Table 1. Metagenomic analysis in the control group vs osteoporosis group

Genus	dataVar.Wilcox.p.val_none	dataVar.wilcox.p.val_fd
Prevotella	0.38225929	0.882626
Roseburia	0.56961814	0.882626
Faecalibacterium	0.72525253	0.962231
Blautia	0.78202284	0.962231
Bifidobacterium	0.36121263	0.882626
Gemmiger	0.58001158	0.882626
Ruminococcus	0.64558630	0.930757
Anaerostipes	0.19843249	0.882626
Bacteroides	0.31380021	0.882626
Dorea	0.14548157	0.882626
Collinsella	1.00000000	1.000000
Escherichia/Shigella	0.82469046	0.962231
Fusicatenibacter	0.52440668	0.882626
Lactobacillus	0.52307056	0.882626
Clostridium_XVIII	0.21282366	0.882626
Enterococcus	0.24847607	0.882626
Streptococcus	0.78173030	0.962231
Coprococcus	0.34109433	0.882626
Holdemanella	0.14070108	0.882626
Ruminococcus2	0.67812298	0.930757
Clostridium_XlVa	0.34109433	0.882626
Dialister	0.32389673	0.882626
Clostridium_IV	0.09684267	0.882626
Romboutsia	0.57978004	0.882626
Butyricicoccus*	0.03794521	0.882626
Alistipes	0.61819394	0.920714
Akkermansia	0.66745796	0.930757
Oscillibacter	0.82476952	0.962231
Parabacteroides	0.31855414	0.882626
Clostridium_sensu_stricto	0.91071370	0.996093
Parasutterella	0.35514427	0.882626
Alloprevotella	0.54173413	0.882626
Intestinibacter	0.95528670	0.998060
Sporobacter	0.15783743	0.882626
Methanobrevibacter	0.44832102	0.882626
Turicibacter	0.88333993	0.996093
Adlercreutzia	0.79830925	0.962231
Enterobacter	0.90923133	0.996093
Hespellia	0.43808824	0.882626
Hydrogenoanaerobacterium	0.66740680	0.930757
Mogibacterium	0.80076988	0.962231
Paraprevotella	0.42480747	0.882626

Senegalimassilia	0.53424617	0.882626
Achromobacter	0.51131515	0.882626
Terrisporobacter	0.50259568	0.882626
Eggerthella	0.82309867	0.962231
Phascolarctobacterium	0.15236734	0.882626
Odoribacter	0.40847010	0.882626
Clostridium_XlVb	0.14915995	0.882626
Haemophilus	1.00000000	1.000000
Bilophila	0.42594295	0.882626
Intestinimonas	0.93373631	0.998060
Barnesiella	0.56229821	0.882626
Flavonifractor	0.40124558	0.882626
Slackia	0.35546090	0.882626
Pseudoflavonifractor	0.25584647	0.882626
Subdoligranulum	0.08680855	0.882626
Howardella	0.11774880	0.882626
Olsenella	0.48238089	0.882626
Butyricimonas	0.81431798	0.962231
Lactococcus	0.45440932	0.882626
Veillonella	0.38602447	0.882626
Allisonella	0.08482705	0.882626
Actinomyces	0.23863576	0.882626
Gordonibacter	0.90755765	0.996093
Pseudobutyrivibrio	0.94277111	0.998060
Clostridium_III	0.97266333	1.000000
Anaerosporobacter	0.05898715	0.882626
Solobacterium	0.42841751	0.882626
Holdemania	0.05934464	0.882626

***:** significant

Table 2. Metagenomic analysis in the control group vs osteopenia group

Genus	dataVar.wilcox.p.val_none	dataVar.wilcox.p.val_fd
Prevotella	0.93817293	0.991782
Roseburia	0.23748361	0.987143
Faecalibacterium	0.74609255	0.987143
Blautia	0.46880398	0.987143
Bifidobacterium	0.49213605	0.987143
Gemmiger	0.40922813	0.987143
Ruminococcus	0.25843593	0.987143
Anaerostipes	0.32848569	0.987143
Bacteroides	0.21769728	0.987143
Dorea	0.41576666	0.987143
Collinsella	0.34112210	0.987143
Escherichia/Shigella	0.95939125	0.999928
Fusicatenibacter	0.68400416	0.987143
Catenibacterium	0.91537370	0.991782
Lactobacillus	0.81808093	0.991782
Clostridium_XVIII	1.00000000	1.000000
Enterococcus	0.61400602	0.987143
Streptococcus	0.40070127	0.987143
Coprococcus	0.16525182	0.987143
Ruminococcus2	0.44544533	0.987143
Clostridium_XlVa	0.24207356	0.987143
Dialister	0.19835953	0.987143
Clostridium_IV	0.52481185	0.987143
Romboutsia	0.59270004	0.987143
Butyricicoccus*	0.02514667	0.987143
Alistipes	0.81886646	0.991782
Akkermansia	0.42137647	0.987143
Oscillibacter	1.00000000	1.000000
Parabacteroides	0.68392225	0.987143
Clostridium_sensu_stricto	0.38336248	0.987143
Parasutterella	0.93392154	0.991782
Alloprevotella	0.09595531	0.987143
Intestinibacter	0.42478959	0.987143
Sporobacter	0.97969462	1.000000
Methanobrevibacter	0.54465482	0.987143
Turicibacter	0.74767086	0.987143
Adlercreutzia	0.85426061	0.991782
Enterobacter	0.85942594	0.991782
Hespellia	0.89872171	0.991782
Hydrogenoanaerobacterium	0.61782367	0.987143
Mogibacterium	0.44000999	0.987143
Paraprevotella	0.75095925	0.987143

Senegalimassilia	0.56159259	0.987143
Achromobacter	0.91330353	0.991782
Terrisporobacter	0.70750317	0.987143
Eggerthella	0.88525401	0.991782
Phascolarctobacterium	0.38428590	0.987143
Odoribacter	0.07523953	0.987143
Clostridium_XlVb	0.81785816	0.991782
Haemophilus	0.74974650	0.987143
Bilophila	0.51956758	0.987143
Intestinimonas	0.40089512	0.987143
Barnesiella	0.34824891	0.987143
Flavonifractor	0.23627043	0.987143
Slackia	0.69265640	0.987143
Pseudoflavonifractor	0.59927111	0.987143
Subdoligranulum	0.76036750	0.987143
Howardella	0.84825688	0.991782
Olsenella	0.66495005	0.987143
Butyricimonas	0.45223678	0.987143
Lactococcus	0.10578403	0.987143
Veillonella	0.64331293	0.987143
Allisonella	0.06590452	0.987143
Actinomyces	0.64299979	0.987143
Gordonibacter	0.34675275	0.987143
Pseudobutyrivibrio	0.47868455	0.987143
Hungatella	0.48255986	0.987143
Coprobacillus	0.27205496	0.987143
Clostridium_III	0.79858491	0.991782
Leuconostoc	0.74988656	0.987143
Anaerosporobacter	0.13998252	0.987143
Finegoldia	0.22822110	0.987143
Holdemania	0.34188217	0.987143
Anaerotruncus	0.26938089	0.987143

***:** significant