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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sample** |  |  | **Total** | **Freq** |  | **Estimated OTU Richnessd** |  |  |
| **ID** | **Group** | **Reada** | **OTUsb** | **OTU2c** | **ESC** | **Chao 1** | **Ace** | **Inv Simpson** | **Shannone** |
| C06S3 | DG | 7237 | 148 | 5625 | 99.0% | 246 (201, 330) | 388 (326, 472) | 1.64 | 1.26 |
| C08S1 | DG | 6961 | 115 | 2321 | 99.4% | 165 (138, 220) | 216 (181, 269) | 4.12 | 2.08 |
| C10S1 | DG | 6578 | 78 | 5880 | 99.4% | 174 (119, 302) | 207 (162, 275) | 1.25 | 0.62 |
| C12S1 | DG | 4209 | 7 | 4202 | 99.9% | 12 (8, 39) | 22 (8, 170) | 1.00 | 0.02 |
| C31S1 | DG | 1203 | 7 | 1178 | 99.6% | 17 (9, 59) | 0 (0,0) | 1.04 | 0.12 |
| C38S1 | DG | 5857 | 133 | 2765 | 98.7% | 306 (223, 467) | 495 (405, 614) | 3.85 | 2.09 |
| C39S3 | DG | 6132 | 132 | 2906 | 99.0% | 230 (182, 327) | 358 (299, 438) | 3.53 | 2.07 |
| C01S1 | UG | 8592 | 354 | 0 | 97.5% | 769 (637, 961) | 1653 (1455, 1885) | 7.00 | 2.84 |
| C02S2 | UG | 6699 | 265 | 3 | 98.1% | 457 (384, 574) | 644 (563, 746) | 8.63 | 3.07 |
| C03S1 | UG | 1752 | 64 | 56 | 97.8% | 249 (132, 568) | 583 (426, 808) | 9.70 | 2.71 |
| C03S4 | UG | 8120 | 251 | 138 | 98.6% | 397 (341, 488) | 556 (487, 646) | 7.30 | 2.93 |
| C05S1 | UG | 4362 | 177 | 0 | 97.6% | 346 (227, 465) | 721 (605, 869) | 5.68 | 2.49 |
| C06S2 | UG | 8141 | 313 | 297 | 97.9% | 610 (508, 764) | 888 (775, 1029) | 11.83 | 3.29 |
| C06S4 | UG | 8426 | 194 | 563 | 98.9% | 402 (310, 568) | 500 (429, 593) | 3.68 | 2.24 |
| C07S1 | UG | 3450 | 168 | 865 | 97.3% | 343 (267, 476) | 541 (452, 658) | 7.27 | 2.70 |
| C08S3 | UG | 8995 | 227 | 33 | 98.9% | 349 (299, 433) | 455 (398, 529) | 5.84 | 2.78 |
| C09S1 | UG | 5163 | 190 | 24 | 97.9% | 443 (334, 633) | 651 (553, 776) | 1.97 | 1.70 |
| C12S2 | UG | 11227 | 553 | 2268 | 97.0% | 1296 (1097, 1569) | 2416 (2181, 2686) | 12.04 | 3.47 |
| C15S2 | UG | 6903 | 266 | 169 | 98.0% | 540 (436, 708) | 814 (713, 938) | 6.58 | 2.87 |
| C17S1 | UG | 3474 | 191 | 17 | 96.5% | 489 (365, 698) | 913 (766, 1098) | 12.48 | 3.06 |
| C18S1 | UG | 3578 | 109 | 0 | 98.3% | 227 (167, 348) | 360 (292, 454) | 3.24 | 1.80 |
| C21S1 | UG | 3666 | 73 | 0 | 99.0% | 163 (109, 299) | 199 (157, 264) | 1.82 | 1.26 |
| C21S2 | UG | 3274 | 166 | 19 | 97.2% | 337 (263, 468) | 508 (426, 616) | 4.41 | 2.31 |
| C21S3 | UG | 2818 | 160 | 18 | 96.8% | 338 (259, 481) | 695 (582, 837) | 8.79 | 3.00 |
| C23S1 | UG | 5686 | 330 | 1507 | 96.6% | 765 (618, 989) | 1225 (1084, 1394) | 8.44 | 3.03 |
| C26S2 | UG | 9457 | 354 | 81 | 98.1% | 605 (522, 729) | 874 (773, 999) | 17.87 | 3.56 |
| C26S3 | UG | 7141 | 257 | 2 | 98.2% | 479 (395, 613) | 706 (613, 824) | 13.69 | 3.28 |
| C30S2 | UG | 4556 | 281 | 0 | 96.3% | 660 (524, 873) | 1174 (1020, 1360) | 11.61 | 3.28 |
| C31S2 | UG | 5885 | 62 | 105 | 99.6% | 90 (72, 137) | 86 (72, 120) | 2.52 | 1.43 |
| C31S3 | UG | 7289 | 257 | 1 | 98.4% | 521 (414, 702) | 737 (644, 851) | 16.39 | 3.54 |
| C31S4 | UG | 4118 | 142 | 0 | 98.6% | 217 (180, 290) | 297 (252, 360) | 5.34 | 2.57 |
| C32S1 | UG | 3243 | 90 | 0 | 98.6% | 166 (125, 257) | 232 (186, 301) | 4.11 | 2.08 |
| C34S1 | UG | 9054 | 357 | 0 | 97.9% | 723, 599, 910) | 975 (866, 1106) | 13.59 | 3.47 |
| C34S2 | UG | 11354 | 196 | 0 | 99.2% | 361 (290, 485) | 470 (405, 556) | 5.00 | 2.38 |
| C39S2 | UG | 7730 | 254 | 14 | 98.3% | 602 (463, 833) | 798 (696, 925) | 6.35 | 2.75 |
| C40S1 | UG | 4348 | 313 | 0 | 95.7% | 726 (585, 940) | 1379 (1212, 1578) | 7.65 | 3.08 |
| C42S1 | UG | 4780 | 150 | 0 | 98.5% | 265 (211, 368) | 358 (303, 432) | 8.45 | 2.70 |
| C33S2 | Outlier | 4770 | 362 | 4 | 96.0% | 695 (586, 858) | 994 (882, 1129) | 20.74 | 3.85 |
| HMP-1 | HMP | 6868 | 361 | 2 | 96.9% | 855 (694, 1094) | 1382 (1219, 1576) | 11.12 | 3.24 |
| HMP-2 | HMP | 7451 | 191 | 0 | 98.7% | 344 (280, 454) | 516 (440, 614) | 6.01 | 2.36 |
| HMP-3 | HMP | 6571 | 389 | 0 | 96.6% | 823 (688, 1021) | 1369 (1215, 1553) | 19.93 | 3.69 |
| HMP-4 | HMP | 5214 | 106 | 0 | 98.8% | 274 (188, 452) | 508 (408, 642) | 4.08 | 1.85 |
| HMP-5 | HMP | 7699 | 145 | 0 | 98.9% | 315 (238, 455) | 615 (507, 755) | 5.26 | 2.13 |
| HMP-6 | HMP | 5138 | 341 | 1 | 96.5% | 699 (576, 886) | 1145 (1015, 1299) | 15.30 | 3.76 |
| HMP-7 | HMP | 6094 | 268 | 0 | 97.5% | 555 (450, 720) | 926 (806, 1073) | 11.33 | 3.17 |
| HMP-8 | HMP | 8696 | 220 | 0 | 98.6% | 520 (397, 728) | 882 (761, 1029) | 9.42 | 2.78 |
| HMP-9 | HMP | 6326 | 162 | 0 | 98.6% | 314 (247, 436) | 395 (334, 478) | 1.54 | 1.14 |
| HMP-10 | HMP | 5322 | 134 | 2 | 98.7% | 281 (208, 426) | 385 (317, 476) | 4.04 | 2.12 |
| HMP-11 | HMP | 6606 | 222 | 0 | 98.2% | 460 (366, 616) | 627 (578, 791) | 7.67 | 2.73 |
| HMP-12 | HMP | 5929 | 282 | 12 | 97.5% | 547 (450, 700) | 874 (764, 1010) | 9.69 | 3.27 |
| HMP-13 | HMP | 6322 | 53 | 3 | 99.6% | 78 (62, 123) | 114 (89, 157) | 2.86 | 1.39 |
| HMP-14 | HMP | 3492 | 54 | 1 | 99.2% | 117 (77, 227) | 172 (129, 240) | 4.85 | 1.87 |
| HMP-15 | HMP | 4425 | 76 | 0 | 99.3% | 107 (89, 151) | 113 (93, 154) | 4.66 | 1.97 |
| HMP-16 | HMP | 3976 | 187 | 0 | 97.5% | 363 (288, 493) | 654 (557, 777) | 9.80 | 3.03 |
| HMP-17 | HMP | 4863 | 126 | 0 | 98.8% | 207 (167, 286) | 294 (245, 363) | 4.93 | 2.24 |
| HMP-18 | HMP | 4361 | 131 | 0 | 98.6% | 245 (188, 360) | 326 (271, 403) | 4.07 | 2.21 |
| HMP-19 | HMP | 11145 | 242 | 0 | 98.9% | 488 (389, 653) | 704 (611, 820) | 11.32 | 3.05 |
| HMP-20 | HMP | 9202 | 281 | 0 | 98.5% | 572 (461, 751) | 669 (585, 778) | 7.52 | 3.02 |
| HMP-21 | HMP | 9883 | 323 | 0 | 98.5% | 544 (466, 663) | 710 (631, 810) | 10.35 | 3.21 |
| HMP-22 | HMP | 17631 | 323 | 9 | 99.0% | 651 (540, 820) | 1170 (1035, 1330) | 4.49 | 2.30 |

 |

Abbreviations: DG, disrupted group - Norovirus patient with a disrupted microbiota; UG, undisrupted group – Norovirus patient with an undisrupted microbiota; HMP, healthy control patient; OTU, operational taxonomic unit; ESC, estimated sample coverage.

aTotal number of sequence reads per sample.

bTotal number of unique OTUs detected (as calculated by mothur at a 3% distance level).

cNumber of times OTU2 was detected per sample.

dValues in brackets for OTU richness estimates represent 95% confidence intervals, as calculated by mothur.

eShannon diversity values are calculated by mothur (at 3% distance).

Sample C33S2 was treated as an outlier and was not included as part of the disrupted or undisrupted patient groups.