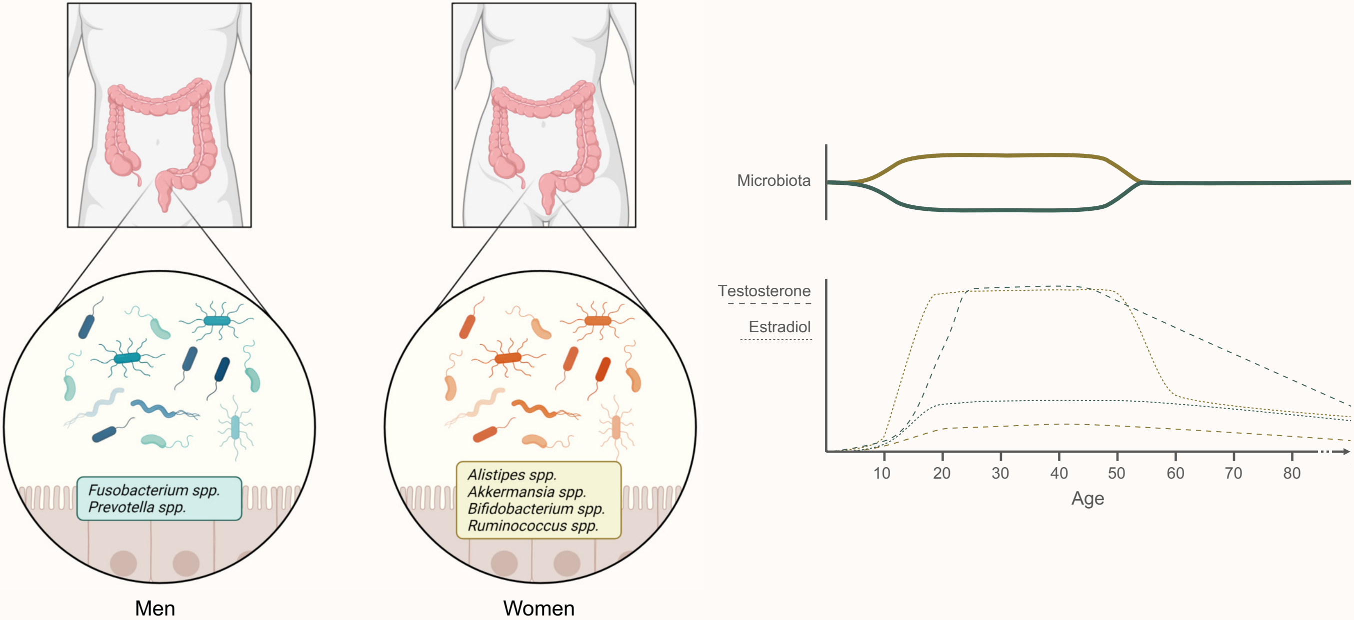
Fusobacterium spp.
Prevotella spp.
Men
Alistipes spp.
Akkermansia spp.
Bifidobacterium spp.
Ruminococcus spp.
Women
Microbiota
Testosterone
Estradiol
10
20
30
40
50
60
70
80
Age

Publication Year	First Author	Cohort Country	No of Participants	Women:Men	Age Range	Women Differing Taxa	Men Differing Taxa	Sequencing Method	Sex-associated Taxa Analysis	Multiple Comparison Correction	Confounding Factors
2019	Takagi	Japan	277	138:139	20 - 89	**↑ *Akkermansia* genus** ↑ *Bifidobacterium* genus **↑ *Ruminococcus* genus**	**↑ *Prevotella* genus** **↑ *Fusobacterium* genus** ↑ *Megamonas* genus ↑ *Megasphaera* genus	16S V3-V4 sRNA Gene sequencing	Student´s paired *t* test	Not Reported	Age
2019	Shin	South Korea	57	26:31	25 - 65	-	-	16S V1-V2 sRNA Gene sequencing	Mann-Whitney test	Not Reported	Not Reported
2019	Sinha	Netherlands	1135	661:474	18 - 81	**↑ *Akkermansia muciniphila***	-	Whole Genome sequencing	General lineal model	Yes, Benjamini-Hochberg (FDR)	83 Factors
2020	Yuan	China	136	66:70	5 - 15	↑ *Alistipes* genus ↑ *Megamonas* genus ↑ *Oscillospira* genus ↑ *Parabacteroides* genus	-	16S V3-V4 sRNA Gene sequencing	Linear discriminant analysis Effect Size	Not Reported	Not Reported
2020	Mayneris-Perxachs	Spain	131	89:42	34.4 - 54.3	**↑ *Akkermansia* spp.** ↑ *Alistipes* spp. ↑ *Bifidobacterium* spp. ↑ *Lachnospiraceae* spp. **↑ *Ruminococcus* spp.** ↓ *Bacteroides* spp. ↓ *Haemophilus* spp. ↓ *Prevotella* spp.	**↑ *Prevotella* spp**. **↑ *Fusobacterium* spp.**	Whole Genome sequencing	General lineal model	Yes, Benjamini-Hochberg (FDR)	Age Obesity Status
2021	Shi	China	1138	567:571	40 - 70	-	-	16S V4 sRNA Gene sequencing	General lineal and logistic regression models	Yes, Benjamini-Hochberg (FDR)	15 factors
2021	Zhang	Pinggu (China)	2338	1191:1147	26 - 76	↑ *Bacteroides* spp. ↑ *Clostridium* spp. ↑ *Eubacterium* spp. **↑ *Ruminococcus* spp.** ↑ *Alistipes* spp. **↑ *Akkermansia muciniphila*** ↑ *Anaerotruncus colihominis* ↑ *Blautia hydrogenotrophica* ↑ *Clostridiales* bacterium 1_7_47FAA ↑ *Erysipelotrichaceae* bacterium 3_1_53 ↑ *Pseudoflavonifractor capillosus*	**↑ *Prevotella spp.*** ↑ *Clostridium perfringens* ↑ *Citrobacter koseri* **↑ *Fusobacterium mortiferum*** ↑ *Lachnospiraceae* ssp. ↑ *Turicibacter sanguinis* ↑ *Solobacterium moorei* ↑ *Streptococcus gordonii* ↑ *Gemella sanguinis* ↑ *Ruminococcus gnavus*	Whole Genome sequencing	General lineal model	Yes, Benjamini-Hochberg (FDR)	14 factors
		China	876	461:415	19 - 86	↑ *Alistipes* spp. **↑ *Akkermansia muciniphila*** ↑ *Anaerotruncus colihominis* ↑ *Blautia hydrogenotrophica* ↑ *Erysipelotrichaceae* bacterium 3_1_53 ↑ *Pseudoflavonifractor capillosus*	**↑ *Fusobacterium mortiferum***	Whole Genome sequencing	General lineal model	Yes, Benjamini-Hochberg (FDR)	Age
		Israel	875	522:353	16 - 70	↑ *Alistipes* sp. HGB5 ↑ *Anaerotruncus colihominis* ↑ *Blautia hydrogenotrophica* ↑ *Clostridiales* bacterium 1_7_47FAA ↑ *Clostridium symbiosum* ↑ *Pseudoflavonifractor capillosus*	**↑ *Prevotella spp.***	Whole Genome sequencing	General lineal model	Yes, Benjamini-Hochberg (FDR)	Age
		Netherlands	281	142:139	6 - 9	-	-	Whole Genome sequencing	General lineal model	Yes, Benjamini-Hochberg (FDR)	10 factors
		Netherlands*	1133	660:473	18 - 81	↑ *Alistipes* spp. **↑ *Akkermansia muciniphila*** ↑ *Anaerotruncus colihominis* ↑ *Blautia hydrogenotrophica* ↑ *Clostridiales* bacterium 1_7_47FAA ↑ *Clostridium symbiosum* ↑ *Erysipelotrichaceae* bacterium 3_1_53 ↑ *Pseudoflavonifractor capillosus*	-	Whole Genome sequencing	General lineal model	Yes, Benjamini-Hochberg (FDR)	Age

* Same cohort as Sinha *et al* (2019) (LifeLine DEEP cohort).