We claim:

1. A method for evaluating efficacy of diet intervention or disease treatment in a subject having type 2 diabetes mellitus, comprising the steps of

a) analyzing DNA extracted from a fecal sample obtained from the subject before and during the diet intervention or disease treatment, to determine abundance of each reference Co-abundance Group (CAG) selected from the group consisting of CAG ID Nos.: 1-64,

A_i (abundance of CAG No: i) = number of reads aligned to CAG No.: i / (size of CAG No.: i × number of total reads;

b) calculating Gut Microbiota Modulation (GMM)-index of each sample using the calculated abundance data,

GMM-index = log ($\sum_{i=1}^{15} A_i$ / $\sum_{i=16}^{64} A_i$); and

c) determining that the subject responds positively to the diet intervention or disease treatment if the GMM-index is increased in the sample collected during the diet intervention or disease treatment,

wherein, CAG NOs.:1-15 comprise nucleic acid sequences set forth in SEQ ID NOs.: 1-191, 192-326, 327-593, 594-835, 836-885, 886-960, 961-1097, 1098-1264, 1265-1433, 1434-1684, 1685-1833, 1834-1979, 1980-2163, 2164-2447, and 2448-2783, respectively, and CAG NOs.:16-64 comprise nucleic acid sequences set forth in SEQ ID NOs.: 2784-2961, 2962-3130, 3131-3525, 3526-3747, 3748-3863, 3864-4068, 4069-4212, 4213-4393, 4394-4532, 4533-4891, 4892-4979, 4980-5116, 5117-5320, 5321-5464, 5465-5781, 5782-6279, 6280-6646, 6647-6954, 6955-7178, 7179-7613, 7614-7758, 7759-8046, 8047-8491, 8492-8546, 8547-9971, 9972-10099, 10100-10392, 10393-10502, 10503-10694, 10695-10986, 10987-11089, 11090-11262, 11263-11466, 11467-11704, 11705-12034, 12035-12113, 12114-12341, 12342-12454, 12455-12664, 12665-12825, 12826-13042, 13403-13500, 13501-13726, 13727-13949, 13950-14014, 14015-14290, 14291-14403, 14404-14686, and 14687-14850, respectively.

2. A method for assessing the presence or the risk of development of type 2 diabetes mellitus in a subject, comprising the steps of:

a) analyzing DNA extracted from a fecal sample obtained from the subject to determine abundance of each reference CAG selected from the group consisting of CAG ID Nos.: 1-64,

A_i (abundance of CAG No: i) = number of reads aligned to CAG No.: i / (size of CAG No.: i × number of total reads;

b) calculating GMM-index of each sample using the calculated abundance data,

GMM-index = log ($\sum_{i=1}^{15} A_i$ / $\sum_{i=16}^{64} A_i$); and

c) determining that the subject suffers from or at a risk of developing type 2 diabetes mellitus if GMM is close to or lower than a predetermined level,

wherein, CAG NOs.:1-15 comprise nucleic acid sequences set forth in SEQ ID NOs.: 1-191, 192-326, 327-593, 594-835, 836-885, 886-960, 961-1097, 1098-1264, 1265-1433, 1434-1684, 1685-1833, 1834-1979, 1980-2163, 2164-2447, and 2448-2783, respectively, and CAG NOs.:16-64 comprise nucleic acid sequences set forth in SEQ ID NOs.: 2784-2961, 2962-3130, 3131-3525, 3526-3747, 3748-3863, 3864-4068, 4069-4212, 4213-4393, 4394-4532, 4533-4891, 4892-4979, 4980-5116, 5117-5320, 5321-5464, 5465-5781, 5782-6279, 6280-6646, 6647-6954, 6955-7178, 7179-7613, 7614-7758, 7759-8046, 8047-8491, 8492-8546, 8547-9971, 9972-10099, 10100-10392, 10393-10502, 10503-10694, 10695-10986, 10987-11089, 11090-11262, 11263-11466, 11467-11704, 11705-12034, 12035-12113, 12114-12341, 12342-12454, 12455-12664, 12665-12825, 12826-13042, 13403-13500, 13501-13726, 13727-13949, 13950-14014, 14015-14290, 14291-14403, 14404-14686, and 14687-14850, respectively.

3. A method for evaluating efficacy of diet intervention or disease treatment in a subject having type 2 diabetes mellitus, comprising the steps of

a) analyzing DNA extracted from a fecal sample obtained from the subject before and during the diet intervention or disease treatment to determine abundance of each reference CAG selected from the group consisting of CAG ID Nos.: 1-15,

A_i (abundance of CAG No.: i)= number of reads aligned to CAG No.: i / (size of CAG No.: i × number of total reads);

b) calculating Ecosystem Service Provider (ESP)-index of each sample using the calculated abundance data,

ESP-Index = $\ln\left(\text{Heip} \times 10^{10} \times \sum_{i=1}^{15} A_i\right)$, wherein Heip= ($e^H$-1)/14, $H = -\sum_{i=1}^{15} A_i \ln A_i$, and

c) determining that the subject responds positively to the diet intervention or disease treatment if the ESP-index is increased in the sample collected during the diet intervention or disease treatment,
wherein, CAG NOs.:1-15 comprise nucleic acid sequences set forth in SEQ ID NOs.: 1-191, 192-326, 327-593, 594-835, 836-885, 886-960, 961-1097, 1098-1264, 1265-1433, 1434-1684, 1685-1833, 1834-1979, 1980-2163, 2164-2447, and 2448-2783, respectively.

4. A method for assessing the presence or the risk of development of type 2 diabetes mellitus in a subject, comprising the steps of:
a) analyzing DNA extracted from a fecal sample obtained from the subject to determine abundance of each reference CAG selected from the group consisting of CAG ID Nos.: 1-15, A_i (abundance of CAG No.: i)= number of reads aligned to CAG No.: i / (size of CAG No.: i × number of total reads);
b) calculating ESP-index of each sample using the calculated abundance data,
ESP-Index = $\ln\left(\text{Heip} \times 10^{10} \times \sum_{i=1}^{15} A_i\right)$, wherein Heip= ($e^H$-1)/14, $H = -\sum_{i=1}^{15} A_i \text{In} A_i$ and
c) determining that the subject suffers from or at a risk of developing type 2 diabetes mellitus if the ESP-index is close to or lower than a predetermined level,
wherein, CAG NOs.:1-15 comprise nucleic acid sequences set forth in SEQ ID NOs.: 1-191, 192-326, 327-593, 594-835, 836-885, 886-960, 961-1097, 1098-1264, 1265-1433, 1434-1684, 1685-1833, 1834-1979, 1980-2163, 2164-2447, and 2448-2783, respectively.

5. The method of claim 1 or 2, wherein, analysis of DNA in step a) comprises the steps of obtaining the DNA sequences and aligning the obtained DNA sequences with the nucleic acid sequences set forth in SEQ ID Nos.: 1-14850.

6. The method of claim 3 or 4, wherein, analysis of DNA in step a) comprises the steps of obtaining the DNA sequences and aligning the obtained DNA sequences with the nucleic acid sequences set forth in SEQ ID Nos.: 1-2783.

7. The method of claim 5, wherein, obtaining of DNA sequences comprises the steps of obtaining raw sequence reads in the sample and processing the raw sequence reads to obtain qualified sequence reads.

8. The method of claim 6, wherein, obtaining of DNA sequences comprises the steps of obtaining raw sequence reads in the sample and processing the raw sequence reads to obtain qualified sequence reads.

9. The method of claim 7 or 8, wherein, the raw sequence reads are obtained by a PCR-based high-throughput sequencing technique.

10. The method of claim 7 or 8, wherein, the processing of the raw sequence reads comprises removal of adapters, trimming of sequences at 3'end until reaching the first nucleotide with a quality threshold higher than 20, removal of short sequences, and removal of sequences aligned to human genome.

11. The method of claim 5 or 6, wherein, the alignment of DNA sequences uses seed-and-extend strategy.

12. The method of claim 11, wherein, the sequences with no mismatch in seed sequence are used to determine the abundance of each reference CAG in step a).

13. The method of claim 11, wherein, the seed sequence is 4-31 bp in length.

14. The method of claim 13, wherein, the seed is 20 bp in length.

15. The method of claim 1 or 3, wherein, during the diet intervention or disease treatment, the fecal sample is obtained from the subject one week, two weeks, three weeks, and/or four weeks after the diet intervention or disease treatment begins.

16. The method of claim 1, wherein, the subject is determined to respond positively to the diet intervention or disease treatment when the GMM-index becomes close to or higher than a predetermined level during the diet intervention or disease treatment.

17. The method of claim 16, the predetermined level is -1.028883.

18. The method of claim 2, wherein, the predetermined level is approximately -1.028883.

19. The method of claim 3, wherein, the subject is determined to respond positively to the diet intervention or disease treatment when the ESP-index becomes close to or higher than a predetermined level during the diet intervention and disease treatment

20. The method of claim 19, the predetermined level is 4.4.

21. The method of claim 4, wherein, the predetermined level is approximately 4.4.

22. A composition, comprising one or more of a bacteria corresponding-CAG NO.1-15, wherein CAG NO.1-4, and 6-15 comprises nucleic acids set forth in SEQ ID NO.: 1-191, 192-326, 327-593, 594-835, 886-960, 961-1097, 1098-1264, 1265-1433, 1434-1684, 1685-1833, 1834-1979, 1980-2163, 2164-2447, and 2448-2783 respectively.