CORRECTION

Correction: Gut microbiome analysis of type 2 diabetic patients from the Chinese minority ethnic groups the Uygurs and Kazaks

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Following publication of this article [1], concerns were raised about the availability of the underlying data. This notice updates readers about the availability of the data with a corrected Data Availability statement.

The Data Availability statement is as follows:

The sequence and assembly data for each of the 40 gut microbiota samples is deposited at the CNGB Sequence Archive (<https://db.cngb.org/cnsa/>) under project accession number CNP0001174. The associated individual-level demographic data is deposited under accession number CNP0001169 (restricted data, for access requests visit https://db.cngb.org/data_access/).

Sample accession numbers are provided as Supporting Information on this notice (S1 File). Samples are grouped as follows:

Kazak, normal glucose tolerance (KNGT) = samples 1–10 (sample accessions CNS0254252–CNS0254261)

Kazak, diabetes mellitus type 2 (KDM2) = samples 11–20 (sample accessions CNS0254262–CNS0254271)

Uygur, normal glucose tolerance (UNGT) = samples 21–30 (sample accessions CNS0254272–CNS0254281)

Uygur, diabetes mellitus type 2 (UDM2) = samples 31–40 (sample accessions CNS0254282–CNS0254291)

Previously published studies on the same samples used 16S rDNA real time PCR to assess correlation between genus-level abundance of bacteria with physical and biochemical indicators in the same four groups [2]. Another previous study on the same samples reported physical and biochemical measurements as well as levels of indirect markers of bacterial exposure in the same four groups [3].

The following additional clarifications are provided regarding statistical analyses in [1]:

Sample size calculation

The sample size calculation uses the following experimental data from [2]:

By 16S rDNA real time PCR in genus level, the abundance of *Veillonella* spp and *C. coccoides* subgroups in Kazaks was obtained (KNGT VS KDM2: 2.10±0.20 VS 3.05±0.39; KNGT VS KDM2: 4.27±0.32 VS 4.80±0.19 Fig 1 and 2 of [2]). According to the following formula, we calculated the sample sizes of Kazaks as 4.47 and 10.35, respectively.

The sample size calculation uses the following formula to compare two sample means:

$$n = \frac{(Z_{\alpha} + Z_{\beta})^2 * 2\sigma^2}{\delta^2}$$

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Where numerator: σ is total variance; denominator: δ is mean difference between two groups. $\alpha = 0.05$, $\beta = 0.9$, $Z_{\alpha} = 1.96$ and $Z_{\beta} = 1.28$

Considering the previously published prevalence of KDM2 (1.47%) [4] and the difficulties collecting KDM2 samples, the number of feces samples for Illumina sequencing was 10 (shown in table 1 and 2 [1]).

Data in Tables 1, 2 and 4 of [1] are reported as mean $\pm$ SD.

Supporting information

S1 File. Sequence data accession numbers.
(DOCX)

References

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