02	-0.01	0.03	-0.21	-0.02
	<i>Fusicatenibacter</i>	-0.06	0.36	-0.08	0.20	0.11	-0.01	-0.02	0.02
	<i>Fusobacterium</i>	-0.27	-0.26	0.01	-0.11	0.25	-0.22	0.00	-0.03
	<i>Holdemanella</i>	0.22	-0.01	-0.02	-0.00	-0.11	0.06	0.20	0.11
	<i>Lachnospira</i>	-0.13	0.37	-0.05	0.09	0.03	0.01	0.04	0.41
	<i>Lactobacillus</i>	-0.17	-0.18	0.03	-0.09	0.08	-0.13	-0.25	-0.39
	<i>Lawsonibacter</i>	0.21	0.14	0.06	-0.15	0.06	0.04	-0.24	-0.08
	<i>Limosilactobacillus</i>	-0.12	-0.18	-0.07	-0.09	-0.18	-0.06	-0.29	-0.28
	<i>Massilimicrobiota</i>	-0.15	-0.00	0.10	0.02	0.08	-0.30	-0.27	-0.26
	<i>Mediterraneibacter</i>	0.05	0.12	-0.27	0.03	0.06	0.09	0.20	0.23
	<i>Megamonas</i>	0.28	-0.00	0.00	0.05	-0.07	0.02	0.16	0.05
	<i>Megasphaera</i>	-0.08	0.01	-0.07	-0.01	-0.30	0.08	-0.06	-0.14
	<i>Merdimonas</i>	-0.09	-0.06	-0.01	-0.04	-0.09	-0.02	-0.41	-0.05
	<i>Mogibacterium</i>	0.03	-0.05	0.05	-0.01	-0.33	0.01	0.01	-0.00
	<i>Negativibacillus</i>	0.31	0.14	0.04	-0.15	-0.09	0.17	-0.01	-0.07
	<i>Neglecta</i>	0.22	0.18	-0.07	0.18	-0.14	0.10	0.00	0.08
	<i>Odoribacter</i>	0.61	0.15	-0.09	0.20	0.18	0.29	0.16	0.26
	<i>Oscillibacter</i>	0.13	0.15	0.19	-0.05	0.00	0.41	0.36	0.60
	<i>Parabacteroides</i>	0.13	0.08	-0.18	-0.02	-0.13	0.07	0.25	-0.12
	<i>Phascolarctobacterium</i>	-0.25	-0.10	-0.04	0.02	0.26	0.04	0.01	-0.05
	<i>Prevotella</i>	0.56	-0.06	0.05	0.06	-0.00	-0.05	0.13	0.14
	<i>Roseburia</i>	0.22	0.45	0.16	0.05	-0.09	-0.04	0.33	0.02
	<i>Ruminococcus</i>	0.48	0.07	-0.02	0.10	-0.16	0.25	0.32	0.30
	<i>Sellimonas</i>	-0.17	0.05	-0.22	-0.09	-0.02	-0.06	-0.15	-0.07
	<i>Streptococcus</i>	-0.37	-0.15	-0.03	-0.26	-0.10	-0.38	-0.54	-0.23
	<i>Turicibacter</i>	0.19	0.20	0.18	0.11	0.12	-0.11	0.28	0.16
	<i>Veillonella</i>	-0.37	-0.06	0.00	-0.01	0.14	-0.38	-0.43	-0.27
		40s_Male	50s_Male	60s_Male	70s_Male				
		40s_Female	50s_Female	60s_Female	70s_Female				
		Age group and sex							

Supplementary Figure S3. The values of ALDEx2 effect size obtained by comparing the liver disease-affected and disease-free Japanese control groups. The comparisons were performed considering age and sex. Negative values of effect size indicate taxa that are more abundant in the disease-affected group than in the control group, and positive values indicate taxa that are less abundant. The values of effect size less than -0.2 are indicated with pink, and the values greater than 0.2 are indicated with light blue.

Taxa (genus level)	<i>Adlercreutzia</i>	0.15	0.22	0.04	0.05	0.12	-0.13
	<i>Akkermansia</i>	0.14	-0.01	0.09	-0.09	-0.21	-0.03
	<i>Anaeromassilibacillus</i>	0.23	-0.05	-0.11	-0.03	-0.04	-0.10
	<i>Anaerofignum</i>	0.26	-0.29	0.05	-0.05	0.07	-0.09
	<i>Bacteroides</i>	0.22	-0.07	-0.08	-0.18	-0.02	-0.07
	<i>Barnesiella</i>	0.12	0.24	0.16	0.20	-0.02	0.00
	<i>Bifidobacterium</i>	0.23	-0.05	0.06	0.07	0.11	0.05
	<i>Blautia</i>	0.11	0.17	-0.27	-0.11	0.01	-0.21
	<i>Butyrivimonas</i>	-0.31	-0.25	0.01	0.11	-0.08	-0.10
	<i>Clostridium_IV</i>	-0.25	-0.19	-0.20	0.05	-0.08	-0.03
	<i>Clostridium_sensu_stricto</i>	-0.09	-0.10	-0.17	-0.10	0.01	0.34
	<i>Clostridium_XIVa</i>	0.10	-0.24	0.02	0.05	0.00	0.09
	<i>Clostridium_XVIII</i>	0.24	-0.10	0.00	-0.08	0.00	-0.14
	<i>Coprobacter</i>	-0.14	0.31	0.14	0.18	-0.02	-0.06
	<i>Coproccoccus</i>	-0.44	0.27	0.07	0.13	0.07	0.19
	<i>Dialister</i>	0.03	0.48	-0.00	-0.03	0.17	0.07
	<i>Dorea</i>	-0.15	0.19	0.02	0.10	0.22	-0.21
	<i>Dysosmobacter</i>	0.09	-0.18	-0.15	-0.01	-0.13	-0.24
	<i>Enterocloster</i>	0.24	-0.50	-0.21	-0.12	-0.36	-0.23
	<i>Erysipelatoclostridium</i>	0.30	-0.25	-0.08	-0.22	-0.13	-0.07
	<i>Faecalibacillus</i>	-0.28	0.08	0.10	0.09	0.16	0.10
	<i>Faecalimonas</i>	0.22	-0.24	-0.02	-0.18	-0.04	-0.11
	<i>Flavonifractor</i>	0.40	-0.27	-0.15	-0.16	-0.25	-0.30
	<i>Frisingicoccus</i>	-0.01	-0.20	0.01	0.01	-0.12	0.02
	<i>Fusobacterium</i>	0.07	-0.47	-0.12	-0.23	-0.15	-0.01
	<i>Holdemanella</i>	-0.58	0.07	0.06	0.05	-0.05	0.07
	<i>Intestinimonas</i>	0.12	-0.35	0.02	0.17	-0.06	0.17
	<i>Lawsonibacter</i>	0.20	0.19	-0.04	0.02	-0.06	-0.06
	<i>Limosilactobacillus</i>	0.05	0.08	-0.19	-0.04	-0.12	-0.22
	<i>Massilimicrobiota</i>	0.29	-0.21	-0.01	0.08	-0.03	-0.07
	<i>Mediterraneibacter</i>	-0.30	0.14	-0.07	-0.02	0.08	0.04
	<i>Mogibacterium</i>	-0.30	0.06	-0.05	-0.07	0.01	-0.00
	<i>Negativibacillus</i>	-0.25	-0.15	0.13	0.00	-0.05	-0.12
	<i>Neglecta</i>	-0.39	0.17	-0.12	-0.08	0.08	0.05
	<i>Oscillibacter</i>	-0.25	0.36	0.17	0.13	0.07	0.08
	<i>Paraprevotella</i>	-0.28	0.13	0.14	0.19	-0.11	-0.12
	<i>Parasutterella</i>	-0.05	0.27	-0.07	0.06	0.02	-0.03
	<i>Phascolarctobacterium</i>	0.00	-0.45	-0.04	0.12	-0.08	-0.17
	<i>Prevotella</i>	-0.21	0.02	0.04	-0.16	0.06	-0.01
	<i>Romboutsia</i>	0.01	-0.22	-0.00	0.11	0.10	0.07
	<i>Roseburia</i>	0.00	-0.31	-0.03	0.00	0.05	0.19
	<i>Ruminococcus</i>	-0.20	0.23	-0.08	0.11	0.01	0.00
	<i>Ruminococcus2</i>	0.05	-0.34	-0.10	-0.19	-0.12	-0.26
	<i>Ruthenibacterium</i>	0.08	0.03	0.01	-0.21	-0.23	-0.21
	<i>Streptococcus</i>	-0.14	-0.26	-0.08	-0.17	-0.16	-0.33
	<i>Turicibacter</i>	-0.36	-0.03	0.04	-0.06	0.09	0.32
		50s_Male	50s_Female	60s_Male	60s_Female	70s_Male	70s_Female
		Age group and sex					

Supplementary Figure S4. The values of ALDEx2 effect size obtained by comparing the arrhythmia disease-affected and disease-free Japanese control groups. The comparisons were performed considering age and sex. Negative values of effect size indicate taxa that are more abundant in the disease-affected group than in the control group, and positive values indicate taxa that are less abundant. The values of effect size less than -0.2 are indicated with pink, and the values greater than 0.2 are indicated with light blue.

Taxa (genus level)	<i>Acidaminococcus</i>	-0.27	0.12	-0.02	-0.04
	<i>Agathobaculum</i>	-0.04	0.07	0.02	0.26
	<i>Alistipes</i>	-0.23	-0.02	-0.09	0.03
	<i>Anaerostipes</i>	0.20	0.19	-0.20	0.06
	<i>Anaerotignum</i>	-0.11	-0.30	-0.06	-0.14
	<i>Clostridium_XVIII</i>	0.08	0.20	-0.16	-0.14
	<i>Dysosmobacter</i>	-0.25	-0.03	-0.19	-0.01
	<i>Enterocloster</i>	-0.07	-0.11	-0.22	0.13
	<i>Faecalibacillus</i>	0.24	0.14	0.15	-0.06
	<i>Flavonifractor</i>	-0.24	-0.06	-0.14	-0.09
	<i>Intestinibacter</i>	0.13	0.10	0.20	-0.01
	<i>Intestinimonas</i>	0.04	0.09	-0.02	-0.25
	<i>Massilimicrobiota</i>	0.03	-0.29	-0.15	-0.13
	<i>Negativibacillus</i>	-0.32	-0.10	-0.16	-0.12
	<i>Odoribacter</i>	-0.07	0.24	-0.04	0.04
	<i>Parabacteroides</i>	-0.24	-0.05	-0.08	-0.01
	<i>Paraprevotella</i>	0.11	0.20	-0.08	-0.08
	<i>Phocaeicola</i>	-0.04	0.22	0.06	0.02
	<i>Roseburia</i>	0.13	0.16	0.39	-0.06
	<i>Ruminococcus2</i>	-0.04	-0.26	-0.10	-0.03
	<i>Ruthenibacterium</i>	-0.25	-0.34	-0.17	-0.01
	<i>Senegalimassilia</i>	-0.03	0.08	0.23	-0.06
	<i>Streptococcus</i>	-0.34	-0.16	-0.25	-0.32
	<i>Turicibacter</i>	0.24	0.09	0.17	0.07
		60s_Male	70s_Male	60s_Female	70s_Female
		Age group and sex			

Supplementary Figure S5. The values of ALDEx2 effect size obtained by comparing the angina pectoris disease-affected and disease-free Japanese control groups. The comparisons were performed considering age and sex. Negative values of effect size indicate taxa that are more abundant in the disease-affected group than in the control group, and positive values indicate taxa that are less abundant. The values of effect size less than -0.2 are indicated with pink, and the values greater than 0.2 are indicated with light blue.

Taxa (genus level)	<i>Agathobacter</i>	-0.08	0.12	-0.00	0.03	0.26	0.63
	<i>Bacteroides</i>	-0.20	-0.03	-0.04	0.06	-0.17	-0.24
	<i>Clostridium_XIVa</i>	-0.04	0.06	-0.11	0.09	-0.05	-0.25
	<i>Clostridium_XIVb</i>	0.12	0.07	0.02	0.08	0.07	0.23
	<i>Clostridium_XVIII</i>	-0.04	-0.05	-0.18	-0.14	-0.26	-0.22
	<i>Coproccoccus</i>	0.01	0.21	0.06	0.14	0.12	0.24
	<i>Eggerthella</i>	-0.06	0.01	-0.04	0.05	-0.10	-0.34
	<i>Enterococcus</i>	-0.01	-0.04	-0.13	-0.13	-0.09	-0.27
	<i>Erysipelatoclostridium</i>	-0.21	-0.07	-0.06	0.03	-0.19	-0.27
	<i>Faecalibacillus</i>	0.11	0.17	-0.06	0.00	0.03	0.21
	<i>Flavonifractor</i>	-0.03	-0.05	-0.14	0.04	-0.14	-0.37
	<i>Fusobacterium</i>	0.04	0.13	-0.07	-0.03	-0.21	-0.02
	<i>Holdemania</i>	-0.08	0.01	-0.02	0.02	-0.02	-0.23
	<i>Intestinibacter</i>	-0.04	-0.22	0.06	0.04	-0.01	-0.24
	<i>Intestinimonas</i>	-0.02	-0.05	0.04	0.06	-0.08	-0.26
	<i>Massilimicrobiota</i>	-0.11	-0.22	-0.02	-0.06	0.03	-0.25
	<i>Negativibacillus</i>	0.13	-0.29	0.18	-0.04	0.05	-0.05
	<i>Oscillibacter</i>	-0.03	0.20	0.13	-0.08	0.30	0.23
	<i>Ruminococcus2</i>	0.19	0.02	-0.07	0.17	0.12	-0.25
	<i>Sellimonas</i>	-0.03	0.00	0.02	0.04	-0.02	-0.31
		50s_Male	50s_Female	60s_Male	60s_Female	70s_Male	70s_Female
		Age group and sex					

Supplementary Figure S6. The values of ALDEx2 effect size obtained by comparing the glaucoma disease-affected and disease-free Japanese control groups. The comparisons were performed considering age and sex. Negative values of effect size indicate taxa that are more abundant in the disease-affected group than in the control group, and positive values indicate taxa that are less abundant. The values of effect size less than -0.2 are indicated with pink, and the values greater than 0.2 are indicated with light blue.

Taxa (genus level)	<i>Adlercreutzia</i>	0.03	0.03	0.17	-0.01	-0.10	0.08	0.11	-0.02	0.05	-0.04	0.10	0.20
	<i>Agathobacter</i>	0.34	0.08	0.00	0.01	-0.04	0.13	-0.10	0.15	-0.23	0.13	0.24	0.09
	<i>Agathobaculum</i>	-0.00	-0.03	0.01	0.04	0.11	0.03	0.10	0.10	0.10	0.05	-0.00	0.25
	<i>Allisonella</i>	0.06	0.03	0.07	-0.01	-0.01	0.03	-0.08	0.03	-0.25	0.07	0.18	0.08
	<i>Amedibacterium</i>	-0.24	-0.04	0.09	0.01	0.06	-0.06	0.08	-0.00	-0.16	-0.02	0.02	0.02
	<i>Anaeromassilibacillus</i>	0.06	-0.07	-0.04	0.04	-0.01	0.01	-0.16	-0.12	-0.09	-0.08	-0.24	-0.00
	<i>Anaerotrignum</i>	-0.05	0.08	-0.03	-0.03	0.06	0.01	0.10	-0.14	0.32	-0.08	-0.16	-0.13
	<i>Bacteroides</i>	0.09	-0.11	-0.13	-0.01	0.02	0.05	-0.21	-0.10	-0.10	-0.29	0.15	-0.07
	<i>Bifidobacterium</i>	-0.11	-0.13	0.04	0.16	-0.08	-0.01	-0.34	0.10	-0.06	-0.26	0.21	-0.03
	<i>Butyrivibrio</i>	-0.12	-0.07	-0.06	0.06	0.02	0.07	0.05	-0.07	0.07	0.31	-0.16	0.03
	<i>Clostridium_sensu_stricto</i>	0.19	-0.19	-0.04	-0.01	0.04	0.06	0.02	-0.14	-0.23	-0.10	0.20	-0.07
	<i>Clostridium_XIVa</i>	0.12	-0.06	-0.16	-0.17	0.02	-0.10	-0.26	-0.15	0.15	-0.23	-0.05	0.03
	<i>Clostridium_XVIII</i>	-0.03	-0.01	-0.06	-0.09	0.11	-0.01	0.14	0.04	0.00	0.02	0.22	-0.12
	<i>Collinsella</i>	0.14	-0.02	0.12	0.06	-0.07	0.04	-0.15	0.08	-0.05	-0.03	0.23	0.08
	<i>Coprobacter</i>	-0.16	0.31	-0.14	0.01	0.06	0.03	0.15	-0.04	0.13	-0.02	0.12	0.10
	<i>Coprococcus</i>	0.02	0.06	0.08	-0.07	-0.05	0.10	0.06	0.09	0.17	-0.00	0.11	0.30
	<i>Dialister</i>	0.17	0.21	0.00	0.07	0.04	-0.00	0.05	0.05	0.25	0.15	-0.13	0.22
	<i>Dysosmabacter</i>	0.02	0.01	-0.06	-0.02	0.01	0.01	-0.29	-0.08	0.15	-0.16	-0.33	-0.09
	<i>Eggerthella</i>	0.23	-0.10	-0.15	-0.08	0.05	-0.09	-0.29	-0.09	-0.01	-0.15	0.16	-0.11
	<i>Eisenbergiella</i>	0.06	-0.01	-0.08	-0.03	0.05	-0.05	-0.00	-0.06	0.10	-0.22	0.02	-0.07
	<i>Enterocloster</i>	0.15	-0.08	-0.06	-0.16	-0.05	-0.07	-0.25	-0.18	0.04	-0.23	-0.27	-0.15
	<i>Enterococcus</i>	-0.02	-0.02	-0.08	-0.04	0.02	-0.02	-0.05	-0.09	-0.01	-0.16	-0.25	0.05
	<i>Erysipelatoclostridium</i>	0.01	-0.11	0.01	-0.20	0.02	-0.13	-0.16	-0.14	0.09	-0.17	0.10	-0.37
	<i>Eubacterium</i>	-0.03	-0.07	-0.01	-0.03	-0.01	-0.04	0.02	-0.05	-0.08	-0.06	-0.12	-0.22
	<i>Faecalibacillus</i>	-0.08	0.01	-0.09	-0.02	0.13	0.05	0.09	0.10	0.28	0.06	0.29	0.50
	<i>Flavonifractor</i>	0.02	-0.06	-0.11	-0.08	0.02	-0.04	-0.37	-0.16	-0.03	-0.09	-0.42	-0.13
	<i>Fusobacterium</i>	-0.08	0.02	-0.11	-0.03	0.06	-0.06	0.02	-0.07	0.25	0.04	0.11	-0.11
	<i>Holdemanella</i>	-0.12	0.01	0.08	-0.01	0.05	0.04	0.16	0.03	0.20	-0.05	0.22	0.11
	<i>Intestinibacter</i>	-0.03	-0.16	-0.07	-0.10	0.14	-0.08	-0.38	-0.06	0.02	-0.01	0.14	0.18
	<i>Intestinimonas</i>	0.27	0.10	-0.03	0.01	0.02	0.01	0.13	-0.02	0.19	0.13	0.09	0.03
	<i>Lachnospira</i>	-0.04	-0.03	0.06	0.00	0.08	0.03	0.14	0.03	-0.22	0.10	0.23	0.12
	<i>Lactobacillus</i>	0.06	0.01	-0.06	-0.02	-0.00	-0.03	0.10	0.01	-0.00	-0.08	-0.34	-0.04
	<i>Lawsonibacter</i>	-0.04	0.04	0.15	0.00	0.07	0.03	0.00	-0.04	0.00	0.17	-0.42	-0.08
	<i>Ligilactobacillus</i>	-0.10	-0.05	-0.00	-0.01	-0.03	-0.03	-0.03	-0.03	-0.11	-0.00	-0.38	-0.01
	<i>Limosilactobacillus</i>	-0.12	0.04	0.02	-0.00	-0.01	-0.02	0.03	-0.00	-0.03	0.09	-0.46	-0.25
	<i>Mediterraneibacter</i>	0.07	-0.07	-0.01	-0.04	-0.03	-0.01	0.35	0.03	-0.24	0.09	0.28	0.28
	<i>Megamonas</i>	-0.19	0.01	0.04	0.00	-0.04	0.06	0.06	0.08	-0.25	0.01	-0.16	0.08
	<i>Megasphaera</i>	0.14	-0.10	-0.00	0.05	-0.07	-0.05	-0.23	0.01	-0.25	-0.08	-0.09	-0.10
	<i>Merdimonas</i>	0.11	-0.17	-0.10	0.04	-0.04	-0.04	0.08	-0.10	-0.04	-0.16	-0.22	0.07
	<i>Negativibacillus</i>	0.06	0.02	-0.06	0.01	-0.02	0.03	0.23	-0.07	0.38	-0.16	-0.18	-0.22
	<i>Odoribacter</i>	-0.02	0.12	-0.17	-0.02	-0.01	0.03	0.04	-0.06	0.24	0.01	-0.04	0.34
	<i>Oscillibacter</i>	0.08	0.08	0.10	0.11	-0.07	0.08	0.24	0.07	0.11	0.04	-0.04	0.09
	<i>Paraprevotella</i>	0.03	0.03	0.02	0.02	0.01	-0.00	0.10	0.07	0.02	0.24	-0.07	-0.34
	<i>Phascolarctobacterium</i>	-0.05	-0.21	0.01	0.03	0.06	0.05	0.08	-0.05	-0.09	-0.14	0.03	-0.40
	<i>Romboutsia</i>	0.16	-0.05	-0.04	0.06	0.19	0.02	-0.05	0.12	-0.43	-0.13	0.14	-0.03
	<i>Roseburia</i>	-0.15	0.03	0.01	0.08	0.06	0.03	0.08	0.20	-0.17	0.25	0.27	-0.15
	<i>Ruminococcus</i>	0.13	0.08	0.03	0.06	0.11	-0.03	0.26	-0.01	0.19	0.08	0.08	0.00
	<i>Ruminococcus2</i>	-0.08	0.04	-0.08	-0.01	0.14	-0.01	-0.18	-0.10	-0.06	-0.03	-0.32	0.33
	<i>Ruthenibacterium</i>	0.02	-0.11	-0.11	-0.02	-0.13	-0.04	-0.19	-0.20	0.01	-0.22	-0.21	-0.05
	<i>Sellimonas</i>	0.05	-0.01	-0.00	0.06	-0.01	-0.09	-0.20	-0.09	0.10	-0.17	-0.00	-0.09
	<i>Senegalimassilia</i>	0.08	-0.02	-0.02	-0.00	-0.03	0.02	-0.13	0.05	0.02	-0.02	0.20	0.04
	<i>Slackia</i>	-0.08	0.06	0.07	-0.01	-0.06	0.05	0.20	0.02	0.23	-0.03	0.14	-0.02
	<i>Streptococcus</i>	-0.05	-0.07	-0.06	-0.04	-0.10	-0.04	-0.20	0.10	0.04	-0.02	-0.36	-0.12
	<i>Sutterella</i>	-0.10	-0.07	0.05	0.05	0.09	0.02	0.05	0.13	0.14	-0.01	0.56	-0.11
	<i>Turicibacter</i>	-0.02	-0.09	-0.05	0.09	0.09	0.10	0.03	0.09	-0.01	0.08	0.29	-0.16
	<i>Veillonella</i>	-0.17	-0.13	-0.02	0.05	0.07	-0.01	-0.03	-0.06	-0.32	0.02	-0.21	-0.02
	<i>Victivallis</i>	-0.01	0.02	0.07	0.03	-0.13	0.03	0.09	-0.06	0.09	-0.08	-0.29	0.13
		20s_Male	30s_Male	40s_Male	50s_Male	60s_Male	70s_Male	20s_Female	30s_Female	40s_Female	50s_Female	60s_Female	70s_Female
		Age group and sex											

Supplementary Figure S7. The values of ALDEx2 effect size obtained by comparing the atopic dermatitis disease-affected and disease-free Japanese control groups. The comparisons were performed considering age and sex. Negative values of effect size indicate taxa that are more abundant in the disease-affected group than in the control group, and positive values indicate taxa that are less abundant. The values of effect size less than -0.2 are indicated with pink, and the values greater than 0.2 are indicated with light blue.