

Supplementary

Table S1. LDA scores and *p*-values associated for species in each group across time.

| Species | Time Point | Group | LDA | <i>p</i> -Value |
|--|------------|-------------|----------|-----------------|
| <i>Bifidobacterium pseudolongum</i> | Month 3 | Neg_Control | 4.962739 | 0.011948 |
| <i>Methanobrevibacter unclassified</i> | Month 3 | Infected | 4.886258 | 0.000113 |
| <i>Butyrivibrio unclassified</i> | Month 3 | Infected | 4.777852 | 0.00039 |
| <i>Alistipes shahii</i> | Month 3 | Neg_Control | 4.478157 | 3.15E-08 |
| <i>Parabacteroides distasonis</i> | Month 3 | Neg_Control | 4.346065 | 0.00015 |
| <i>Bifidobacterium angulatum</i> | Month 3 | Infected | 4.33015 | 0.002528 |
| <i>Prevotella stercorea</i> | Month 3 | Neg_Control | 4.134405 | 0.000184 |
| <i>Bacteroides vulgatus</i> | Month 3 | Neg_Control | 4.097004 | 0.015093 |
| <i>Subdoligranulum unclassified</i> | Month 3 | Neg_Control | 4.093583 | 0.030568 |
| <i>Alistipes unclassified</i> | Month 3 | Neg_Control | 4.076705 | 0.011057 |
| <i>Bifidobacterium adolescentis</i> | Month 3 | Infected | 4.071279 | 0.000218 |
| <i>Bifidobacterium pseudolongum</i> | Month 6 | Neg_Control | 5.08208 | 3.44E-07 |
| <i>Methanobrevibacter unclassified</i> | Month 6 | Infected | 4.946584 | 0.025121 |
| <i>Butyrivibrio unclassified</i> | Month 6 | Infected | 4.933534 | 0.005116 |
| <i>Butyrivibrio unclassified</i> | Month 9 | Infected | 4.656766 | 0.046088 |
| <i>Lactobacillus buchneri</i> | Month 9 | Neg_Control | 4.651226 | 0.016779 |

Table S2. PERMANOVA and betadisper analysis for microbial community.

| PERMANOVA | | Betadisper | | |
|--|----------------|------------|--|---------|
| | R ² | p-value | p-value | |
| Exposed vs. Control | 0.05509 | 0.001 | Exposed vs. Control | 0.00516 |
| Sero-positive vs. Sero-negative | 0.01083 | 0.05 | Sero-positive vs. sero-negative | 0.03714 |
| Month 3 vs. Month 6 vs. Month 9 | 0.23819 | 0.001 | Month 3 vs. Month 6 | 0.001 |
| | | | Month 3 vs. Month 9 | 0.001 |
| | | | Month 6 vs. Month 9 | 0.857 |
| Ileocecal valve enlargement present vs. absent | 0.0065 | 0.207 | Ileocecal valve enlargement present vs. absent | 0.34892 |

Table S3. Superfocus level 1.

| Pathway Level 1 | Time Point | Group | LDA | p-Value |
|---|------------|-------------|--------------|----------|
| Membrane Transport | Month 3 | Neg_Control | 3.33315 4 | 6.36E-06 |
| Cofactors, Vitamins, Prosthetic Groups, Pigments | Month 3 | Infected | 2.82187 2 | 0.022913 |
| Phages, Prophages, Transposable elements Plasmids | Month 3 | Neg_Control | 2.74275 4 | 0.000169 |
| Clustering based subsystems | Month 3 | Infected | 2.69593 1 | 0.001186 |
| Potassium metabolism | Month 3 | Neg_Control | 2.68032 | 7.54E-05 |
| RNA Metabolism | Month 3 | Infected | 2.65086 3 | 0.019879 |
| Virulence | Month 3 | Neg_Control | 2.64941 3 | 0.001114 |
| Stress Response | Month 3 | Infected | 2.58610 5 | 0.00846 |
| Respiration | Month 3 | Infected | 2.57890 4 | 0.025152 |
| Miscellaneous | Month 3 | Infected | 2.57625 | 0.04115 |
| Predictions based on plant prokaryote comparative analysis | Month 3 | Infected | 2.47444 8 | 0.015598 |
| Phages, Prophages Transposable elements | Month 3 | Neg_Control | 2.41896 7 | 0.007609 |
| Iron acquisition and metabolism | Month 3 | Neg_Control | 2.38718 6 | 0.022913 |
| Sulfur Metabolism | Month 3 | Infected | 2.36710 2 | 0.046781 |
| Virulence, Disease and Defense | Month 3 | Neg_Control | 2.35646 2 | 0.014847 |
| Regulation and Cell signaling | Month 3 | Neg_Control | 2.24122 6 | 0.01278 |
| Carbohydrates | Month 6 | Neg_Control | 4.72467 5 | 0.006332 |
| Protein Metabolism | Month 6 | Infected | 4.65829 | 9.88E-05 |
| Cofactors, Vitamins, Prosthetic Groups, Pigments | Month 6 | Infected | 4.33813 4 | 0.018525 |
| Nucleosides and Nucleotides | Month 6 | Neg_Control | 4.28415 9 | 1.28E-05 |
| RNA Metabolism | Month 6 | Infected | 4.26824 4 | 1.70E-05 |
| Respiration | Month 6 | Infected | 4.10926 1 | 0.003931 |
| Fatty Acids Lipids and Isoprenoids | Month 6 | Neg_Control | 3.75605 5 | 0.0202 |
| Phosphorus Metabolism | Month 6 | Neg_Control | 3.66710 3 | 2.41E-07 |

| | | | | |
|---|---------|-------------|--------------|----------|
| Phages, Prophages, Transposable elements, Plasmids | Month 6 | Infected | 3.52112 6 | 0.001005 |
| Motility and Chemotaxis | Month 6 | Neg_Control | 3.31324 1 | 3.19E-05 |
| Iron acquisition and metabolism | Month 6 | Neg_Control | 3.31270 5 | 0.001713 |
| Nitrogen Metabolism | Month 6 | Neg_Control | 3.31247 1 | 5.45E-08 |
| Virulence, Disease and Defense | Month 6 | Neg_Control | 2.97241 1 | 0.000673 |
| Metabolism of Aromatic Compounds | Month 6 | Neg_Control | 2.80881 1 | 0.015362 |
| Metabolism of Aromatic Compounds | Month 9 | Infected | 2.01245 6 | 0.00512 |
| Phosphorus Metabolism | Month 9 | Neg_Control | 2.30226 | 0.027486 |
| Nucleosides and Nucleotides | Month 9 | Neg_Control | 2.40555 7 | 0.025121 |
| Cell Wall and Capsule | Month 9 | Neg_Control | 2.45773 3 | 0.027486 |
| Motility and Chemotaxis | Month 9 | Neg_Control | 2.67589 | 6.16E-05 |

Table S4. Level 3 Pathways.

| Pathway | Timepoint | Group | LDA | p Value |
|---|-----------|-------------|----------|----------|
| Ton and Tol transport systems | Month 3 | Neg_Control | 3.397796 | 6.37E-07 |
| Cellulosome | Month 3 | Neg_Control | 2.852431 | 2.07E-06 |
| Conjugative transposon | Month 3 | Neg_Control | 2.765266 | 1.05E-05 |
| Bacteroidales | | | | |
| Mannose Metabolism | Month 3 | Neg_Control | 2.725044 | 2.47E-06 |
| DNA replication | Month 3 | Neg_Control | 2.496932 | 0.000711 |
| Multidrug Resistance Efflux | Month 3 | Neg_Control | 2.462527 | 0.000109 |
| Pumps | | | | |
| Peptidoglycan Biosynthesis | Month 3 | Neg_Control | 2.442976 | 0.000258 |
| Translation elongation factor G family | Month 3 | Neg_Control | 2.423262 | 2.81E-08 |

| | | | | |
|---|---------|-------------|----------|----------|
| Maltose and Maltodextrin Utilization | Month 3 | Infected | 2.346961 | 0.027579 |
| Hydrogenases | Month 3 | Infected | 2.319713 | 0.04115 |
| Aromatic amino acid interconversions with aryl acids | Month 3 | Infected | 2.31549 | 0.000297 |
| ABC transporter oligopeptide | Month 3 | Infected | 2.28926 | 0.018949 |
| TC3_A_1_5_1_ | | | | |
| Glycogen metabolism | Month 3 | Infected | 2.279149 | 0.048796 |
| Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Month 3 | Neg_Control | 2.260514 | 0.008917 |
| RNA polymerase bacterial Universal GTPases Ribosome LSU bacterial Formate hydrogenase Potassium homeostasis Histidine Degradation DNA Repair Base Excision Glycolysis and Gluconeogenesis Branched Chain Amino Acid Ammonia assimilation Single copy ribosomal proteins Fructooligosaccharides FOS and Raffinose Utilization | Month 3 | Infected | 2.24884 | 0.013439 |
| | Month 3 | Infected | 2.245888 | 0.00492 |
| | Month 3 | Infected | 2.245667 | 0.025152 |
| | Month 3 | Infected | 2.241678 | 0.002063 |
| | Month 3 | Neg_Control | 2.224955 | 8.12E-05 |
| | Month 3 | Neg_Control | 2.221785 | 0.02401 |
| | Month 3 | Infected | 2.215552 | 8.19E-06 |
| | Month 3 | Infected | 2.214637 | 0.001263 |
| | Month 3 | Neg_Control | 2.206725 | 0.02401 |
| Biosynthesis | | | | |
| | Month 3 | Neg_Control | 2.189119 | 0.027579 |
| | Month 3 | Infected | 2.187243 | 0.002191 |
| | Month 3 | Infected | 2.175969 | 0.014847 |

| | | | | |
|--|---------|-------------|----------|----------|
| Restriction Modification System | Month 3 | Neg_Control | 2.173854 | 0.00492 |
| Competence or DNA damage | Month 3 | Infected | 2.168221 | 0.000169 |
| inducible protein CinA and related protein families | | | | |
| Cobalt, zinc, cadmium resistance | | | | |
| Multi drug Resistance, Tripartite | Month 3 | Neg_Control | 2.14152 | 3.64E-07 |
| Systems Found in Gram Negative Bacteria | | | | |
| tRNA mods Archaea | Month 3 | Infected | 2.133358 | 0.003307 |
| DNA topoisomerases Type II ATP | Month 3 | Infected | 2.130945 | 0.000195 |
| dependent | | | | |
| CBSS_350688_3_peg_1509 | Month 3 | Infected | 2.129998 | 0.030204 |
| DNA repair bacterial UvrD and | Month 3 | Infected | 2.126481 | 3.99E-07 |
| related helicases | | | | |
| Fatty Acid Biosynthesis FASII | Month 3 | Neg_Control | 2.12425 | 0.013439 |
| Translation termination factors | Month 3 | Infected | 2.122664 | 0.000277 |
| bacterial | | | | |
| Respiratory dehydrogenases 1 | Month 3 | Neg_Control | 2.105421 | 0.000809 |
| Resistance to fluoroquinolones | Month 3 | Infected | 2.102699 | 0.001114 |
| DNA repair bacterial | Month 3 | Infected | 2.09602 | 0.001618 |
| DNA repair UvrABC system | Month 3 | Infected | 2.092834 | 0.001522 |
| At5g37530_CsdL protein family | Month 3 | Infected | 2.08672 | 0.002777 |

| | | | | |
|--|---------|-------------|----------|----------|
| Two cell division clusters | Month 3 | Infected | 2.070994 | 0.016383 |
| relating to chromosome partitioning | | | | |
| GroupII intron associated genes | | | | |
| At5g63290 | | | | |
| Heatshock dnaK gene cluster extended | Month 3 | Infected | 2.069919 | 0.005201 |
| EC3_4_11_Aminopeptidases | Month 3 | Neg_Control | 2.02731 | 0.001114 |
| Na translocating NADH quinone oxidoreductase and rnf_like group of electron transport complexes | Month 9 | Neg_Control | 2.339701 | 0.001069 |
| Maltose and Maltodextrin Utilization | Month 9 | Neg_Control | 2.28345 | 0.001636 |
| Glycogen metabolism | Month 9 | Neg_Control | 2.236263 | 0.020915 |
| Carbon monoxide induced hydrogenase | Month 9 | Neg_Control | 2.234515 | 0.003289 |
| Phosphate metabolism | Month 9 | Neg_Control | 2.227462 | 0.004849 |
| Flagellum | Month 9 | Neg_Control | 2.207519 | 2.89E-05 |
| Multidrug Resistance Efflux Pumps | Month 9 | Neg_Control | 2.182279 | 0.015757 |
| Flagellar motility | Month 9 | Neg_Control | 2.15775 | 1.26E-06 |
| CBSS_393121_3_peg_2760 | Month 9 | Neg_Control | 2.145124 | 0.001285 |
| Inositol catabolism | Month 9 | Infected | 2.142067 | 0.000437 |
| DeNovo Purine Biosynthesis | Month 9 | Neg_Control | 2.140344 | 0.001137 |
| Lactose and Galactose Uptake and Utilization | Month 9 | Neg_Control | 2.121676 | 0.010635 |
| Restriction Modification System | Month 9 | Neg_Control | 2.089932 | 0.015757 |
| Copper homeostasis | Month 9 | Infected | 2.086014 | 0.000645 |
| Omega_amidaseKE2 | Month 9 | Neg_Control | 2.073458 | 0.000944 |
| Translation elongation factor G family | Month 9 | Neg_Control | 2.067573 | 0.000208 |
| Lacto_N_Biosel and Galacto_N_Biose Metabolic Pathway | Month 9 | Neg_Control | 2.041006 | 0.000467 |
| Methionine Biosynthesis | Month 9 | Infected | 2.03467 | 0.000103 |
| Ni Fehydrogenase maturation | Month 9 | Infected | 2.01025 | 0.003108 |
| Xylose utilization | Month 9 | Neg_Control | 2.004691 | 0.032797 |

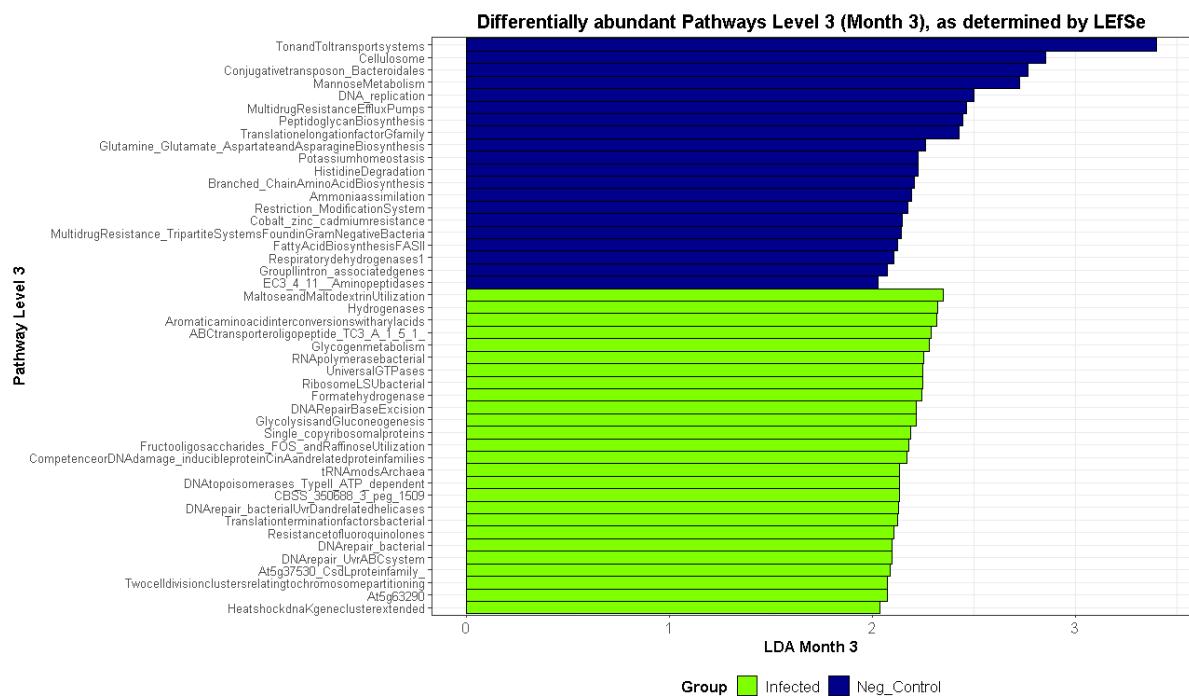


Figure S1. LEfSE analysis of Level 3 SUPER-FOCUS pathways in month 3.

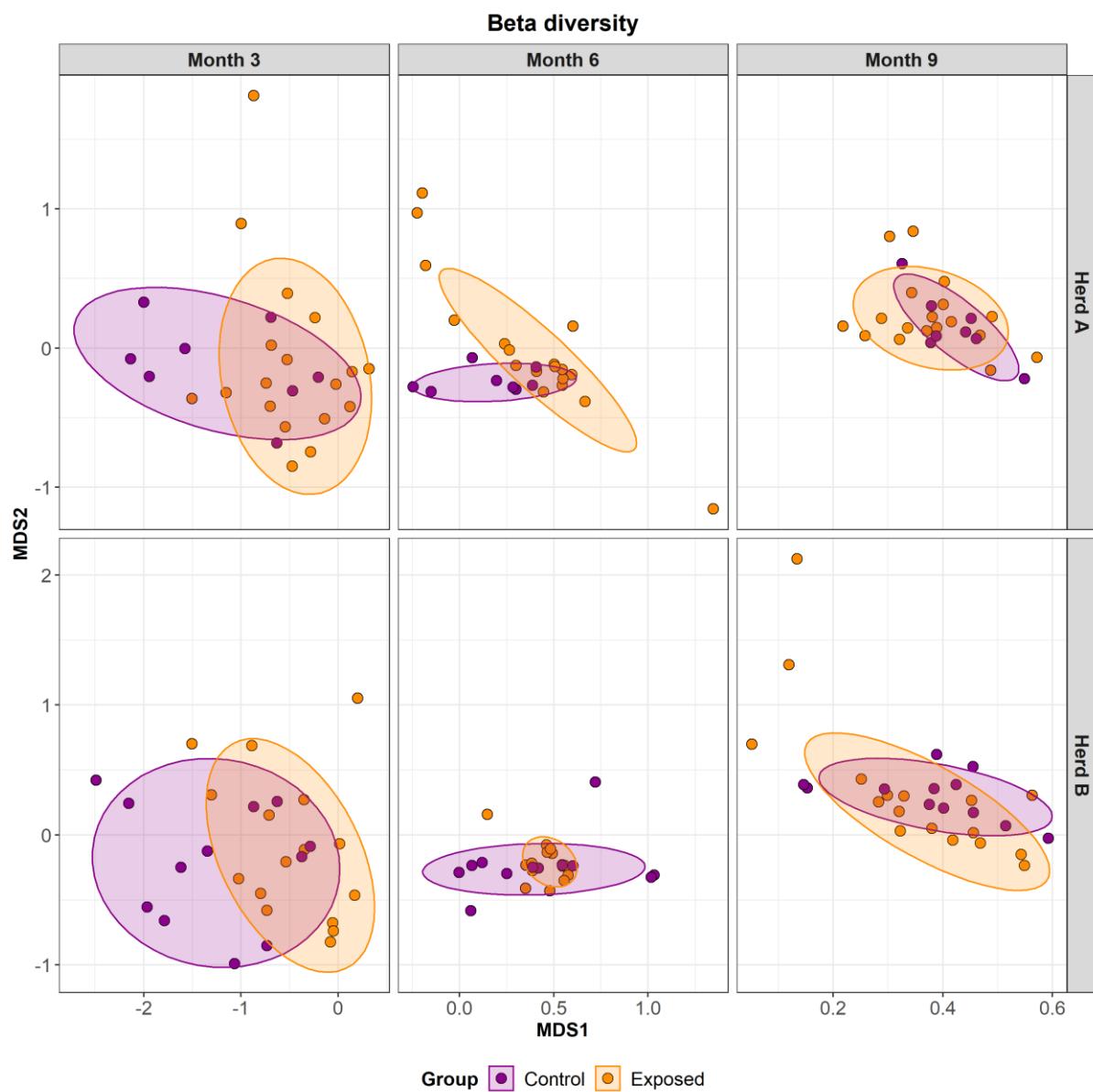


Figure S2. Bray-Curtis beta diversity among animals in both the exposed and control groups, across both time and herd. Month 6 shows the microbiome becoming more stable in herd B, where samples in the exposed group are most similar. However, results were non-significant.

Table S5. A summary of the positive and inconclusive IDEX ELISA results during the course of the experimental challenge study, with S/P% provided. Animals which remained negative are not included. This table has been adapted from Britton, 2017.

| Group | ID | Pre | M3 | M6 | M10 | M12 | M15 | M16 | M20 | M21 | M24 | M27 | M28 | M30 | M31 | M33 |
|------------|------|-----|----|----|-----------|-----|-----|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|
| Challenged | 2155 | - | - | - | - | - | - | ✓ 68.3 | ✓ 95.0 | ✓ 55.6 | ✓ 82.6 | ✓ 86.9 | ✓ 109.4 | - | - | - |
| | 2176 | - | - | - | - | - | - | - | ✓ 56.8 | - | I 52.5 | - | - | - | - | - |
| | 2194 | - | - | - | - | - | - | I 50.2 | - | I 51.4 | ✓ 60.7 | - | I 48.7 | - | I 49.2 | - |
| | 2199 | - | - | - | - | - | - | - | ✓ 61.6 | I 50.2 | - | | | | | |
| | 2201 | - | - | - | - | - | - | - | I 48.4 | - | - | - | - | - | - | - |
| | 2390 | - | - | - | - | - | - | - | ✓ 63.0 | ✓ 63.0 | - | ✓ 64.8 | ✓ 67.6 | I 50.4 | - | - |
| | 2402 | - | - | - | - | - | - | ✓ 93.9 | ✓ 84.9 | ✓ 68.7 | - | ✓ 84.8 | ✓ 99.0 | ✓ 70.8 | - | - |
| | 2413 | - | - | - | - | - | - | - | - | - | - | I 45.3 | - | - | - | - |
| | 2415 | - | - | - | - | - | - | - | I 50.0 | - | - | - | - | - | - | - |
| | 2420 | - | - | - | - | - | - | - | ✓ 68.1 | ✓ 76.1 | ✓ 70.8 | ✓ 67.2 | ✓ 85.2 | ✓ 56.8 | - | ✓ 81.8 |
| Control | 2170 | - | - | - | ✓ 56.2 | - | | | | | | | | | | |
| | 2454 | - | - | - | - | - | - | - | - | - | - | ✓ 93.4 | ✓ 78.3 | ✓ 82.5 | ✓ 68 | ✓ 64.8 |

Pre = preimmune testing; M = month post-challenge; ✓ = Positive, - = Negative; I = Inconclusive. Blacked out cells represent animals that were necropsied during the previous timepoint.

Table S6. IGRA PPDj ΔOD readings from animals at 3 months post inoculation.

| Group | ID | PPDj | | ID | PPDj | | ID | PPDj |
|------------|------|-------|--|------|-------|--|------|--------|
| Challenged | 2149 | 0.369 | | 2194 | 0.195 | | 2403 | 0.012 |
| | 2152 | 2.947 | | 2199 | 0.024 | | 2404 | 0.315 |
| | 2154 | 1.817 | | 2200 | 0.202 | | 2407 | 0.161 |
| | 2155 | 0.005 | | 2201 | 1.240 | | 2408 | 0.439 |
| | 2158 | 0.248 | | 2209 | 0.165 | | 2410 | 0.116 |
| | 2162 | 0.115 | | 2212 | 0.307 | | 2412 | 0.193 |
| | 2164 | 0.087 | | 2387 | 0.183 | | 2413 | 0.051 |
| | 2169 | 0.141 | | 2388 | 1.898 | | 2415 | 0.148 |
| | 2176 | 0.222 | | 2390 | 0.973 | | 2416 | 0.204 |
| | 2182 | 0.512 | | 2392 | 0.121 | | 2420 | 0.411 |
| | 2183 | 0.072 | | 2393 | 1.635 | | 2422 | 0.140 |
| | 2185 | 0.061 | | 2402 | 0.220 | | | |
| | ID | PPDj | | ID | PPDj | | ID | PPDj |
| Control | 2163 | 0.254 | | 2218 | 0.011 | | 2401 | -0.010 |
| | 2168 | 2.636 | | 2389 | 0.166 | | 2405 | 0.681 |
| | 2170 | 0.022 | | 2391 | 0.019 | | 2406 | 0.398 |
| | 2172 | 0.148 | | 2395 | 1.203 | | 2409 | 0.062 |
| | 2175 | 0.324 | | 2397 | 0.068 | | 2425 | 0.191 |
| | 2213 | 1.377 | | 2398 | 0.129 | | 2454 | 0.771 |
| | 2215 | 0.212 | | 2399 | 0.646 | | | |