The Authors have attempted a research study of relevance in contemporary area of interest for a large section of readers, as it is directly focused on sustaining a desirable gut microbiota in the long run for better bone health. Considering the relevance of topic, the manuscript under submission *is appropriate for publication* in 'Peer J'. However, there are certain suggestions / corrections given below for the Authors to provide precise answers. Further, Reviewer's concern about the merit of study is also included in the last.

Abstract

Lines 14-15: Avoid mentioning that no researchers have explored the gut

microbiota changes in osteoporosis patients, unless it is doubly

sure and checked not from all sources.

<u>Line 32</u>: Replace 'understanding' with 'understand'

Introduction

<u>Line 60</u>: Evidence for the statement "However no previous study has

performed diversity analysis of the gut microbiota in

osteoporosis patients".

Authors are to check from all sources about the authentication

of the statement included in the manuscript.

Lines 71-73: The purpose of study with focused objective is missing. Mere

mention of performing gene sequencing to assess microbial community does not reflect any importance or innovativeness of the study. The objective mentioned in the manuscript is more like someone participating in an event with many others

and reach the end point in my own time.

It is important that any research study should bring into focus the need for present study undertaken in the background literature or existing information on a scientific basis. Also, it should give an indication as to what the study finally would lead to the understanding of ------

Methods

<u>Lines 107-</u> Give the details of source for software QIIME 9version 1.17) and UPARSE (version 7.1)

There is no documentation of analytical method for bone mass density (BMD) which is of relevance to the data presented

Discussion

<u>Lines 232-</u> Authors state that they found that bone mass could be normalized after gut microbiota transplantation in GF mice

The Reviewer is not able to locate any experimental evidence

for this statement of Authors in the present manuscript

<u>Table 2</u>: Data in Table 2 is already documented in running text – <u>Lines</u>

136-137

Reviewer's concern

In the opinion of Reviewer, the Authors have failed to provide the requisite basic understanding of relating microbes and health condition through well established biochemical benchmarkers.

There are no biochemical analytical characterization undertaken in the study specific to the subjects of primary osteoporosis (OP), primary osteopenia (ON) and normal controls (NC). In other words, there should be some benchmark for those disease conditions and also in normal controls some other differentiation character will be prevalent. These benchmarks need to be based on well established attributes. Such biochemical analytical data is very important to relate the gut microbiota to any health parameter. This would give an understanding to the relationship between microflora and the requisite biochemical benchmark with supporting data of bone mass density.

The relationship between gut microbiota diversity and BMD in select subjects is based on the taxonomic data generated based on molecular biology tool. In fact, it would have been of interest, if experimental trials were designed in appropriate models to evaluate the proposed relationship by altering microbial taxa or phylum as required and get the data of BMD. This would definitely confirm the interpretation of Authors. In the absence of experimental data of biochemical parameters, it is very difficult to accept the microbiota diversity as a strong evidence.

Human health is related to a complex human physiology, wherein gut microflora has multi-dimensional approach to play in sustaining human health. In the absence of well established experimental approaches supporting the inference of study under review, it is difficult to accept the interpretation of Authors relating BMD to gut microbiota in select subjects. In fact, microbial diversity of gut may be in-place to sustain better health through functioning of other living systems in the body.