**Characteristics of the whole cohort**

| **Study group** | **HC** | **PD** | **iRBD** |
|---|---|---|---|
| N | 78 | 76 | 21 |
| **Demographics** | | | |
| Male/female (% male) | 46/32 (59%) | 50/26 (66%) | 12/9 (57%) |
| age, years [mean +/- standard deviation] | 68.45 +/- 6.71 | 68.04 +/- 9.7 | 66.14 +/- 7.93 |
| **Anthropometrics** | | | |
| weight, kg [mean +/- standard deviation] | 80.15 +/- 16.02 | 83.68 +/- 15.52 | 78.01 +/- 14.28 |
| height, cm [mean +/- standard deviation] | 173.26 +/- 8.84 | 171.4 +/- 9.66 | 172.38 +/- 10.05 |
| BMI, kg/(m*m) [mean +/- standard deviation] | 26.54 +/- 4.07 | 28.46 +/- 4.52 | 26.15 +/- 3.44 |
| **Motor Symptoms** | | | |
| Hoehn and Yahr staging [mean +/- standard deviation] | 0 +/- 0 | 2.13 +/- 0.8 | 0.05 +/- 0.22 |
| MDS-UPDRS II, sum [mean +/- standard deviation] | 1.47 +/- 2.04 | 13.15 +/- 7.43 | 3.19 +/- 2.98 |
| MDS-UPDRS III, sum [mean +/- standard deviation] | 1.54 +/- 2.8 | 29.69 +/- 13.58 | 3.76 +/- 3.24 |
| MDS-UPDRS IV, sum [mean +/- standard deviation] | 0 +/- 0 | 1.06 +/- 1.81 | 0 +/- 0 |
| MDS-UPDRS, sum [mean +/- standard deviation] | 8.47 +/- 7.76 | 55.62 +/- 24.84 | 18.81 +/- 9.35 |
| **Non-motor symptoms** | | | |
| MDS-UPDRS I, sum [mean +/- standard deviation] | 5.46 +/- 4.3 | 11.72 +/- 7.22 | 11.86 +/- 6 |
| MDS-UPDRS anxiety (Question I.4) [mean +/- standard deviation] | 0.23 +/- 0.53 | 0.67 +/- 0.84 | 1.05 +/- 0.97 |
| MDS-UPDRS pain (Question I.9) [mean +/- standard deviation] | 0.69 +/- 0.83 | 1.28 +/- 1.12 | 0.9 +/- 0.7 |
| MDS-UPDRS constipation (Question I.11) [mean +/- standard deviation] | 0.27 +/- 0.7 | 1.23 +/- 1.13 | 0.95 +/- 1.2 |
| Scopa-AUT, sum [mean +/- standard deviation] | 8.37 +/- 5.67 | 13.09 +/- 7.09 | 12.38 +/- 5.45 |
| Scopa-AUT gastrointestinal part (Questions 1-7), sum [mean +/- standard deviation] | 0.91 +/- 1.11 | 3.18 +/- 2.36 | 3 +/- 1.97 |
| Scopa-AUT constipation (Question 5) | often:2 (3%);<br>sometimes:5 (6%);<br>never:71 (91%) | often:4 (5%);<br>regularly:2 (3%);<br>sometimes:25 (34%);<br>never:43 (58%);<br>2 n.d. | often:1 (5%);<br>regularly:1 (5%);<br>sometimes:9 (43%);<br>never:10 (48%); |
| NMS-Quest constipation (Question 5), yes/no (%) | 9/69 (12%) | 38/38 (50%) | 8/13 (38%) |
| Non-motor symptom assessment scale (NMSS) constipation (Question 21, strength*frequency) [mean +/- standard deviation] | 0.04 +/- 0.25 | 0.45 +/- 1.52 | 0.67 +/- 1.43 |
| constipation by interview, N (%) | 1 (1%) | 15 (20%) | n.d. |
| other GI dysfunction by interview, N (%) | 17 (22%) | 24 (32%) | n.d. |
| Beck depression inventory (BDI), sum [mean +/- standard deviation] | 3.71 +/- 4.47 | 7.35 +/- 5.92 | 6.79 +/- 5.55 |
| Geriatric Depression Scale (GDS), sum [mean +/- standard deviation] | 1.34 +/- 2.2 | 2.55 +/- 2.61 | 2.62 +/- 2.36 |
| Epworth Sleepiness Scale (ESS), sum [mean +/- standard deviation] | 6.02 +/- 3.69 | 7.86 +/- 3.84 | 9.5 +/- 4.36 |
| Mini-Mental-State-Examination (MMSE), total score [mean +/- standard deviation] | 28.71 +/- 1.53 | 27.72 +/- 2.35 | 28.67 +/- 0.86 |
| Montreal Cognitive Assessment (MoCa), total score [mean +/- standard deviation] | 26.1 +/- 2.73 | 24.32 +/- 4.2 | 23.81 +/- 3.2 |
| Montgomery-Åsberg Depression Rating Scale (MADRS), sum [mean +/- standard deviation] | 1.89 +/- 5.05 | 2.79 +/- 3.78 | 5.24 +/- 6.14 |
| RBD by polysomnography, N | 0 | 40; 6 n.d. | 21 |
| Smell identification test (by 16 item Sniffin Sticks) [mean +/- standard deviation] | 11.81 +/- 2.59 | 5.91 +/- 3.45 | 6.4 +/- 3.93 |
| **Intake of PD medication** | | | |
| Azilect, N (%) | 0 (0%) | 50 (66%) | 0 (0%) |
| any MAO-B inhibitors, N (%) | 0 (0%) | 52 (68%) | 0 (0%) |
| Levodopa, N (%) | 0 (0%) | 66, (87%) | 0 (0%) |
| L-Dopa agonists, N (%) | 0 (0%) | 52 (68%) | 0 (0%) |
| COMT inhibitors, N (%) | 0 (0%) | 4 (5%) | 0 (0%) |
| OTHER: macrogol intake, N (%) | 1 (1%) | 8 (11%) | 0 (0%) |
| **Medical history** | | | |
| depression, N (%) | 11 (14%) | 7 (9%) | 6 (29%) |
| anxiety, N (%) | 2 (3%) | 4 (5%) | 3, 1 n.d. (15%) |
| sleep apnoe, N (%) | 8 (10%) | 2 (3%) | 3 (14%) |
| periodic limb movement disorder, N (%) | 0 (0%) | 1 (1%) | 1 (5%) |
| hypertension, N (%) | 36 (46%) | 43 (56%) | 10 (48%) |
| hyperlipidemia, N (%) | 46 (59%) | 31 (41%) | 7 (33%) |
| diabetes mellitus, N (%) | 4 (5%) | 6 (8%) | 3 (14%) |
| osteoathritis, N (%) | 37 (47%) | 19 (25%) | 11 (52%) |
| rheumatoid arthritis, N (%) | 1 (1%) | 6 (8%) | 0 (0%) |
| coronary artery disease, N (%) | 2 (3%) | 8 (11%) | 2 (10%) |
| congestive heart disease, N (%) | 2 (3%) | 3 (4%) | 1 (5%) |
| hypotheroidism, N (%) | 7 (9%) | 7 (9%) | 3 (14%) |
| asthma/COPD, N (%) | 9 (12%) | 6 (8%) | 5 (24%) |
| cancer, N (%) | 4 (5%) | 5 (7%) | 0 (0%) |
| antidepressant intake, N (%) | 5, 1 n.d. (6%) | 5 (7%) | 0 (0%) |
| current diabetes and/or metformin intake, N (%) | 6 (8%) | 7 (9%) | 3 (14%) |
| metformin intake, N (%) | 3 (4%) | 4 (5%) | 3 (14%) |

**Characteristics of the cohort with nasal wash samples**

| **Study group** | **HC** | **PD** | **iRBD** |
|---|---|---|---|
| N | 65 | 70 | 12 |
| **Demographics** | | | |
| Male/female (% male) | 36/29 (55%) | 47/23 (67%) | 7/5 (58%) |
| age, years [mean +/- standard deviation] | 68.32 +/- 6.28 | 68.14 +/- 10.06 | 68 +/- 7.32 |
| **Anthropometrics** | | | |
| weight, kg [mean +/- standard deviation] | 80.31 +/- 16.36 | 83.59 +/- 15.58 | 79.54 +/- 16.14 |
| height, cm [mean +/- standard deviation] | 172.89 +/- 8.56 | 171.64 +/- 9.69 | 172.17 +/- 10.94 |
| BMI, kg/(m*m) [mean +/- standard deviation] | 26.71 +/- 4.26 | 28.34 +/- 4.44 | 26.65 +/- 3.48 |
| **Motor Symptoms** | | | |
| Hoehn and Yahr staging [mean +/- standard deviation] | 0 +/- 0 | 2.16 +/- 0.82 | 0.08 +/- 0.29 |
| MDS-UPDRS II, sum [mean +/- standard deviation] | 1.45 +/- 1.93 | 13.54 +/- 7.56 | 3.08 +/- 3.09 |
| MDS-UPDRS III, sum [mean +/- standard deviation] | 1.62 +/- 2.72 | 29.99 +/- 13.91 | 3.83 +/- 3.38 |
| MDS-UPDRS IV, sum [mean +/- standard deviation] | 0 +/- 0 | 1.12 +/- 1.87 | 0 +/- 0 |
| MDS-UPDRS, sum [mean +/- standard deviation] | 8.6 +/- 7.75 | 56.35 +/- 25.5 | 17.17 +/- 9.79 |
| **Non-motor symptoms** | | | |
| MDS-UPDRS I, sum [mean +/- standard deviation] | 5.54 +/- 4.49 | 11.71 +/- 7.36 | 10.25 +/- 5.03 |
| MDS-UPDRS anxiety (Question I.4) [mean +/- standard deviation] | 0.28 +/- 0.57 | 0.64 +/- 0.82 | 0.92 +/- 1 |
| MDS-UPDRS pain (Question I.9) [mean +/- standard deviation] | 0.68 +/- 0.85 | 1.26 +/- 1.13 | 0.83 +/- 0.72 |
| MDS-UPDRS constipation (Question I.11) [mean +/- standard deviation] | 0.31 +/- 0.75 | 1.26 +/- 1.13 | 0.5 +/- 0.9 |
| Scopa-AUT, sum [mean +/- standard deviation] | 8.72 +/- 5.67 | 13.05 +/- 7.29 | 10.42 +/- 4.72 |
| Scopa-AUT gastrointestinal part (Questions 1-7), sum [mean +/- standard deviation] | 0.98 +/- 1.17 | 3.14 +/- 2.35 | 2.08 +/- 1.51 |
| Scopa-AUT constipation (Question 5) | often:2 (3%);<br>sometimes:4 (6%);<br>never:59 (91%) | often:4 (6%);<br>regularly:1 (1%);<br>sometimes:25 (37%);<br>never:38 (56%);<br>2 n.d. | sometimes:4 (33%);<br>never:8 (67%); |
| NMS-Quest constipation (Question 5), yes/no (%) | 9/56 (16%) | 36/34 (51%) | 3/9 (25%) |
| Non-motor symptom assessment scale (NMSS) constipation (Question 21, strength*frequency) [mean +/- standard deviation] | 0.05 +/- 0.28 | 0.49 +/- 1.58 | 0.67 +/- 1.56 |
| constipation by interview, N (%) | 1 (2%) | 13 (19%) | n.d. |
| other GI dysfunction by interview, N (%) | 16 (25%) | 23 (33%) | n.d. |
| Beck depression inventory (BDI), sum [mean +/- standard deviation] | 3.89 +/- 4.77 | 7.17 +/- 5.7 | 5.25 +/- 4.64 |
| Geriatric Depression Scale (GDS), sum [mean +/- standard deviation] | 1.44 +/- 2.35 | 2.55 +/- 2.67 | 1.76 +/- 1.43 |
| Epworth Sleepiness Scale (ESS), sum [mean +/- standard deviation] | 6.15 +/- 3.83 | 7.72 +/- 3.71 | n.d. |
| Mini-Mental-State-Examination (MMSE), total score [mean +/- standard deviation] | 28.71 +/- 1.53 | 27.72 +/- 2.35 | 28.67 +/- 0.86 |
| Montreal Cognitive Assessment (MoCa), total score [mean +/- standard deviation] | 26.02 +/- 2.48 | 24.21 +/- 4.29 | 23.33 +/- 3.68 |
| Montgomery-Åsberg Depression Rating Scale (MADRS), sum [mean +/- standard deviation] | 1.97 +/- 5.46 | 2.74 +/- 3.66 | 3.25 +/- 3.19 |
| RBD by polysomnography, N | 0 | 37; 5 n.d. | 12 |
| Smell identification test (by 16 item Sniffin Sticks) [mean +/- standard deviation] | 11.88 +/- 2.56 | 5.8 +/- 3.52 | 7 +/- 3.22 |
| **Intake of PD medication** | | | |
| Azilect, N (%) | 0 (0%) | 44 (63%) | 0 (0%) |
| any MAO-B inhibitors, N (%) | 0 (0%) | 46 (66%) | 0 (0%) |
| Levodopa, N (%) | 0 (0%) | 62, (89%) | 0 (0%) |
| L-Dopa agonists, N (%) | 0 (0%) | 46 (66%) | 0 (0%) |
| COMT inhibitors, N (%) | 0 (0%) | 4 (6%) | 0 (0%) |
| OTHER: macrogol intake, N (%) | 1 (2%) | 7 (10%) | 0 (0%) |
| **Medical history** | | | |
| depression, N (%) | 11 (17%) | 7 (10%) | 1 (8%) |
| anxiety, N (%) | 2 (3%) | 4 (6%) | 0, 1 n.d. (0%) |
| sleep apnoe, N (%) | 7 (11%) | 2 (3%) | 2 (17%) |
| periodic limb movement disorder, N (%) | 0 (0%) | 1 (1%) | 1 (8%) |
| hypertension, N (%) | 30 (46%) | 39 (56%) | 6 (50%) |
| hyperlipidemia, N (%) | 39 (60%) | 28 (40%) | 3 (25%) |
| diabetes mellitus, N (%) | 4 (6%) | 6 (9%) | 2 (17%) |
| osteoathritis, N (%) | 34 (52%) | 18 (26%) | 8 (67%) |
| rheumatoid arthritis, N (%) | 1 (2%) | 6 (9%) | 0 (0%) |
| coronary artery disease, N (%) | 2 (3%) | 6 (9%) | 1 (8%) |
| congestive heart disease, N (%) | 2 (3%) | 3 (4%) | 1 (8%) |
| hypotheroidism, N (%) | 7 (6%) | 5 (7%) | 3 (25%) |
| asthma/COPD, N (%) | 9 (14%) | 6 (9%) | 3 (25%) |
| cancer, N (%) | 4 (6%) | 5 (7%) | 0, 2 n.d. (0%) |
| antidepressant intake, N (%) | 5, 1 n.d. (6%) | 5 (7%) | 0 (0%) |
| current diabetes and/or metformin intake, N (%) | 6 (9%) | 6 (9%) | 2 (17%) |
| metformin intake, N (%) | 3 (5%) | 3 (4%) | 2 (17%) |

**Characteristics of the cohort with stool samples analyzed by 16S rRNA gene amplicon sequencing**

| **Study group** | **HC** | **PD** | **iRBD** |
|---|---|---|---|
| N | 38 | 26 | 20 |
| **Demographics** | | | |
| Male/female (% male) | 25/13 (66%) | 19/7 (73%) | 12/8 (60%) |
| age, years [mean +/- standard deviation] | 69.84 +/- 6.6 | 65.96 +/- 8.01 | 66.05 +/- 8.13 |
| **Anthropometrics** | | | |
| weight, kg [mean +/- standard deviation] | 80.55 +/- 14.92 | 85.09 +/- 13.69 | 78.76 +/- 14.22 |
| height, cm [mean +/- standard deviation] | 172.55 +/- 8.92 | 173.17 +/- 9.19 | 172.75 +/- 10.17 |
| BMI, kg/(m*m) [mean +/- standard deviation] | 26.9 +/- 3.68 | 28.47 +/- 4.05 | 26.3 +/- 3.46 |
| **Motor Symptoms** | | | |
| Hoehn and Yahr staging [mean +/- standard deviation] | 0 +/- 0 | 2 +/- 0.58 | 0.05 +/- 0.22 |
| MDS-UPDRS II, sum [mean +/- standard deviation] | 1.42 +/- 1.93 | 11.38 +/- 5.39 | 3.35 +/- 2.96 |
| MDS-UPDRS III, sum [mean +/- standard deviation] | 1.5 +/- 2.83 | 27.46 +/- 11.81 | 3.95 +/- 3.2 |
| MDS-UPDRS IV, sum [mean +/- standard deviation] | 0 +/- 0 | 0.69 +/- 1.26 | 0 +/- 0 |
| MDS-UPDRS, sum [mean +/- standard deviation] | 8.97 +/- 7.33 | 49.81 +/- 20.11 | 19.55 +/- 8.94 |
| **Non-motor symptoms** | | | |
| MDS-UPDRS I, sum [mean +/- standard deviation] | 6.05 +/- 4.05 | 10.27 +/- 6.35 | 12.25 +/- 5.87 |
| MDS-UPDRS anxiety (Question I.4) [mean +/- standard deviation] | 0.26 +/- 0.6 | 0.5 +/- 0.76 | 1.1 +/- 0.97 |
| MDS-UPDRS pain (Question I.9) [mean +/- standard deviation] | 0.68 +/- 0.77 | 1.08 +/- 1.2 | 0.95 +/- 0.69 |
| MDS-UPDRS constipation (Question I.11) [mean +/- standard deviation] | 0.32 +/- 0.77 | 0.77 +/- 0.95 | 1 +/- 1.21 |
| Scopa-AUT, sum [mean +/- standard deviation] | 7.58 +/- 5.58 | 13 +/- 6.41 | 12.3 +/- 5.58 |
| Scopa-AUT gastrointestinal part (Questions 1-7), sum [mean +/- standard deviation] | 0.82 +/- 1.09 | 3.16 +/- 2.36 | 3.1 +/- 1.97 |
| Scopa-AUT constipation (Question 5) | often:2 (5%);<br>sometimes:4 (11%);<br>never:32 (84%) | often:1 (4%);<br>regularly:1 (4%);<br>sometimes:8 (31%);<br>never:16 (62%) | often:1 (5%);<br>regularly:1 (5%);<br>sometimes:9 (45%);<br>never:9 (45%); |
| NMS-Quest constipation (Question 5), yes/no (%) | 4/34 (11%) | 11/15 (42%) | 8/12 (40%) |
| Non-motor symptom assessment scale (NMSS) constipation (Question 21, strength*frequency) [mean +/- standard deviation] | 0.08 +/- 0.36 | 0 +/- 0 | 0.7 +/- 1.45 |
| constipation by interview, N (%) | 1 (3%) | 4 (15%) | n.d. |
| other GI dysfunction by interview, N (%) | 6 (16%) | 8 (33%) | n.d. |
| Beck depression inventory (BDI), sum [mean +/- standard deviation] | 2.95 +/- 3.02 | 6.76 +/- 7.01 | 6.47 +/- 5.51 |
| Geriatric Depression Scale (GDS), sum [mean +/- standard deviation] | 1.11 +/- 1.54 | 2.53 +/- 2.57 | 2.55 +/- 2.4 |
| Epworth Sleepiness Scale (ESS), sum [mean +/- standard deviation] | 5.56 +/- 3.21 | 8.27 +/- 3.69 | 9.5 +/- 4.36 |
| Mini-Mental-State-Examination (MMSE), total score [mean +/- standard deviation] | 28.5 +/- 1.91 | 28.5 +/- 1.7 | 28.75 +/- 0.79 |
| Montreal Cognitive Assessment (MoCa), total score [mean +/- standard deviation] | 25.76 +/- 3.03 | 25.46 +/- 3.54 | 23.75 +/- 3.27 |
| Montgomery-Åsberg Depression Rating Scale (MADRS), sum [mean +/- standard deviation] | 1.69 +/- 4.6 | 3.19 +/- 4.31 | 5.15 +/- 6.29 |
| RBD by polysomnography, N | 0 | 13; 2 n.d. | 20 |
| Smell identification test (by 16 item Sniffin Sticks) [mean +/- standard deviation] | 11.5 +/- 2.86 | 5.35 +/- 2.99 | 6.21 +/- 3.94 |
| **Intake of PD medication** | | | |
| Azilect, N (%) | 0 (0%) | 20 (77%) | 0 (0%) |
| any MAO-B inhibitors, N (%) | 0 (0%) | 21 (81%) | 0 (0%) |
| Levodopa, N (%) | 0 (0%) | 20, (77%) | 0 (0%) |
| L-Dopa agonists, N (%) | 0 (0%) | 22 (85%) | 0 (0%) |
| COMT inhibitors, N (%) | 0 (0%) | 1 (4%) | 0 (0%) |
| OTHER: macrogol intake, N (%) | 1 (3%) | 2 (8%) | 0 (0%) |
| **Medical history** | | | |
| depression, N (%) | 4 (11%) | 0 (0%) | 6 (30%) |
| anxiety, N (%) | 0 (0%) | 0 (0%) | 3, 1 n.d. (16%) |
| sleep apnoe, N (%) | 6 (16%) | 1 (4%) | 3 (15%) |
| periodic limb movement disorder, N (%) | 0 (0%) | 0 (0%) | 1 (5%) |
| hypertension, N (%) | 18 (47%) | 12 (46%) | 10 (50%) |
| hyperlipidemia, N (%) | 23 (61%) | 7 (27%) | 7 (35%) |
| diabetes mellitus, N (%) | 3 (8%) | 0 (0%) | 3 (15%) |
| osteoathritis, N (%) | 14 (37%) | 3 (12%) | 10 (50%) |
| rheumatoid arthritis, N (%) | 1 (3%) | 2 (8%) | 0 (0%) |
| coronary artery disease, N (%) | 1 (3%) | 2 (8%) | 2 (10%) |
| congestive heart disease, N (%) | 2 (5%) | 2 (8%) | 1 (5%) |
| hypotheroidism, N (%) | 4 (11%) | 3 (12%) | 3 (15%) |
| asthma/COPD, N (%) | 4 (11%) | 0 (0%) | 5 (25%) |
| cancer, N (%) | 1 (3%) | 0 (0%) | 0 (0%) |
| antidepressant intake, N (%) | 2, 1 n.d. (6%) | 1 (4%) | 0 (0%) |
| current diabetes and/or metformin intake, N (%) | 3 (8%) | 1 (4%) | 3 (15%) |
| metformin intake, N (%) | 1 (3%) | 1 (4%) | 3 (15%) |

**Characteristics of the cohort with stool samples analyzed by 18S rRNA gene amplicon sequencing**

| **Study group** | **HC** | **PD** | **iRBD** |
|---|---|---|---|
| N | 32 | 14 | 15 |
| **Demographics** | | | |
| Male/female (% male) | 20/12 (63%) | 10/4 (71%) | 9/6 (50%) |
| age, years [mean +/- standard deviation] | 69.31 +/- 5.9 | 65.43 +/- 6.57 | 65.87 +/- 7.86 |
| **Anthropometrics** | | | |
| weight, kg [mean +/- standard deviation] | 79.89 +/- 14.92 | 84.27 +/- 13.42 | 81.75 +/- 14.74 |
| height, cm [mean +/- standard deviation] | 173.12 +/- 8.43 | 173.61 +/- 10.66 | 173.73 +/- 11.1 |
| BMI, kg/(m*m) [mean +/- standard deviation] | 26.51 +/- 3.77 | 28 +/- 4.12 | 27.02 +/- 3.69 |
| **Motor Symptoms** | | | |
| Hoehn and Yahr staging [mean +/- standard deviation] | 0 +/- 0 | 2.04 +/- 0.66 | 0.07 +/- 0.26 |
| MDS-UPDRS II, sum [mean +/- standard deviation] | 1.16 +/- 1.55 | 10.29 +/- 4.87 | 3.27 +/- 2.55 |
| MDS-UPDRS III, sum [mean +/- standard deviation] | 1.34 +/- 2.39 | 26.93 +/- 12.72 | 3.67 +/- 3.31 |
| MDS-UPDRS IV, sum [mean +/- standard deviation] | 0 +/- 0 | 0.93 +/- 1.49 | 0 +/- 0 |
| MDS-UPDRS, sum [mean +/- standard deviation] | 8.59 +/- 6.67 | 48.57 +/- 21.06 | 19.6 +/- 8.85 |
| **Non-motor symptoms** | | | |
| MDS-UPDRS I, sum [mean +/- standard deviation] | 6.09 +/- 4.21 | 10.43 +/- 7.23 | 12.67 +/- 5.89 |
| MDS-UPDRS anxiety (Question I.4) [mean +/- standard deviation] | 0.28 +/- 0.63 | 0.64 +/- 0.84 | 1.2 +/- 0.86 |
| MDS-UPDRS pain (Question I.9) [mean +/- standard deviation] | 0.75 +/- 0.8 | 0.93 +/- 1.27 | 1.07 +/- 0.59 |
| MDS-UPDRS constipation (Question I.11) [mean +/- standard deviation] | 0.38 +/- 0.83 | 0.86 +/- 1.03 | 1 +/- 1.2 |
| Scopa-AUT, sum [mean +/- standard deviation] | 7.72 +/- 5.85 | 13.18 +/- 6.29 | 12.27 +/- 6.31 |
| Scopa-AUT gastrointestinal part (Questions 1-7), sum [mean +/- standard deviation] | 0.84 +/- 1.14 | 3.08 +/- 2.5 | 3.33 +/- 2.16 |
| Scopa-AUT constipation (Question 5) | often:2 (6%);<br>sometimes:3 (9%);<br>never:27 (84%) | regularly:1 (8%);<br>sometimes:5 (38%);<br>never:8 (62%);<br>1 n.d. | often:1 (7%);<br>regularly:1 (7%);<br>sometimes:7 (47%);<br>never:6 (40%); |
| NMS-Quest constipation (Question 5), yes/no (%) | 4/28 (13%) | 6/8 (43%) | 7/8 (47%) |
| Non-motor symptom assessment scale (NMSS) constipation (Question 21, strength*frequency) [mean +/- standard deviation] | 0.09 +/- 0.39 | 0 +/- 0 | 0.67 +/- 1.4 |
| constipation by interview, N (%) | 1 (3%) | 2 (14%) | n.d. |
| other GI dysfunction by interview, N (%) | 6 (19%) | 4 (29%) | n.d. |
| Beck depression inventory (BDI), sum [mean +/- standard deviation] | 3.1 +/- 3.16 | 7.67 +/- 7.89 | 6.37 +/- 6.26 |
| Geriatric Depression Scale (GDS), sum [mean +/- standard deviation] | 1.1 +/- 1.51 | 3.26 +/- 3.13 | 2.94 +/- 2.61 |
| Epworth Sleepiness Scale (ESS), sum [mean +/- standard deviation] | 5.62 +/- 3.17 | 8.36 +/- 3.1 | 9.5 +/- 4.36 |
| Mini-Mental-State-Examination (MMSE), total score [mean +/- standard deviation] | 28.91 +/- 1.38 | 28.57 +/- 2.03 | 28.67 +/- 0.82 |
| Montreal Cognitive Assessment (MoCa), total score [mean +/- standard deviation] | 26.19 +/- 2.26 | 25 +/- 3.74 | 23.33 +/- 3.39 |
| Montgomery-Åsberg Depression Rating Scale (MADRS), sum [mean +/- standard deviation] | 1.87 +/- 4.92 | 3.5 +/- 4.82 | 6.53 +/- 6.67 |
| RBD by polysomnography, N | 0 | 9; 1 n.d. | 15 |
| Smell identification test (by 16 item Sniffin Sticks) [mean +/- standard deviation] | 11.47 +/- 2.66 | 5.43 +/- 2.98 | 5.86 +/- 3.84 |
| **Intake of PD medication** | | | |
| Azilect, N (%) | 0 (0%) | 9 (64%) | 0 (0%) |
| any MAO-B inhibitors, N (%) | 0 (0%) | 10 (71%) | 0 (0%) |
| Levodopa, N (%) | 0 (0%) | 12 (86%) | 0 (0%) |
| L-Dopa agonists, N (%) | 0 (0%) | 12 (86%) | 0 (0%) |
| COMT inhibitors, N (%) | 0 (0%) | 1 (7%) | 0 (0%) |
| OTHER: macrogol intake, N (%) | 1 (3%) | 2 (14%) | 0 (0%) |
| **Medical history** | | | |
| depression, N (%) | 4 (13%) | 0 (0%) | 4 (27%) |
| anxiety, N (%) | 0 (0%) | 0 (0%) | 2, 1 n.d. (14%) |
| sleep apnoe, N (%) | 4 (13%) | 0 (0%) | 3 (20%) |
| periodic limb movement disorder, N (%) | 0 (0%) | 0 (0%) | 1 (7%) |
| hypertension, N (%) | 14 (44%) | 5 (36%) | 6 (40%) |
| hyperlipidemia, N (%) | 20 (63%) | 3 (21%) | 4 (27%) |
| diabetes mellitus, N (%) | 2 (6%) | 0 (0%) | 1 (7%) |
| osteoathritis, N (%) | 14 (44%) | 2 (14%) | 7 (47%) |
| rheumatoid arthritis, N (%) | 1 (3%) | 2 (14%) | 0 (0%) |
| coronary artery disease, N (%) | 1 (3%) | 0 (0%) | 1 (7%) |
| congestive heart disease, N (%) | 2 (6%) | 1 (7%) | 1 (7%) |
| hypotheroidism, N (%) | 3 (9%) | 2 (14%) | 3 (20%) |
| asthma/COPD, N (%) | 3 (9%) | 0 (0%) | 4 (27%) |
| cancer, N (%) | 0 (0%) | 0 (0%) | 0 (0%) |
| antidepressant intake, N (%) | 1, 1 n.d. (6%) | 1 (7%) | 0 (0%) |
| current diabetes and/or metformin intake, N (%) | 2 (6%) | 1 (7%) | 1 (7%) |
| metformin intake, N (%) | 1 (3%) | 1 (7%) | 1 (7%) |

**comparison PD versus HC**

| KEGG orthologous group | HC mean % abundan | greater median in | estimate of location parameter | P-Value (Wilcoxon rank sum test) | adjusted P-value | KEGG description |
|---|---|---|---|---|---|---|
| K13038 | 0.069% | HC | -0.0049% | 0.004 | 1.0 | dfp; fused 4'-phosphopantothenoylcysteine decarboxylase/phosphopantothenoylcysteine synthetase, FMN-binding (EC:4.1.1.36 6.3.2.5); K13038 phosphopantothenoylcysteine decarboxylase / phosphopantothenate--cysteine ligase [EC:4.1.1.36 6.3.2.5] (A) |
| K01749 | 0.022% | PD | 0.0032% | 0.009 | 1.0 | HMBS, PBG-D, PBGD, PORC, UPS; hydroxymethylbilane synthase (EC:2.5.1.61); K01749 hydroxymethylbilane synthase [EC:2.5.1.61] (A) |
| K01845 | 0.032% | PD | 0.0019% | 0.006 | 1.0 | GSA2; glutamate-1-semialdehyde 2,1-aminomutase 2; K01845 glutamate-1-semialdehyde 2,1-aminomutase [EC:5.4.3.8] (A) |
| K00925 | 0.078% | HC | 0.0005% | 0.007 | 1.0 | similar to acetate kinase; K00925 acetate kinase [EC:2.7.2.1] (A) |
| K02492 | 0.025% | PD | 0.0042% | 0.004 | 1.0 | HEMA2; glutamyl-tRNA reductase 2; K02492 glutamyl-tRNA reductase [EC:1.2.1.70] (A) |
| K09812 | 0.073% | HC | -0.0057% | 0.005 | 1.0 | ftsE; predicted transporter subunit: ATP-binding component of ABC superfamily; K09812 cell division transport system ATP-binding protein (A) |
| K06998 | 0.013% | PD | 0.0027% | 0.007 | 1.0 | PBLD, MAWBP, MAWDBP; phenazine biosynthesis-like protein domain containing; K06998 (A) |
| K02049 | 0.027% | PD | 0.0034% | 0.004 | 1.0 | putative ABC transporter; K02049 NitT/TauT family transport system ATP-binding protein (A) |
| K01607 | 0.028% | PD | 0.0030% | 0.005 | 1.0 | AO090038000029; 4-carboxymuconolactone decarboxylase; K01607 4-carboxymuconolactone decarboxylase [EC:4.1.1.44] (A) |
| K00537 | 0.011% | PD | 0.0027% | 0.003 | 1.0 | arsenate reductase-like; K00537 arsenate reductase [EC:1.20.4.1] (A) |
| K03783 | 0.065% | HC | 0.0004% | 0.009 | 1.0 | PNP, NP, PRO1837, PUNP; purine nucleoside phosphorylase (EC:2.4.2.1); K03783 purine-nucleoside phosphorylase [EC:2.4.2.1] (A) |
| K02652 | 0.019% | PD | 0.0033% | 0.004 | 1.0 | pilus biogenesis protein; K02652 type IV pilus assembly protein PilB (A) |
| K02669 | 0.035% | PD | 0.0030% | 0.005 | 1.0 | yggR; predicted pilus retraction ATPase; K02669 twitching motility protein PilT (A) |
| K00100 | 0.016% | PD | 0.0029% | 0.001 | 1.0 | Akr1c6, 3alpha-HSD, Akr1c1, Hsd17b5; aldo-keto reductase family 1, member C6; K00100 [EC:1.1.1.-] (A) |
| K01966 | 0.003% | PD | 0.0027% | 0.005 | 1.0 | PCCB; propionyl CoA carboxylase, beta polypeptide (EC:6.4.1.3); K01966 propionyl-CoA carboxylase beta chain [EC:6.4.1.3] (A) |
| K01447 | 0.007% | PD | 0.0060% | 0.007 | 1.0 | N-acetylmuramoyl-L-alanine amidase; K01447 N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28] (A) |
| K00955 | 0.008% | PD | 0.0018% | 0.001 | 1.0 | nodQ; bifunctional sulfate adenylyltransferase/adenylyl-sulfate kinase (EC:2.7.1.25 2.7.7.4); K00955 bifunctional enzyme CysN/CysC [EC:2.7.7.4 2.7.1.25] (A) |
| K13542 | 0.020% | PD | 0.0035% | 0.006 | 1.0 | hemD; uroporphyrinogen III C2,C7-methyltransferase and uroporphyrinogen III synthase; K13542 uroporphyrinogen III methyltransferase / synthase [EC:2.1.1.107 4.2.1.75] (A) |
| K07192 | 0.018% | PD | 0.0008% | 0.009 | 1.0 | FLOT1; flotillin 1; K07192 flotillin (A) |
| K09940 | 0.002% | PD | 0.0028% | 0.009 | 1.0 | hypothetical protein; K09940 hypothetical protein (A) |
| K03818 | 0.002% | PD | 0.0026% | 0.007 | 1.0 | wcaF; predicted acyl transferase; K03818 putative colanic acid biosynthesis acetyltransferase WcaF [EC:2.3.1.-] (A) |
| K16870 | 0.000% | PD | 0.0000% | 0.007 | 1.0 | N-acetylglucosaminyl-diphospho-decaprenol L-rhamnosyltransferase [EC:2.4.1.289] |

**comparison iRBD versus HC**

| KEGG orthologous group | HC mean % abundan | greater median in | estimate of location parameter | P-Value (Wilcoxon rank sum test) | adjusted P-value | KEGG description |
|---|---|---|---|---|---|---|
| K02863 | 0.080% | HC | -0.0022% | 0.009 | 0.4 | PRPL1; Plastid ribosomal protein L1 large ribosomal subunit; K02863 large subunit ribosomal protein L1 (A) |
| K02906 | 0.080% | HC | -0.0022% | 0.009 | 0.4 | 50S ribosomal protein L3-1; K02906 large subunit ribosomal protein L3 (A) |
| K02933 | 0.072% | HC | -0.0014% | 0.007 | 0.4 | emb2394; 50S ribosomal protein L6; K02933 large subunit ribosomal protein L6 (A) |
| K02950 | 0.080% | HC | -0.0022% | 0.008 | 0.4 | rps12; ribosomal protein S12; K02950 small subunit ribosomal protein S12 (A) |
| K02967 | 0.079% | HC | -0.0024% | 0.010 | 0.4 | rps2; 30S ribosomal protein S2; K02967 small subunit ribosomal protein S2 (A) |
| K02996 | 0.061% | HC | -0.0056% | 0.010 | 0.4 | RPS9; 30S ribosomal protein S9; K02996 small subunit ribosomal protein S9 (A) |
| K01533 | 0.080% | HC | -0.0008% | 0.008 | 0.4 | ATP7A, DSMAX, MK, MNK, SMAX3; ATPase, Cu++ transporting, alpha polypeptide (EC:3.6.3.4); K01533 Cu2+-exporting ATPase [EC:3.6.3.4] (A) |
| K00600 | 0.076% | HC | -0.0036% | 0.009 | 0.4 | SHMT1, CSHMT, SHMT; serine hydroxymethyltransferase 1 (soluble) (EC:2.1.2.1); K00600 glycine hydroxymethyltransferase [EC:2.1.2.1] (A) |
| K00820 | 0.082% | HC | -0.0031% | 0.005 | 0.4 | GFPT1, GFA, GFAT, GFAT_1, GFAT1, GFAT1m, GFPT, GFPT1L, MSLG; glutamine--fructose-6-phosphate transaminase 1 (EC:2.6.1.16); K00820 glucosamine--fructose-6-phosphate aminotransferase (isomerizing) [EC:2.6.1.16] (A) |
| K04077 | 0.082% | HC | -0.0027% | 0.008 | 0.4 | HSPD1, CPN60, GROEL, HLD4, HSP-60, HSP60, HSP65, HuCHA60, SPG13; heat shock 60kDa protein 1 (chaperonin); K04077 chaperonin GroEL (A) |
| K03168 | 0.073% | HC | -0.0005% | 0.007 | 0.4 | DNA topoisomerase-like protein (EC:5.99.1.2); K03168 DNA topoisomerase I [EC:5.99.1.2] (A) |
| K00609 | 0.080% | HC | -0.0026% | 0.007 | 0.4 | PYRB; aspartate carbamoyltransferase; K00609 aspartate carbamoyltransferase catalytic subunit [EC:2.1.3.2] (A) |
| K04078 | 0.082% | HC | -0.0026% | 0.003 | 0.3 | HSPE1, CPN10, EPF, GROES, HSP10; heat shock 10kDa protein 1 (chaperonin 10); K04078 chaperonin GroES (A) |
| K00602 | 0.084% | HC | -0.0037% | 0.003 | 0.3 | ATIC, AICAR, AICARFT, IMPCHASE, PURH; 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase (EC:2.1.2.3 3.5.4.10); K00602 phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP cyclohydrolase [EC:2.1.2.3 3.5.4.10] (A) |
| K02887 | 0.080% | HC | -0.0023% | 0.010 | 0.4 | rpl20; 50S ribosomal protein L20; K02887 large subunit ribosomal protein L20 (A) |
| K02355 | 0.127% | HC | -0.0047% | 0.009 | 0.4 | GFM2, EF-G2mt, EFG2, MRRF2, MST027, RRF2, RRF2mt, hEFG2, mEF-G_2; G elongation factor, mitochondrial 2; K02355 elongation factor G (A) |
| K02358 | 0.084% | HC | -0.0033% | 0.004 | 0.4 | TUFM, COXPD4, EF-TuMT, EFTU, P43; Tu translation elongation factor, mitochondrial; K02358 elongation factor Tu (A) |
| K02926 | 0.079% | HC | -0.0023% | 0.010 | 0.4 | RPL4; 50S ribosomal protein L4; K02926 large subunit ribosomal protein L4 (A) |
| K03086 | 0.131% | HC | -0.0141% | 0.001 | 0.3 | SIGA; sigma factor A; K03086 RNA polymerase primary sigma factor (A) |
| K03977 | 0.079% | HC | -0.0023% | 0.009 | 0.4 | GTPase Der-like; K03977 GTP-binding protein (A) |
| K01924 | 0.081% | HC | -0.0021% | 0.004 | 0.3 | murC; UDP-N-acetylmuramate:L-alanine ligase (EC:6.3.2.8); K01924 UDP-N-acetylmuramate--alanine ligase [EC:6.3.2.8] (A) |
| K03723 | 0.081% | HC | -0.0023% | 0.004 | 0.3 | mfd; transcription-repair coupling factor; K03723 transcription-repair coupling factor (superfamily II helicase) [EC:3.6.4.-] (A) |
| K06997 | 0.080% | HC | -0.0029% | 0.007 | 0.4 | PROSC; proline synthetase co-transcribed homolog (bacterial); K06997 (A) |
| K02907 | 0.078% | HC | -0.0010% | 0.007 | 0.4 | large subunit ribosomal protein L30; K02907 large subunit ribosomal protein L30 (A) |
| K02860 | 0.081% | HC | -0.0024% | 0.004 | 0.3 | RimM-like protein; K02860 16S rRNA processing protein RimM (A) |
| K00817 | 0.082% | HC | -0.0035% | 0.002 | 0.3 | HISN6B; Histidinol-phosphate aminotransferase; K00817 histidinol-phosphate aminotransferase [EC:2.6.1.9] (A) |
| K01262 | 0.089% | HC | -0.0023% | 0.001 | 0.3 | XPNPEP3, APP3, NPHPL1; X-prolyl aminopeptidase (aminopeptidase P) 3, putative (EC:3.4.11.9); K01262 Xaa-Pro aminopeptidase [EC:3.4.11.9] (A) |
| K06287 | 0.082% | HC | -0.0027% | 0.004 | 0.4 | 1810009N02Rik; RIKEN cDNA 1810009N02 gene; K06287 septum formation protein (A) |
| K02013 | 0.144% | RBD | 0.0055% | 0.003 | 0.3 | fhuC; iron-hydroxamate transporter subunit; K02013 iron complex transport system ATP-binding protein [EC:3.6.3.34] (A) |
| K06966 | 0.049% | HC | -0.0082% | 0.004 | 0.4 | LOG1; cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG1; K06966 (A) |
| K02015 | 0.189% | RBD | 0.0057% | 0.003 | 0.3 | fhuB; fused iron-hydroxamate transporter subunits of ABC superfamily: membrane components; K02015 iron complex transport system permease protein (A) |
| K00645 | 0.082% | HC | -0.0029% | 0.006 | 0.4 | MCAT, FASN2C, MCT, MT, NET62, fabD; malonyl CoA:ACP acyltransferase (mitochondrial) (EC:2.3.1.39); K00645 [acyl-carrier-protein] S-malonyltransferase [EC:2.3.1.39] (A) |
| K04485 | 0.075% | HC | -0.0036% | 0.003 | 0.3 | DNA repair protein RadA homolog; K04485 DNA repair protein RadA/Sms (A) |
| K01776 | 0.066% | HC | -0.0046% | 0.003 | 0.3 | murI; glutamate racemase (EC:5.1.1.3); K01776 glutamate racemase [EC:5.1.1.3] (A) |
| K01652 | 0.115% | RBD | 0.0053% | 0.006 | 0.4 | similar to 2-hydroxyacyl-CoA lyase 1; K01652 acetolactate synthase I/II/III large subunit [EC:2.2.1.6] (A) |
| K00648 | 0.083% | HC | -0.0052% | 0.004 | 0.3 | KAS_III; 3-oxoacyl-[acyl-carrier-protein] synthase III; K00648 3-oxoacyl-[acyl-carrier-protein] synthase III [EC:2.3.1.180] (A) |
| K01778 | 0.090% | RBD | 0.0072% | 0.009 | 0.4 | diaminopimelate epimerase; K01778 diaminopimelate epimerase [EC:5.1.1.7] (A) |
| K00640 | 0.110% | HC | -0.0051% | 0.003 | 0.3 | SERAT2;1; serine O-acetyltransferase; K00640 serine O-acetyltransferase [EC:2.3.1.30] (A) |
| K01662 | 0.088% | HC | -0.0054% | 0.001 | 0.3 | DXPS1; 1-deoxy-D-xylulose 5-phosphate synthase 1; K01662 1-deoxy-D-xylulose-5-phosphate synthase [EC:2.2.1.7] (A) |

| | | | | | | |
|---|---|---|---|---|---|---|
| K00759 | 0.058% | HC | -0.0068% | 0.003 | 0.3 | APRT, AMP; adenine phosphoribosyltransferase (EC:2.4.2.7); K00759 adenine phosphoribosyltransferase [EC:2.4.2.7] (A) |
| K01897 | 0.108% | HC | -0.0108% | 0.008 | 0.4 | ACSL1, ACS1, FACL1, FACL2, LACS, LACS1, LACS2; acyl-CoA synthetase long-chain family member 1 (EC:6.2.1.3); K01897 long-chain acyl-CoA synthetase [EC:6.2.1.3] (A) |
| K00616 | 0.050% | RBD | 0.0038% | 0.006 | 0.4 | TALDO1, TAL, TAL-H, TALDOR, TALH; transaldolase 1 (EC:2.2.1.2); K00616 transaldolase [EC:2.2.1.2] (A) |
| K00950 | 0.023% | HC | -0.0050% | 0.010 | 0.4 | DHPS, PPPK; dihydropteroate synthetase (EC:2.5.1.15); K00796 dihydropteroate synthase [EC:2.5.1.15] K00950 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase [EC:2.7.6.3] (A) |
| K07560 | 0.071% | HC | -0.0037% | 0.005 | 0.4 | DTD1, C20orf88, DUEB, HARS2, bA379J5.3, bA555E18.1, pqn-68; D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae) (EC:6.1.1.21); K07560 D-tyrosyl-tRNA(Tyr) deacylase [EC:3.1.-.-] (A) |
| K07567 | 0.075% | HC | -0.0015% | 0.009 | 0.4 | endoribonuclease L-PSP, putative; K07567 TdcF protein (A) |
| K01752 | 0.122% | RBD | 0.0076% | 0.007 | 0.4 | SDS, SDH; serine dehydratase (EC:4.3.1.17 4.3.1.19); K01752 L-serine dehydratase [EC:4.3.1.17] (A) |
| K00831 | 0.078% | HC | -0.0021% | 0.006 | 0.4 | PSAT1, EPIP, PSA, PSAT; phosphoserine aminotransferase 1 (EC:2.6.1.52); K00831 phosphoserine aminotransferase [EC:2.6.1.52] (A) |
| K03786 | 0.047% | HC | -0.0084% | 0.009 | 0.4 | DEHA2F23584p; K03786 3-dehydroquinate dehydratase II [EC:4.2.1.10] (A) |
| K01953 | 0.105% | RBD | 0.0049% | 0.003 | 0.3 | ASNS, TS11; asparagine synthetase (glutamine-hydrolyzing) (EC:6.3.5.4); K01953 asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4] (A) |
| K02687 | 0.077% | HC | -0.0030% | 0.004 | 0.4 | prmA; methyltransferase for 50S ribosomal subunit protein L11 (EC:2.1.1.-); K02687 ribosomal protein L11 methyltransferase [EC:2.1.1.-] (A) |
| K03978 | 0.080% | HC | -0.0025% | 0.004 | 0.3 | GTP-binding protein At2g22870-like; K03978 GTP-binding protein (A) |
| K03570 | 0.078% | HC | -0.0024% | 0.001 | 0.3 | mreC; cell wall structural complex MreBCD transmembrane component MreC; K03570 rod shape-determining protein MreC (A) |
| K02970 | 0.079% | HC | -0.0025% | 0.009 | 0.4 | rpsU; 30S ribosomal subunit protein S21; K02970 small subunit ribosomal protein S21 (A) |
| K01719 | 0.013% | HC | -0.0052% | 0.006 | 0.4 | UROS, UROIIIS; uroporphyrinogen III synthase (EC:4.2.1.75); K01719 uroporphyrinogen-III synthase [EC:4.2.1.75] (A) |
| K02837 | 0.064% | HC | -0.0055% | 0.003 | 0.3 | prfC; peptide chain release factor RF-3; K02837 peptide chain release factor 3 (A) |
| K07636 | 0.077% | HC | -0.0005% | 0.009 | 0.4 | phoR; sensory histidine kinase in two-component regulatory system with PhoB (EC:2.7.3.-); K07636 two-component system, OmpR family, phosphate regulon sensor histidine kinase PhoR [EC:2.7.13.3] (A) |
| K06950 | 0.129% | HC | -0.0104% | 0.006 | 0.4 | Metal-dependent phosphohydrolase; K06950 uncharacterized protein (A) |
| K09760 | 0.042% | HC | -0.0060% | 0.008 | 0.4 | rmuC; predicted recombination limiting protein; K09760 DNA recombination protein RmuC (A) |
| K01187 | 0.099% | RBD | 0.0098% | 0.008 | 0.4 | sucrase-isomaltase, intestinal-like; K01187 alpha-glucosidase [EC:3.2.1.20] (A) |
| K03699 | 0.047% | RBD | 0.0067% | 0.004 | 0.3 | tlyC; hemolysin; K03699 putative hemolysin (A) |
| K05366 | 0.079% | HC | -0.0082% | 0.000 | 0.3 | mrcA; fused penicillin-binding protein 1a: murein transglycosylase/murein transpeptidase (EC:2.4.2.- 3.4.-.-); K05366 penicillin-binding protein 1A [EC:2.4.1.- 3.4.-.-] (A) |
| K01433 | 0.006% | HC | -0.0011% | 0.003 | 0.3 | Formyl transferase; K01433 formyltetrahydrofolate deformylase [EC:3.5.1.10] (A) |
| K07053 | 0.105% | RBD | 0.0053% | 0.003 | 0.3 | Polymerase/histidinol phosphatase-like protein; K07053 (A) |
| K03547 | 0.045% | RBD | 0.0081% | 0.006 | 0.4 | sbcD; exonuclease, dsDNA, ATP-dependent; K03547 exonuclease SbcD (A) |
| K03294 | 0.025% | RBD | 0.0036% | 0.005 | 0.4 | uncharacterized LOC100776671; K03294 basic amino acid/polyamine antiporter, APA family (A) |
| K03581 | 0.045% | RBD | 0.0040% | 0.008 | 0.4 | recD; exonuclease V (RecBCD complex), alpha chain (EC:3.1.11.5); K03581 exodeoxyribonuclease V alpha subunit [EC:3.1.11.5] (A) |
| K06890 | 0.034% | HC | -0.0084% | 0.004 | 0.4 | GRINA, HNRGW, LFG1, NMDARA1, TMBIM3; glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding); K06890 (A) |
| K01259 | 0.004% | HC | -0.0013% | 0.002 | 0.3 | PIP; proline iminopeptidase; K01259 proline iminopeptidase [EC:3.4.11.5] (A) |
| K09125 | 0.011% | HC | -0.0053% | 0.005 | 0.4 | yhhQ; inner membrane protein, DUF165 family; K09125 hypothetical protein (A) |
| K07054 | 0.004% | HC | -0.0027% | 0.000 | 0.3 | ypfJ; conserved protein; K07054 (A) |
| K05794 | 0.003% | HC | -0.0006% | 0.000 | 0.3 | terC; phage inhibition, colicin resistance and tellurite resistance protein; K05794 tellurite resistance protein TerC (A) |
| K03316 | 0.004% | HC | -0.0006% | 0.004 | 0.4 | CPA1 family transporter: sodium ion/proton; K03316 monovalent cation:H+ antiporter, CPA1 family (A) |
| K01151 | 0.047% | RBD | 0.0043% | 0.001 | 0.3 | DNA LYASE/ENDONUCLEASE 4; K01151 deoxyribonuclease IV [EC:3.1.21.2] (A) |
| K00782 | 0.009% | HC | -0.0036% | 0.006 | 0.4 | ykgG; predicted transporter; K00782 hypothetical protein (A) |
| K07727 | 0.042% | RBD | 0.0034% | 0.007 | 0.4 | XRE family transcriptional regulator; K07727 putative transcriptional regulator (A) |
| K05521 | 0.016% | HC | -0.0071% | 0.003 | 0.3 | yegU; predicted hydrolase; K05521 ADP-ribosylglycohydrolase [EC:3.2.-.-] (A) |
| K03549 | 0.005% | HC | -0.0007% | 0.005 | 0.4 | KT2; potassium transporter 2; K03549 KUP system potassium uptake protein (A) |
| K08281 | 0.005% | HC | -0.0040% | 0.000 | 0.3 | pncA; nicotinamidase/pyrazinamidase (EC:3.5.1.19 3.5.1.-); K08281 nicotinamidase/pyrazinamidase [EC:3.5.1.19 3.5.1.-] (A) |
| K03929 | 0.012% | HC | -0.0009% | 0.008 | 0.4 | putative esterase; K03929 para-nitrobenzyl esterase [EC:3.1.1.-] (A) |
| K01654 | 0.022% | RBD | 0.0029% | 0.007 | 0.4 | neuB; sialic acid synthase NeuB (EC:1.2.4.1); K01654 N-acetylneuraminate synthase [EC:2.5.1.56] (A) |
| K06177 | 0.010% | HC | -0.0053% | 0.003 | 0.3 | rluA; pseudouridine synthase for 23S rRNA (position 746) and tRNAphe(position 32) (EC:4.2.1.70); K06177 tRNA pseudouridine32 synthase / 23S rRNA pseudouridine746 synthase [EC:5.4.99.28 5.4.99.29] (A) |
| K07259 | 0.012% | HC | -0.0065% | 0.001 | 0.3 | dacB; D-alanyl-D-alanine carboxypeptidase (EC:3.4.16.4); K07259 D-alanyl-D-alanine carboxypeptidase / D-alanyl-D-alanine-endopeptidase (penicillin-binding protein 4) [EC:3.4.16.4 3.4.21.-] (A) |
| K08963 | 0.028% | RBD | 0.0050% | 0.008 | 0.4 | MRI1, MTNA, Ypr118w; methylthioribose-1-phosphate isomerase homolog (S. cerevisiae) (EC:5.3.1.23); K08963 methylthioribose-1-phosphate isomerase [EC:5.3.1.23] (A) |
| K04651 | 0.036% | RBD | 0.0037% | 0.004 | 0.4 | hypA; protein involved in nickel insertion into hydrogenases 3; K04651 hydrogenase nickel incorporation protein HypA/HybF (A) |
| K04652 | 0.034% | RBD | 0.0038% | 0.003 | 0.3 | hypB; GTP hydrolase involved in nickel liganding into hydrogenases; K04652 hydrogenase nickel incorporation protein HypB (A) |
| K01417 | 0.009% | RBD | 0.0023% | 0.007 | 0.4 | ATP-dependent Zn protease FtsH2; K01417 [EC:3.4.24.-] (A) |

| | | | | | | |
|---|---|---|---|---|---|---|
| K07023 | 0.036% | RBD | 0.0039% | 0.010 | 0.4 | HDDC2, C6orf74, NS5ATP2, dJ167O5.2; HD domain containing 2; K07023 putative hydrolases of HD superfamily (A) |
| K07185 | 0.013% | RBD | 0.0011% | 0.003 | 0.3 | TspO/MBR family protein; K07185 tryptophan-rich sensory protein (A) |
| K05516 | 0.011% | HC | -0.0059% | 0.004 | 0.4 | cbpA; curved DNA-binding protein, DnaJ homologue that functions as a co-chaperone of DnaK; K05516 curved DNA-binding protein (A) |
| K00983 | 0.023% | RBD | 0.0033% | 0.007 | 0.4 | CMAS, CSS; cytidine monophosphate N-acetylneuraminic acid synthetase (EC:2.7.7.43); K00983 N-acylneuraminate cytidylyltransferase [EC:2.7.7.43] (A) |
| K10536 | 0.023% | RBD | 0.0047% | 0.008 | 0.4 | EMB1873; agmatine deiminase; K10536 agmatine deiminase [EC:3.5.3.12] (A) |
| K07456 | 0.075% | HC | -0.0017% | 0.009 | 0.4 | DNA mismatch repair protein MutS2; K07456 DNA mismatch repair protein MutS2 (A) |
| K07334 | 0.006% | HC | -0.0017% | 0.001 | 0.3 | putative toxin-plasmid maintenance system killer protein; K07334 proteic killer suppression protein (A) |
| K07213 | 0.012% | HC | -0.0047% | 0.008 | 0.4 | ATOX1, ATX1, HAH1; ATX1 antioxidant protein 1 homolog (yeast) (EC:6.2.1.2); K07213 copper chaperone (A) |
| K00231 | 0.005% | HC | -0.0033% | 0.002 | 0.3 | PPOX, PPO, V290M, VP; protoporphyrinogen oxidase (EC:1.3.3.4); K00231 oxygen-dependent protoporphyrinogen oxidase [EC:1.3.3.4] (A) |
| K01734 | 0.099% | RBD | 0.0102% | 0.004 | 0.4 | mgsA; methylglyoxal synthase (EC:4.2.3.3); K01734 methylglyoxal synthase [EC:4.2.3.3] (A) |
| K02007 | 0.029% | RBD | 0.0027% | 0.001 | 0.3 | cbiM; cobalamin biosynthesis protein CbiM; K02007 cobalt/nickel transport system permease protein (A) |
| K02006 | 0.029% | RBD | 0.0029% | 0.001 | 0.3 | ABC transporter ATP-binding protein; K02006 cobalt/nickel transport system ATP-binding protein (A) |
| K01858 | 0.006% | HC | -0.0007% | 0.002 | 0.3 | ISYNA1, INO1, INOS, IPS, IPS_1, IPS-1; inositol-3-phosphate synthase 1 (EC:5.5.1.4); K01858 myo-inositol-1-phosphate synthase [EC:5.5.1.4] (A) |
| K01442 | 0.059% | RBD | 0.0099% | 0.006 | 0.4 | choloylglycine hydrolase; K01442 choloylglycine hydrolase [EC:3.5.1.24] (A) |
| K03387 | 0.012% | HC | -0.0033% | 0.008 | 0.4 | ahpF; alkyl hydroperoxide reductase, F52a subunit, FAD/NAD(P)-binding (EC:1.11.1.15); K03387 alkyl hydroperoxide reductase subunit F [EC:1.6.4.-] (A) |
| K03286 | 0.005% | HC | -0.0009% | 0.010 | 0.4 | ompA; outer membrane protein A (3a;II*;G;d); K03286 OmpA-OmpF porin, OOP family (A) |
| K02843 | 0.005% | HC | -0.0023% | 0.006 | 0.4 | rfaF; ADP-heptose:LPS heptosyltransferase II (EC:2.-.-.-); K02843 heptosyltransferase II [EC:2.4.-.-] (A) |
| K03718 | 0.019% | HC | -0.0016% | 0.007 | 0.4 | asnC; DNA-binding transcriptional dual regulator; K03718 Lrp/AsnC family transcriptional regulator, regulator for asnA, asnC and gidA (A) |
| K08987 | 0.002% | HC | 0.0040% | 0.002 | 0.3 | integral membrane protein; K08987 putative membrane protein (A) |
| K01552 | 0.013% | RBD | 0.0022% | 0.007 | 0.4 | PfATPase7; P-type ATPase, putative (EC:3.6.3.-); K01552 [EC:3.6.3.-] (A) |
| K04764 | 0.004% | HC | -0.0033% | 0.001 | 0.3 | ihfA; integration host factor (IHF), DNA-binding protein, alpha subunit; K04764 integration host factor subunit alpha (A) |
| K06973 | 0.049% | RBD | 0.0091% | 0.002 | 0.3 | peptidase membrane zinc metallopeptidase; K06973 (A) |
| K08974 | 0.036% | RBD | 0.0077% | 0.006 | 0.4 | membrane protein; K08974 putative membrane protein (A) |
| K00282 | 0.011% | HC | -0.0013% | 0.006 | 0.4 | glycine cleavage system protein P; K00282 glycine dehydrogenase subunit 1 [EC:1.4.4.2] (A) |
| K00283 | 0.011% | HC | -0.0013% | 0.006 | 0.4 | glycine cleavage system protein P; K00283 glycine dehydrogenase subunit 2 [EC:1.4.4.2] (A) |
| K07214 | 0.007% | HC | -0.0001% | 0.006 | 0.4 | fes; enterobactin/ferric enterobactin esterase; K07214 enterochelin esterase and related enzymes (A) |
| K02361 | 0.009% | HC | -0.0005% | 0.003 | 0.3 | entC; isochorismate synthase 1 (EC:5.4.4.2); K02361 isochorismate synthase [EC:5.4.4.2] (A) |
| K12960 | 0.029% | RBD | 0.0038% | 0.009 | 0.4 | chlorohydrolase family protein; K12960 5-methylthioadenosine/S-adenosylhomocysteine deaminase [EC:3.5.4.31 3.5.4.28] (A) |
| K07273 | 0.012% | HC | -0.0003% | 0.001 | 0.3 | yegX; predicted hydrolase; K07273 lysozyme (A) |
| K08217 | 0.037% | RBD | 0.0035% | 0.004 | 0.3 | macrolide-efflux protein; K08217 MFS transporter, DHA3 family, macrolide efflux protein (A) |
| K05801 | 0.010% | HC | -0.0023% | 0.003 | 0.3 | djlA; DnaJ-like protein, membrane anchored; K05801 DnaJ like chaperone protein (A) |
| K07284 | 0.011% | RBD | 0.0020% | 0.004 | 0.4 | LPXTG-site transpeptidase; K07284 sortase A [EC:3.4.22.70] (A) |
| K07192 | 0.018% | RBD | 0.0020% | 0.009 | 0.4 | FLOT1; flotillin 1; K07192 flotillin (A) |
| K07454 | 0.003% | HC | -0.0028% | 0.001 | 0.3 | HNH nuclease; K07454 putative restriction endonuclease (A) |
| K01278 | 0.019% | HC | -0.0066% | 0.004 | 0.3 | DPP4, ADABP, ADCP2, CD26, DPPIV, TP103; dipeptidyl-peptidase 4 (EC:3.4.14.5); K01278 dipeptidyl-peptidase 4 [EC:3.4.14.5] (A) |
| K09702 | 0.022% | RBD | 0.0050% | 0.007 | 0.4 | REE1; Ree1p; K09702 hypothetical protein (A) |
| K01185 | 0.003% | HC | -0.0063% | 0.001 | 0.3 | LYZL2; lysozyme-like 2 (EC:3.2.1.17); K01185 lysozyme [EC:3.2.1.17] (A) |
| K03773 | 0.012% | HC | -0.0022% | 0.008 | 0.4 | FBP11-1; peptidyl-prolyl cis-trans isomerase, FKBP-type; K03773 FKBP-type peptidyl-prolyl cis-trans isomerase FklB [EC:5.2.1.8] (A) |
| K07979 | 0.032% | RBD | 0.0042% | 0.009 | 0.4 | GntR family transcriptional regulator; K07979 GntR family transcriptional regulator (A) |
| K07218 | 0.001% | HC | 0.0016% | 0.000 | 0.3 | NosD, nitrous oxidase accessory protein; K07218 nitrous oxidase accessory protein (A) |
| K03816 | 0.060% | HC | -0.0028% | 0.006 | 0.4 | xanthine phosphoribosyltransferase (EC:2.4.2.22); K03816 xanthine phosphoribosyltransferase [EC:2.4.2.22] (A) |
| K06990 | 0.002% | HC | 0.0020% | 0.003 | 0.3 | MEMO1, C2orf4, MEMO, NS5ATP7; mediator of cell motility 1; K06990 (A) |
| K00376 | 0.001% | HC | 0.0016% | 0.000 | 0.3 | nitrous-oxide reductase (EC:1.7.99.6); K00376 nitrous-oxide reductase [EC:1.7.2.4] (A) |
| K13626 | 0.022% | RBD | 0.0026% | 0.010 | 0.4 | flagellar assembly protein FliW; K13626 flagellar assembly factor FliW (A) |
| K05364 | 0.012% | RBD | 0.0005% | 0.005 | 0.4 | peptidoglycan glycosyltransferase (EC:2.4.1.129); K05364 peptidoglycan glycosyltransferase [EC:2.4.1.129] (A) |
| K16922 | 0.002% | HC | -0.0047% | 0.000 | 0.3 | putative peptide zinc metalloprotease protein |
| K08984 | 0.002% | HC | 0.0020% | 0.000 | 0.3 | yjdF; conserved inner membrane protein; K08984 putative membrane protein (A) |
| K05499 | 0.001% | HC | -0.0044% | 0.001 | 0.3 | cytR; DNA-binding transcriptional dual regulator; K05499 LacI family transcriptional regulator, repressor for deo operon, udp, cdd, tsx, nupC, and nupG (A) |
| K07000 | 0.003% | HC | -0.0014% | 0.006 | 0.4 | ycfP; conserved protein; K07000 (A) |
| K03385 | 0.008% | HC | -0.0051% | 0.008 | 0.4 | nrfA; nitrite reductase, formate-dependent, cytochrome; K03385 cytochrome c-552 [EC:1.7.2.2] (A) |

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|---|---|---|---|---|---|---|
| K00096 | 0.025% | RBD | 0.0020% | 0.007 | 0.4 | glycerol dehydrogenase; K00096 glycerol-1-phosphate dehydrogenase [NAD(P)] [EC:1.1.1.261] (A) |
| K00690 | 0.013% | RBD | 0.0007% | 0.004 | 0.3 | ycjM; predicted glucosyltransferase; K00690 sucrose phosphorylase [EC:2.4.1.7] (A) |
| K17318 | 0.137% | RBD | 0.0217% | 0.008 | 0.4 | putative aldouronate transport system substrate-binding protein |
| K17319 | 0.101% | RBD | 0.0146% | 0.007 | 0.4 | putative aldouronate transport system permease protein |
| K17320 | 0.101% | RBD | 0.0146% | 0.007 | 0.4 | putative aldouronate transport system permease protein |
| K09155 | 0.013% | HC | -0.0047% | 0.005 | 0.4 | PAS/PAC sensor protein; K09155 hypothetical protein (A) |
| K07079 | 0.068% | RBD | 0.0085% | 0.006 | 0.4 | aldo/keto reductase; K07079 (A) |
| K01713 | 0.002% | HC | 0.0023% | 0.002 | 0.3 | cyclohexadienyl dehydratase; K01713 cyclohexadienyl dehydratase [EC:4.2.1.51 4.2.1.91] (A) |
| K02385 | 0.020% | RBD | 0.0025% | 0.007 | 0.4 | flbD; flagellar protein FlbD; K02385 flagellar protein FlbD (A) |
| K08364 | 0.001% | HC | 0.0014% | 0.002 | 0.3 | mercuric transport protein periplasmic componentprecursor MerP; K08364 periplasmic mercuric ion binding protein (A) |
| K09474 | 0.006% | HC | -0.0028% | 0.001 | 0.3 | acid phosphatase; K09474 acid phosphatase (class A) [EC:3.1.3.2] (A) |
| K15876 | 0.006% | HC | -0.0052% | 0.004 | 0.3 | NRFH; small subunit of cytochrome c nitrite reductase; K15876 cytochrome c-type protein (A) |
| K03716 | 0.014% | RBD | 0.0001% | 0.010 | 0.4 | DNA repair photolyase; K03716 spore photoproduct lyase [EC:4.1.99.14] (A) |
| K05792 | 0.001% | HC | -0.0045% | 0.002 | 0.3 | terA; phage inhibition, colicin resistance and tellurite resistance protein; K05792 tellurite resistance protein TerA (A) |
| K05791 | 0.001% | HC | 0.0014% | 0.001 | 0.3 | terZ; phage inhibition, colicin resistance and tellurite resistance protein; K05791 tellurium resistance protein TerZ (A) |
| K07791 | 0.006% | HC | -0.0027% | 0.008 | 0.4 | dcuA; C4-dicarboxylate antiporter; K07791 anaerobic C4-dicarboxylate transporter DcuA (A) |
| K07792 | 0.003% | HC | -0.0032% | 0.008 | 0.4 | dcuB; C4-dicarboxylate transporter, anaerobic; DcuS co-sensor; K07792 anaerobic C4 dicarboxylate transporter DcuB (A) |
| K00113 | 0.002% | HC | 0.0023% | 0.001 | 0.3 | glpC; anaerobic sn-glycerol-3-phosphate dehydrogenase, C subunit, 4Fe-4S iron-sulfur cluster; K00113 glycerol-3-phosphate dehydrogenase subunit C [EC:1.1.5.3] (A) |
| K00895 | 0.008% | HC | -0.0007% | 0.004 | 0.3 | pyrophosphate--fructose-6-phosphate 1-phosphotransferase; K00895 pyrophosphate--fructose-6-phosphate 1-phosphotransferase [EC:2.7.1.90] (A) |
| K00112 | 0.002% | HC | 0.0023% | 0.001 | 0.3 | glpB; sn-glycerol-3-phosphate dehydrogenase (anaerobic), membrane anchor subunit (EC:1.1.5.3); K00112 glycerol-3-phosphate dehydrogenase subunit B [EC:1.1.5.3] (A) |
| K11921 | 0.003% | HC | -0.0037% | 0.003 | 0.3 | cynR; transcriptional activator of cyn operon; autorepressor; K11921 LysR family transcriptional regulator (A) |
| K07014 | 0.002% | HC | -0.0031% | 0.001 | 0.3 | yejM; predicted hydrolase, inner membrane; K07014 (A) |
| K09805 | 0.002% | HC | -0.0048% | 0.000 | 0.3 | hypothetical protein; K09805 hypothetical protein (A) |
| K07720 | 0.188% | RBD | 0.0212% | 0.008 | 0.4 | yesN; two-component response regulator YesM; K07720 two-component system, response regulator YesN (A) |
| K03810 | 0.001% | HC | -0.0043% | 0.001 | 0.3 | yceM; predicted oxidoreductase with NAD(P)-binding Rossmann-fold domain; K03810 virulence factor (A) |
| K07718 | 0.186% | RBD | 0.0218% | 0.008 | 0.4 | yesM; two-component sensor histidine kinase YesN; K07718 two-component system, sensor histidine kinase YesM [EC:2.7.13.3] (A) |
| K06610 | 0.001% | HC | -0.0044% | 0.002 | 0.3 | major facilitator superfamily protein; K06610 MFS transporter, SP family, inositol transporter (A) |
| K11031 | 0.002% | HC | 0.0023% | 0.006 | 0.4 | Thiol-activated cytolysin; K11031 thiol-activated cytolysin (A) |
| K06374 | 0.023% | RBD | 0.0026% | 0.009 | 0.4 | spmB; spore maturation protein B; K06374 spore maturation protein B (A) |
| K06373 | 0.029% | RBD | 0.0047% | 0.009 | 0.4 | spore maturation protein A; K06373 spore maturation protein A (A) |
| K01085 | 0.003% | HC | -0.0044% | 0.001 | 0.3 | agp; glucose-1-phosphatase/inositol phosphatase (EC:3.1.3.10); K01085 glucose-1-phosphatase [EC:3.1.3.10] (A) |
| K04835 | 0.001% | HC | 0.0017% | 0.001 | 0.3 | methylaspartate ammonia-lyase C-terminal domain protein; K04835 methylaspartate ammonia-lyase [EC:4.3.1.2] (A) |
| K12962 | 0.001% | HC | -0.0044% | 0.003 | 0.3 | arnE; undecaprenyl phosphate-alpha-L-ara4N exporter; flippase ArnEF subunit; K12962 undecaprenyl phosphate-alpha-L-ara4N flippase subunit ArnE (A) |
| K09680 | 0.013% | HC | -0.0015% | 0.004 | 0.3 | PANK1, PANK; pantothenate kinase 1 (EC:2.7.1.33); K09680 type II pantothenate kinase [EC:2.7.1.33] (A) |
| K03146 | 0.002% | HC | -0.0029% | 0.003 | 0.3 | THI1; thiazole biosynthetic enzyme; K03146 thiamine biosynthetic enzyme (A) |
| K10797 | 0.010% | RBD | 0.0015% | 0.008 | 0.4 | NADH:flavin oxidoreductase; K10797 2-enoate reductase [EC:1.3.1.31] (A) |
| K15974 | 0.001% | HC | 0.0014% | 0.003 | 0.3 | mprA; DNA-binding transcriptional repressor of microcin B17 synthesis and multidrug efflux; K15974 MarR family transcriptional regulator, negative regulator of the multidrug operon emrRAB (A) |
| K15855 | 0.001% | HC | -0.0044% | 0.001 | 0.3 | similar to exo-beta-D-glucosaminidase; K15855 exo-1,4-beta-D-glucosaminidase [EC:3.2.1.165] (A) |
| K03289 | 0.005% | HC | -0.0026% | 0.001 | 0.3 | nupG; nucleoside transporter; K03289 MFS transporter, NHS family, nucleoside permease (A) |

| | | | nose | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ID | analyzed samples | comment | Sample ID | extraction batch | sequencing run | sequencing coordinate | library PCR yield | qPCR human DNA | qPCR bacterial yield | fastq Files | Forward Primer | Reverse Primer |
| HC001 | nose | | HC001.n | L2.n | P5 | D06 | 3.5 | 0.01 | 0.24 | L-106-HC001-P5-D06_S42_L001_R1_001.fastq.gz,L-106-HC001-P5-D06_S42_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC002 | nose & stool | | HC002.n | D2.n | P4 | D03 | 6.49 | 0 | 0 | D03-D-103-HC002_S39_L001_R1_001.fastq.gz,D03-D-103-HC002_S39_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC003 | stool | too few reads in 18S stool | | | | | | | | | | |
| HC004 | nose | | HC004.n | D2.n | P4 | D02 | 10.63 | 0.03 | 0.38 | D02-D-102-HC004_S38_L001_R1_001.fastq.gz,D02-D-102-HC004_S38_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC005 | nose | | HC005.n | A2.n | P4 | A04 | 4.29 | 0.01 | 0.68 | A04-A-104-HC005_S4_L001_R1_001.fastq.gz,A04-A-104-HC005_S4_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC006 | nose | | HC006.n | F2.n | P4 | F10 | 3.58 | 0 | 0.04 | F10-F-110-HC006_S70_L001_R1_001.fastq.gz,F10-F-110-HC006_S70_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC007 | nose & stool | | HC007.n | D1.n | P2 | D11 | | 0.21 | 2.01 | D11-HC007-09b_S121_L001_R1_001.fastq,D11-HC007-09b_S121_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC008 | nose | | HC008.n | O2.n | P3 | B01 | 7.82 | 0.01 | 0.04 | O-101-HC008-945-3-16S_S13_L001_R1_001.fastq.gz,O-101-HC008-945-3-16S_S13_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC009 | nose & stool | | HC009.n | E1.n | P2 | E10 | | 0.06 | 0.12 | E10-HC009-09b_S132_L001_R1_001.fastq,E10-HC009-09b_S132_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC010 | nose | | HC010.n | I2.n | P5 | B07 | 9.7 | 0 | 0.13 | I-107-HC010-P5-B07_S19_L001_R1_001.fastq.gz,I-107-HC010-P5-B07_S19_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC011 | nose & stool | | HC011.n | N2.n | P3 | A01 | 16.27 | 0.07 | 1.79 | N-101-HC011-1294-3-16S_S1_L001_R1_001.fastq.gz,N-101-HC011-1294-3-16S_S1_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC012 | nose | | HC012.n | O2.n | P3 | B03 | 3.01 | 0.01 | 0.52 | O-103-HC012-1161-3-16S_S15_L001_R1_001.fastq.gz,O-103-HC012-1161-3-16S_S15_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC013 | nose & stool | | HC013.n | M2.n | P5 | E05 | 14.7 | 0 | 0.88 | M-105-HC013-P5-E05_S53_L001_R1_001.fastq.gz,M-105-HC013-P5-E05_S53_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC014 | nose | | HC014.n | L2.n | P5 | D04 | 35.5 | 0.01 | 0.08 | L-104-HC014-P5-D04_S40_L001_R1_001.fastq.gz,L-104-HC014-P5-D04_S40_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC015 | stool | too few reads in 18S stool | | | | | | | | | | |
| HC016 | nose & stool | | HC016.n | A2.n | P4 | A05 | 14.91 | 0.03 | 4.02 | A05-A-105-HC016_S5_L001_R1_001.fastq.gz,A05-A-105-HC016_S5_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC017 | nose & stool | | HC017.n | O2.n | P3 | B12 | 21.82 | 0.01 | 0 | O-112-HC017-1164-3-16S_S24_L001_R1_001.fastq.gz,O-112-HC017-1164-3-16S_S24_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC018 | nose | | HC018.n | H2.n | P9 | B10 | 76.7 | 0 | 0.05 | H-110-HC018-P9-B10_S94_L001_R1_001.fastq.gz,H-110-HC018-P9-B10_S94_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC019 | nose & stool | | HC019.n | E2.n | P4 | E11 | 6.53 | 0.01 | 0 | E11-E-111-HC019_S59_L001_R1_001.fastq.gz,E11-E-111-HC019_S59_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC020 | nose & stool | | HC020.n | P2.n | P3 | C12 | 2.82 | 0 | 0.27 | P-112-HC020-1228-3-16S_S36_L001_R1_001.fastq.gz,P-112-HC020-1228-3-16S_S36_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC021 | nose | | HC021.n | L2.n | P5 | D03 | 11.9 | 0.01 | 0.82 | L-103-HC021-P5-D03_S39_L001_R1_001.fastq.gz,L-103-HC021-P5-D03_S39_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC022 | nose | | HC022.n | L2.n | P5 | D07 | 4.4 | 0.03 | 3.85 | L-107-HC022-P5-D07_S43_L001_R1_001.fastq.gz,L-107-HC022-P5-D07_S43_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC023 | stool | | | | | | | | | | | |
| HC024 | nose & stool | | HC024.n | H2.n | P9 | B08 | 114.6 | 0 | 2.59 | H-108-HC024-P9-B08_S92_L001_R1_001.fastq.gz,H-108-HC024-P9-B08_S92_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC025 | nose & stool | | HC025.n | E2.n | P4 | E10 | 10.37 | 0.01 | 0.18 | E10-E-110-HC025_S58_L001_R1_001.fastq.gz,E10-E-110-HC025_S58_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC026 | nose | | HC026.n | H2.n | P9 | B07 | 37.3 | 0.01 | 0 | H-107-HC026-P9-B07_S91_L001_R1_001.fastq.gz,H-107-HC026-P9-B07_S91_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC027 | nose & stool | | HC027.n | T2.n | P9 | A12 | 39.4 | 0.01 | 0.06 | T-112-HC027-P9-A12_S84_L001_R1_001.fastq.gz,T-112-HC027-P9-A12_S84_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC028 | nose & stool | | HC028.n | B2.n | P4 | B02 | 20.98 | 0.01 | 2.35 | B02-B-102-HC028_S14_L001_R1_001.fastq.gz,B02-B-102-HC028_S14_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC029 | stool | | | | | | | | | | | |
| HC030 | nose | | HC030.n | E2.n | P4 | E01 | 10.7 | 0.01 | 0.07 | E01-E-101-HC030_S49_L001_R1_001.fastq.gz,E01-E-101-HC030_S49_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC031 | nose | | HC031.n | C2.n | P4 | C01 | 5.03 | 0.01 | 0.12 | C01-C-101-HC031_S25_L001_R1_001.fastq.gz,C01-C-101-HC031_S25_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC032 | stool | | | | | | | | | | | |
| HC033 | nose & stool | | HC033.n | Q2.n | P3 | D01 | 4.23 | 0.02 | 0.14 | Q-101-HC033-2060-3-16S_S37_L001_R1_001.fastq.gz,Q-101-HC033-2060-3-16S_S37_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC034 | stool | | | | | | | | | | | |
| HC035 | stool | | | | | | | | | | | |
| HC037 | nose & stool | | HC037.n | G2.n | P4 | G11 | 3.69 | 0 | 0.02 | G11-G-111-HC037_S83_L001_R1_001.fastq.gz,G11-G-111-HC037_S83_L001_R1_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC038 | nose | | HC038.n | J2.n | P5 | A07 | 107.4 | 0.02 | 1.03 | J-107-HC038-P5-A07_S7_L001_R1_001.fastq.gz,J-107-HC038-P5-A07_S7_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC039 | nose | | HC039.n | B2.n | P4 | B05 | 4.67 | 0 | 0.1 | B05-B-105-HC039_S17_L001_R1_001.fastq.gz,B05-B-105-HC039_S17_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC040 | nose & stool | | HC040.n | D1.n | P2 | D08 | | 0.04 | 0.12 | D08-HC040-09b_S118_L001_R1_001.fastq,D08-HC040-09b_S118_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC041 | nose | | HC041.n | E2.n | P4 | E12 | 5.59 | 0 | 0 | E12-E-112-HC041_S60_L001_R1_001.fastq.gz,E12-E-112-HC041_S60_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC042 | stool | | | | | | | | | | | |
| HC043 | nose | | HC043.n | G2.n | P4 | G10 | 4.16 | 0 | 0.05 | G10-G-110-HC043_S82_L001_R1_001.fastq.gz,G10-G-110-HC043_S82_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC044 | nose & stool | | HC044.n | P2.n | P3 | C02 | 11.14 | 0 | 0 | P-102-HC044-1286-3-16S_S26_L001_R1_001.fastq.gz,P-102-HC044-1286-3-16S_S26_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC045 | nose | | HC045.n | I2.n | P5 | B08 | 6.5 | 0 | 0.25 | I-108-HC045-P5-B08_S20_L001_R1_001.fastq.gz,I-108-HC045-P5-B08_S20_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC046 | nose & stool | | HC046.n | A2.n | P4 | A03 | 0.9 | 0 | 0 | A03-A-103-HC046_S3_L001_R1_001.fastq.gz,A03-A-103-HC046_S3_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC047 | nose & stool | too few reads in 18S stool | HC047.n | M2.n | P5 | E03 | 98.6 | 0.04 | 0.17 | M-103-HC047-P5-E03_S51_L001_R1_001.fastq.gz,M-103-HC047-P5-E03_S51_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC048 | nose | | HC048.n | K2.n | P5 | C07 | 4.9 | 0 | 0.03 | K-107-HC048-P5-C07_S31_L001_R1_001.fastq.gz,K-107-HC048-P5-C07_S31_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC049 | stool | | | | | | | | | | | |
| HC050 | nose | | HC050.n | Q2.n | P3 | D05 | 3.08 | 0 | 0.17 | Q-105-HC050-1323-3-16S_S41_L001_R1_001.fastq.gz,Q-105-HC050-1323-3-16S_S41_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC051 | nose & stool | | HC051.n | C1.n | P2 | C11 | | 0.33 | 2.41 | C11-HC051-09b_S109_L001_R1_001.fastq,C11-HC051-09b_S109_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC052 | nose | | HC052.n | P2.n | P3 | C01 | 20.27 | 0.09 | 2.17 | P-101-HC052-942-3-16S_S25_L001_R1_001.fastq.gz,P-101-HC052-942-3-16S_S25_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC053 | nose | | HC053.n | M2.n | P5 | E02 | 28.3 | 0.01 | 0.07 | M-102-HC053-P5-E02_S50_L001_R1_001.fastq.gz,M-102-HC053-P5-E02_S50_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC054 | nose | | HC054.n | B2.n | P4 | B04 | 1.54 | 0 | 0.11 | B04-B-104-HC054_S16_L001_R1_001.fastq.gz,B04-B-104-HC054_S16_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC055 | nose | | HC055.n | F2.n | P4 | F12 | 8.23 | 0 | 0.09 | F12-F-112-HC055_S72_L001_R1_001.fastq.gz,F12-F-112-HC055_S72_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC056 | nose & stool | too few reads in 18S stool | HC056.n | J2.n | P5 | A09 | 34.1 | 0.01 | 0 | J-109-HC056-P5-A09_S9_L001_R1_001.fastq.gz,J-109-HC056-P5-A09_S9_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC057 | nose | | HC057.n | Q2.n | P3 | D10 | 0 | 0 | 0 | Q-110-HC057-958-3-16S_S46_L001_R1_001.fastq.gz,Q-110-HC057-958-3-16S_S46_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC058 | nose | | HC058.n | A2.n | P4 | A02 | 0.42 | 0 | 0 | A02-A-102-HC058_S2_L001_R1_001.fastq.gz,A02-A-102-HC058_S2_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC059 | nose & stool | | HC059.n | J2.n | P5 | A08 | 29.8 | 0.01 | 0 | J-108-HC059-P5-A08_S8_L001_R1_001.fastq.gz,J-108-HC059-P5-A08_S8_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC060 | nose & stool | | HC060.n | T2.n | P9 | A11 | 34.2 | 0.01 | 0.36 | T-111-HC060-P9-A11_S83_L001_R1_001.fastq.gz,T-111-HC060-P9-A11_S83_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC061 | stool | | | | | | | | | | | |
| HC062 | nose & stool | | HC062.n | K2.n | P5 | C04 | 61.4 | 0.09 | 0.25 | K-104-HC062-P5-C04_S28_L001_R1_001.fastq.gz,K-104-HC062-P5-C04_S28_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC063 | nose | | HC063.n | N2.n | P3 | A02 | 0 | 0.02 | 1.02 | N-102-HC063-931-3-16S_S2_L001_R1_001.fastq.gz,N-102-HC063-931-3-16S_S2_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC064 | nose | | HC064.n | J2.n | P710 | G05 | | 0.01 | 0.09 | P10-G05-J-105-HC064_S51_L001_R1_001.fastq.gz,P10-G05-J-105-HC064_S51_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC065 | nose | | HC065.n | K2.n | P5 | C05 | 14.8 | 0.01 | 0.26 | K-105-HC065-P5-C05_S29_L001_R1_001.fastq.gz,K-105-HC065-P5-C05_S29_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC066 | nose | | HC066.n | I2.n | P5 | B06 | 25.8 | 0.01 | 0.46 | I-106-HC066-P5-B06_S18_L001_R1_001.fastq.gz,I-106-HC066-P5-B06_S18_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC068 | nose & stool | | HC068.n | I2.n | P5 | B09 | 79.9 | 0.04 | 0.93 | I-109-HC068-P5-B09_S21_L001_R1_001.fastq.gz,I-109-HC068-P5-B09_S21_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC069 | nose | | HC069.n | N2.n | P3 | A05 | 37.4 | 0.04 | 0.21 | N-105-HC069-918-3-16S_S5_L001_R1_001.fastq.gz,N-105-HC069-918-3-16S_S5_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC070 | nose | | HC070.n | F2.n | P4 | F01 | 3.25 | 0 | 0.12 | F01-F-101-HC070_S61_L001_R1_001.fastq.gz,F01-F-101-HC070_S61_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC071 | nose | | HC071.n | D2.n | P4 | D12 | 7.94 | 0 | 0.3 | D12-D-112-HC071_S48_L001_R1_001.fastq.gz,D12-D-112-HC071_S48_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC072 | nose | | HC072.n | D2.n | P4 | D11 | 8.31 | 0.01 | 0 | D11-D-111-HC072_S47_L001_R1_001.fastq.gz,D11-D-111-HC072_S47_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC073 | stool | | | | | | | | | | | |
| HC074 | stool | | | | | | | | | | | |
| HC075 | nose | | HC075.n | H2.n | P9 | B09 | 52.1 | 0 | 0.02 | H-109-HC075-P9-B09_S93_L001_R1_001.fastq.gz,H-109-HC075-P9-B09_S93_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC076 | nose | | HC076.n | J2.n | P5 | A06 | 19.9 | 0 | 0.23 | J-106-HC076-P5-A06_S6_L001_R1_001.fastq.gz,J-106-HC076-P5-A06_S6_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC077 | stool | | | | | | | | | | | |
| HC078 | nose | | HC078.n | M2.n | P5 | E04 | 37.9 | 0 | 3.42 | M-104-HC078-P5-E04_S52_L001_R1_001.fastq.gz,M-104-HC078-P5-E04_S52_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC079 | nose | | HC079.n | N2.n | P3 | A03 | 13.93 | 0 | 0.49 | N-103-HC079-1220-3-16S_S3_L001_R1_001.fastq.gz,N-103-HC079-1220-3-16S_S3_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC080 | nose | | HC080.n | H2.n | P9 | B11 | 57.2 | 0.02 | 0.16 | H-111-HC080-P9-B11_S95_L001_R1_001.fastq.gz,H-111-HC080-P9-B11_S95_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD002 | nose & stool | | PD002.n | M2.n | P5 | E07 | 33.4 | 0 | 0 | M-107-PD002-P5-E07_S55_L001_R1_001.fastq.gz,M-107-PD002-P5-E07_S55_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD003 | stool | | | | | | | | | | | |
| PD004 | nose | | PD004.n | E2.n | P4 | E03 | 17.14 | 0.02 | 0.04 | E03-E-103-PD004_S51_L001_R1_001.fastq.gz,E03-E-103-PD004_S51_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD005 | nose | | PD005.n | O2.n | P3 | B05 | 14.25 | 0.04 | 1.18 | O-105-PD005-1061-3-16S_S17_L001_R1_001.fastq.gz,O-105-PD005-1061-3-16S_S17_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD006 | nose | | PD006.n | A2.n | P4 | A08 | 0.3 | 0 | 0 | A08-A-108-PD006_S8_L001_R1_001.fastq.gz,A08-A-108-PD006_S8_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD007 | nose & stool | | PD007.n | C1.n | P2 | C08 | | 0.05 | 5.54 | C08-PD007-09l_S106_L001_R1_001.fastq,C08-PD007-09l_S106_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| | | reads were merged with PD007.n | PD007-09r.n | D1.n | P2 | D03 | | 0.02 | 0.73 | D03-PD007-09r_S113_L001_R1_001.fastq,D03-PD007-09r_S113_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| | | reads were merged with PD007.n | PD007-09r-2.n | F1.n | P2 | F03 | | | | F03-PD007-09r-2_S137_L001_R1_001.fastq,F03-PD007-09r-2_S137_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| | | reads were merged with PD007.n | PD007-09r-3.n | H1.n | P2 | H03 | | | | H03-PD007-09r-3_S160_L001_R1_001.fastq,H03-PD007-09r-3_S160_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD008 | nose | | PD008.n | M2.n | P5 | E09 | 18.9 | 0.07 | 0.95 | M-109-PD008-P5-E09_S57_L001_R1_001.fastq.gz,M-109-PD008-P5-E09_S57_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD010 | nose | | PD010.n | L2.n | P5 | D08 | 7.6 | 0 | 0 | L-108-PD010-P5-D08_S44_L001_R1_001.fastq.gz,L-108-PD010-P5-D08_S44_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD011 | nose & stool | | PD011.n | A1.n | P2 | A02 | | 0.11 | 0.2 | A02-PD011-09r_S76_L001_R1_001.fastq,A02-PD011-09r_S76_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD012 | stool | | | | | | | | | | | |
| PD013 | nose (& stool) | too few reads in 16S and 18S stool | PD013.n | C2.n | P4 | C07 | 18.17 | 0.09 | 0.14 | C07-C-107-PD013_S31_L001_R1_001.fastq.gz,C07-C-107-PD013_S31_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD014 | nose | | PD014.n | L2.n | P5 | D11 | 40.9 | 0.17 | 0.06 | L-111-PD014-P5-D11_S47_L001_R1_001.fastq.gz,L-111-PD014-P5-D11_S47_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD021 | nose | | PD021.n | K2.n | P5 | C11 | 61.3 | 0 | 0.23 | K-111-PD021-P5-C11_S35_L001_R1_001.fastq.gz,K-111-PD021-P5-C11_S35_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD022 | nose | | PD022.n | N2.n | P3 | A06 | 24.1 | 0 | 0 | N-106-PD022-1291-3-16S_S6_L001_R1_001.fastq.gz,N-106-PD022-1291-3-16S_S6_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD023 | nose | | PD023.n | L2.n | P5 | D10 | 7 | 0.03 | 0.2 | L-110-PD023-P5-D10_S46_L001_R1_001.fastq.gz,L-110-PD023-P5-D10_S46_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD024 | nose | | PD024.n | B2.n | P4 | B06 | 1.3 | 0.01 | 0 | B06-B-106-PD024_S18_L001_R1_001.fastq.gz,B06-B-106-PD024_S18_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD025 | stool | too few reads in 18S stool | | | | | | | | | | |
| PD026 | nose | | PD026.n | B2.n | P4 | B07 | 4.13 | 0.01 | 4.02 | B07-B-107-PD026_S19_L001_R1_001.fastq.gz,B07-B-107-PD026_S19_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD027 | nose | | PD027.n | E2.n | P4 | E02 | 5.5 | 0.04 | 0.06 | E02-E-102-PD027_S50_L001_R1_001.fastq.gz,E02-E-102-PD027_S50_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD028 | nose | | PD028.n | H2.n | P9 | B01 | 88.7 | 0 | 0.15 | H-101-PD028-P9-B01_S85_L001_R1_001.fastq.gz,H-101-PD028-P9-B01_S85_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD029 | nose & stool | too few reads in 18S stool | PD029.n | B2.n | P4 | B09 | 11.17 | 0.01 | 0 | B09-B-109-PD029_S21_L001_R1_001.fastq.gz,B09-B-109-PD029_S21_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD030 | nose | | PD030.n | P2.n | P3 | C04 | 27.71 | 0.12 | 0.12 | P-104-PD030-1108-3-16S_S28_L001_R1_001.fastq.gz,P-104-PD030-1108-3-16S_S28_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD033 | nose | | PD033.n | O2.n | P3 | B08 | 9.82 | 0.01 | 0.02 | O-108-PD033-1027-3-16S_S20_L001_R1_001.fastq.gz,O-108-PD033-1027-3-16S_S20_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD034 | nose | | PD034.n | P2.n | P3 | C03 | 12.14 | 0.01 | 0.18 | P-103-PD034-834-3-16S_S27_L001_R1_001.fastq.gz,P-103-PD034-834-3-16S_S27_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD035 | nose & stool | | PD035.n | K2.n | P5 | C12 | 42 | 0.02 | 0.06 | K-112-PD035-P5-C12_S36_L001_R1_001.fastq.gz,K-112-PD035-P5-C12_S36_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD036 | nose & stool | | PD036.n | E1.n | P2 | E08 | | 0.05 | 0.25 | E08-PD036-09b_S130_L001_R1_001.fastq,E08-PD036-09b_S130_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD037 | nose & stool | | PD037.n | A2.n | P4 | A07 | 7.01 | 0.01 | 0.06 | A07-A-107-PD037_S7_L001_R1_001.fastq.gz,A07-A-107-PD037_S7_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD038 | nose | | PD038.n | G2.n | P4 | G12 | 29.35 | 0 | 0.03 | G12-G-112-PD038_S84_L001_R1_001.fastq.gz,G12-G-112-PD038_S84_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD043 | nose | | PD043.n | C2.n | P4 | C04 | 6.41 | 0.01 | 0.04 | C04-C-104-PD043_S28_L001_R1_001.fastq.gz,C04-C-104-PD043_S28_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD044 | nose & stool | | PD044.n | K2.n | P5 | C10 | 181.7 | 0.86 | 3.25 | K-110-PD044-P5-C10_S34_L001_R1_001.fastq.gz,K-110-PD044-P5-C10_S34_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD045 | nose | | PD045.n | O2.n | P3 | B04 | 5.42 | 0.04 | 1.58 | O-104-PD045-870-3-16S_S16_L001_R1_001.fastq.gz,O-104-PD045-870-3-16S_S16_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD046 | nose | | PD046.n | P2.n | P3 | C05 | 26.48 | 0.03 | 0.5 | P-105-PD046-797-3-16S_S29_L001_R1_001.fastq.gz,P-105-PD046-797-3-16S_S29_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD051 | nose | | PD051.n | J2.n | P710 | G01 | | 0 | 0.69 | P10-G01-J-101-PD051_S5_L001_R1_001.fastq.gz,P10-G01-J-101-PD051_S5_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD054 | nose | | PD054.n | C2.n | P4 | C05 | 24.54 | 0.03 | 0.05 | C05-C-105-PD054_S29_L001_R1_001.fastq.gz,C05-C-105-PD054_S29_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD055 | nose & stool | | PD055.n | A1.n | P2 | A04 | | 0.04 | 1 | A04-PD055-09l_S78_L001_R1_001.fastq,A04-PD055-09l_S78_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| | | reads were merged with PD055.n | PD055-09r.n | A1.n | P2 | A11 | | 0.03 | 0.24 | A11-PD055-09r_S85_L001_R1_001.fastq,A11-PD055-09r_S85_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD056 | nose | | PD056.n | F2.n | P4 | F03 | 15.02 | 0.03 | 1.04 | F03-F-103-PD056_S63_L001_R1_001.fastq.gz,F03-F-103-PD056_S63_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD057 | nose | | PD057.n | M2.n | P5 | E08 | 26.1 | 0 | 0.08 | M-108-PD057-P5-E08_S56_L001_R1_001.fastq.gz,M-108-PD057-P5-E08_S56_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD058 | nose | | PD058.n | D2.n | P4 | D06 | 1.68 | 0 | 0.07 | D06-D-106-PD058_S42_L001_R1_001.fastq.gz,D06-D-106-PD058_S42_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD059 | nose | | PD059.n | R2.n | P3 | E08 | 17.4 | 0 | 1.79 | R-108-PD059-1034-3-16S_S56_L001_R1_001.fastq.gz,R-108-PD059-1034-3-16S_S56_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD060 | nose | | PD060.n | C2.n | P4 | C06 | 14.45 | 0.02 | 0.14 | C06-C-106-PD060_S30_L001_R1_001.fastq.gz,C06-C-106-PD060_S30_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD062 | nose | | PD062.n | N2.n | P3 | A07 | 42.33 | 0.02 | 15.44 | N-107-PD062-1042-3-16S_S7_L001_R1_001.fastq.gz,N-107-PD062-1042-3-16S_S7_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD063 | nose & stool | | PD063.n | N2.n | P3 | A09 | 3.32 | 0.01 | 1.47 | N-109-PD063-1232-3-16S_S9_L001_R1_001.fastq.gz,N-109-PD063-1232-3-16S_S9_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD064 | nose | | PD064.n | J2.n | P5 | A12 | 108.8 | 0 | 1.14 | J-112-PD064-P5-A12_S12_L001_R1_001.fastq.gz,J-112-PD064-P5-A12_S12_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD065 | nose & stool | too few reads in 18S stool | PD065.n | T2.n | P9 | A08 | 133.4 | 0.18 | 1.02 | T-108-PD065-P9-A08_S80_L001_R1_001.fastq.gz,T-108-PD065-P9-A08_S80_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD066 | nose | | PD066.n | I2.n | P5 | B01 | 68.9 | 0.02 | 1.64 | I-101-PD066-P5-B01_S13_L001_R1_001.fastq.gz,I-101-PD066-P5-B01_S13_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD067 | nose & stool | | PD067.n | J2.n | P710 | G03 | | 0.02 | 0.13 | P10-G03-J-103-PD067_S29_L001_R1_001.fastq.gz,P10-G03-J-103-PD067_S29_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD068 | stool | | | | | | | | | | | |
| PD069 | nose & stool | | PD069.n | F2.n | P4 | F04 | 4.24 | 0.01 | 0.05 | F04-F-104-PD069_S64_L001_R1_001.fastq.gz,F04-F-104-PD069_S64_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD070 | nose | | PD070.n | I2.n | P5 | B02 | 23.3 | 0 | 1.28 | I-102-PD070-P5-B02_S14_L001_R1_001.fastq.gz,I-102-PD070-P5-B02_S14_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD071 | nose | | PD071.n | Q2.n | P3 | D12 | 19.07 | 0 | 0 | Q-112-PD071-776-3-16S_S48_L001_R1_001.fastq.gz,Q-112-PD071-776-3-16S_S48_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD072 | stool | too few reads in 18S stool | | | | | | | | | | |
| PD073 | nose | | PD073.n | L2.n | P5 | D09 | 18.9 | 0.01 | 0.17 | L-109-PD073-P5-D09_S45_L001_R1_001.fastq.gz,L-109-PD073-P5-D09_S45_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD074 | nose & stool | | PD074.n | N2.n | P3 | A08 | 13.02 | 0 | 0 | N-108-PD074-998-3-16S_S8_L001_R1_001.fastq.gz,N-108-PD074-998-3-16S_S8_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD075 | nose & stool | | PD075.n | J2.n | P5 | A10 | 90.2 | 0.05 | 3.88 | J-110-PD075-P5-A10_S10_L001_R1_001.fastq.gz,J-110-PD075-P5-A10_S10_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD076 | nose (& stool) | too few reads in 16S and 18S stool | PD076.n | D2.n | P4 | D07 | 9.79 | 0.01 | 0 | D07-D-107-PD076_S43_L001_R1_001.fastq.gz,D07-D-107-PD076_S43_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD077 | nose | | PD077.n | G2.n | P4 | G03 | 21.66 | 0.02 | 0.15 | G03-G-103-PD077_S75_L001_R1_001.fastq.gz,G03-G-103-PD077_S75_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD079 | nose | | PD079.n | H2.n | P9 | B03 | 66.6 | 0.02 | 0.23 | H-103-PD079-P9-B03_S87_L001_R1_001.fastq.gz,H-103-PD079-P9-B03_S87_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD080 | nose | | PD080.n | T2.n | P9 | A10 | 80.3 | 0.05 | 1 | T-110-PD080-P9-A10_S82_L001_R1_001.fastq.gz,T-110-PD080-P9-A10_S82_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD081 | nose | | PD081.n | G2.n | P4 | G02 | 1.95 | 0.01 | 1.51 | G02-G-102-PD081_S74_L001_R1_001.fastq.gz,G02-G-102-PD081_S74_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD082 | nose & stool | | PD082.n | U2.n | P710 | A10 | | 0.32 | 0.01 | P7-A10-U-110-PD082_S14_L001_R1_001.fastq.gz,P7-A10-U-110-PD082_S14_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD083 | stool | | | | | | | | | | | |
| PD084 | nose | | PD084.n | B2.n | P4 | B08 | 28.57 | 0.14 | 4.48 | B08-B-108-PD084_S20_L001_R1_001.fastq.gz,B08-B-108-PD084_S20_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD085 | nose & stool | | PD085.n | D1.n | P2 | D04 | | 1.38 | 352.58 | D04-PD085-09b_S114_L001_R1_001.fastq,D04-PD085-09b_S114_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| | | reads were merged with PD085.n | PD085-2.n | F1.n | P2 | F04 | | | | F04-PD085-09b-2_S138_L001_R1_001.fastq,F04-PD085-09b-2_S138_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| | | reads were merged with PD085.n | PD085-3.n | H1.n | P2 | H04 | | | | H04-PD085-09b-3_S161_L001_R1_001.fastq,H04-PD085-09b-3_S161_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD086 | nose & stool | | PD086.n | Q2.n | P3 | D04 | 24.65 | 0.22 | 27.85 | Q-104-PD086-1276-3-16S_S40_L001_R1_001.fastq.gz,Q-104-PD086-1276-3-16S_S40_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD087 | nose | | PD087.n | P2.n | P3 | C06 | 21.11 | 0 | 0 | P-106-PD087-1368-3-16S_S30_L001_R1_001.fastq.gz,P-106-PD087-1368-3-16S_S30_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD088 | nose | | PD088.n | O2.n | P3 | B07 | 30.64 | 0.13 | 4.47 | O-107-PD088-1212-3-16S_S19_L001_R1_001.fastq.gz,O-107-PD088-1212-3-16S_S19_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD089 | nose | | PD089.n | V2.n | P710 | B01 | | 0.11 | 0.12 | P7-B01-V-101-PD089_S49_L001_R1_001.fastq.gz,P7-B01-V-101-PD089_S49_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD090 | nose | | PD090.n | T2.n | P9 | A09 | 52.3 | 0.03 | 0 | T-109-PD090-P9-A09_S81_L001_R1_001.fastq.gz,T-109-PD090-P9-A09_S81_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD091 | nose | | PD091.n | J2.n | P5 | A11 | 53.6 | 0.02 | 0.06 | J-111-PD091-P5-A11_S11_L001_R1_001.fastq.gz,J-111-PD091-P5-A11_S11_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD092 | nose | | PD092.n | H2.n | P9 | B02 | 144.9 | 0.08 | 1 | H-102-PD092-P9-B02_S86_L001_R1_001.fastq.gz,H-102-PD092-P9-B02_S86_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD093 | nose | | PD093.n | A2.n | P4 | A06 | 2.64 | 0 | 0.05 | A06-A-106-PD093_S6_L001_R1_001.fastq.gz,A06-A-106-PD093_S6_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD094 | nose | | PD094.n | F2.n | P4 | F05 | 7.67 | 0.01 | 0.03 | F05-F-105-PD094_S65_L001_R1_001.fastq.gz,F05-F-105-PD094_S65_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD095 | nose | | PD095.n | R2.n | P3 | E01 | 5.89 | 0.02 | 0.32 | R-101-PD095-1117-3-16S_S49_L001_R1_001.fastq.gz,R-101-PD095-1117-3-16S_S49_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD097 | nose & stool | | PD097.n | P2.n | P3 | C07 | 29.09 | 0.05 | 0.28 | P-107-PD097-811-3-16S_S31_L001_R1_001.fastq.gz,P-107-PD097-811-3-16S_S31_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD098 | nose | | PD098.n | D2.n | P4 | D05 | 20.82 | 0.03 | 0.73 | D05-D-105-PD098_S41_L001_R1_001.fastq.gz,D05-D-105-PD098_S41_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD100 | nose & stool | too few reads in 18S stool | PD100.n | K2.n | P5 | C09 | 27.2 | 0 | 0.56 | K-109-PD100-P5-C09_S33_L001_R1_001.fastq.gz,K-109-PD100-P5-C09_S33_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD002 | nose & stool | | RBD002.n | C1.n | P2 | C07 | | 0.02 | 0 | C07-RBD002-09r_S105_L001_R1_001.fastq,C07-RBD002-09r_S105_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| | | reads were merged with RBD002.n | RBD002-09l.n | C1.n | P2 | C10 | | 0.03 | 0.38 | C10-RBD002-09l_S108_L001_R1_001.fastq,C10-RBD002-09l_S108_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD003 | nose & stool | too few reads in 18S stool | RBD003.n | B2.n | P4 | B10 | 2.14 | 0 | 0 | B10-B-110-RBD003_S22_L001_R1_001.fastq.gz,B10-B-110-RBD003_S22_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD004 | stool | | | | | | | | | | | |
| RBD005 | stool | | | | | | | | | | | |
| RBD006 | stool | | | | | | | | | | | |
| RBD007 | stool | too few reads in 18S stool | | | | | | | | | | |
| RBD008 | nose & stool | | RBD008.n | O2.n | P3 | B09 | 17.53 | 0.8 | 28.34 | O-109-RBD008-2111-16S_S21_L001_R1_001.fastq.gz,O-109-RBD008-2111-16S_S21_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD009 | nose & stool | | RBD009.n | I2.n | P5 | B03 | 30.9 | 0.04 | 0.03 | I-103-RBD009-P5-B03_S15_L001_R1_001.fastq.gz,I-103-RBD009-P5-B03_S15_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD010 | stool | | | | | | | | | | | |
| RBD012 | stool | | | | | | | | | | | |
| RBD013 | nose & stool | | RBD013.n | T2.n | P9 | A01 | 6.6 | 0 | 0.51 | T-101-RBD013-P9-A01_S73_L001_R1_001.fastq.gz,T-101-RBD013-P9-A01_S73_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD014 | nose & stool | too few reads in 18S stool | RBD014-v1.n | G1.n | P2 | G06 | | 0.03 | 0 | G06-RBD014-09b_S152_L001_R1_001.fastq,G06-RBD014-09b_S152_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD015 | stool | too few reads in 18S stool | | | | | | | | | | |
| RBD017 | nose & stool | | RBD017.n | Q2.n | P3 | D07 | 44.44 | 0.02 | 0.97 | Q-107-RBD017-1929-1928-16S_S43_L001_R1_001.fastq.gz,Q-107-RBD017-1929-1928-16S_S43_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD018 | nose & stool | | RBD018.n | T2.n | P9 | A02 | 36.6 | 0.01 | 2.28 | T-102-RBD018-P9-A02_S74_L001_R1_001.fastq.gz,T-102-RBD018-P9-A02_S74_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD019 | nose & stool | | RBD019.n | D2.n | P4 | D08 | 5.77 | 0 | 0 | D08-D-108-RBD019_S44_L001_R1_001.fastq.gz,D08-D-108-RBD019_S44_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD020 | stool | | | | | | | | | | | |
| RBD021 | nose & stool | | RBD021.n | U2.n | P710 | A05 | | 0.16 | 0.01 | P7-A05-U-105-RBD021_S48_L001_R1_001.fastq.gz,P7-A05-U-105-RBD021_S48_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD022 | nose & stool | | RBD022.n | B1.n | P2 | B05 | | 0.09 | 0.25 | B05-RBD022-09r_S91_L001_R1_001.fastq,B05-RBD022-09r_S91_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| | | reads were merged with RBD022.n | RBD022-09l.n | B1.n | P2 | B11 | | 0.04 | 0 | B11-RBD022-09l_S97_L001_R1_001.fastq,B11-RBD022-09l_S97_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| | | reads were merged with RBD022.n | RBD022-09r-2.n | F1.n | P2 | F06 | | | | F06-RBD022-09r-2_S140_L001_R1_001.fastq,F06-RBD022-09r-2_S140_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| | | reads were merged with RBD022.n | RBD022-09r-3.n | H1.n | P2 | H06 | | | | H06-RBD022-09r-3_S163_L001_R1_001.fastq,H06-RBD022-09r-3_S163_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD023 | stool | | | | | | | | | | | |
| RBD025 | nose (& stool) | too few reads in 16S and 18S stool | RBD025.n | L2.n | P5 | D12 | 28.4 | 0 | 0 | L-112-RBD025-P5-D12_S48_L001_R1_001.fastq.gz,L-112-RBD025-P5-D12_S48_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |

| | stool 16S | | | | | | |
|---|---|---|---|---|---|---|---|
| ID | Sample ID | extraction batch | sequencing run | sequencing coordinate | fastq Files | Forward Primer | Reverse Primer |
| HC002 | HC002.f | A2.f | P11 | D12 | P11.D12-113-HC002-16S_S48_L001_R1_001.fastq.gz,P11.D12-113-HC002-16S_S48_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC003 | HC003.f | B2.f | P11 | B03 | P11.B03-118-HC003-16S_S15_L001_R1_001.fastq.gz,P11.B03-118-HC003-16S_S15_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC007 | HC007.f | A2.f | P11 | G06 | P11.G06-120-HC007-16S_S75_L001_R1_001.fastq.gz,P11.G06-120-HC007-16S_S75_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC009 | HC009.f | A1.f | P1 | B05 | B05-HC009F-DA3-16s_S15_L001_R1_001.fastq,B05-HC009F-DA3-16s_S15_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC011 | HC011.f | D2.f | P11 | D09 | P11.D09-120-HC011-16S_S45_L001_R1_001.fastq.gz,P11.D09-120-HC011-16S_S45_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC013 | HC013.f | E2.f | P11 | D11 | P11.D11-112-HC013-16S_S47_L001_R1_001.fastq.gz,P11.D11-112-HC013-16S_S47_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC015 | HC015.f | D2.f | P11 | C06 | P11.C06-119-HC015-16S_S30_L001_R1_001.fastq.gz,P11.C06-119-HC015-16S_S30_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC016 | HC016.f | D2.f | P11 | A09 | P11.A09-117-HC016-16S_S9_L001_R1_001.fastq.gz,P11.A09-117-HC016-16S_S9_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC017 | HC017.f | D2.f | P11 | E08 | P11.E08-113-HC017-16S_S56_L001_R1_001.fastq.gz,P11.E08-113-HC017-16S_S56_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC019 | HC019.f | B2.f | P11 | F02 | P11.F02-114-HC019-16S_S61_L001_R1_001.fastq.gz,P11.F02-114-HC019-16S_S61_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC020 | HC020.f | D2.f | P11 | H08 | P11.H08-116-HC020-16S_S86_L001_R1_001.fastq.gz,P11.H08-116-HC020-16S_S86_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC023 | HC023.f | C2.f | P11 | H05 | P11.H05-116-HC023-16S_S84_L001_R1_001.fastq.gz,P11.H05-116-HC023-16S_S84_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC024 | HC024.f | A2.f | P11 | F12 | P11.F12-115-HC024-16S_S70_L001_R1_001.fastq.gz,P11.F12-115-HC024-16S_S70_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC025 | HC025.f | B2.f | P11 | G02 | P11.G02-115-HC025-16S_S72_L001_R1_001.fastq.gz,P11.G02-115-HC025-16S_S72_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC027 | HC027.f | E2.f | P11 | E11 | P11.E11-113-HC027-16S_S58_L001_R1_001.fastq.gz,P11.E11-113-HC027-16S_S58_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC028 | HC028.f | A2.f | P11 | E06 | P11.E06-118-HC028-16S_S54_L001_R1_001.fastq.gz,P11.E06-118-HC028-16S_S54_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC029 | HC029.f | C2.f | P11 | B06 | P11.B06-118-HC029-16S_S18_L001_R1_001.fastq.gz,P11.B06-118-HC029-16S_S18_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC032 | HC032.f | A1.f | P1 | H02 | H02-HC032F-DA-16s_S68_L001_R1_001.fastq,H02-HC032F-DA-16s_S68_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC033 | HC033.f | D2.f | P11 | F08 | P11.F08-114-HC033-16S_S67_L001_R1_001.fastq.gz,P11.F08-114-HC033-16S_S67_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC034 | HC034.f | B2.f | P11 | H02 | P11.H02-116-HC034-16S_S82_L001_R1_001.fastq.gz,P11.H02-116-HC034-16S_S82_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC035 | HC035.f | C2.f | P11 | A06 | P11.A06-117-HC035-16S_S6_L001_R1_001.fastq.gz,P11.A06-117-HC035-16S_S6_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC037 | HC037.f | A2.f | P11 | G12 | P11.G12-116-HC037-16S_S80_L001_R1_001.fastq.gz,P11.G12-116-HC037-16S_S80_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC040 | HC040.f | A1.f | P1 | H04 | H04-HC040F-DA3-16s_S70_L001_R1_001.fastq,H04-HC040F-DA3-16s_S70_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC042 | HC042.f | B2.f | P11 | D03 | P11.D03-120-HC042-16S_S39_L001_R1_001.fastq.gz,P11.D03-120-HC042-16S_S39_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC044 | HC044.f | D2.f | P11 | C09 | P11.C09-119-HC044-16S_S33_L001_R1_001.fastq.gz,P11.C09-119-HC044-16S_S33_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC046 | HC046.f | D2.f | P11 | G08 | P11.G08-115-HC046-16S_S77_L001_R1_001.fastq.gz,P11.G08-115-HC046-16S_S77_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC047 | HC047.f | A2.f | P11 | E12 | P11.E12-114-HC047-16S_S59_L001_R1_001.fastq.gz,P11.E12-114-HC047-16S_S59_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC049 | HC049.f | C2.f | P11 | G05 | P11.G05-115-HC049-16S_S74_L001_R1_001.fastq.gz,P11.G05-115-HC049-16S_S74_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC051 | HC051.f | A1.f | P1 | F01 | F01-HC051F-DA-16s_S50_L001_R1_001.fastq,F01-HC051F-DA-16s_S50_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC056 | HC056.f | A2.f | P11 | F06 | P11.F06-119-HC056-16S_S65_L001_R1_001.fastq.gz,P11.F06-119-HC056-16S_S65_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC059 | HC059.f | B2.f | P11 | E02 | P11.E02-113-HC059-16S_S50_L001_R1_001.fastq.gz,P11.E02-113-HC059-16S_S50_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC060 | HC060.f | E2.f | P11 | G11 | P11.G11-115-HC060-16S_S79_L001_R1_001.fastq.gz,P11.G11-115-HC060-16S_S79_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC061 | HC061.f | C2.f | P11 | D06 | P11.D06-120-HC061-16S_S42_L001_R1_001.fastq.gz,P11.D06-120-HC061-16S_S42_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC062 | HC062.f | A2.f | P11 | H12 | P11.H12-117-HC062-16S_S89_L001_R1_001.fastq.gz,P11.H12-117-HC062-16S_S89_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC068 | HC068.f | E2.f | P11 | C11 | P11.C11-111-HC068-16S_S35_L001_R1_001.fastq.gz,P11.C11-111-HC068-16S_S35_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC073 | HC073.f | C2.f | P11 | C03 | P11.C03-119-HC073-16S_S27_L001_R1_001.fastq.gz,P11.C03-119-HC073-16S_S27_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC074 | HC074.f | C2.f | P11 | F05 | P11.F05-114-HC074-16S_S64_L001_R1_001.fastq.gz,P11.F05-114-HC074-16S_S64_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| HC077 | HC077.f | E2.f | P11 | F11 | P11.F11-114-HC077-16S_S69_L001_R1_001.fastq.gz,P11.F11-114-HC077-16S_S69_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD002 | PD002.f | A2.f | P710 | H05 | P10-H05-FA-105-PD002_S52_L001_R1_001.fastq.gz,P10-H05-FA-105-PD002_S52_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD003 | PD003.f | D2.f | P11 | C07 | P11.C07-103-PD003-16S_S31_L001_R1_001.fastq.gz,P11.C07-103-PD003-16S_S31_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD007 | PD007.f | B2.f | P11 | E01 | P11.E01-105-PD007-16S_S49_L001_R1_001.fastq.gz,P11.E01-105-PD007-16S_S49_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD011 | PD011.f | A1.f | P1 | E01 | E01-PD011F-DA-16s_S41_L001_R1_001.fastq,E01-PD011F-DA-16s_S41_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD012 | PD012.f | A1.f | P1 | G02 | G02-PD012F-DA-16s_S60_L001_R1_001.fastq,G02-PD012F-DA-16s_S60_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD013 | PD013.f | C2.f | P11 | A04 | P11.A04-101-PD013-16S_S4_L001_R1_001.fastq.gz,P11.A04-101-PD013-16S_S4_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD025 | PD025.f | B2.f | P11 | B01 | P11.B01-102-PD025-16S_S13_L001_R1_001.fastq.gz,P11.B01-102-PD025-16S_S13_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD029 | PD029.f | D2.f | P11 | B07 | P11.B07-102-PD029-16S_S19_L001_R1_001.fastq.gz,P11.B07-102-PD029-16S_S19_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD035 | PD035.f | E2.f | P11 | B10 | P11.B10-102-PD035-16S_S22_L001_R1_001.fastq.gz,P11.B10-102-PD035-16S_S22_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD036 | PD036.f | A1.f | P1 | E02 | E02-PD036F-DA-16s_S42_L001_R1_001.fastq,E02-PD036F-DA-16s_S42_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD037 | PD037.f | A2.f | P710 | H06 | P10-H06-FA-106-PD037_S62_L001_R1_001.fastq.gz,P10-H06-FA-106-PD037_S62_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD044 | PD044.f | B2.f | P11 | C01 | P11.C01-103-PD044-16S_S25_L001_R1_001.fastq.gz,P11.C01-103-PD044-16S_S25_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD055 | PD055.f | B1.f | P1 | F04 | F04-PD055F-DB2-16s_S53_L001_R1_001.fastq,F04-PD055F-DB2-16s_S53_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD063 | PD063.f | D2.f | P11 | D07 | P11.D07-104-PD063-16S_S43_L001_R1_001.fastq.gz,P11.D07-104-PD063-16S_S43_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD065 | PD065.f | E2.f | P11 | E10 | P11.E10-105-PD065-16S_S57_L001_R1_001.fastq.gz,P11.E10-105-PD065-16S_S57_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD067 | PD067.f | A2.f | P710 | H02 | P10-H02-FA-102-PD067_S18_L001_R1_001.fastq.gz,P10-H02-FA-102-PD067_S18_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD068 | PD068.f | D2.f | P11 | E07 | P11.E07-105-PD068-16S_S55_L001_R1_001.fastq.gz,P11.E07-105-PD068-16S_S55_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD069 | PD069.f | B2.f | P11 | D01 | P11.D01-104-PD069-16S_S37_L001_R1_001.fastq.gz,P11.D01-104-PD069-16S_S37_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD072 | PD072.f | A2.f | P710 | H04 | P10-H04-FA-104-PD072_S41_L001_R1_001.fastq.gz,P10-H04-FA-104-PD072_S41_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD074 | PD074.f | C2.f | P11 | D04 | P11.D04-104-PD074-16S_S40_L001_R1_001.fastq.gz,P11.D04-104-PD074-16S_S40_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD075 | PD075.f | C2.f | P11 | F04 | P11.F04-106-PD075-16S_S63_L001_R1_001.fastq.gz,P11.F04-106-PD075-16S_S63_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD076 | PD076.f | C2.f | P11 | G04 | P11.G04-107-PD076-16S_S73_L001_R1_001.fastq.gz,P11.G04-107-PD076-16S_S73_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD082 | PD082.f | E2.f | P11 | C10 | P11.C10-103-PD082-16S_S34_L001_R1_001.fastq.gz,P11.C10-103-PD082-16S_S34_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD083 | PD083.f | E2.f | P11 | D10 | P11.D10-104-PD083-16S_S46_L001_R1_001.fastq.gz,P11.D10-104-PD083-16S_S46_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD085 | PD085.f | A1.f | P1 | D02 | D02-PD085F-DA-16s_S32_L001_R1_001.fastq,D02-PD085F-DA-16s_S32_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD086 | PD086.f | E2.f | P11 | A10 | P11.A10-101-PD086-16S_S10_L001_R1_001.fastq.gz,P11.A10-101-PD086-16S_S10_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD097 | PD097.f | A2.f | P710 | H01 | P10-H01-FA-101-PD097_S6_L001_R1_001.fastq.gz,P10-H01-FA-101-PD097_S6_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| PD100 | PD100.f | C2.f | P11 | C04 | P11.C04-103-PD100-16S_S28_L001_R1_001.fastq.gz,P11.C04-103-PD100-16S_S28_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD002 | RBD002.f | B1.f | P1 | F05 | F05-RBD002F-DB3-16s_S54_L001_R1_001.fastq,F05-RBD002F-DB3-16s_S54_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD003 | RBD003.f | B2.f | P11 | F01 | P11.F01-106-RBD003-16S_S60_L001_R1_001.fastq.gz,P11.F01-106-RBD003-16S_S60_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD004 | RBD004.f | A2.f | P11 | C12 | P11.C12-112-RBD004-16S_S36_L001_R1_001.fastq.gz,P11.C12-112-RBD004-16S_S36_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD005 | RBD005.f | E2.f | P11 | A11 | P11.A11-109-RBD005-16S_S11_L001_R1_001.fastq.gz,P11.A11-109-RBD005-16S_S11_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD006 | RBD006.f | A2.f | P710 | H08 | P10-H08-FA-108-RBD006_S82_L001_R1_001.fastq.gz,P10-H08-FA-108-RBD006_S82_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD007 | RBD007.f | C2.f | P11 | C05 | P11.C05-111-RBD007-16S_S29_L001_R1_001.fastq.gz,P11.C05-111-RBD007-16S_S29_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD008 | RBD008.f | D2.f | P11 | H07 | P11.H07-108-RBD008-16S_S85_L001_R1_001.fastq.gz,P11.H07-108-RBD008-16S_S85_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD009 | RBD009.f | D2.f | P11 | A08 | P11.A08-109-RBD009-16S_S8_L001_R1_001.fastq.gz,P11.A08-109-RBD009-16S_S8_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD010 | RBD010.f | A2.f | P710 | H10 | P10-H10-FA-110-RBD010_S19_L001_R1_001.fastq.gz,P10-H10-FA-110-RBD010_S19_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD012 | RBD012.f | A2.f | P710 | H09 | P10-H09-FA-109-RBD012_S7_L001_R1_001.fastq.gz,P10-H09-FA-109-RBD012_S7_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD013 | RBD013.f | E2.f | P11 | F10 | P11.F10-106-RBD013-16S_S68_L001_R1_001.fastq.gz,P11.F10-106-RBD013-16S_S68_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD014 | RBD014.f | A1.f | P1 | F03 | F03-RBD014F-DA-16s_S52_L001_R1_001.fastq,F03-RBD014F-DA-16s_S52_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD015 | RBD015.f | C2.f | P11 | D05 | P11.D05-112-RBD015-16S_S41_L001_R1_001.fastq.gz,P11.D05-112-RBD015-16S_S41_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD017 | RBD017.f | C2.f | P11 | A05 | P11.A05-109-RBD017-16S_S5_L001_R1_001.fastq.gz,P11.A05-109-RBD017-16S_S5_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD018 | RBD018.f | E2.f | P11 | G10 | P11.G10-107-RBD018-16S_S78_L001_R1_001.fastq.gz,P11.G10-107-RBD018-16S_S78_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD019 | RBD019.f | D2.f | P11 | G07 | P11.G07-107-RBD019-16S_S76_L001_R1_001.fastq.gz,P11.G07-107-RBD019-16S_S76_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD020 | RBD020.f | E2.f | P11 | H10 | P11.H10-108-RBD020-16S_S87_L001_R1_001.fastq.gz,P11.H10-108-RBD020-16S_S87_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD021 | RBD021.f | D2.f | P11 | C08 | P11.C08-111-RBD021-16S_S32_L001_R1_001.fastq.gz,P11.C08-111-RBD021-16S_S32_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD022 | RBD022.f | B1.f | P1 | E03 | E03-RBD022F-DB-16s_S43_L001_R1_001.fastq,E03-RBD022F-DB-16s_S43_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD023 | RBD023.f | A2.f | P710 | H07 | P10-H07-FA-107-RBD023_S72_L001_R1_001.fastq.gz,P10-H07-FA-107-RBD023_S72_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| RBD025 | RBD025.f | B2.f | P11 | D02 | P11.D02-112-RBD025-16S_S38_L001_R1_001.fastq.gz,P11.D02-112-RBD025-16S_S38_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |

| | stool 18S | | | | | | |
|---|---|---|---|---|---|---|---|
| ID | Sample ID | extraction batch | sequencing run | sequencing coordinate | fastq Files | Forward Primer | Reverse Primer |
| HC002 | HC002.f | A2.f | P12 | E02 | E02_113_HC002_18S_ATCTCAGG-CCTAGAGT_L001_R1_001.fastq,E02_113_HC002_18S_ATCTCAGG-CCTAGAGT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC003 | HC003.f | B2.f | P12 | B06 | B06_118_HC003_18S_CGGAGCCT-TCTCTCCG_L001_R1_001.fastq,B06_118_HC003_18S_CGGAGCCT-TCTCTCCG_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC007 | HC007.f | A2.f | P12 | D03 | D03_120_HC007_18S_ACTCGCTA-TTCTAGCT_L001_R1_001.fastq,D03_120_HC007_18S_ACTCGCTA-TTCTAGCT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC009 | HC009.f | B2.f | P12 | A06 | A06_117_HC009_18S_CGGAGCCT-CGTCTAAT_L001_R1_001.fastq,A06_117_HC009_18S_CGGAGCCT-CGTCTAAT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC011 | HC011.f | D2.f | P13 | D06 | P13D06-120-HC011_S69_L001_R1_001.fastq,P13D06-120-HC011_S69_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC013 | HC013.f | E2.f | P12 | F06 | F06_112_HC013_18S_CGGAGCCT-GCGTAAGA_L001_R1_001.fastq,F06_112_HC013_18S_CGGAGCCT-GCGTAAGA_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC015 | HC015.f | C2.f | P13 | C03 | P13C03-119-HC015_S59_L001_R1_001.fastq,P13C03-119-HC015_S59_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC016 | HC016.f | D2.f | P13 | A06 | P13A06-117-HC016_S46_L001_R1_001.fastq,P13A06-117-HC016_S46_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC017 | HC017.f | D2.f | P13 | E05 | P13E05-113-HC017_S75_L001_R1_001.fastq,P13E05-113-HC017_S75_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC019 | HC019.f | B2.f | P12 | F05 | F05_114_HC019_18S_GCGTAGTA-GCGTAAGA_L001_R1_001.fastq,F05_114_HC019_18S_GCGTAGTA-GCGTAAGA_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC020 | HC020.f | D2.f | P13 | H05 | P13H05-116-HC020_S91_L001_R1_001.fastq,P13H05-116-HC020_S91_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC023 | HC023.f | C2.f | P13 | H02 | P13H02-116-HC023_S89_L001_R1_001.fastq,P13H02-116-HC023_S89_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC024 | HC024.f | A2.f | P12 | G02 | G02_115_HC024_18S_ATCTCAGG-CTATTAAG_L001_R1_001.fastq,G02_115_HC024_18S_ATCTCAGG-CTATTAAG_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC025 | HC025.f | B2.f | P12 | G05 | G05_115_HC025_18S_GCGTAGTA-CTATTAAG_L001_R1_001.fastq,G05_115_HC025_18S_GCGTAGTA-CTATTAAG_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC027 | HC027.f | E2.f | P12 | G06 | G06_113_HC027_18S_CGGAGCCT-CTATTAAG_L001_R1_001.fastq,G06_113_HC027_18S_CGGAGCCT-CTATTAAG_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC028 | HC028.f | A2.f | P12 | B03 | B03_118_HC028_18S_ACTCGCTA-TCTCTCCG_L001_R1_001.fastq,B03_118_HC028_18S_ACTCGCTA-TCTCTCCG_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC029 | HC029.f | C2.f | P13 | B03 | P13B03-118-HC029_S51_L001_R1_001.fastq,P13B03-118-HC029_S51_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC032 | HC032.f | D2.f | P13 | D05 | P13D05-112-HC032_S68_L001_R1_001.fastq,P13D05-112-HC032_S68_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC033 | HC033.f | D2.f | P13 | F05 | P13F05-114-HC033_S81_L001_R1_001.fastq,P13F05-114-HC033_S81_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC034 | HC034.f | B2.f | P12 | H05 | H05_116_HC034_18S_GCGTAGTA-AAGGCTAT_L001_R1_001.fastq,H05_116_HC034_18S_GCGTAGTA-AAGGCTAT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC035 | HC035.f | C2.f | P13 | A03 | P13A03-117-HC035_S43_L001_R1_001.fastq,P13A03-117-HC035_S43_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC037 | HC037.f | A2.f | P12 | H02 | H02_116_HC037_18S_ATCTCAGG-AAGGCTAT_L001_R1_001.fastq,H02_116_HC037_18S_ATCTCAGG-AAGGCTAT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC042 | HC042.f | B2.f | P12 | D06 | D06_120_HC042_18S_CGGAGCCT-TTCTAGCT_L001_R1_001.fastq,D06_120_HC042_18S_CGGAGCCT-TTCTAGCT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC044 | HC044.f | D2.f | P13 | C06 | P13C06-119-HC044_S62_L001_R1_001.fastq,P13C06-119-HC044_S62_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC046 | HC046.f | D2.f | P13 | G05 | P13G05-115-HC046_S86_L001_R1_001.fastq,P13G05-115-HC046_S86_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC047 | HC047.f | A2.f | P12 | F02 | F02_114_HC047_18S_ATCTCAGG-GCGTAAGA_L001_R1_001.fastq,F02_114_HC047_18S_ATCTCAGG-GCGTAAGA_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC049 | HC049.f | C2.f | P13 | G02 | P13G02-115-HC049_S84_L001_R1_001.fastq,P13G02-115-HC049_S84_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC056 | HC056.f | A2.f | P12 | C03 | C03_119_HC056_18S_ACTCGCTA-TCGACTAG_L001_R1_001.fastq,C03_119_HC056_18S_ACTCGCTA-TCGACTAG_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC059 | HC059.f | B2.f | P12 | E05 | E05_113_HC059_18S_GCGTAGTA-CCTAGAGT_L001_R1_001.fastq,E05_113_HC059_18S_GCGTAGTA-CCTAGAGT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC060 | HC060.f | E2.f | P12 | A07 | A07_115_HC060_18S_TACGCTGC-CGTCTAAT_L001_R1_001.fastq,A07_115_HC060_18S_TACGCTGC-CGTCTAAT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC061 | HC061.f | C2.f | P13 | D03 | P13D03-120-HC061_S66_L001_R1_001.fastq,P13D03-120-HC061_S66_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC062 | HC062.f | A2.f | P12 | A03 | A03_117_HC062_18S_ACTCGCTA-CGTCTAAT_L001_R1_001.fastq,A03_117_HC062_18S_ACTCGCTA-CGTCTAAT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC068 | HC068.f | E2.f | P12 | E06 | E06_111_HC068_18S_CGGAGCCT-CCTAGAGT_L001_R1_001.fastq,E06_111_HC068_18S_CGGAGCCT-CCTAGAGT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC073 | HC073.f | B2.f | P12 | C06 | C06_119_HC073_18S_CGGAGCCT-TCGACTAG_L001_R1_001.fastq,C06_119_HC073_18S_CGGAGCCT-TCGACTAG_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC074 | HC074.f | C2.f | P13 | F02 | P13F02-114-HC074_S78_L001_R1_001.fastq,P13F02-114-HC074_S78_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| HC077 | HC077.f | E2.f | P12 | H06 | H06_114_HC077_18S_CGGAGCCT-AAGGCTAT_L001_R1_001.fastq,H06_114_HC077_18S_CGGAGCCT-AAGGCTAT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD003 | PD003.f | D2.f | P13 | C04 | P13C04-103-PD003_S60_L001_R1_001.fastq,P13C04-103-PD003_S60_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD007 | PD007.f | B2.f | P12 | E04 | E04_105_PD007_18S_GGAGCTAC-CCTAGAGT_L001_R1_001.fastq,E04_105_PD007_18S_GGAGCTAC-CCTAGAGT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD013 | PD013.f | C2.f | P13 | A01 | P13A01-101-PD013_S41_L001_R1_001.fastq,P13A01-101-PD013_S41_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD025 | PD025.f | B2.f | P12 | B04 | B04_102_PD025_18S_GGAGCTAC-TCTCTCCG_L001_R1_001.fastq,B04_102_PD025_18S_GGAGCTAC-TCTCTCCG_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD029 | PD029.f | D2.f | P13 | B04 | P13B04-102-PD029_S52_L001_R1_001.fastq,P13B04-102-PD029_S52_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD035 | PD035.f | E2.f | P13 | B07 | P13B07-102-PD035_S55_L001_R1_001.fastq,P13B07-102-PD035_S55_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD044 | PD044.f | B2.f | P12 | C04 | C04_103_PD044_18S_GGAGCTAC-TCGACTAG_L001_R1_001.fastq,C04_103_PD044_18S_GGAGCTAC-TCGACTAG_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD055 | PD055.f | B2.f | P12 | A04 | A04_101_PD055_18S_GGAGCTAC-CGTCTAAT_L001_R1_001.fastq,A04_101_PD055_18S_GGAGCTAC-CGTCTAAT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD063 | PD063.f | D2.f | P13 | D04 | P13D04-104-PD063_S67_L001_R1_001.fastq,P13D04-104-PD063_S67_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD065 | PD065.f | E2.f | P13 | E07 | P13E07-105-PD065_S76_L001_R1_001.fastq,P13E07-105-PD065_S76_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD068 | PD068.f | D2.f | P13 | E04 | P13E04-105-PD068_S74_L001_R1_001.fastq,P13E04-105-PD068_S74_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD069 | PD069.f | B2.f | P12 | D04 | D04_104_PD069_18S_GGAGCTAC-TTCTAGCT_L001_R1_001.fastq,D04_104_PD069_18S_GGAGCTAC-TTCTAGCT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD072 | PD072.f | A2.f | P12 | D01 | D01_104_PD072_18S_GCTCATGA-TTCTAGCT_L001_R1_001.fastq,D01_104_PD072_18S_GCTCATGA-TTCTAGCT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD074 | PD074.f | C2.f | P13 | D01 | P13D01-104-PD074_S64_L001_R1_001.fastq,P13D01-104-PD074_S64_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD075 | PD075.f | C2.f | P13 | F01 | P13F01-106-PD075_S77_L001_R1_001.fastq,P13F01-106-PD075_S77_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD076 | PD076.f | C2.f | P13 | G01 | P13G01-107-PD076_S83_L001_R1_001.fastq,P13G01-107-PD076_S83_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD082 | PD082.f | E2.f | P13 | C07 | P13C07-103-PD082_S63_L001_R1_001.fastq,P13C07-103-PD082_S63_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD083 | PD083.f | E2.f | P13 | D07 | P13D07-104-PD083_S70_L001_R1_001.fastq,P13D07-104-PD083_S70_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD086 | PD086.f | E2.f | P13 | A07 | P13A07-101-PD086_S47_L001_R1_001.fastq,P13A07-101-PD086_S47_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD097 | PD097.f | A2.f | P12 | A01 | A01_101_PD097_18S_GCTCATGA-CGTCTAAT_L001_R1_001.fastq,A01_101_PD097_18S_GCTCATGA-CGTCTAAT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| PD100 | PD100.f | C2.f | P13 | C01 | P13C01-103-PD100_S57_L001_R1_001.fastq,P13C01-103-PD100_S57_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| RBD002 | RBD002.f | C2.f | P13 | H01 | P13H01-108-RBD002_S88_L001_R1_001.fastq,P13H01-108-RBD002_S88_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| RBD003 | RBD003.f | B2.f | P12 | F04 | F04_106_RBD003_18S_GGAGCTAC-GCGTAAGA_L001_R1_001.fastq,F04_106_RBD003_18S_GGAGCTAC-GCGTAAGA_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| RBD004 | RBD004.f | A2.f | P12 | D02 | D02_112_RBD004_18S_ATCTCAGG-TTCTAGCT_L001_R1_001.fastq,D02_112_RBD004_18S_ATCTCAGG-TTCTAGCT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| RBD005 | RBD005.f | E2.f | P13 | A08 | P13A08-109-RBD005_S48_L001_R1_001.fastq,P13A08-109-RBD005_S48_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| RBD006 | RBD006.f | A2.f | P12 | H01 | H01_108_RBD006_18S_GCTCATGA-AAGGCTAT_L001_R1_001.fastq,H01_108_RBD006_18S_GCTCATGA-AAGGCTAT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| RBD007 | RBD007.f | C2.f | P13 | C02 | P13C02-111-RBD007_S58_L001_R1_001.fastq,P13C02-111-RBD007_S58_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| RBD008 | RBD008.f | D2.f | P13 | H04 | P13H04-108-RBD008_S90_L001_R1_001.fastq,P13H04-108-RBD008_S90_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| RBD009 | RBD009.f | D2.f | P13 | A05 | P13A05-109-RBD009_S45_L001_R1_001.fastq,P13A05-109-RBD009_S45_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| RBD010 | RBD010.f | A2.f | P12 | B02 | B02_110_RBD010_18S_ATCTCAGG-TCTCTCCG_L001_R1_001.fastq,B02_110_RBD010_18S_ATCTCAGG-TCTCTCCG_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| RBD012 | RBD012.f | A2.f | P12 | A02 | A02_109_RBD012_18S_ATCTCAGG-CGTCTAAT_L001_R1_001.fastq,A02_109_RBD012_18S_ATCTCAGG-CGTCTAAT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| RBD013 | RBD013.f | E2.f | P13 | F07 | P13F07-106-RBD013_S82_L001_R1_001.fastq,P13F07-106-RBD013_S82_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| RBD014 | RBD014.f | B2.f | P12 | A05 | A05_109_RBD014_18S_GCGTAGTA-CGTCTAAT_L001_R1_001.fastq,A05_109_RBD014_18S_GCGTAGTA-CGTCTAAT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| RBD015 | RBD015.f | C2.f | P13 | D02 | P13D02-112-RBD015_S65_L001_R1_001.fastq,P13D02-112-RBD015_S65_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| RBD017 | RBD017.f | C2.f | P13 | A02 | P13A02-109-RBD017_S42_L001_R1_001.fastq,P13A02-109-RBD017_S42_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| RBD018 | RBD018.f | E2.f | P13 | G07 | P13G07-107-RBD018_S87_L001_R1_001.fastq,P13G07-107-RBD018_S87_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| RBD019 | RBD019.f | D2.f | P13 | G04 | P13G04-107-RBD019_S85_L001_R1_001.fastq,P13G04-107-RBD019_S85_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| RBD020 | RBD020.f | E2.f | P13 | H07 | P13H07-108-RBD020_S92_L001_R1_001.fastq,P13H07-108-RBD020_S92_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| RBD021 | RBD021.f | D2.f | P13 | C05 | P13C05-111-RBD021_S61_L001_R1_001.fastq,P13C05-111-RBD021_S61_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| RBD023 | RBD023.f | A2.f | P12 | G01 | G01_107_RBD023_18S_GCTCATGA-CTATTAAG_L001_R1_001.fastq,G01_107_RBD023_18S_GCTCATGA-CTATTAAG_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| RBD025 | RBD025.f | B2.f | P12 | D05 | D05_112_RBD025_18S_GCGTAGTA-TTCTAGCT_L001_R1_001.fastq,D05_112_RBD025_18S_GCGTAGTA-TTCTAGCT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |

| ID | comment | Sample ID | extraction batch | sequencing run | sequencing coordinate | fastq Files | Forward Primer | Reverse Primer |
|---|---|---|---|---|---|---|---|---|
| none | mock-extraction control | exCA0D.f | A1.f | P1 | A04 | A04-exCFAD-16s_S4_L001_R1_001.fastq,A04-exCFAD-16s_S4_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCB0D.f | B1.f | P1 | B04 | B04-exCFBD-16s_S14_L001_R1_001.fastq,B04-exCFBD-16s_S14_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCA0cD.f | A1.f | P1 | G08 | G08-exCFAcD-16s_S65_L001_R1_001.fastq,G08-exCFAcD-16s_S65_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCB0cD.f | B1.f | P1 | H08 | H08-exCFBcD-16s_S73_L001_R1_001.fastq,H08-exCFBcD-16s_S73_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCE1D.f | E2.f | P11 | A12 | P11.A12-117-exCFE-16S_S12_L001_R1_001.fastq.gz,P11.A12-117-exCFE-16S_S12_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCC1D.f | C2.f | P11 | B04 | P11.B04-102-exCFC-16S_S16_L001_R1_001.fastq.gz,P11.B04-102-exCFC-16S_S16_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | elu-P11.f | NA | P11 | B09 | P11.B09-ntc-16S_S21_L001_R1_001.fastq.gz,P11.B09-ntc-16S_S21_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCB1D.f | B2.f | P11 | C02 | P11.C02-111-exCFB-16S_S26_L001_R1_001.fastq.gz,P11.C02-111-exCFB-16S_S26_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCA0.n | A1.n | P2 | A12 | A12-eCA_S86_L001_R1_001.fastq,A12-eCA_S86_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCB0.n | B1.n | P2 | B12 | B12-eCB_S98_L001_R1_001.fastq,B12-eCB_S98_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCC0.n | C1.n | P2 | C12 | C12-eCC_S110_L001_R1_001.fastq,C12-eCC_S110_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCD0.n | D1.n | P2 | D12 | D12-eCD_S122_L001_R1_001.fastq,D12-eCD_S122_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCE0.n | E1.n | P2 | E12 | E12-eCE_S134_L001_R1_001.fastq,E12-eCE_S134_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCG0.n | G1.n | P2 | G10 | G10-eCG_S156_L001_R1_001.fastq,G10-eCG_S156_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCN1.n | N2.n | P3 | A12 | N-112-exN1-16S_S12_L001_R1_001.fastq.gz,N-112-exN1-16S_S12_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCO1.n | O2.n | P3 | B11 | O-111-exO1-16S_S23_L001_R1_001.fastq.gz,O-111-exO1-16S_S23_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCP1.n | P2.n | P3 | C10 | P-110-exP1-16S_S34_L001_R1_001.fastq.gz,P-110-exP1-16S_S34_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCQ1.n | Q2.n | P3 | D09 | Q-109-exQ1-16S_S45_L001_R1_001.fastq.gz,Q-109-exQ1-16S_S45_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCR1.n | R2.n | P3 | E02 | R-102-exR1-16S_S50_L001_R1_001.fastq.gz,R-102-exR1-16S_S50_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCA1.n | A2.n | P4 | A01 | A01-A-101_S1_L001_R1_001.fastq.gz,A01-A-101_S1_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCB1.n | B2.n | P4 | B12 | B12-B-112_S24_L001_R1_001.fastq.gz,B12-B-112_S24_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCC1.n | C2.n | P4 | C11 | C11-C-111_S35_L001_R1_001.fastq.gz,C11-C-111_S35_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCD1.n | D2.n | P4 | D10 | D10-D-110_S46_L001_R1_001.fastq.gz,D10-D-110_S46_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCE1.n | E2.n | P4 | E09 | E09-E-109_S57_L001_R1_001.fastq.gz,E09-E-109_S57_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCF1.n | F2.n | P4 | F08 | F08-F-108_S68_L001_R1_001.fastq.gz,F08-F-108_S68_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCG1.n | G2.n | P4 | G07 | G07-G-107_S79_L001_R1_001.fastq.gz,G07-G-107_S79_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCT1.n | T2.n | P59 | A04 | T-104-P9-A04_S76_L001_R1_001.fastq.gz,T-104-P9-A04_S76_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCI1.n | I2.n | P59 | B05 | I-105-P5-B05_S17_L001_R1_001.fastq.gz,I-105-P5-B05_S17_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCH1.n | H2.n | P59 | B06 | H-106-P9-B06_S90_L001_R1_001.fastq.gz,H-106-P9-B06_S90_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCK1.n | K2.n | P59 | C03 | K-103-P5-C03_S27_L001_R1_001.fastq.gz,K-103-P5-C03_S27_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCL1.n | L2.n | P59 | D02 | L-102-P5-D02_S38_L001_R1_001.fastq.gz,L-102-P5-D02_S38_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCM1.n | M2.n | P59 | E01 | M-101-P5-E01_S49_L001_R1_001.fastq.gz,M-101-P5-E01_S49_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCJ1.n | J2.n | P710 | G04 | P10-G04-J-104_S40_L001_R1_001.fastq.gz,P10-G04-J-104_S40_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCU1.n | U2.n | P710 | A11 | P7-A11-U-111_S26_L001_R1_001.fastq.gz,P7-A11-U-111_S26_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCV1.n | V2.n | P710 | B06 | P7-B06-V-106_S15_L001_R1_001.fastq.gz,P7-B06-V-106_S15_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCA1D.f | A2.f | P710 | H03 | P10-H03-FA-103-exCFA_S30_L001_R1_001.fastq.gz,P10-H03-FA-103-exCFA_S30_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | mock-extraction control | exCB1D.f | B2.f | P12 | C05 | C05_111_exCFB_18S_GCGTAGTA-TCGACTAG_L001_R1_001.fastq,C05_111_exCFB_18S_GCGTAGTA-TCGACTAG_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| none | mock-extraction control | exCC1D.f | C2.f | P13 | B01 | P13B01-102-exCFC_S49_L001_R1_001.fastq,P13B01-102-exCFC_S49_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| none | mock-extraction control | exCE1D.f | E2.f | P12 | C07 | C07_117_exCFE_18S_TACGCTGC-TCGACTAG_L001_R1_001.fastq,C07_117_exCFE_18S_TACGCTGC-TCGACTAG_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| none | nasal wash solution | saline09 | Saline | P2 | G11 | G11-saline09_S157_L001_R1_001.fastq,G11-saline09_S157_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | no template control | NTC-P1 | NA | P1 | H09 | H09-NTC-16s_S74_L001_R1_001.fastq,H09-NTC-16s_S74_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | no template control | NTC-P2 | NA | P2 | F02 | F02-NTC_S136_L001_R1_001.fastq,F02-NTC_S136_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | no template control | NTC-P3 | NA | P3 | F10 | S-110-16S_S70_L001_R1_001.fastq.gz,S-110-16S_S70_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | reagent control | elu-P2.n | NA | P2 | F07 | F07-elu_S141_L001_R1_001.fastq,F07-elu_S141_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | reagent control | elu-P3-1.n | NA | P3 | D03 | NTC-16S_S39_L001_R1_001.fastq.gz,NTC-16S_S39_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | reagent control | elu-P3-2.n | NA | P3 | H01 | NTC2-16S_S73_L001_R1_001.fastq.gz,NTC2-16S_S73_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | reagent control | elu-P4-1.n | NA | P4 | E05 | E05-E-105_S53_L001_R1_001.fastq.gz,E05-E-105_S53_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | reagent control | elu-P4-2.n | NA | P4 | H01 | H01-NTC_S85_L001_R1_001.fastq.gz,H01-NTC_S85_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | reagent control | elu-P5o.n | NA | P59 | C01 | NTCo-P9-C01_S69_L001_R1_001.fastq.gz,NTCo-P9-C01_S69_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | reagent control | elu-P5n.n | NA | P59 | C02 | NTCn-P9-C02_S70_L001_R1_001.fastq.gz,NTCn-P9-C02_S70_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | reagent control | elu-P7n.n | NA | P710 | G06 | P10-G06-NTCn_S61_L001_R1_001.fastq.gz,P10-G06-NTCn_S61_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | reagent control | elu-P7.n | NA | P710 | C01 | P7-C01-NTC_S4_L001_R1_001.fastq.gz,P7-C01-NTC_S4_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| none | reagent control | elu-P13.f | NA | P13 | B06 | P13B06-ntc_S54_L001_R1_001.fastq,P13B06-ntc_S54_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| generous donor A | internal standard | GDAcD-P1 | GDA | P1 | A09 | A09-GDAcD-16s_S9_L001_R1_001.fastq,A09-GDAcD-16s_S9_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| generous donor A | internal standard | GDA-2-P1 | GDA | P1 | A10 | A10-GDAD-16s_S10_L001_R1_001.fastq,A10-GDAD-16s_S10_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| generous donor A | internal standard | GDA-0.2-P1 | GDA | P1 | B10 | B10-GDAD0-1-16s_S20_L001_R1_001.fastq,B10-GDAD0-1-16s_S20_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| generous donor A | internal standard | GDA-0.02-P1 | GDA | P1 | C10 | C10-GDAD0-01-16s_S30_L001_R1_001.fastq,C10-GDAD0-01-16s_S30_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| generous donor A | internal standard | GDA-0.002-P1 | GDA | P1 | D10 | D10-GDAD0001-16s_S40_L001_R1_001.fastq,D10-GDAD0001-16s_S40_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| generous donor A | internal standard | GDA1-P11 | GDA | P11 | E03 | P11.E03-GDA1-16S_S51_L001_R1_001.fastq.gz,P11.E03-GDA1-16S_S51_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| generous donor A | internal standard | GDA2-P11 | GDA | P11 | F03 | P11.F03-GDA2-16S_S62_L001_R1_001.fastq.gz,P11.F03-GDA2-16S_S62_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| generous donor A | internal standard | GDA2-P2 | GDA | P2 | H09 | H09-GD1_S165_L001_R1_001.fastq,H09-GD1_S165_L001_R2_001.fastq | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| generous donor A | internal standard | GDA0.3-P3 | GDA | P3 | H02 | GDA0-3-16S_S74_L001_R1_001.fastq.gz,GDA0-3-16S_S74_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| generous donor A | internal standard | GDA0.03-P3 | GDA | P3 | H03 | GDA0-03-16S_S75_L001_R1_001.fastq.gz,GDA0-03-16S_S75_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| generous donor A | internal standard | GDA0.3-P4 | GDA | P4 | H02 | H02-GDA0-3_S86_L001_R1_001.fastq.gz,H02-GDA0-3_S86_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| generous donor A | internal standard | GDA0.03-P4 | GDA | P4 | H03 | H03-GDA0-03_S87_L001_R1_001.fastq.gz,H03-GDA0-03_S87_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| generous donor A | internal standard | GDA0.3-P10 | GDA | P710 | G07 | P10-G07-GDA0-3_S71_L001_R1_001.fastq.gz,P10-G07-GDA0-3_S71_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| generous donor A | internal standard | GDA0.03-P10 | GDA | P710 | G08 | P10-G08-GDA0-03_S81_L001_R1_001.fastq.gz,P10-G08-GDA0-03_S81_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| generous donor A | internal standard | GDA0.3-P7 | GDA | P710 | C02 | P7-C02-GDA0-3_S16_L001_R1_001.fastq.gz,P7-C02-GDA0-3_S16_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| generous donor A | internal standard | GDA0.03-P7 | GDA | P710 | C03 | P7-C03-GDA0-03_S28_L001_R1_001.fastq.gz,P7-C03-GDA0-03_S28_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| generous donor A | internal standard | GDA1-P10 | GDA | P710 | H11 | P10-H11-GDA1-GDA1_S31_L001_R1_001.fastq.gz,P10-H11-GDA1-GDA1_S31_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| generous donor A | internal standard | GDA2-P10 | GDA | P710 | H12 | P10-H12-GDA2-GDA2_S42_L001_R1_001.fastq.gz,P10-H12-GDA2-GDA2_S42_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| generous donor A | internal standard | GDA0.3-P9 | GDA | P9 | C03 | GDA0-3-P9-C03_S71_L001_R1_001.fastq.gz,GDA0-3-P9-C03_S71_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| generous donor A | internal standard | GDA0.03-P9 | GDA | P9 | C04 | GDA0-03-P9-C04_S72_L001_R1_001.fastq.gz,GDA0-03-P9-C04_S72_L001_R2_001.fastq.gz | GTGBCAGCMGCCGCGGTAA | GACTACHVGGGTATCTAATCC |
| generous donor A | internal standard | GDA1-P12 | GDA | P12 | F03 | F03__GDA1_18S_ACTCGCTA-GCGTAAGA_L001_R1_001.fastq,F03__GDA1_18S_ACTCGCTA-GCGTAAGA_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| generous donor A | internal standard | GDA1-P13 | GDA | P13 | F03 | P13F03-GDA1_S79_L001_R1_001.fastq,P13F03-GDA1_S79_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| generous donor A | internal standard | GDA2-P12 | GDA | P12 | E03 | E03__GDA2_18S_ACTCGCTA-CCTAGAGT_L001_R1_001.fastq,E03__GDA2_18S_ACTCGCTA-CCTAGAGT_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |
| generous donor A | internal standard | GDA2-P13 | GDA | P13 | E03 | P13E03-GDA2_S73_L001_R1_001.fastq,P13E03-GDA2_S73_L001_R2_001.fastq | CGGTAAYTCCAGCTCYV | CCGTCAATTHCTTYAART |