**Supplementary Table 1** MR estimates for the association between gut microbiota and HZ

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Exposure  | Outcome | NO.ofSNP | Methods | *β* | *OR* | *P* | *P* ofPleiotropy  | *P* ofHeterogeneity |
| class Deltaproteobacteria | HZ | 12 | IVW | -0.271 | 0.762 | 0.016 | 0.255 | 0.595 |
|  |  | 12 | MR-Egger | -0.869 | 0.419 | 0.510 |  |  |
|  |  | 12 | Weighted median | -0.377 | 0.686 | 0.421 |  |  |
|  |  | 12 | Weighted mode | -0.399 | 0.671 | 0.602 |  |  |
| order Desulfovibrionales |  | 11 | IVW | -0.280 | 0.755 | 0.016 | 0.103 | 0.760 |
|  |  | 11 | MR-Egger | -1.157 | 0.314 | 0.045 |  |  |
|  |  | 11 | Weighted median | -0.377 | 0.685 | 0.018 |  |  |
| family Desulfovibrionaceaegenus Coprococcus2phylum Cyanobacteriagenus Eubacterium rectale group |  | 119999888888888888 | Weighted modeIVWMR-EggerWeighted medianWeighted modeIVWMR-EggerWeighted medianWeighted modeIVWMR-EggerWeighted medianWeighted modeIVWMR-EggerWeighted medianWeighted mode | -0.399-0.361-0.976-0.387-0.391-0.362-0.976-0.387-0.3910.2060.0800.2880.3270.3100.4030.2770.293 | 0.6710.6970.3770.6790.6760.6970.9580.6930.6931.2281.0831.3331.3871.3631.4961.3191.340 | 0.1310.0040.1020.0220.1340.0020.9660.0220.1830.0220.8100.0140.1010.0250.4740.1540.379 | 0.2610.7470.6960.860 | 0.7520.4010.4540.371 |

Abbreviations: HZ- herpes zoster; IVW-inverse variance weighting; MR-mendelian randomization; OR—odds ratio.

**Supplementary Table 3** MR estimates for the association between gut microbiota and PHN

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Exposure  | Outcome | NO.ofSNP | Methods | *β* | *OR* | *P* | *P* ofPleiotropy  | *P* ofHeterogeneity |
| class Coriobacteriiaorder Coriobacterialesfamily Coriobacteriaceaegenus Lachnospiraceae NK4A136 groupgenus Ruminococcaceae UCG011genus Candidatus Soleaferreagenus Eubacterium rectale groupgenus Methanobrevibacter | PHN | 141414141414141414141414151515158888999988886666 | IVWMR-EggerWeighted medianWeighted modeIVWMR-EggerWeighted medianWeighted modeIVWMR-EggerWeighted medianWeighted modeIVWMR-EggerWeighted medianWeighted modeIVWMR-EggerWeighted medianWeighted modeIVWMR-EggerWeighted medianWeighted modeIVWMR-EggerWeighted medianWeighted modeIVWMR-EggerWeighted medianWeighted mode | -0.838-1.906-1.249-1.456-0.838-1.906-1.249-1.456-0.838-1.906-1.249-1.456-0.694-0.138-0.005-0.039-0.563-0.586-0.242-0.0670.6531.3240.5680.4951.1480.6190.9441.0950.7600.8590.8130.707 | 0.4320.1490.2870.2330.1870.0050.0940.0390.4330.1490.2870.2330.5000.8700.9940.9620.5700.5570.7850.9351.9213.7621.7631.6403.1531.8572.5722.9902.1372.3612.2542.029 | 0.0490.2950.0310.1400.0490.2960.0280.1350.0490.2960.0300.1270.0430.8430.9920.9480.0470.7150.4900.9190.0500.7260.1910.4810.0350.7700.1860.3500.0180.5580.0620.250 | 0.5390.5390.5390.3640.9880.8580.7950.943 | 0.7340.7340.7340.7100.1670.2600.4020.285 |

Abbreviations: IVW-inverse variance weighting; MR-mendelian randomization; OR—odds ratio; PHN- postherpetic neuralgia.

**Supplementary Table 4** Reverse causal association between HZ and gut microbiota

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Exposure  | Outcome | NO.ofSNP | Methods | *β* | *OR* | *P* | *P* ofPleiotropy  | *P* ofHeterogeneity |
| HZ | class Deltaproteobacteria | 11 | IVW | -0.007 | 0.992 | 0.862 | 0.865 | 0.064 |
|  |  | 11 | MR-Egger | -0.114 | 0.886 | 0.315 |  |  |
|  |  | 11 | Weighted median | -0.051 | 0.986 | 0.785 |  |  |
|  |  | 11 | Weighted mode | -0.066 | 0.979 | 0.756 |  |  |
|  | order Desulfovibrionales | 11 | IVW | -0.010 | 0.990 | 0.825 | 0.271 | 0.078 |
|  |  | 11 | MR-Egger | -0.129 | 0.879 | 0.272 |  |  |
|  |  | 11 | Weighted median | -0.018 | 0.983 | 0.736 |  |  |
|  | family Desulfovibrionaceaegenus Coprococcus2phylum Cyanobacteriagenus Eubacterium rectale group | 1111111111111111111111111111111111 | Weighted modeIVWMR-EggerWeighted medianWeighted modeIVWMR-EggerWeighted medianWeighted modeIVWMR-EggerWeighted medianWeighted modeIVWMR-EggerWeighted medianWeighted mode | -0.028-0.010-0.130-0.018-0.027-0.065-0.026-0.078-0.0750.063-0.0380.0740.0760.0640.1260.0590.093 | 0.9730.9900.8780.9810.9730.9370.9740.9250.9271.0650.9621.0771.0791.0661.1331.0601.097 | 0.6870.8150.2650.7140.6820.1090.8170.1740.3370.2070.7680.2420.4330.0440.1550.1700.163 | 0.2640.6990.4040.428 | 0.0860.3610.4250.885 |

Abbreviations: HZ- herpes zoster; IVW-inverse variance weighting; MR-mendelian randomization; OR—odds ratio.

**Supplementary Table 5** Reverse causal association between PHN and gut microbiota

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Exposure  | Outcome | NO.ofSNP | Methods | *β* | *OR* | *P* | *P* ofPleiotropy  | *P* ofHeterogeneity |
| PHN | class Coriobacteriiaorder Coriobacterialesfamily Coriobacteriaceaegenus Lachnospiraceae NK4A136 groupgenus Ruminococcaceae UCG011genus Candidatus Soleaferreagenus Eubacterium rectale groupgenus Methanobrevibacter | 33333333333333333333333333333333 | IVWMR-EggerWeighted medianWeighted modeIVWMR-EggerWeighted medianWeighted modeIVWMR-EggerWeighted medianWeighted modeIVWMR-EggerWeighted medianWeighted modeIVWMR-EggerWeighted medianWeighted modeIVWMR-EggerWeighted medianWeighted modeIVWMR-EggerWeighted medianWeighted modeIVWMR-EggerWeighted medianWeighted mode | -0.0180.046-0,016-0.012-0.0180.046-0.016-0.011-0.0180.046-0.016-0.0120.008-0.0380.0020.0000.0290.1700.0440.0510.016-0.0190.0230.0300.012-0.0410.0160.0240.1010.4030.0650.047 | 0.9821.0470.9840.9880.9821.0470.9840.9880.9821.0470.9840.9881.0080.9631.0021.0001.0301.1861.0461.0521.0160.9811.0231.0301.0110.9601.0161.0241.1061.4961.0681.048 | 0.2570.6050.4320.6760.0490.2570.4400.6940.2570.6050.4320.7030.6120.6650.9130.9850.4050.4460.2780.4250.5520.8920.4920.5060.4700.6400.4410.4520.1230.2930.2370.557 | 0.4910.4910.4910.5990.4960.7980.5550.363 | 0.4280.4280.4280.7450.5980.8060.5470.039 |

Abbreviations: IVW-inverse variance weighting; MR-mendelian randomization; OR-odds ratio; PHN- postherpetic neuralgia.