

Table S1: Bias assessment criteria

JBIChecklist/Study	Were the criteria for inclusion in the sample clearly defined?	Were the study subjects and the setting described in detail?	Was the exposure measured in a valid and reliable way?	Were objective, standard criteria used for measurement of the condition?	Were confounding factors identified?	Were strategies to deal with confounding factors stated?	Were the outcomes measured in a valid and reliable way?	Was appropriate statistical analysis used?	Overall	Risk
Diener et.al.	1	1	1	1	1	1	1	1	8	Low risk of bias
Maskarinec et.al.	1	1	1	1	1	1	0	1	7	Low risk of bias
Shen et.al	1	1	1	1	1	1	1	1	8	Low risk of bias
Li Qian	1	1	1	1	0	0	1	1	6	Moderate risk of bias
Karlsson	1	1	1	1	0	0	1	1	6	Moderate risk of bias
Ruuskanen	1	1	1	1	1	0	1	1	7	Low risk of bias
Wang	1	1	1	1	1	1	1	1	8	Low risk of bias
Vals-Delgado	1	1	1	1	1	1	1	1	8	Low risk of bias
Hao Wu	1	1	1	1	1	0	1	1	7	Low risk of bias
Allin	1	1	1	1	0	0	1	1	6	Moderate risk of bias
Kwan	1	1	1	1	1	1	1	1	8	Low risk of bias
Chen Z	1	1	1	1	1	1	1	1	8	Low risk of bias
Kitten AK	1	1	1	1	0	0	1	1	6	Moderate risk of bias
Larsen et al	1	1	1	1	0	0	1	1	6	Moderate risk of bias
Sedighi et al.	1	1	1	1	1	0	1	1	7	Moderate risk of bias
Ahmad et.al.	1	1	1	1	0	1	1	1	7	Low risk of bias
Neri-Rosario et al	0	0	1	1	0	0	1	1	4	High risk of bias
Carrizales-Sánchez	1	1	1	1	0	0	1	1	6	Moderate risk of bias
Guo et.al	1	1	1	1	1	1	1	1	8	Low risk of bias
Chang et.al	1	1	1	1	1	0	1	1	7	Low risk of bias
Wu et.al	1	1	1	0	0	0	1	1	5	High risk of bias

Criteria used to rank the risk of bias:	
≤49%=high risk of bias	
50-69%=Moderate risk of bias	
above 70% = low risk of Bias	
Coded answer numerical	
Yes	1
No	0

# Table S2: Selected studies overview

	Paper 1	Paper 2	Paper 3	Paper 4	Paper 5	Paper 6	Paper 7	Paper 8	Paper 9	Paper 10	Paper 11	Paper 12	Paper 13	Paper 14	Paper 15	Paper 16	Paper 17	Paper 18	Paper 19	Paper 20	Paper 21	Totals
Author	Diener et al.	Maskarinec et al.	Shen et al.	Li Qian	Karlsson	Ruuskanen	Wang	Vals-Delgado	Hao Wu	Allin	Kwan	Chen Z	Kitten AK	Larsen et al.	Sedighi et al.	Ahmad et al.	Neri-Rosario et al.	Carrizales-Sánchez	Guo et al.	Chang et al.	Wu et al.	
Date of publication	2021	2020	2020	2021	2020	2013	2022	2022	2020	2018	2022	2021	2021	2010	2017	2019	2019	2023	2023	2024	2024	2010
Country /population	Mexico	USA	China	China	China	Finland	China	Spain	Sweden	Denmark	Mexico	Netherlands	USA	Denmark	Iran	Pakistan	Mexico	Mexico	China	Taiwan	China	
Type of study	cohort study /cross sectiona;	Retrospective coh		retrospective cohort for m cohort	China cohort	Finland Cohort observational	China Populational longit	Spain cross sectional	Sweden discovery cohort	Denmark case control stud	Mexico Cohort	Netherlands populational cro	USA cross section	Denmark cross section	Iran cohort	Pakistan cohort	Mexico Machine learning associ	Mexico cohort	China cohort	Taiwan cohort	China cohort	
Significant changes in microbiome in T2D?	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
T2D sample size	48	315	229	30	30	432	123	107	46	46	75	193	14	18	18	40	40	21	21	93	16	1800
Control group size (normal glucose)	214	765	50251	30	30	5140	2772	523	134	134	141	1056	23	18	18	20	20	20	20	60	12	61184
Prediabetic sample size	42	518	462	60	60	2895	462	569	268	268	216	2166	37	36	36	60	60	410	41	118	117	28
Total size of the study	405	1756	53970	60	145	5572	2895	462	569	268	216	2166	37	36	36	60	60	410	41	118	117	28
16 s rRNA sequencing type	illumia						illumia			illumia												
Primers	V4	V1-V3		V4 V5			V4			V4			V4	V4		V3 V4		V3 V4	V3V4	V3 V4	V3	
Bioinformatic tool for data processing	QIIME																					
Alpha diversity Shannon index	Yes	Yes			yes and Chao index			Yes		yes		yes	yes					yes				
Alpha diversity higher or lower in T2D?	Lower	Lower		Lower				No difference		lower		Lower	no significant difference					higher				
Genera positively associated with T2D (unhealthy)					Faecalibacterium, Dorea, Fusobacterium, Lactobacillus gasseri, Streptococcus mutans, Clostridium clostridioforme	Lachnospiraceae, Clostridium (ruminococcus, Eggertella, coprococcus, blautia, anaerostipes)	Dorea	Prevotella, Sutterella, Paraprevotella, Dialister, Lactobacillus, Anaerostipes	[Ruminococcus], Sutterella and Streptococcus, Faecalibacterium	Dorea, [Ruminococcus], Sutterella and Streptococcus, Faecalibacterium	Enterobacteriaceae, Escherichia/Shigella, Gammaproteobacteria, proteobacteria, Fusicatenaibacter, Lactobacillus	Acetitomaculum, Christensenella ceae R7 group, Marvinbryantia, Ruminococcaceae	Proteobacteria, Verrucobacteria	Bacteroidetes, Proteobacteria, Lactobacillus spp.	Lactobacillus group	Firmicutes, Clostridia, Negativibacterium, Eubacterium coprostanaligenes group, Dialister, Allisonella, Bacillus, Sparothermodurans, and Staphylococcus sp. SV3	Enterobacteriaceae, Escherichia/Shigella, Gammaproteobacteria, proteobacteria, Fusicatenaibacter, Lactobacillus, Dielma, and Allisonella	Faecalibacterium, Prevotella, Dorea, and Lactobacillus	Bacteroides, Parabacteroides, Phascolarctobacterium, [Ruminococcus], Dorea, Ruminococcus, Collinsella	Bacteroides, Phascolarctobacterium, Parabacteroides, and Paraprevotella	Clostridium leptum	
Genera negatively associated with T2DM (healthy)					Parabacteroides, Streptococcus, Bifidobacterium and Akkermansia, Roseburia	Alistipes, sutterella	Erysipelatoclostridium, Parabacteroides, Paraprevotella, Dialister	Akkermansia, Faecalibacterium, Clostridiaceae, Porphyromonadaceae, Ruminococcaceae, Odoribacter, Butyrivomax, Barnesiella, Parabacteroides, Bacteroidetes, Collinsella, Lachnospira	Faecalibacterium spp., Clostridium spp., Alistipes spp., Pseudoflavonifractor spp., and Oscillibacter, Clostridiales bacterium, Flavonifractor plautii, Coprococcus eutactus, Alistipes obesi, and Intestinimonas butyriciproducens;	Clostridium, Akkermansia muciniphila,	Faecalibacterium prausnitzii, Peptostreptococcaceae, Romboutsia and Clostridium sensu stricto 1	Clostridium sensu stricto 1, Peptostreptococcaceae, In testinibacter, Romboutsia	Bacteroidetes, Bifidobacterium, Firmicutes phylum, Roseburia genus, Streptococcus genus	Firmicutes, Clostridia spp.	Bifidobacterium group	Bacteroidetes, Verrucobacteria, Elusimicrobia, and Prevotella_9	Lachnospiraceae UCG.004, Holdemania, Ruminococcus 1, and Anaerostipes	[Ruminococcus], Succinivibrio, and Bacteroides	Blautia, [Ruminococcus], Dorea, Ruminococcus, Faecalibacterium, Bifidobacterium, Collinsella	Blautia, Faecalibacterium, Bifidobacterium, Anaerostipes, Mediterraneibacter, Streptococcus, Eggertella, Butyrivomax	Bacteroides vulgatus and Bifidobacterium genus	
Type of treatment	Metformin												Metformin					Metformin				

Table S3: Bacteria reported in both groups across the studies.

Bacteria reported in both groups across the studies			
	Positively associated with T2DM	Negatively associated with T2DM (healthy)	Comment
<i>Blautia</i>	Shen et.al and Ruuskanen et.al	Diener et.al.	Ruuskanen et.al. conducted large observational cohort of 5572 participants, however T2D sample size was relatively low as most of the participants observed in this study belonged to control group. Nevertheless, the increase in <i>Blautia</i> has also been confirmed in Shen at.al. study , which is a multi-ethnic study with a sample size of 53970 participants. The study by Shen et.al included Mexican population (n=405) which might not be exact representation of ethnical diversities.
<i>Collinsella</i>	Guo et.al	Vals-Delgado et.al.	Vals-Delgado reported the species as healthy. However, the results are based on relatively low sample size. Interestingly study by Vals-Delgado et.al the T2DM group is 3 times smaller than a control group, whilst in Gu et.al study the ratio of T2D:Control was 3.72 ,on the contrary to Vals-Delgado which may explain the discrepant results of these two reports.
<i>Dialister</i>	Vals-Delgado et.al. and Ahmad et.al.	Wang et.al.	Ahmad et.al. compared T2D versus prediabetic and also seen the statistically significant difference in these bacteria, suggesting positive association with T2DM.
<i>Dorea</i>	Shen et.al , Li Qian, Karlsson et.al, Wang et.al. , Allin et.al,Carrizales-Sánchez et.al; Guo et.al	Guo et.al	Positively associated with T2DM in 7 independent studies and only 1 study found it on the contrary.
<i>Paraprevotella</i>	Vals-Delgado and Chang et.al	Wang et.al.	2 studies of total sample size 579 found the species to be positively associated with T2D, whilst Wang et al. study of n=2895 found the species negatively correlated. These differences observed might be due to geographic locations/ethnicity.
<i>Prevotella</i>	Vals-Delgado, Kwan, Larsen et al , Carrizales-Sánchez et.al.	Ahmad et.al.	Only one study of a low sample size showed negative association with T2DM.
<i>Proteobacteria</i>	Kitten AK, 14 Larsen et al , Ahmad et.al., Neri-Rosario et al	Ruuskanen et.al.	Only 1 study found these bacteria healthy, with 4 different cohorts reporting positive correlation with T2DM
<i>Sutterella</i>	Vals-Delgado and Allin et.al reported both as unhealthy species positively associated with T2DM, with much smaller sample size of 462 and 268 participants	Kitten AK et.al	Very low sample size , results reported as percentages rather than differential abundance therefore questionable. Also <i>Akkermansia</i> belongs to genus <i>Verrucomicrobia</i> ,but it is well recognized for its beneficial effects on glucose balance , therefore one needs to look more into lower taxonomic level to make better conclusions.
<i>Anaerostipes</i>	Shen et.al, Ruuskanen, Vals-Delgado	Diener et.al. ;Neri-Rosario et.al ; Chang et.al	
<i>Faecalibacterium</i>	Karlsson et.al;Allin et.al; Carrizales-Sánchez et.al.	Shen et.al ;Vals-Delgado et.al ; Hao Wu et.al ;11 Kwan et.al ; Guo et.al; Chang et.al	