Table S1. List of studies used in the data analysis.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Study** | **Authors** | **Abbreviation** | **Age** | **Sex** | **Country** | **Sample Type** | **# of Samples** | **# of** **Sequences** | **Reference** |
| 1 | A core gut microbiome in obese and lean twins | Turnbaugh *et al.* | Turn | 11.7±1.2child | F | USA | Feces | 154 | 817,556 | [1] |
| 2 | Association between composition of the human gastrointestinal microbiome and development of fatty liver with choline deﬁciency | Spencer *et al.* | Fatty | 59±13.7Adult | F | USA | Feces | 74 | 173,215 | [2] |
| 3 | Bacterial community variation in human body habitats across space and time | Costello *et al*. | CWB | Adult(30-35, 60) | M+F | USA | Feces, Skin, Oral, External auditory canal, Nostril and Hair | 815 | 699,431 | [3] |
| 4 | Characterization of bacteria in biopsies of colon and stools by high throughput sequencing of the V2 region of bacterial 16S rRNA gene in human | Momozawa *et al.* | MOMO | Adult(25-62) | M+F | Europe | Cecum, Ascending colon, Transverse colon, Sigmoid colon, Colonoscopy stool, and Feces | 70 | 63,999 | [4] |
| 5 | Composition, variability, and temporal stability of the intestinal microbiota of the elderly | Claesson *et al.* | Eld | Elderly(78±7) | M+F | Europe (Ireland) | Feces | 168 | 2,400,407 | [5] |
| 6 | Delivery mode shapes the acquisition and structure of the initial microbiota across multiple body habitats in newborns | Dominguez-Bello *et al.* | DOM | Adults (21-33)Infants | F | Venezuela | Skin, Oral and Vagina | 187 | 145,055 | [6] |
| 7 | Disordered microbial communities in the upper respiratory tract of cigarette smokers | Charlson *et al.* | SMOKE | Adults (20-61) | M+F | USA | Nose and Throat | 291 | 284,535 | [7] |
| 8 | Forensic identification using skin bacterial communities | Fierer *et al.* | FFOR | Adults (20-35) | M+F | USA | Skin | 40 | 44,848 | [8] |
| 9 | Human oral, gut, and plaque microbiota in patients with atherosclerosis | Koren *et al.* | Kor | Adult68 | M+F | Europe(Sweden) | Feces, Oral, Atherosclerotic plaques | 73 | 320,494 | [9] |
| 10 | Impact of diet in shaping gut microbiota revealed by a comparative study in children from Europe and rural Africa | De Filippo *et al.* | Def | Children(1-6) | M+F | Africa (Burkina Faso)Europe (Italy) | Feces | 29 | 74,032 | [10] |
| 11 | Incomplete recovery and individualized responses of the human distal gut microbiota to repeated antibiotic perturbation | Dethlefsen and Relman | Deth | Adults(28-54) | F | USA | Feces | 198 | 3,087,840 | [11] |
| 12 | Resistant starches types 2 and 4 have differential effects on the composition of the fecal microbiota in human subjects | Martinez *et al.* | STAR | Adults(28-38) | M+F | USA | Feces | 162 | 180,341 | [12] |
| 13 | Short-term antibiotic treatment has differing long-term impacts on the human throat and gut microbiome | Jakobsson *et al.* | ABX | Adults(66±9.3) | M+F | Europe (Sweden) | Feces and throat | 58 | 95,491 | [13] |
| 14 | Succession of microbial consortia in the developing infant gut microbiome | Koenig *et al.* | Koen | Infant | M | USA | Feces | 62 | 272,327 | [14] |
| 15 | The influence of sex, handedness, and washing on the diversity of hand surface bacteria | Fierer *et al.* | FUND | Adults | M+F | USA | Skin | 102 | 336,212 | [15] |
| 16 | Vaginal microbiome of reproductive-age women | Ravel *et al.* | UMIGS | Adults(30.6±7.34) | F | USA | Vagina | 394 | 796,280 | [16] |
| 17 | Metahit | Metahit | MH | Adults | M+F | Denmark | Feces | 85 | 3,977,682,656 | [17] |
| 18 | Human Microbiome Project 16S rRNA data | The human Microbiome Project Consortium | HMP | Adults(27±5) | M+F | USA | Feces, Vagina, Skin, Oral, Airway | 10,213 | 20,472,845 | [18] |
| 19 | Human Microbiome Project WGS data | The human Microbiome Project Consortium | HMP | Adults(27±5) | M+F | USA | Feces, Vagina, Skin, Oral, Airway | 690 |  > 35,000,000,000 | [18] |

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