**Supplementary Table 2**: Characteristics of the included studies on Major Depressive Disorders (MDD).

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| Study | Country | Participants | Microbiota analysis method |
| Naseribafrouei et al. 2014(Naseribafrouei et al., 2014) | Norway | 37 MDD patients (49.2 ± 14 years old, 25.2 ± 4kg/m²,19 female)18 control (46.1 ± 14 years old, 24.7 ± 3 kg/m², 10 female). | 16S rRNA amplicon (V4 regions) sequencing analysis |
| Jiang et al. 2015(Jiang et al., 2015) | China | 29 MDD patients (25.3 ± 5 years old, 20.3 ± 3kg/m²,10 female)30 control (27.1 ± 5 years old, 19.6 ± 3 kg/m², 15 female). | 16S rRNA amplicon (V4 regions) sequencing analysis |
| Aizawa et al. 2016(Aizawa et al., 2016) | Japan | 43 MDD patients (39.4 ± 10 years old, 23.2 ± 4kg/m²,20 female)57 control (42.8 ± 13 years old, 22.3 ± 4 kg/m², 35female). | 16S rRNA amplicon (V3-V4 regions) sequencing analysis |
| Zheng et al. 2016(Zheng et al., 2016) | China | 58 MDD patients (40.6 ± 12 years old, 22.0 ± 3kg/m²,36 female)63 control (41.8 ± 12 years old, 22.6 ± 3 kg/m², 40 female). | 16S rRNA amplicon (V4 regions) sequencing analysis |
| Kelly et al. 2016(Kelly et al., 2019) | Ireland | 34 MDD patients (41.8 ± 12 years old, 26.2 ± 4 kg/m², 13 female)34 control (45.8 ± 12 years old, 24.6 ± 3kg/m², 14 female). | 16S rRNA amplicon (V3-V4 regions) sequencing analysis |
| Liu et al. 2016(Liu et al., 2016) | China | 15 MDD patients (44.8 ± 15 years old, 22.0 ± 3 kg/m², 11 female)20 control (43.9 ± 11 years old, 24.6 ± 3kg/m², 13 female). | 16S rRNA amplicon (V1-V3 regions) sequencing analysis |
| Lin et al. 2017(Lin et al., 2017) | China | 10 MDD patients (36.2 ± 10 years old, 23.8 ± 2kg/m²,4 female)10 control (38.1 ± 3 years old, 24.2 ± 2 kg/m², 4 female). | 16S rRNA amplicon (V4 regions) sequencing analysis |
| Chen et al. 2018(Chen et al., 2018b) | China | 10 MDD patients (43.9 ± 14 years old, 23.5 ± 2kg/m², 5 female)10 control (39.6 ± 9 years old, 22.6 ± 2 kg/m², 5 female). | 16S rRNA amplicon (V4 regions) sequencing analysis |
| Valles-Colomer et al. 2019(Valles-Colomer et al., 2019) | Belgium | 121 MDD patients933 controls (50 years old, 24.9 kg/m²) | 16S rRNA amplicon (V4 regions) sequencing analysis |
| Lai et al. 2019(Lai et al., 2019) | China | 26 MDD patients (43.7 ± 11 years old, 21.1 ± 2kg/m², 18 female)29 control (39.4 ± 11 years old, 21.1 ± 2 kg/m², 16 female). | shotgun metagenomic sequencing |
| Chen et al. 2019(Chen et al., 2018a) | China | 44 MDD patients (41.7 ± 11 years old, 22.2 ± 2kg/m², 24 female)44 control (39.4 ± 11 years old, 22.1 ± 2 kg/m², 24 female). | 16S rRNA amplicon (V3-V5 regions) sequencing analysis |
| Chung et al. 2019(Chung et al., 2019) | China | 36 MDD patients (45.8 ± 14 years old, 22.8 ± 4kg/m², 28 female)37 control (41.2 ± 13 years old, 23.9 ± 4 kg/m², 23 female). | 16S rRNA amplicon (V4 regions) sequencing analysis |
| Rong et al. 2019(Rong et al., 2019) | China | 31 MDD patients (41.6 ± 10 years old, 21.4 ± 2kg/m², 22 female)30 control (49.5 ± 10 years old, 21.9 ± 3 kg/m², 14 female). | Shotgun metagenomic sequencing |
| Mason et al. 2020(Mason et al., 2020) | USA | 38 MDD patients (39.2 ± 12 years old, 22.8 ± 4kg/m², 31 female)10 control (33.1 ± 8 years old, 25.6 ± 4 kg/m², 23 female). | 16S rRNA amplicon (V4 regions) sequencing analysis |
| Fontana et al. 2020(Fontana et al., 2020) | Italy | 34 MDD patients (57 [43 - 61] years old, 23.1 [21.9 – 28.1] kg/m², 24 female)20 control (37.7 [30.6 – 58.0] years old, 22.7 [21.1 – 23.8] kg/m², 7 female). | 16S rRNA amplicon (V3-V4 regions) sequencing analysis |
| Liu et al. 2020(Liu et al., 2020) | USA | 43 MDD patients (21.9 ± 2 years old, BMI unknown, 38 female)47 control (22.1 ± 2 years old, BMI unknown, 34 female). | 16S rRNA amplicon (V4 regions) sequencing analysis |
| Chen et al. 2020(Chen et al., 2020) | China | 70 MDD patients (39.2 ± 12 years old, 22.8 ± 4kg/m², 31 female)71 control (33.1 ± 8 years old, 25.6 ± 4 kg/m², 23 female). | 16S rRNA amplicon (V4 regions) sequencing analysis |
| Zheng et al. 2020(Zheng et al., 2020) | China | 122 MDD patients (26.5 ± 4 years old, 22.4 ± 4 kg/m², 78 female)171 control (26.8 ± 6 years old, 22.1 ± 3kg/m², 101 female). | 16S rRNA amplicon (V4 regions) sequencing analysis |

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