

Dietary contamination with neonicotinoid (Clothianidin) gradient triggers specific dysbiosis signatures of microbiota activity along the honeybee (*Apis mellifera*) digestive tract

Supplementary information file

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Table S1 : Information regarding the reads tracking process using *dada2* and the number of ASVs per sample

Sample Name	Experimental group	Input reads	Filtration step	Dereplication step	Chimera removal	Number of ASVs
1-1A	Control	33613	21532	21464	18325	615
1-1V	Control	25563	15537	15486	13298	497
1-1X	Control	26019	14838	14815	13229	326
1-2A	Control	19322	6228	6108	5674	270
1-2V	Control	41578	20508	20459	17929	197
1-2X	Control	18821	11514	11480	10507	252
2-1A	Control	21870	13824	13764	11045	581
2-1V	Control	29357	17716	17631	14891	623
2-1X	Control	24504	11738	11708	9616	399
2-2A	Control	25328	16046	15951	14558	575
2-2V	Control	26700	11595	11547	9540	578
2-2X	Control	22684	11957	11916	10189	702
3-1A	Control	27932	14444	14409	11895	480
3-1V	Control	27825	18792	18753	16161	402
3-1X	Control	25342	16878	16811	13388	726
3-2A	Control	23429	15223	15134	10520	808
3-2V	Control	20283	6707	6662	5136	527
3-2X	Control	26392	14378	14300	10965	832
4-1A	Control	22348	14183	14111	10820	849
4-1V	Control	15	5	2	2	2
4-1X	Control	24007	12648	12604	11141	499
4-2A	Control	23432	14679	14625	11928	753
4-2V	Control	21944	6905	6866	5312	560
4-2X	Control	28505	9743	9702	8292	559

5-1A	Control	25893	14671	14621	11619	746
5-1V	Control	35263	10951	10909	9718	383
5-1X	Control	45860	18083	18025	16607	400
5-2A	Control	22718	14215	14140	10731	919
5-2V	Control	28764	13177	13127	10221	401
5-2X	Control	20123	10143	10077	8106	486
6-1A	Clothianidin_0.1	27584	18413	18320	15116	796
6-1V	Clothianidin_0.1	37584	14145	14084	11401	781
6-1X	Clothianidin_0.1	39917	16315	16238	13145	718
6-2A	Clothianidin_0.1	16233	7996	7941	7052	436
6-2V	Clothianidin_0.1	32763	14725	14588	11507	767
6-2X	Clothianidin_0.1	26553	12548	12436	10746	574
7-1A	Clothianidin_0.1	23238	13248	13187	10411	765
7-1V	Clothianidin_0.1	10581	6855	6832	5529	483
7-1X	Clothianidin_0.1	20639	11033	10957	7994	775
7-2A	Clothianidin_0.1	24471	13888	13845	10415	533
7-2V	Clothianidin_0.1	26217	17021	16944	13935	704
7-2X	Clothianidin_0.1	39759	18530	18394	13410	929
8-1A	Clothianidin_0.1	29541	19188	19092	16497	531
8-1V	Clothianidin_0.1	22913	14000	13920	11699	665

8-1X	Clothianidin_0. 1	22604	5054	5038	4377	352
8-2A	Clothianidin_0. 1	28043	12532	12441	9078	780
8-2V	Clothianidin_0. 1	22618	8179	8128	5578	648
8-2X	Clothianidin_0. 1	26242	11590	11539	10032	434
9-1A	Clothianidin_0. 1	30002	19123	19045	15665	616
9-1V	Clothianidin_0. 1	31172	12871	12760	10189	830
9-1X	Clothianidin_0. 1	24606	13738	13640	11342	805
9-2A	Clothianidin_0. 1	22372	14186	14081	10216	853
9-2V	Clothianidin_0. 1	24507	11185	11131	9281	693
9-2X	Clothianidin_0. 1	27768	16513	16422	12872	827
10-1A	Clothianidin_0. 1	20909	13211	13122	9341	816
10-1V	Clothianidin_0. 1	34691	14555	14502	11965	539
10-1X	Clothianidin_0. 1	34273	11859	11733	10087	593
10-2A	Clothianidin_0. 1	21256	12227	12148	9216	640
10-2V	Clothianidin_0. 1	20466	8383	8342	5872	675
10-2X	Clothianidin_0. 1	28865	13911	13856	11737	752
11-1A	Clothianidin_1	41975	23960	23802	17786	1093
11-1V	Clothianidin_1	24817	9966	9908	7525	786
11-1X	Clothianidin_1	30467	14297	14210	11164	754

11-2A	Clothianidin_1	32112	18671	18540	13215	991
11-2V	Clothianidin_1	38629	20572	20452	15045	1043
11-2X	Clothianidin_1	34542	17916	17829	14421	863
12-1A	Clothianidin_1	21659	13446	13354	8636	881
12-1V	Clothianidin_1	38808	12745	12671	10170	676
12-1X	Clothianidin_1	33594	16764	16590	12547	811
12-2A	Clothianidin_1	18249	11080	11026	8559	785
12-2V	Clothianidin_1	23170	11395	11337	7446	714
12-2X	Clothianidin_1	25247	11731	11664	10085	500
13-1A	Clothianidin_1	15651	9447	9393	6961	799
13-1V	Clothianidin_1	23720	10964	10921	8437	681
13-1X	Clothianidin_1	15282	8049	8007	6673	494
13-2A	Clothianidin_1	17717	12175	12103	9244	704
13-2V	Clothianidin_1	18047	10469	10424	8151	635
13-2X	Clothianidin_1	17316	9906	9859	8609	528
14-1A	Clothianidin_1	28221	17378	17288	13924	575
14-1V	Clothianidin_1	21136	10562	10514	8348	455
14-1X	Clothianidin_1	21994	9321	9256	7589	418
14-2A	Clothianidin_1	15190	9606	9538	7173	493
14-2V	Clothianidin_1	24423	13912	13814	11097	504
14-2X	Clothianidin_1	17460	8017	7973	6846	354
15-1A	Clothianidin_1	10945	6539	6518	5485	395
15-1V	Clothianidin_1	21205	10765	10695	7798	587
15-1X	Clothianidin_1	21505	10931	10866	8714	518
15-2A	Clothianidin_1	28260	17115	16975	12212	902
15-2V	Clothianidin_1	22502	12827	12774	10780	515
15-2X	Clothianidin_1	27472	15506	15435	12643	690

16-1A	Clothianidin_10	16004	10573	10490	7204	719
16-1V	Clothianidin_10	19102	10672	10596	8107	632
16-1X	Clothianidin_10	18991	11496	11439	9227	645
16-2A	Clothianidin_10	17387	11090	11023	8658	604
16-2V	Clothianidin_10	21864	10631	10568	8483	589
16-2X	Clothianidin_10	26506	11667	11595	9095	684
17-1A	Clothianidin_10	33351	18797	18697	13507	907
17-1V	Clothianidin_10	38559	22461	22316	16346	1071
17-1X	Clothianidin_10	26032	11471	11380	8108	875
17-2A	Clothianidin_10	13990	8648	8596	6033	761
17-2V	Clothianidin_10	35580	15248	15128	10299	776
17-2X	Clothianidin_10	95943	26069	25890	18959	1000
18-1A	Clothianidin_10	27329	17448	17342	14320	658
18-1V	Clothianidin_10	7857	4670	4638	3276	601
18-1X	Clothianidin_10	25536	14914	14837	10498	983
18-2A	Clothianidin_10	21676	10783	10738	8449	665
18-2V	Clothianidin_10	27071	14799	14661	9257	1089
18-2X	Clothianidin_10	33271	13416	13335	10560	743
19-1A	Clothianidin_10	31118	14356	14254	9577	1049
19-1V	Clothianidin_10	23864	10494	10421	7599	954
19-1X	Clothianidin_10	27201	12648	12542	8529	702
19-2A	Clothianidin_10	11745	6436	6411	5284	542
19-2V	Clothianidin_10	26463	16568	16490	12650	778
19-2X	Clothianidin_10	26445	15723	15644	12266	965
20-1A	Clothianidin_10	18961	11581	11534	8952	558
20-1V	Clothianidin_10	32368	12709	12604	9885	783
20-1X	Clothianidin_10	49720	27283	27047	19112	1188

20-2A	Clothianidin_10	26318	14951	14873	10688	819
20-2V	Clothianidin_10	43259	19891	19761	13844	958
20-2X	Clothianidin_10	22924	12722	12638	7639	973

Table S2: Cox Proportional Hazards model comparisons between the survival of honeybees exposed vs. unexposed to clothianidin for 28 days

Days	6	7	14	21	22	25	26	27	28
Ctrl vs:									
[0.1 ppb]	< 0.05	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001
[1 ppb]	-	-	< 0.05	-	< 0.001	< 0.05	< 0.05	-	0.001
[10 ppb]	< 0.001	-	-	-	-	-	-	< 0.05	< 0.05

Significant

P-values < 0.05 (orange);

P-values = 0.001 (green);

P-values < 0.001 (yellow).

Table S3: Syrup consumption average levels per honeybee between the experimental groups compared to the control group overtime

Treatment	[0.1 ppb]	[1 ppb]	[10 ppb]
Control	0.001	< 0.001	< 0.001

Wilcoxon rank sum test

Significant p-values < 0.05

Table S4: Syrup consumption average levels per honeybee between the experimental groups compared to the control group at specific time points

Days	6	8	11	13	15	25	
Ctrl vs:							
[0.1 ppb]	< 0.05	-	-	-		-	-
[1 ppb]	-				-	< 0.05	
[10 ppb]	-	-	-	-	-	-	-

Kruskal-Wallis test

Significant p-values < 0.05

Table S5: Mean quantification of the clothianidin levels (ng/mL per bee) with the standard deviation (S.D.) in the honeybee gut

Concentration	Mean (S.D.) Day 7	R.T.	Mean (S.D.) Day 14	R.T.	Mean (S.D.) Day 21	R.T.	Mean (S.D.) Day 28	R.T.
Control	-	-	-	-	-	-	-	-
[0.1 ppb]	0.013 (0.0046)	6.26	0.009 (0.0023)	6.24	0.008 (0.0007)	6.12	0.006 (0.0039)	6.20
[1 ppb]	0.004 (0.0009)	6.19	0.007 (0.0017)	6.22	0.005 (0.0047)	6.25	0.005 (0.0038)	6.09
[10 ppb]	0.009 (0.0007)	6.20	0.021 (0.0033)	6.19	0.011 (0.0061)	6.17	0.015 (0.0063)	6.09

R.T. (Retention Time)

Table S6 : Total taxonomic distribution of active ASVs in midgut exposed at 0 ppb

ASV Species	ASV activity
<i>[Clostridium] saccharolyticum</i>	1
<i>Achromobacter insolitus</i>	23
<i>Actinomyces johnsonii</i>	6
<i>Arthrobacter russicus</i>	10
<i>Bacteroides caccae</i>	1
<i>Bacteroides plebeius DSM 17135</i>	4
<i>Bartonella apis</i>	6004
<i>Bifidobacterium asteroides</i>	31
<i>Bifidobacterium callitrichos DSM 23973</i>	1
<i>Bifidobacterium coryneforme</i>	44
<i>Bombella apis</i>	44
<i>Bosea vaviloviae</i>	7
<i>Bradyrhizobium oligotrophicum S58</i>	1
<i>Bradyrhizobium vignae</i>	27
<i>Brevundimonas albigilva</i>	56
<i>Brevundimonas lenta</i>	12
<i>Chryseobacterium hispanicum</i>	1
<i>Delftia acidovorans</i>	102
<i>Dermacoccus profundi</i>	4
<i>Dialister invisus</i>	6
<i>Escherichia fergusonii ATCC 35469</i>	1

<i>Faecalibacterium prausnitzii</i>	1
<i>Frischella perrara</i>	25666
<i>Gilliamella apicola</i>	4405
<i>Gilliamella bombicola</i>	1
<i>Gilliamella intestini</i>	17
<i>Intestinibacter bartlettii</i>	82
<i>Lachnoclostridium pacaense</i>	18
<i>Lactobacillus apis</i>	18339
<i>Lactobacillus helsingborgensis</i>	3718
<i>Lactobacillus kimbladii</i>	1843
<i>Lactobacillus kullabergensis</i>	133
<i>Lactobacillus kunkeei</i>	8
<i>Lactobacillus mellifer</i>	111
<i>Lactobacillus mellis</i>	1077
<i>Lactobacillus melliventris</i>	635
<i>Leifsonia shinshuensis</i>	1
<i>Lysinibacillus parviboronicapiens</i>	8
<i>Moraxella osloensis</i>	36
<i>Morganella morganii subsp. sibonii</i>	6
<i>Oceanobacillus chironomi</i>	4
<i>Parasaccharibacter apium</i>	270
<i>Pediococcus stilesii</i>	180
<i>Pelomonas saccharophila</i>	37
<i>Pseudaminobacter manganicus</i>	155
<i>Pseudomonas canadensis</i>	50
<i>Pseudomonas cerasi</i>	74

<i>Pseudomonas songnenensis</i>	29
<i>Pseudoxanthomonas jiangsuensis</i>	27
<i>Psychrobacter cryohalolentis</i> K5	82
<i>Ralstonia pickettii</i>	165
<i>Romboutsia timonensis</i>	519
<i>Roseburia faecis</i>	770
<i>Rothia dentocariosa</i> ATCC 17931	162
<i>Shinella fusca</i>	2138
<i>Skermanella aerolata</i>	848
<i>Snodgrassella alvi</i> wkB2	10265
<i>Sphingomonas echinoides</i>	3628
<i>Staphylococcus epidermidis</i>	9005
<i>Streptococcus oralis</i> subsp. <i>dentisani</i>	6983
<i>Streptococcus salivarius</i>	7593
<i>Unassigned</i>	10788

Table S7: Total taxonomic distribution of active ASVs in midgut exposed at 0.1 ppb

ASV Species	ASV activity
<i>[Clostridium] saccharolyticum</i>	1
<i>Bacillus licheniformis</i>	1
<i>Bacillus wiedmannii</i>	2
<i>Bacteroides caccae</i>	2
<i>Bacteroides plebeius</i> DSM 17135	1
<i>Bartonella apis</i>	6052
<i>Bifidobacterium asteroides</i>	12
<i>Bifidobacterium callitrichos</i> DSM 23973	1
<i>Bifidobacterium coryneforme</i>	23
<i>Bombella apis</i>	236
<i>Bradyrhizobium oligotrophicum</i> S58	4
<i>Bradyrhizobium vignae</i>	4
<i>Dermaococcus profundus</i>	10
<i>Dialister invisus</i>	4
<i>Frischella perrara</i>	9582
<i>Gemmiger formicilis</i>	0
<i>Gilliamella apicola</i>	2772
<i>Intestinibacter bartlettii</i>	2
<i>Lachnoclostridium pacaense</i>	20
<i>Lactobacillus apis</i>	3492
<i>Lactobacillus helsingborgensis</i>	480
<i>Lactobacillus kimbladii</i>	89
<i>Lactobacillus kullabergensis</i>	19

<i>Lactobacillus kunkeei</i>	1
<i>Lactobacillus mellifer</i>	42
<i>Lactobacillus mellis</i>	185
<i>Lactobacillus melliventris</i>	487
<i>Lysinibacillus parviboronicapiens</i>	10
<i>Methylobacterium populi BJ001</i>	1
<i>Oceanobacillus chironomi</i>	28
<i>Parasaccharibacter apium</i>	1
<i>Pediococcus stilesii</i>	1
<i>Pelomonas saccharophila</i>	71
<i>Phascolarctobacterium faecium</i>	114
<i>Pseudaminobacter manganicus</i>	9
<i>Pseudomonas canadensis</i>	254
<i>Pseudomonas cerasi</i>	114
<i>Pseudomonas songnenensis</i>	146
<i>Pseudoxanthomonas jiangsuensis</i>	17
<i>Psychrobacter cryohalolentis K5</i>	440
<i>Ralstonia insidiosa</i>	232
<i>Ralstonia pickettii</i>	436
<i>Romboutsia timonensis</i>	994
<i>Roseburia faecis</i>	1577
<i>Rothia dentocariosa ATCC 17931</i>	171
<i>Shinella fusca</i>	4467
<i>Skermanella aerolata</i>	2
<i>Snodgrassella alvi wkb2</i>	16055
<i>Sphingomonas echinoides</i>	8777

<i>Staphylococcus epidermidis</i>	11709
<i>Streptococcus oralis subsp. dentisani</i>	9801
<i>Streptococcus salivarius</i>	19617
<i>Unassigned</i>	12379

Table S8: Total taxonomic distribution of active ASVs in midgut exposed at 1 ppb

ASV Species	ASV activity
<i>Actinomyces johnsonii</i>	3
<i>Bacillus wiedmannii</i>	2
<i>Bacteroides caccae</i>	1
<i>Bacteroides dorei</i>	4
<i>Bartonella apis</i>	2029
<i>Bifidobacterium asteroides</i>	33
<i>Bifidobacterium callitrichos DSM 23973</i>	6
<i>Bifidobacterium coryneforme</i>	111
<i>Blautia wexlerae DSM 19850</i>	1
<i>Bombella apis</i>	118
<i>Bradyrhizobium oligotrophicum S58</i>	8
<i>Bradyrhizobium vignae</i>	6
<i>Dermacoccus profundi</i>	6
<i>Escherichia fergusonii ATCC 35469</i>	4
<i>Faecalibacterium prausnitzii</i>	1
<i>Flavobacterium acidificum</i>	15
<i>Frischella perrara</i>	1931
<i>Gemmiger formicilis</i>	1

<i>Gilliamella apicola</i>	2077
<i>Intestinibacter bartlettii</i>	2
<i>Lactobacillus apis</i>	10196
<i>Lactobacillus helsingborgensis</i>	1562
<i>Lactobacillus kimbladii</i>	132
<i>Lactobacillus kullabergensis</i>	16
<i>Lactobacillus kunkeei</i>	31
<i>Lactobacillus mellifer</i>	28
<i>Lactobacillus mellis</i>	303
<i>Lactobacillus melliventris</i>	209
<i>Leifsonia shinshuensis</i>	5
<i>Lysinibacillus parviboronicapiens</i>	9
<i>Methylobacterium populi BJ001</i>	1
<i>Oceanobacillus chironomi</i>	3
<i>Parasaccharibacter apium</i>	275
<i>Pediococcus stilesii</i>	2
<i>Pelomonas saccharophila</i>	73
<i>Phascolarctobacterium faecium</i>	7
<i>Pseudaminobacter manganicus</i>	26
<i>Pseudomonas canadensis</i>	180
<i>Pseudomonas cerasi</i>	67
<i>Pseudomonas songnenensis</i>	30
<i>Pseudoxanthomonas jiangsuensis</i>	86
<i>Psychrobacter cryohalolentis K5</i>	294
<i>Ralstonia insidiosa</i>	369
<i>Ralstonia pickettii</i>	322

<i>Romboutsia timonensis</i>	1226
<i>Roseburia faecis</i>	1137
<i>Rothia dentocariosa ATCC 17931</i>	164
<i>Shinella fusca</i>	6860
<i>Skermanella aerolata</i>	6777
<i>Snodgrassella alvi wkb2</i>	15599
<i>Sphingomonas echinoides</i>	13694
<i>Staphylococcus epidermidis</i>	8321
<i>Streptococcus oralis subsp. dentisani</i>	1493
<i>Streptococcus salivarius</i>	23362
<i>Unassigned</i>	13742

Table S9: Total taxonomic distribution of active ASVs in midgut exposed at 10 ppb

ASV Species	ASV activity
<i>Achromobacter insolitus</i>	4
<i>Actinomyces johnsonii</i>	1
<i>Bacillus wiedmannii</i>	54
<i>Bartonella apis</i>	5560
<i>Bifidobacterium asteroides</i>	139
<i>Bifidobacterium callitrichos DSM 23973</i>	6
<i>Bifidobacterium coryneforme</i>	138
<i>Bombella apis</i>	2
<i>Bradyrhizobium vignae</i>	2
<i>Delftia acidovorans</i>	5
<i>Dermacoccus profundi</i>	11

<i>Faecalibacterium prausnitzii</i>	2
<i>Frischella perrara</i>	7093
<i>Gilliamella apicola</i>	16389
<i>Gilliamella bombicola</i>	4
<i>Gilliamella intestini</i>	5
<i>Intestinibacter bartlettii</i>	2
<i>Lactobacillus apis</i>	24330
<i>Lactobacillus helsingborgensis</i>	3054
<i>Lactobacillus kimbladii</i>	1081
<i>Lactobacillus kullabergensis</i>	244
<i>Lactobacillus kunkeei</i>	9
<i>Lactobacillus mellifer</i>	112
<i>Lactobacillus mellis</i>	760
<i>Lactobacillus melliventris</i>	1753
<i>Lawsonella clevelandensis</i>	4
<i>Leifsonia shinshuensis</i>	1
<i>Parasaccharibacter apium</i>	1161
<i>Pediococcus stilesii</i>	24
<i>Pelomonas saccharophila</i>	117
<i>Pseudaminobacter manganicus</i>	102
<i>Pseudomonas canadensis</i>	95
<i>Pseudomonas cerasi</i>	191
<i>Pseudomonas songnenensis</i>	22
<i>Pseudoxanthomonas jiangsuensis</i>	8
<i>Psychrobacter cryohalolentis K5</i>	185
<i>Ralstonia insidiosa</i>	9

<i>Ralstonia pickettii</i>	168
<i>Romboutsia timonensis</i>	772
<i>Roseburia faecis</i>	1487
<i>Rothia dentocariosa ATCC 17931</i>	1
<i>Shinella fusca</i>	2589
<i>Skermanella aerolata</i>	1159
<i>Snodgrassella alvi wkb2</i>	10116
<i>Sphingomonas echinoides</i>	3775
<i>Staphylococcus epidermidis</i>	9959
<i>Streptococcus oralis subsp. dentisani</i>	3399
<i>Streptococcus salivarius</i>	10126
<i>Unassigned</i>	14842

Table S10 : Total taxonomic distribution of active ASVs in ileum exposed at 0 ppb

ASV Species	ASV activity
<i>Achromobacter insolitus</i>	3
<i>Acinetobacter defluvii</i>	2
<i>Arthrobacter russicus</i>	5
<i>Bacillus wiedmannii</i>	1
<i>Bacteroides caccae</i>	3
<i>Bartonella apis</i>	5211
<i>Bifidobacterium asteroides</i>	10
<i>Bifidobacterium callitrichos DSM 23973</i>	1
<i>Bifidobacterium coryneforme</i>	48
<i>Blautia wexlerae DSM 19850</i>	21

<i>Bombella apis</i>	39
<i>Bradyrhizobium vignae</i>	4
<i>Brevundimonas albigilva</i>	4
<i>Dermacoccus profundus</i>	2
<i>Escherichia fergusonii</i> ATCC 35469	1
<i>Faecalibacterium prausnitzii</i>	3
<i>Frischella perrara</i>	23313
<i>Gilliamella apicola</i>	5795
<i>Gilliamella bombicola</i>	6
<i>Gilliamella intestini</i>	3
<i>Lachnoclostridium pacaense</i>	4
<i>Lactobacillus apis</i>	23973
<i>Lactobacillus helsingborgensis</i>	3255
<i>Lactobacillus kimbladii</i>	580
<i>Lactobacillus kullabergensis</i>	54
<i>Lactobacillus kunkeei</i>	3
<i>Lactobacillus mellifer</i>	98
<i>Lactobacillus mellis</i>	609
<i>Lactobacillus melliventris</i>	641
<i>Lactobacillus rogosae</i>	1
<i>Lysinibacillus parviboronicapiens</i>	4
<i>Oceanobacillus chironomi</i>	3
<i>Parasaccharibacter apium</i>	17
<i>Pediococcus stilesii</i>	159
<i>Pelomonas saccharophila</i>	21
<i>Pseudaminobacter manganicus</i>	1

<i>Pseudomonas canadensis</i>	82
<i>Pseudomonas cerasi</i>	35
<i>Pseudomonas songnenensis</i>	71
<i>Pseudoxanthomonas jiangsuensis</i>	5
<i>Psychrobacter cryohalolentis K5</i>	26
<i>Ralstonia pickettii</i>	428
<i>Romboutsia timonensis</i>	511
<i>Roseburia faecis</i>	437
<i>Rothia dentocariosa ATCC 17931</i>	85
<i>Shinella fusca</i>	2336
<i>Skermanella aerolata</i>	235
<i>Snodgrassella alvi wkb2</i>	19553
<i>Sphingomonas echinoides</i>	8825
<i>Staphylococcus epidermidis</i>	4802
<i>Streptococcus oralis subsp. dentisani</i>	1645
<i>Streptococcus salivarius</i>	12975
<i>Unassigned</i>	8837

Table S11 : Total taxonomic distribution of active ASVs in ileum exposed at 0.1 ppb

ASV Species	ASV activity
<i>Achromobacter insolitus</i>	3
<i>Acinetobacter defluvii</i>	6
<i>Actinomyces johnsonii</i>	1
<i>Bacillus wiedmannii</i>	14
<i>Bacteroides caccae</i>	2
<i>Bacteroides dorei</i>	2

<i>Bartonella apis</i>	7950
<i>Bifidobacterium asteroides</i>	15
<i>Bifidobacterium callitrichos</i> DSM 23973	3
<i>Bifidobacterium coryneforme</i>	110
<i>Bradyrhizobium oligotrophicum</i> S58	1
<i>Bradyrhizobium vignae</i>	10
<i>Brevundimonas albigilva</i>	2
<i>Chryseobacterium hispanicum</i>	1
<i>Delftia acidovorans</i>	8
<i>Dermacoccus profundi</i>	6
<i>Flavobacterium acidificum</i>	7
<i>Frischella perrara</i>	9153
<i>Gilliamella apicola</i>	5041
<i>Gilliamella bombicola</i>	4
<i>Gilliamella intestini</i>	11
<i>Lachnoclostridium pacaense</i>	4
<i>Lactobacillus apis</i>	29174
<i>Lactobacillus helsingborgensis</i>	4113
<i>Lactobacillus kimbladii</i>	446
<i>Lactobacillus kullabergensis</i>	80
<i>Lactobacillus mellifer</i>	83
<i>Lactobacillus mellis</i>	311
<i>Lactobacillus melliventris</i>	1320
<i>Lawsonella clevelandensis</i>	3
<i>Leifsonia shinshuensis</i>	1
<i>Lysinibacillus parviboronicapiens</i>	3

<i>Methylobacterium populi</i> BJ001	5
<i>Morganella morganii</i> subsp. <i>sibonii</i>	2
<i>Parasaccharibacter apium</i>	1
<i>Pediococcus stilesii</i>	216
<i>Pelomonas saccharophila</i>	23
<i>Phascolarctobacterium faecium</i>	122
<i>Pseudaminobacter manganicus</i>	11
<i>Pseudomonas canadensis</i>	95
<i>Pseudomonas cerasi</i>	131
<i>Pseudomonas songnenensis</i>	53
<i>Pseudoxanthomonas jiangsuensis</i>	252
<i>Psychrobacter cryohalolentis</i> K5	186
<i>Ralstonia insidiosa</i>	252
<i>Ralstonia pickettii</i>	886
<i>Romboutsia timonensis</i>	275
<i>Roseburia faecis</i>	430
<i>Rothia dentocariosa</i> ATCC 17931	2316
<i>Shinella fusca</i>	2918
<i>Skermanella aerolata</i>	64
<i>Snodgrassella alvi</i> wkB2	17322
<i>Sphingomonas echinoides</i>	6272
<i>Staphylococcus epidermidis</i>	5320
<i>Streptococcus oralis</i> subsp. <i>dentisani</i>	2809
<i>Streptococcus salivarius</i>	12297
Unassigned	9726

Table S12 : Total taxonomic distribution of active ASVs in ileum exposed at 1 ppb

ASV Species	ASV activity
<i>[Clostridium] saccharolyticum</i>	5
<i>Achromobacter insolitus</i>	6
<i>Arthrobacter russicus</i>	1
<i>Bacillus wiedmannii</i>	182
<i>Bacteroides caccae</i>	1
<i>Bacteroides dorei</i>	5
<i>Bartonella apis</i>	4793
<i>Bifidobacterium asteroides</i>	22
<i>Bifidobacterium callitrichos DSM 23973</i>	4
<i>Bifidobacterium coryneforme</i>	49
<i>Bradyrhizobium oligotrophicum S58</i>	7
<i>Bradyrhizobium vignae</i>	39
<i>Brevundimonas albigilva</i>	6
<i>Brevundimonas lenta</i>	9
<i>Chryseobacterium hispanicum</i>	6
<i>Delftia acidovorans</i>	10
<i>Dermaococcus profundus</i>	3
<i>Dialister invisus</i>	5
<i>Escherichia fergusonii ATCC 35469</i>	4
<i>Flavobacterium acidificum</i>	2
<i>Frischella perrara</i>	16368
<i>Gemmiger formicilis</i>	1
<i>Gilliamella apicola</i>	1903

<i>Gilliamella bombicola</i>	1
<i>Lachnoclostridium pacaense</i>	5
<i>Lactobacillus apis</i>	15168
<i>Lactobacillus helsingborgensis</i>	2745
<i>Lactobacillus kimbladii</i>	237
<i>Lactobacillus kullabergensis</i>	20
<i>Lactobacillus kunkeei</i>	15
<i>Lactobacillus mellifer</i>	34
<i>Lactobacillus mellis</i>	334
<i>Lactobacillus melliventris</i>	611
<i>Lactobacillus rogosae</i>	1
<i>Lawsonella clevelandensis</i>	2
<i>Lysinibacillus parviboronicapiens</i>	2
<i>Methylobacterium populi BJ001</i>	8
<i>Morganella morganii subsp. sibonii</i>	6
<i>Oceanobacillus chironomi</i>	2
<i>Parasaccharibacter apium</i>	339
<i>Pediococcus stilesii</i>	76
<i>Pelomonas saccharophila</i>	11
<i>Phascolarctobacterium faecium</i>	16
<i>Phascolarctobacterium succinatutens</i>	122
<i>Pseudaminobacter manganicus</i>	5
<i>Pseudomonas canadensis</i>	54
<i>Pseudomonas cerasi</i>	35
<i>Pseudomonas songnenensis</i>	20
<i>Pseudoxanthomonas jiangsuensis</i>	31

<i>Psychrobacter cryohalolentis</i> K5	95
<i>Ralstonia insidiosa</i>	15
<i>Ralstonia pickettii</i>	150
<i>Romboutsia timonensis</i>	450
<i>Roseburia faecis</i>	626
<i>Shinella fusca</i>	3512
<i>Skermanella aerolata</i>	163
<i>Snodgrassella alvi</i> wkB2	9250
<i>Sphingomonas echinoides</i>	16699
<i>Staphylococcus epidermidis</i>	6428
<i>Streptococcus oralis</i> subsp. <i>dentisani</i>	499
<i>Streptococcus salivarius</i>	18116
Unassigned	12014

Table S13 : Total taxonomic distribution of active ASVs in ileum exposed at 10 ppb

ASV Species	ASV activity
<i>Bacillus wiedmannii</i>	80
<i>Bacteroides caccae</i>	5
<i>Bacteroides dorei</i>	2
<i>Bartonella apis</i>	5718
<i>Bifidobacterium asteroides</i>	95
<i>Bifidobacterium callitrichos</i> DSM 23973	6
<i>Bifidobacterium coryneforme</i>	237
<i>Bradyrhizobium vignae</i>	2
<i>Dermacoccus profundi</i>	13
<i>Escherichia fergusonii</i> ATCC 35469	1

<i>Flavobacterium acidificum</i>	1
<i>Frischella perrara</i>	5725
<i>Gilliamella apicola</i>	9200
<i>Gilliamella bombicola</i>	17
<i>Gilliamella intestini</i>	29
<i>Lachnoclostridium pacaense</i>	19
<i>Lactobacillus apis</i>	27304
<i>Lactobacillus helsingborgensis</i>	2839
<i>Lactobacillus kimbladii</i>	869
<i>Lactobacillus kullabergensis</i>	176
<i>Lactobacillus kunkeei</i>	8
<i>Lactobacillus mellifer</i>	83
<i>Lactobacillus mellis</i>	643
<i>Lactobacillus melliventris</i>	1297
<i>Lawsonella clevelandensis</i>	5
<i>Methylobacterium populi BJ001</i>	3
<i>Parasaccharibacter apium</i>	37
<i>Pediococcus stilesii</i>	180
<i>Pelomonas saccharophila</i>	29
<i>Phascolarctobacterium faecium</i>	5
<i>Pseudomonas canadensis</i>	168
<i>Pseudomonas cerasi</i>	119
<i>Pseudomonas songnenensis</i>	39
<i>Pseudoxanthomonas jiangsuensis</i>	3
<i>Psychrobacter cryohalolentis K5</i>	103
<i>Ralstonia insidiosa</i>	7

<i>Ralstonia pickettii</i>	393
<i>Romboutsia timonensis</i>	271
<i>Roseburia faecis</i>	1225
<i>Rothia dentocariosa ATCC 17931</i>	4
<i>Shinella fusca</i>	2841
<i>Skermanella aerolata</i>	59
<i>Snodgrassella alvi wkb2</i>	14705
<i>Sphingomonas echinoides</i>	10557
<i>Staphylococcus epidermidis</i>	8745
<i>Streptococcus oralis subsp. dentisani</i>	7369
<i>Streptococcus salivarius</i>	17734
<i>Unassigned</i>	17326

Table S14 : Total taxonomic distribution of active ASVs in rectum exposed at 0 ppb

ASV Species	ASV activity
<i>Arthrobacter russicus</i>	3
<i>Bacteroides caccae</i>	1
<i>Bacteroides plebeius DSM 17135</i>	2
<i>Bartonella apis</i>	9066
<i>Bifidobacterium asteroides</i>	30
<i>Bifidobacterium callitrichos DSM 23973</i>	9
<i>Bifidobacterium coryneforme</i>	49
<i>Bradyrhizobium vignae</i>	1
<i>Brevundimonas albigilva</i>	2
<i>Brevundimonas lenta</i>	1
<i>Chryseobacterium hispanicum</i>	10

<i>Delftia acidovorans</i>	1
<i>Dermaococcus profundus</i>	11
<i>Dialister invisus</i>	1
<i>Escherichia fergusonii</i> ATCC 35469	13
<i>Faecalibacterium prausnitzii</i>	12
<i>Flavobacterium acidificum</i>	10
<i>Frischella perrara</i>	6051
<i>Gemmiger formicilis</i>	15
<i>Gilliamella apicola</i>	4582
<i>Gilliamella bombicola</i>	2
<i>Lachnoclostridium pacaense</i>	58
<i>Lactobacillus apis</i>	19221
<i>Lactobacillus helsingborgensis</i>	5750
<i>Lactobacillus kimbladii</i>	475
<i>Lactobacillus kullabergensis</i>	206
<i>Lactobacillus kunkeei</i>	8
<i>Lactobacillus mellifer</i>	66
<i>Lactobacillus mellis</i>	1447
<i>Lactobacillus melliventris</i>	1278
<i>Lactobacillus rogosae</i>	1
<i>Lysinibacillus parviboronicapiens</i>	3
<i>Methylobacterium populi</i> BJ001	3
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1
<i>Oceanobacillus chironomi</i>	3
<i>Parasaccharibacter apium</i>	41
<i>Pediococcus stilesii</i>	2

<i>Pelomonas saccharophila</i>	51
<i>Pseudaminobacter manganicus</i>	19
<i>Pseudomonas canadensis</i>	21
<i>Pseudomonas cerasi</i>	152
<i>Pseudomonas songnenensis</i>	138
<i>Pseudoxanthomonas jiangsuensis</i>	46
<i>Psychrobacter cryohalolentis K5</i>	71
<i>Ralstonia pickettii</i>	827
<i>Romboutsia timonensis</i>	1015
<i>Roseburia faecis</i>	810
<i>Rothia dentocariosa ATCC 17931</i>	2121
<i>Shinella fusca</i>	7158
<i>Skermanella aerolata</i>	18
<i>Snodgrassella alvi wkb2</i>	16394
<i>Sphingomonas echinoides</i>	4781
<i>Staphylococcus epidermidis</i>	9962
<i>Streptococcus oralis subsp. dentisani</i>	4892
<i>Streptococcus salivarius</i>	22122
<i>Unassigned</i>	13213

Table S15 : Total taxonomic distribution of active ASVs in rectum exposed at 0.1 ppb

ASV Species	ASV activity
<i>Achromobacter insolitus</i>	1
<i>Bacillus licheniformis</i>	2
<i>Bacillus wiedmannii</i>	1
<i>Bacteroides dorei</i>	3

<i>Bartonella apis</i>	4194
<i>Bifidobacterium asteroides</i>	22
<i>Bifidobacterium coryneforme</i>	181
<i>Bosea vaviloviae</i>	1
<i>Dermaococcus profundi</i>	16
<i>Faecalibacterium prausnitzii</i>	1
<i>Frischella perrara</i>	1336
<i>Gemmiger formicilis</i>	1
<i>Gilliamella apicola</i>	3217
<i>Lactobacillus apis</i>	28894
<i>Lactobacillus helsingborgensis</i>	3699
<i>Lactobacillus kimbladii</i>	642
<i>Lactobacillus kullabergensis</i>	43
<i>Lactobacillus kunkei</i>	4
<i>Lactobacillus mellifer</i>	35
<i>Lactobacillus mellis</i>	314
<i>Lactobacillus melliventris</i>	1990
<i>Lawsonella clevelandensis</i>	5
<i>Lysinibacillus parviboronicapiens</i>	2
<i>Morganella morganii subsp. sibonii</i>	2
<i>Oceanobacillus chironomi</i>	2
<i>Pediococcus stilesii</i>	3
<i>Pelomonas saccharophila</i>	86
<i>Pseudaminobacter manganicus</i>	31
<i>Pseudomonas canadensis</i>	2
<i>Pseudomonas cerasi</i>	99

<i>Pseudomonas songnenensis</i>	299
<i>Pseudoxanthomonas jiangsuensis</i>	7
<i>Psychrobacter cryohalolentis</i> K5	247
<i>Ralstonia insidiosa</i>	16
<i>Ralstonia pickettii</i>	685
<i>Romboutsia timonensis</i>	670
<i>Roseburia faecis</i>	948
<i>Rothia dentocariosa</i> ATCC 17931	14
<i>Shinella fusca</i>	6266
<i>Snodgrassella alvi</i> wkB2	15445
<i>Sphingomonas echinoides</i>	7055
<i>Staphylococcus epidermidis</i>	10553
<i>Streptococcus oralis</i> subsp. <i>dentisani</i>	5059
<i>Streptococcus salivarius</i>	16578
Unassigned	21276

Table S16 : Total taxonomic distribution of active ASVs in rectum exposed at 1 ppb

ASV Species	ASV activity
<i>[Clostridium] saccharolyticum</i>	3
<i>Bacteroides caccae</i>	1
<i>Bartonella apis</i>	7534
<i>Bifidobacterium asteroides</i>	21
<i>Bifidobacterium callitrichos</i> DSM 23973	7
<i>Bifidobacterium coryneforme</i>	62
<i>Blautia wexlerae</i> DSM 19850	1
<i>Bradyrhizobium vignae</i>	2

<i>Dermaococcus profundus</i>	14
<i>Frischella perrara</i>	4818
<i>Gilliamella apicola</i>	2004
<i>Gilliamella bombicola</i>	3
<i>Gilliamella intestini</i>	1
<i>Lachnoclostridium pacaense</i>	41
<i>Lactobacillus apis</i>	25179
<i>Lactobacillus helsingborgensis</i>	3021
<i>Lactobacillus kimbladii</i>	569
<i>Lactobacillus kullabergensis</i>	59
<i>Lactobacillus kunkeei</i>	12
<i>Lactobacillus mellifer</i>	115
<i>Lactobacillus mellis</i>	677
<i>Lactobacillus melliventris</i>	776
<i>Lactobacillus rogosae</i>	1
<i>Lysinibacillus parviboronicapiens</i>	8
<i>Morganella morganii subsp. sibonii</i>	1
<i>Oceanobacillus chironomi</i>	1
<i>Pediococcus stilesii</i>	6
<i>Pelomonas saccharophila</i>	38
<i>Pseudaminobacter manganicus</i>	36
<i>Pseudomonas canadensis</i>	5
<i>Pseudomonas cerasi</i>	113
<i>Pseudomonas songnenensis</i>	54
<i>Pseudoxanthomonas jiangsuensis</i>	3
<i>Psychrobacter cryohalolentis K5</i>	106

<i>Ralstonia pickettii</i>	434
<i>Romboutsia timonensis</i>	1316
<i>Roseburia faecis</i>	1781
<i>Shinella fusca</i>	4981
<i>Skermanella aerolata</i>	5
<i>Snodgrassella alvi wkb2</i>	17562
<i>Sphingomonas echinoides</i>	6088
<i>Staphylococcus epidermidis</i>	5581
<i>Streptococcus oralis subsp. dentisani</i>	1182
<i>Streptococcus salivarius</i>	18194
<i>Unassigned</i>	19626

Table S17 : Total taxonomic distribution of active ASVs in rectum exposed at 10 ppb

ASV Species	ASV activity
<i>[Clostridium] saccharolyticum</i>	3
<i>Bacteroides caccae</i>	1
<i>Bartonella apis</i>	7534
<i>Bifidobacterium asteroides</i>	21
<i>Bifidobacterium callitrichos DSM 23973</i>	7
<i>Bifidobacterium coryneforme</i>	62
<i>Blautia wexlerae DSM 19850</i>	1
<i>Bradyrhizobium vignae</i>	2
<i>Dermacoccus profundus</i>	14
<i>Frischella perrara</i>	4818
<i>Gilliamella apicola</i>	2004
<i>Gilliamella bombicola</i>	3

<i>Gilliamella intestini</i>	1
<i>Lachnoclostridium pacaense</i>	41
<i>Lactobacillus apis</i>	25179
<i>Lactobacillus helsingborgensis</i>	3021
<i>Lactobacillus kimbladii</i>	569
<i>Lactobacillus kullabergensis</i>	59
<i>Lactobacillus kunkeei</i>	12
<i>Lactobacillus mellifer</i>	115
<i>Lactobacillus mellis</i>	677
<i>Lactobacillus melliventris</i>	776
<i>Lactobacillus rogosae</i>	1
<i>Lysinibacillus parviboronicapiens</i>	8
<i>Morganella morganii subsp. sibonii</i>	1
<i>Oceanobacillus chironomi</i>	1
<i>Pediococcus stilesii</i>	6
<i>Pelomonas saccharophila</i>	38
<i>Pseudaminobacter manganicus</i>	36
<i>Pseudomonas canadensis</i>	5
<i>Pseudomonas cerasi</i>	113
<i>Pseudomonas songnenensis</i>	54
<i>Pseudoxanthomonas jiangsuensis</i>	3
<i>Psychrobacter cryohalolentis K5</i>	106
<i>Ralstonia pickettii</i>	434
<i>Romboutsia timonensis</i>	1316
<i>Roseburia faecis</i>	1781
<i>Shinella fusca</i>	4981

<i>Skermanella aerolata</i>	5
<i>Snodgrassella alvi wkb2</i>	17562
<i>Sphingomonas echinoides</i>	6088
<i>Staphylococcus epidermidis</i>	5581
<i>Streptococcus oralis subsp. dentisani</i>	1182
<i>Streptococcus salivarius</i>	18194
<i>Unassigned</i>	19626

Table S18 : Network metrics for gut microbiome taxa in midgut exposed to 0 ppb clothianidin

CC = Closeness centrality, DG = Degree, NC = Neighborhood Connectivity

Taxa name (spp.)	ASV classification	CC	DG	NC	ASV activity
<i>Bartonella</i>	Non-core	0.65671642	22	14.22727273	15007
<i>Pediococcus</i>	Low abundant	0.61971831	22	12.04545455	230
<i>Pelomonas</i>	Low abundant	0.61111111	17	16.41176471	1
<i>Acinetobacter</i>	Low abundant	0.61111111	17	16.41176471	4
<i>Leifsonia</i>	Low abundant	0.61111111	17	16.41176471	6
<i>Morganella</i>	Low abundant	0.61111111	17	16.41176471	2
<i>Phascolarctobacterium</i>	Low abundant	0.61111111	17	16.41176471	10
<i>Staphylococcus</i>	Low abundant	0.61111111	17	15.64705882	8
<i>Devosia</i>	Low abundant	0.61111111	17	16.41176471	17
<i>Snodgrassella</i>	Core	0.60273973	18	14.61111111	10367
<i>Bradyrhizobium</i>	Low abundant	0.58666667	15	16.13333333	43
<i>Lachnoclostridium</i>	Low abundant	0.57894737	16	14.375	155

<i>Rothia</i>	Low abundant	0.57142857	13	13.38461538	1
<i>Streptococcus</i>	Low abundant	0.57142857	13	13.38461538	36
<i>Intestinibacter</i>	Low abundant	0.57142857	13	13.38461538	63
<i>Escherichia</i>	Low abundant	0.56410256	12	11.41666667	1
Unassigned	unassigned	0.55696203	12	12.5	14420
<i>Flavobacterium</i>	Low abundant	0.55	16	14.375	10
<i>Achromobacter</i>	Low abundant	0.55	12	11.41666667	42
<i>Prevotella</i>	Low abundant	0.55	16	14.375	32
<i>Frischella</i>	Non-core	0.55	12	12.75	29145
<i>Arthrobacter</i>	Low abundant	0.54320988	15	15.33333333	29
<i>Bosea</i>	Low abundant	0.54320988	15	15.33333333	37
<i>Lactobacillus</i>	Core	0.54320988	12	13.08333333	38528
<i>Pseudoxanthomonas</i>	Low abundant	0.53012048	11	15.36363636	6
<i>Brevundimonas</i>	Low abundant	0.53012048	13	12.92307692	65
<i>Delftia</i>	Low abundant	0.53012048	10	12.4	96
<i>Bifidobacterium</i>	Core	0.51764706	11	10.36363636	195
<i>Bombella</i>	Non-core	0.51764706	7	13.28571429	204
<i>Acidocella</i>	Low abundant	0.51162791	8	12	10
<i>Barnesiella</i>	Low abundant	0.50574713	10	13	4
<i>Dialister</i>	Low abundant	0.50574713	10	13	7
<i>Commensalibacter</i>	Non-core	0.50574713	8	10	28
<i>Roseburia</i>	Low abundant	0.50574713	9	12.77777778	85
<i>Pseudomonas</i>	Low abundant	0.50574713	10	13	1
<i>Actinomyces</i>	Low abundant	0.49438202	6	13	6
<i>Gilliamella</i>	Non-core	0.49438202	9	12.77777778	11407

<i>Gemmiger</i>	Low abundant	0.48888889	6	11	1
<i>Anaerobiospirillum</i>	Low abundant	0.48888889	6	11	1
<i>Phyllobacterium</i>	Low abundant	0.48888889	6	11	2
<i>Shinella</i>	Low abundant	0.48351648	11	12.72727273	3
<i>Parasaccharibacter</i>	Non-core	0.46808511	10	11.1	1117
<i>Faecalibacterium</i>	Low abundant	0.44897959	8	11.5	6
<i>Dermacoccus</i>	Low abundant	0.44444444	3	14	2
<i>Pseudaminobacter</i>	Low abundant	0.40366972	3	9.33333333	2

Table S19 : Network metrics for gut microbiome taxa in midgut exposed to 0.1 ppb clothianidin

CC = Closeness centrality, DG = Degree, NC = Neighborhood Connectivity

Taxa name (spp.)	ASV Classification	CC	DG	NC	ASV activity
<i>Frischella</i>	Non-core	0.56666667	8	10.625	20817
<i>Bartonella</i>	Non-core	0.61818182	14	10.42857143	17761
<i>Lactobacillus</i>	Core	0.66666667	17	9.70588235	34363
<i>Snodgrassella</i>	Core	0.59649123	11	10.45454545	12928
Unassigned	unassigned	0.60714286	12	10.5	20940
<i>Gilliamella</i>	Non-core	0.53125	8	9.875	12598
<i>Parasaccharibacter</i>	Non-core	0.60714286	12	10.25	3
<i>Bombella</i>	Non-core	0.5862069	11	10.36363636	404
<i>Bacillus</i>	Low abundant	0.56666667	10	10.1	266
<i>Bifidobacterium</i>	Core	0.5483871	8	11.125	544
<i>Pediococcus</i>	Low abundant	0.5862069	11	10.54545455	256
<i>Lachnoclostridium</i>	Low abundant	0.60714286	13	10	31

<i>Ralstonia</i>	Low abundant	0.60714286	13	10.61538462	122
<i>Pseudomonas</i>	Low abundant	0.55737705	9	9.66666667	4
<i>Delftia</i>	Low abundant	0.53968254	7	9.85714286	6
<i>Bradyrhizobium</i>	Low abundant	0.51515152	7	10.85714286	17
<i>Streptococcus</i>	Low abundant	0.5862069	10	9.9	1
<i>Commensalibacter</i>	Non-core	0.61818182	13	9.92307692	72
<i>Prevotella</i>	Low abundant	0.5862069	10	12.2	1
<i>Methylobacterium</i>	Low abundant	0.5862069	11	10.63636364	3
<i>Oceanobacillus</i>	Low abundant	0.5862069	10	12.2	22
<i>Lysinibacillus</i>	Low abundant	0.52307692	7	11.42857143	1
<i>Blautia</i>	Low abundant	0.5483871	8	10.5	3
<i>Faecalibacterium</i>	Low abundant	0.5483871	8	10.5	1
<i>Acidocella</i>	Low abundant	0.55737705	8	11.5	26
<i>Achromobacter</i>	Low abundant	0.53125	7	10.42857143	2
<i>Anaerobiospirillum</i>	Low abundant	0.55737705	9	9.33333333	4
<i>Staphylococcus</i>	Low abundant	0.55737705	11	10	4
<i>Shinella</i>	Low abundant	0.53968254	10	9.7	12
<i>Flavobacterium</i>	Low abundant	0.5483871	10	10.4	3
<i>Escherichia</i>	Low abundant	0.5483871	8	10.625	1
<i>Thiohalobacter</i>	Low abundant	0.56666667	9	11.33333333	10
<i>Acinetobacter</i>	Low abundant	0.53125	7	10.42857143	1
<i>Pelomonas</i>	Low abundant	0.61818182	13	10.46153846	3
<i>Moraxella</i>	Low abundant	0.48571429	4	13.5	1

Table S20 : Network metrics for gut microbiome taxa in midgut exposed to 1 ppb clothianidin

CC = Closeness centrality, DG = Degree, NC = Neighborhood Connectivity

Taxa name (spp.)	ASV Classification	CC	DG	NC	ASV activity
<i>Frischella</i>	Non-core	0.66037736	18	9.77777778	11964
<i>Lactobacillus</i>	Core	0.57377049	11	10.90909091	49115
<i>Gilliamella</i>	Non-core	0.55555556	9	10.11111111	3576
Unassigned	unassigned	0.64814815	16	10.125	20649
<i>Snodgrassella</i>	Core	0.5	6	9.66666667	19115
<i>Parasaccharibacter</i>	Non-core	0.57377049	11	10.54545455	7050
<i>Bombella</i>	Non-core	0.58333333	11	10.54545455	282
<i>Bacillus</i>	Low abundant	0.47297297	7	9.71428571	372
<i>Bifidobacterium</i>	Core	0.56451613	13	9.84615385	522
<i>Pediococcus</i>	Low abundant	0.55555556	10	10.6	182
<i>Lachnoclostridium</i>	Low abundant	0.46666667	5	10	41
<i>Ralstonia</i>	Low abundant	0.57377049	11	9.45454545	10
<i>Bartonella</i>	Non-core	0.43209877	3	9.66666667	10349
<i>Roseburia</i>	Low abundant	0.55555556	10	10.4	2
<i>Delftia</i>	Low abundant	0.45454545	6	8.5	3
<i>Bradyrhizobium</i>	Low abundant	0.5	8	10.625	12
<i>Streptococcus</i>	Low abundant	0.56451613	11	10.90909091	5
<i>Commensalibacter</i>	Non-core	0.55555556	10	10.4	98
<i>Bacteroides</i>	Low abundant	0.58333333	10	9.8	5
<i>Pseudoxanthomonas</i>	Low abundant	0.53846154	8	8.875	6
<i>Prevotella</i>	Low abundant	0.56451613	10	9.5	1

<i>Methylobacterium</i>	Low abundant	0.546875	9	10.77777777 8	6
<i>Phyllobacterium</i>	Low abundant	0.53030303	11	9	32
<i>Lysinibacillus</i>	Low abundant	0.53030303	9	10.33333333 3	30
<i>Faecalibacterium</i>	Low abundant	0.33653846	1	6	4
<i>Acidocella</i>	Low abundant	0.53030303	9	10	46
<i>Achromobacter</i>	Low abundant	0.52238806	9	10.44444444 4	2
<i>Anaerobiospirillum</i>	Low abundant	0.42682927	4	8.75	5
<i>Shinella</i>	Low abundant	0.50724638	6	11.16666666 7	7
<i>Flavobacterium</i>	Low abundant	0.58333333	10	10.6	3
<i>Dermacoccus</i>	Low abundant	0.52238806	9	10.44444444 4	6
<i>Chryseobacterium</i>	Low abundant	0.5	7	10.1428571 4	1
<i>Escherichia</i>	Low abundant	0.58333333	11	10.7272727 3	3
<i>Lawsonella</i>	Low abundant	0.52238806	9	10.44444444 4	1
<i>Porphyromonas</i>	Low abundant	0.5	7	10.1428571 4	2
<i>Mycobacterium</i>	Low abundant	0.47297297	7	8.42857143	3

Table S21 : Network metrics for gut microbiome taxa in midgut exposed to 10 ppb clothianidin

CC = Closeness centrality, DG = Degree, NC = Neighborhood Connectivity

Taxa name (spp.)	ASV Classification	CC	DG	NC	ASV activity
<i>Snodgrassella</i>	Core	0.62745098	13	8.38461538	7386

<i>Bifidobacterium</i>	Core	0.60377358	14	9.5	595
<i>Parasaccharibacter</i>	Non-core	0.59259259	14	8.57142857	2317
<i>Acidocella</i>	Low abundant	0.59259259	10	9.4	58
<i>Anaerobiospirillum</i>	Low abundant	0.59259259	12	8.41666667	45
<i>Rothia</i>	Low abundant	0.59259259	11	9.90909091	1
<i>Bartonella</i>	Non-core	0.58181818	10	10.6	15516
<i>Leifsonia</i>	Low abundant	0.58181818	10	9.5	1
<i>Thiohalobacter</i>	Low abundant	0.58181818	10	9.5	1
<i>Pelomonas</i>	Low abundant	0.58181818	10	9.5	1
<i>Commensalibacter</i>	Non-core	0.57142857	9	10.11111111	111
<i>Staphylococcus</i>	Low abundant	0.56140351	9	9.66666667	3
<i>Lactobacillus</i>	Core	0.55172414	8	9.125	51835
Unassigned	unassigned	0.55172414	9	9.88888889	28981
<i>Roseburia</i>	Low abundant	0.55172414	8	10	3
<i>Shinella</i>	Low abundant	0.55172414	8	7.625	14
<i>Bombella</i>	Non-core	0.54237288	10	10.4	3
<i>Achromobacter</i>	Low abundant	0.54237288	10	10.4	6
<i>Ralstonia</i>	Low abundant	0.53333333	10	9.1	9
<i>Pediococcus</i>	Low abundant	0.49230769	6	8.83333333	121
<i>Streptococcus</i>	Low abundant	0.49230769	8	10.125	4
<i>Phyllobacterium</i>	Low abundant	0.49230769	8	10.125	3
<i>Lawsonella</i>	Low abundant	0.49230769	8	10.125	4
<i>Actinomyces</i>	Low abundant	0.49230769	8	10.125	1
<i>Bacillus</i>	Low abundant	0.48484848	7	8.28571429	54

<i>Frischella</i>	Non-core	0.48484848	7	8.57142857	10132
<i>Pseudomonas</i>	Low abundant	0.48484848	7	8	3
<i>Lachnoclostridium</i>	Low abundant	0.47761194	4	9.75	102
<i>Flavobacterium</i>	Low abundant	0.47761194	4	9.75	2
<i>Gilliamella</i>	Core	0.47058824	7	8.57142857	19862
<i>Pseudoxanthomonas</i>	Low abundant	0.45714286	4	8.5	1
<i>Delftia</i>	Low abundant	0.44444444	5	10.2	5
<i>Faecalibacterium</i>	Low abundant	0.4	2	7.5	3

Table S22 : Network metrics for gut microbiome taxa in ileum exposed to 0 ppb clothianidin

CC = Closeness centrality, DG = Degree, NC = Neighborhood Connectivity

Taxa name (spp.)	ASV Classification	CC	DG	NC	ASV activity
<i>Bartonella</i>	Non-core	0.62962963	19	11.10526316	10013
<i>Lactobacillus</i>	Core	0.61818182	13	10	48171
<i>Commensalibacter</i>	Non-core	0.59649123	16	10.875	48
<i>Pediococcus</i>	Low abundant	0.59649123	13	10.38461538	236
<i>Bifidobacterium</i>	Core	0.59649123	17	10.82352941	108
Unassigned	Unassigned	0.59649123	16	10.875	9830
<i>Frischella</i>	Low abundant	0.59649123	12	11.5	30344
<i>Snodgrassella</i>	Core	0.5862069	14	10.92857143	24749

<i>Gilliamella</i>	Core	0.57627119	12	9.25	7453
<i>Lachnoclostridium</i>	Low abundant	0.56666667	8	8.75	5
<i>Blautia</i>	Low abundant	0.55737705	9	12.22222222	21
<i>Parasaccharibacter</i>	Non-core	0.55737705	8	9.5	252
<i>Sphingomonas</i>	Low abundant	0.53968254	8	10.625	1
<i>Brevundimonas</i>	Low abundant	0.53968254	12	11.75	4
<i>Acinetobacter</i>	Low abundant	0.53125	11	13.81818182	2
<i>Escherichia</i>	Low abundant	0.53125	11	13.81818182	1
<i>Faecalibacterium</i>	Low abundant	0.53125	11	13.81818182	3
<i>Bacteroides</i>	Low abundant	0.53125	11	13.81818182	2
<i>Achromobacter</i>	Low abundant	0.52307692	7	11.42857143	1
<i>Acidocella</i>	Low abundant	0.51515152	8	12.125	10
<i>Pelomonas</i>	Low abundant	0.50746269	7	12	1
<i>Arthrobacter</i>	Low abundant	0.50746269	9	13	5
<i>Shinella</i>	Low abundant	0.5	7	13.71428571	2
<i>Delftia</i>	Low abundant	0.5	7	13.71428571	1
<i>Bombella</i>	Non-core	0.5	6	11.33333333	123
<i>Oceanobacillus</i>	Low abundant	0.47887324	6	11.33333333	2

<i>Pseudaminobacter</i>	Low abundant	0.45945946	4	10.25	3
<i>Methylobacterium</i>	Low abundant	0.45333333	4	7.75	25
<i>Flavobacterium</i>	Low abundant	0.44736842	3	9.66666667	3
<i>Anaerobiospirillum</i>	Low abundant	0.44155844	5	7	3
<i>Rothia</i>	Low abundant	0.41975309	3	7.33333333	2
<i>Streptococcus</i>	Low abundant	0.4047619	5	5.4	2
<i>Roseburia</i>	Low abundant	0.4047619	5	5.4	2
<i>Pseudomonas</i>	Low abundant	0.4047619	5	5.4	5
<i>Bradyrhizobium</i>	Low abundant	0.34693878	4	4.75	5

Table S23 : Network metrics for gut microbiome taxa in ileum exposed to 0.1 ppb clothianidin

CC = Closeness centrality, DG = Degree, NC = Neighborhood Connectivity

Taxa name (spp.)	ASV Classification	CC	DG	NC	ASV activity
Unassigned	unassigned	0.6507936 5	19	10.84210 526	14500
<i>Bifidobacterium</i>	Core	0.6307692 3	17	9.647058 82	318
<i>Acidocella</i>	Low abundant	0.6029411 8	14	12.35714 286	13
<i>Streptococcus</i>	Low abundant	0.6029411 8	15	11.4	7
<i>Bartonella</i>	Non-core	0.6029411 8	15	11.8	13269

<i>Actinomyces</i>	Low abundant	0.5774647 9	12	11.16666 667	1
<i>Lawsonella</i>	Low abundant	0.5774647 9	12	11.16666 667	3
<i>Pediococcus</i>	Low abundant	0.5774647 9	12	11	283
<i>Bacillus</i>	Low abundant	0.5774647 9	14	10.64285 714	116
<i>Oceanobacillus</i>	Low abundant	0.5694444 4	14	10.92857 143	1
<i>Phyllobacterium</i>	Low abundant	0.5694444 4	14	10.92857 143	3
<i>Delftia</i>	Low abundant	0.5694444 4	12	11.16666 667	8
<i>Pelomonas</i>	Low abundant	0.5616438 4	10	12.6	2
<i>Shinella</i>	Low abundant	0.5616438 4	11	10.81818 182	12
<i>Acinetobacter</i>	Low abundant	0.5540540 5	11	10.63636 364	4
<i>Flavobacterium</i>	Low abundant	0.5466666 7	11	12.90909 091	10
<i>Lactobacillus</i>	Core	0.5466666 7	12	11.66666 667	55511
<i>Sphingomonas</i>	Low abundant	0.5394736 8	10	10.4	6
<i>Ralstonia</i>	Low abundant	0.5394736 8	11	8.545454 55	285
<i>Lachnoclostridium</i>	Low abundant	0.5394736 8	8	13.875	12
<i>Frischella</i>	Non-core	0.5394736 8	11	9	15057
<i>Polynucleobacter</i>	Low abundant	0.5324675 3	7	13.57142 857	4

<i>Leifsonia</i>	Low abundant	0.5324675 3	7	13.57142 857	1
<i>Commensalibacter</i>	Non-core	0.5324675 3	10	10.3	44
<i>Anaerobiospirillum</i>	Low abundant	0.5256410 3	9	13.44444 444	6
<i>Rothia</i>	Low abundant	0.5189873 4	8	12.875	1
<i>Psychrobacter</i>	Low abundant	0.5189873 4	8	9.5	18
<i>Bradyrhizobium</i>	Low abundant	0.5125	8	10.875	12
<i>Roseburia</i>	Low abundant	0.5125	7	11	2
<i>Chryseobacterium</i>	Low abundant	0.5061728 4	8	9.625	1
<i>Achromobacter</i>	Low abundant	0.5061728 4	9	10.44444 444	3
<i>Methylobacterium</i>	Low abundant	0.5061728 4	8	9.625	1
<i>Bombella</i>	Non-core	0.5061728 4	7	11	2316
<i>Gilliamella</i>	Core	0.5061728 4	10	9.8	7918
<i>Parasaccharibacter</i>	Non-core	0.5061728 4	7	11	64
<i>Thiohalobacter</i>	Low abundant	0.5	6	11.33333 333	2
<i>Bacteroides</i>	Low abundant	0.5	6	11	1
<i>Snodgrassella</i>	Core	0.5	7	11.14285 714	20309
<i>Staphylococcus</i>	Low abundant	0.4767441 9	6	12.66666 667	1
<i>Lysinibacillus</i>	Low abundant	0.4767441 9	6	12.66666 667	2

<i>Pseudomonas</i>	Low abundant	0.4659090 9	8	10	122
<i>Brevundimonas</i>	Low abundant	0.4606741 6	5	9.8	4

Table S24 : Network metrics for gut microbiome taxa in ileum exposed to 1 ppb clothianidin

CC = Closeness centrality, DG = Degree, NC = Neighborhood Connectivity

Taxa name (spp.)	ASV Classification	CC	DG	NC	ASV activity
<i>Methylobacterium</i>	Low abundant	0.6842105 3	22	14.31818 182	10
<i>Bifidobacterium</i>	Core	0.6724137 9	20	13.5	177
<i>Flavobacterium</i>	Low abundant	0.6610169 5	19	15.15789 474	7
<i>Morganella</i>	Low abundant	0.6610169 5	19	15.15789 474	12
<i>Staphylococcus</i>	Low abundant	0.6393442 6	18	14.44444 444	18
<i>Sphingomonas</i>	Low abundant	0.6190476 2	17	17.17647 059	1
<i>Escherichia</i>	Low abundant	0.6190476 2	17	17.17647 059	4
<i>Chryseobacterium</i>	Low abundant	0.6190476 2	17	17.17647 059	6
<i>Psychrobacter</i>	Low abundant	0.6190476 2	17	17.17647 059	4
<i>Achromobacter</i>	Low abundant	0.6190476 2	17	17.17647 059	6
<i>Arthrobacter</i>	Low abundant	0.6190476 2	17	17.17647 059	1
<i>Pseudoxanthomonas</i>	Low abundant	0.6190476 2	17	17.17647 059	29
<i>Ralstonia</i>	Low abundant	0.6190476 2	18	14.05555 556	34
<i>Bradyrhizobium</i>	Low abundant	0.609375	16	15.3125	42
<i>Pediococcus</i>	Low abundant	0.609375	17	16	126

<i>Bartonella</i>	Non-core	0.609375	14	11.14285 714	11207
<i>Frischella</i>	Non-core	0.609375	15	12.86666 667	25966
<i>Pseudomonas</i>	Low abundant	0.6	14	14.64285 714	12
<i>Commensalibacter</i>	Non-core	0.5909090 9	14	15.64285 714	96
<i>Acidocella</i>	Low abundant	0.5820895 5	12	12.91666 667	20
<i>Lawsonella</i>	Low abundant	0.5735294 1	11	14.81818 182	1
<i>Romboutsia</i>	Low abundant	0.5735294 1	11	14.81818 182	122
<i>Moraxella</i>	Low abundant	0.5571428 6	11	13.45454 545	2
<i>Pelomonas</i>	Low abundant	0.5571428 6	11	13.45454 545	1
<i>Shinella</i>	Low abundant	0.5571428 6	9	13.11111 111	7
<i>Prevotella</i>	Low abundant	0.5571428 6	11	13.45454 545	2
<i>Anaerobiospirillum</i>	Low abundant	0.5492957 7	10	13.8	9
<i>Parasaccharibacter</i>	Non-core	0.5492957 7	11	13.54545 455	502
Unassigned	unassigned	0.5416666 7	13	13.84615 385	14462
<i>Delftia</i>	Low abundant	0.5416666 7	7	9.571428 57	12
<i>Lachnoclostridium</i>	Low abundant	0.5342465 8	8	15.375	13
<i>Snodgrassella</i>	Core	0.5270270 3	9	12.66666 667	21301

<i>Gilliamella</i>	Core	0.52	8	11.125	2408
<i>Gemmiger</i>	Low abundant	0.5131578 9	6	10.16666 667	1
<i>Streptococcus</i>	Low abundant	0.5131578 9	9	13.44444 444	9
<i>Brevundimonas</i>	Low abundant	0.5064935 1	5	10.6	9
<i>Lysinibacillus</i>	Low abundant	0.4936708 9	5	15.6	16
<i>Bacillus</i>	Low abundant	0.4875	5	9.4	196
<i>Lactobacillus</i>	Core	0.4642857 1	6	8.166666 67	44837
<i>Thiohalobacter</i>	Low abundant	0.4239130 4	3	10	1

Table S25 : Network metrics for gut microbiome taxa in ileum exposed to 10 ppb clothianidin

CC = Closeness centrality, DG = Degree, NC = Neighborhood Connectivity

Taxa name (spp.)	ASV Classification	CC	DG	NC	ASV activity
<i>Frischella</i>	Non-core	0.58	11	6.72727 273	16636
<i>Blautia</i>	Low abundant	0.5686274 5	9	6.33333 333	1
<i>Lactobacillus</i>	Core	0.5471698 1	7	7.71428 571	61901
<i>Pediococcus</i>	Low abundant	0.5370370 4	10	7	356
<i>Bombella</i>	Non-core	0.5370370 4	7	6.28571 429	1
<i>Snodgrassella</i>	Core	0.5370370 4	7	7.85714 286	20535

<i>Commensalibacter</i>	Non-core	0.5272727 3	6	7.16666 667	115
<i>Gilliamella</i>	Core	0.5272727 3	7	6.85714 286	16658
<i>Bifidobacterium</i>	Core	0.5178571 4	8	6.25	474
Unassigned	unassigned	0.5178571 4	8	6.125	24882
<i>Thiohalobacter</i>	Low abundant	0.5087719 3	6	6.66666 667	1
<i>Acidocella</i>	Low abundant	0.5	5	7.6	31
<i>Rothia</i>	Low abundant	0.4915254 2	8	8.625	3
<i>Escherichia</i>	Low abundant	0.4915254 2	8	8.625	1
<i>Skermanella</i>	Low abundant	0.4915254 2	8	8.625	20
<i>Bradyrhizobium</i>	Low abundant	0.4915254 2	8	8.625	1
<i>Pseudomonas</i>	Low abundant	0.4915254 2	8	8.625	1
<i>Pelomonas</i>	Low abundant	0.4833333 3	6	7.16666 667	10
<i>Staphylococcus</i>	Low abundant	0.4754098 4	8	7.875	4
<i>Methylobacterium</i>	Low abundant	0.4754098 4	8	7.875	3
<i>Ralstonia</i>	Low abundant	0.4754098 4	7	6.14285 714	11
<i>Roseburia</i>	Low abundant	0.4393939 4	4	6	2
<i>Bartonella</i>	Non-core	0.4393939 4	4	7.25	14459

<i>Bacillus</i>	Low abundant	0.4328358 2	3	6	86
<i>Flavobacterium</i>	Low abundant	0.4264705 9	4	6.25	2
<i>Anaerobiospirillum</i>	Low abundant	0.4264705 9	4	6	32
<i>Lachnoclostridium</i>	Low abundant	0.4142857 1	3	6	20
<i>Parasaccharibacter</i>	Non-core	0.4142857 1	4	5	75
<i>Shinella</i>	Low abundant	0.4027777 8	3	6	20
<i>Streptococcus</i>	Low abundant	0.3918918 9	3	5.66666 667	5

Table S26 : Network metrics for gut microbiome taxa in rectum exposed to 0 ppb clothianidin

CC = Closeness centrality, DG = Degree, NC = Neighborhood Connectivity

Taxa name (spp.)	ASV Classification	CC	DG	NC	ASV activity
<i>Dialister</i>	Low abundant	0.75	22	19.772727 27	2
<i>Morganella</i>	Low abundant	0.75	22	19.772727 27	1
<i>Gemmiger</i>	Low abundant	0.75	22	19.772727 27	10
<i>Phascolarctobacterium</i>	Low abundant	0.75	22	19.772727 27	4
<i>Staphylococcus</i>	Low abundant	0.75	22	19.772727 27	1
<i>Faecalibacterium</i>	Low abundant	0.75	22	19.772727 27	21

<i>Blautia</i>	Low abundant	0.75	22	19.772727 27	11
<i>Bacteroides</i>	Low abundant	0.75	22	19.772727 27	32
<i>Streptococcus</i>	Low abundant	0.75	22	19.772727 27	3
<i>Brevundimonas</i>	Low abundant	0.75	22	19.772727 27	1
<i>Ralstonia</i>	Low abundant	0.75	22	19.772727 27	1
<i>Acidocella</i>	Low abundant	0.7333333 3	21	17.238095 24	48
<i>Roseburia</i>	Low abundant	0.7021276 6	20	19.1	33
<i>Prevotella</i>	Low abundant	0.6875	19	18.526315 79	3
Unassigned	unassigned	0.6734693 9	19	18.684210 53	26229
<i>Bartonella</i>	Non-core	0.6734693 9	18	17.388888 89	19028
<i>Bifidobacterium</i>	Core	0.66	18	17.611111 11	199
<i>Delftia</i>	Low abundant	0.6470588 2	17	19.588235 29	3
<i>Snodgrassella</i>	Core	0.6470588 2	16	19.75	9248
<i>Escherichia</i>	Low abundant	0.6346153 8	17	19.647058 82	7
<i>Commensalibacter</i>	Non-core	0.6346153 8	18	18.722222 22	59
<i>Lachnoclostridium</i>	Low abundant	0.6346153 8	17	18.529411 76	81
<i>Lactobacillus</i>	Core	0.6111111 1	15	18.466666 67	65178

<i>Pediococcus</i>	Low abundant	0.55	7	9	23
<i>Anaerobiospirillum</i>	Low abundant	0.5409836 1	6	16.166666 67	12
<i>Shinella</i>	Low abundant	0.5322580 6	7	17.285714 29	17
<i>Bradyrhizobium</i>	Low abundant	0.515625	6	10.166666 67	3
<i>Bombella</i>	Non-core	0.515625	6	10.166666 67	2121
<i>Gilliamella</i>	Core	0.5076923 1	5	13.4	9502
<i>Flavobacterium</i>	Low abundant	0.4852941 2	4	18.75	7
<i>Frischella</i>	Non-core	0.4782608 7	3	14.333333 33	12408
<i>Pelomonas</i>	Low abundant	0.4647887 3	4	13.75	1
<i>Acinetobacter</i>	Low abundant	0.4647887 3	4	13.75	2
<i>Parasaccharibacter</i>	Non-core	0.44	3	9.3333333 3	28

Table S27 : Network metrics for gut microbiome taxa in rectum exposed to 0.1 ppb clothianidin

CC = Closeness centrality, DG = Degree, NC = Neighborhood Connectivity

Taxa name (spp.)	ASV Classification	CC	DG	NC	ASV activity
<i>Bifidobacterium</i>	Core	0.5853658 5	11	6.818181 82	544
<i>Bacillus</i>	Low abundant	0.5714285 7	9	6.777777 78	20
<i>Pseudaminobacter</i>	Non-core	0.5581395 3	7	7.142857 14	1
<i>Lysinibacillus</i>	Low abundant	0.5581395 3	7	7.142857 14	4
<i>Frischella</i>	Non-core	0.5581395 3	8	5	10075
<i>Lactobacillus</i>	Core	0.5106383	8	6.375	65373
<i>Staphylococcus</i>	Low abundant	0.5	5	7.6	1
Unassigned	unassigned	0.5	8	6.125	30672
<i>Acidocella</i>	Low abundant	0.48	6	7	50
<i>Bartonella</i>	Non-core	0.4705882 4	7	6	14746
<i>Actinomyces</i>	Low abundant	0.4615384 6	7	8	2
<i>Leifsonia</i>	Low abundant	0.4615384 6	7	8	1
<i>Streptococcus</i>	Low abundant	0.4615384 6	7	8	3
<i>Bradyrhizobium</i>	Low abundant	0.4615384 6	7	8	2
<i>Brevundimonas</i>	Low abundant	0.4615384 6	7	8	2

<i>Lachnospirillum</i>	Low abundant	0.4615384 6	3	6.666666 67	38
<i>Snodgrassella</i>	Core	0.4615384 6	8	6.875	13233
<i>Shinella</i>	Low abundant	0.4528301 9	4	7.5	24
<i>Bacteroides</i>	Low abundant	0.4285714 3	3	6	1
<i>Commensalibacter</i>	Non-core	0.4210526 3	4	6.5	107
<i>Pediococcus</i>	Low abundant	0.4	2	8	5
<i>Gilliamella</i>	Core	0.3870967 7	3	5.333333 33	8282
<i>Delftia</i>	Low abundant	0.3692307 7	2	5	2
<i>Bombella</i>	Non-core	0.3692307 7	2	5	14
<i>Anaerobiospirillum</i>	Low abundant	0.3529411 8	2	3.5	20

Table S28 : Network metrics for gut microbiome taxa in rectum exposed to 1 ppb clothianidin

CC = Closeness centrality, DG = Degree, NC = Neighborhood Connectivity

Taxa name (spp.)	ASV Classification	CC	DG	NC	ASV activity
<i>Lactobacillus</i>	Core	0.6470588 2	11	6.90909 091	63263
<i>Commensalibacter</i>	Non-core	0.6285714 3	10	7.9	167
<i>Lachnospirillum</i>	Low abundant	0.6111111 1	8	7.375	79

Unassigned	unassigned	0.6111111 1	8	9	33295
<i>Bartonella</i>	Non-core	0.6111111 1	9	7	13115
<i>Snodgrassella</i>	Core	0.6111111 1	10	7.3	13936
<i>Anaerobiospirillum</i>	Low abundant	0.5945945 9	8	6.875	23
<i>Acidocella</i>	Low abundant	0.5945945 9	8	6.75	51
<i>Escherichia</i>	Low abundant	0.5641025 6	6	7.5	1
<i>Oceanobacillus</i>	Low abundant	0.5641025 6	6	7.5	1
<i>Bifidobacterium</i>	Core	0.55	8	7	239
<i>Parasaccharibacter</i>	Non-core	0.5365853 7	5	8	5
<i>Pseudaminobacter</i>	Low abundant	0.5238095 2	6	7.66666 667	1
<i>Morganella</i>	Low abundant	0.5238095 2	6	7.66666 667	1
<i>Shinella</i>	Low abundant	0.5238095 2	5	5.4	31
<i>Bacteroides</i>	Low abundant	0.5116279 1	5	7	2
<i>Gilliamella</i>	Core	0.5116279 1	6	6.5	3188
<i>Lysinibacillus</i>	Low abundant	0.5	5	6	15
<i>Frischella</i>	Non-core	0.4888888 9	5	7.6	11109
<i>Blautia</i>	Low abundant	0.4782608 7	3	9	1

<i>Flavobacterium</i>	Low abundant	0.4583333 3	4	6.25	2
<i>Delftia</i>	Low abundant	0.4583333 3	4	6.25	1
<i>Pediococcus</i>	Low abundant	0.4150943 4	2	8.5	11

Table S29 : Network metrics for gut microbiome taxa in rectum exposed to 10 ppb clothianidin

CC = Closeness centrality, DG = Degree, NC = Neighborhood Connectivity

Taxa name (spp.)	ASV Classification	CC	DG	NC	ASV activity
<i>Snodgrassella</i>	Core	0.6774193 5	12	7.66666667	7242
<i>Bifidobacterium</i>	Core	0.65625	11	8.54545455	642
<i>Frischella</i>	Non-core	0.65625	11	7.36363636	6984
<i>Commensalibacter</i>	Non-core	0.6176470 6	9	8.88888889	87
<i>Bradyrhizobium</i>	Low abundant	0.6176470 6	8	8.75	1
Unassigned	unassigned	0.6176470 6	9	8.44444444	26387
<i>Acidocella</i>	Low abundant	0.6	10	7.3	43
<i>Shinella</i>	Low abundant	0.5675675 7	7	9	15
<i>Psychrobacter</i>	Low abundant	0.5675675 7	6	7.5	1
<i>Staphylococcus</i>	Low abundant	0.5526315 8	7	9.71428571	1

<i>Faecalibacterium</i>	Low abundant	0.5526315 8	7	9.71428571	1
<i>Pediococcus</i>	Low abundant	0.5526315 8	8	7.5	7
<i>Bacillus</i>	Low abundant	0.5526315 8	5	7.2	1
<i>Lachnoclostridium</i>	Low abundant	0.5384615 4	7	6.42857143	59
<i>Anaerobiospirillum</i>	Low abundant	0.525	6	5.16666667	18
<i>Bartonella</i>	Non-core	0.525	5	7.6	11244
<i>Gilliamella</i>	Core	0.5121951 2	6	5.83333333	12959
<i>Pseudaminobacter</i>	Low abundant	0.5	5	9.2	1
<i>Streptococcus</i>	Low abundant	0.5	5	9.2	2
<i>Lactobacillus</i>	Core	0.4772727 3	3	7.33333333	58212
<i>Parasaccharibacter</i>	Non-core	0.4468085 1	2	7	50
<i>Flavobacterium</i>	Low abundant	0.4117647 1	3	6.33333333	1

Table S30 : Number of positive (+) and/or negative (-) interactions at the genus level in the microbial network depending on each honeybee gut section (midgut, ileum and rectum) and clothianidin concentrations (Ctrl (0 ppb), 0.1, 1 and 10 ppb)

Clothianidin Concentration	(+)			(-)		
	Midgut	Ileum	Rectum	Midgut	Ileum	Rectum
Control (0 ppb)	96	27	108	1	6	5
0.1 ppb	28	52	21	5	5	1
1 ppb	30	73	13	5	4	0
10 ppb	40	29	17	4	2	3

Figure S1 : Violin plot of Degree from taxa in midgut microbial networks

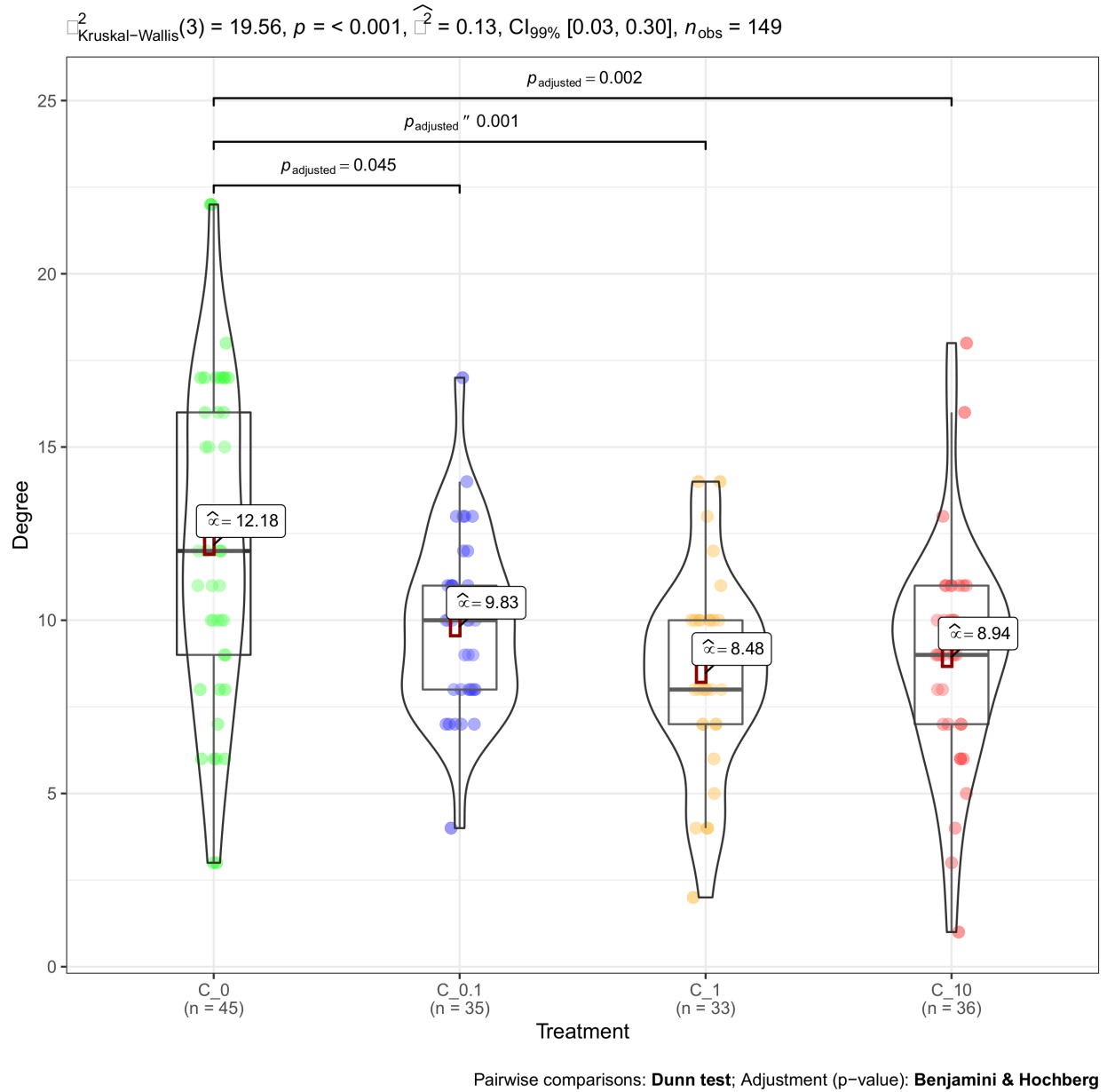
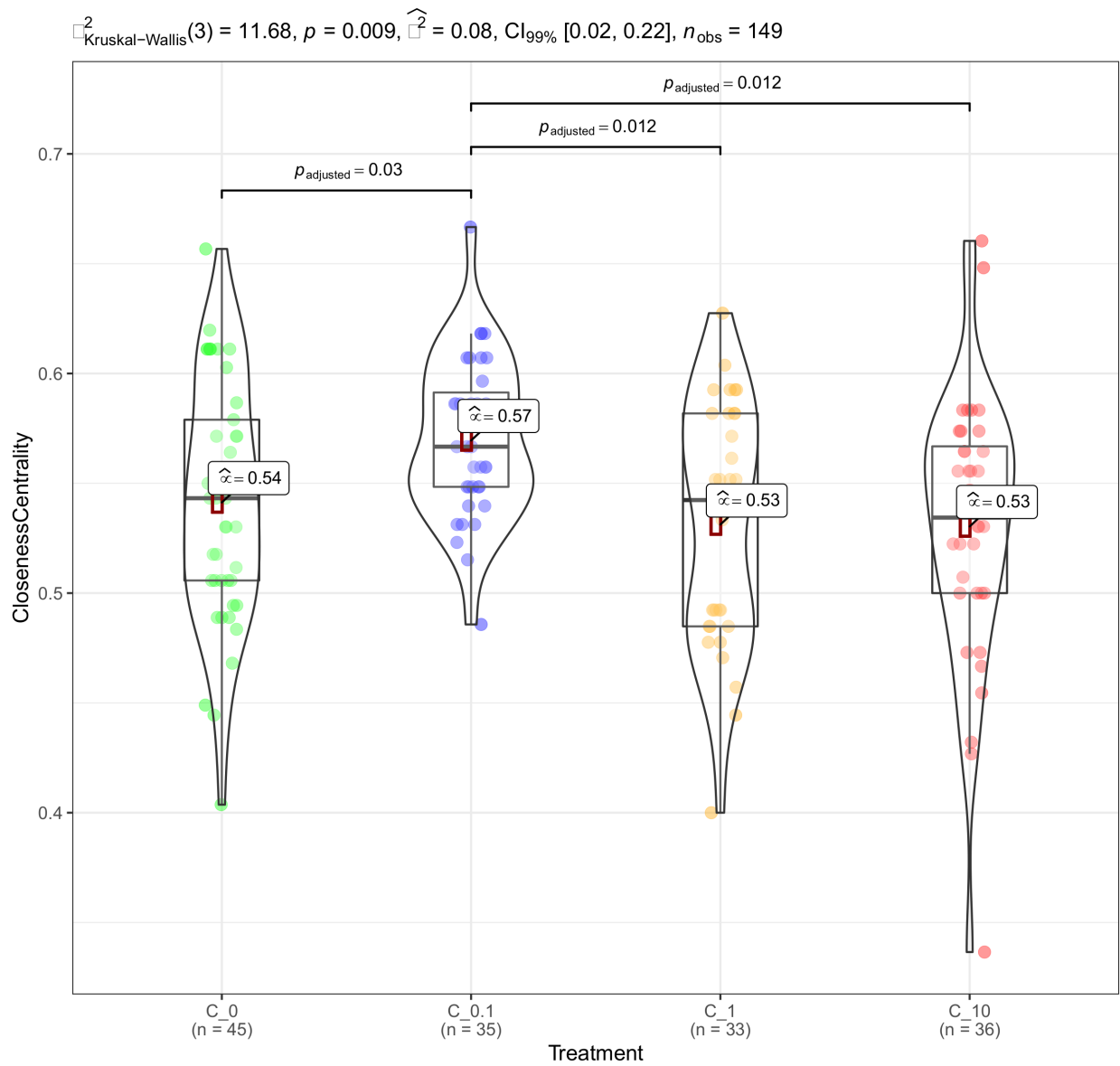
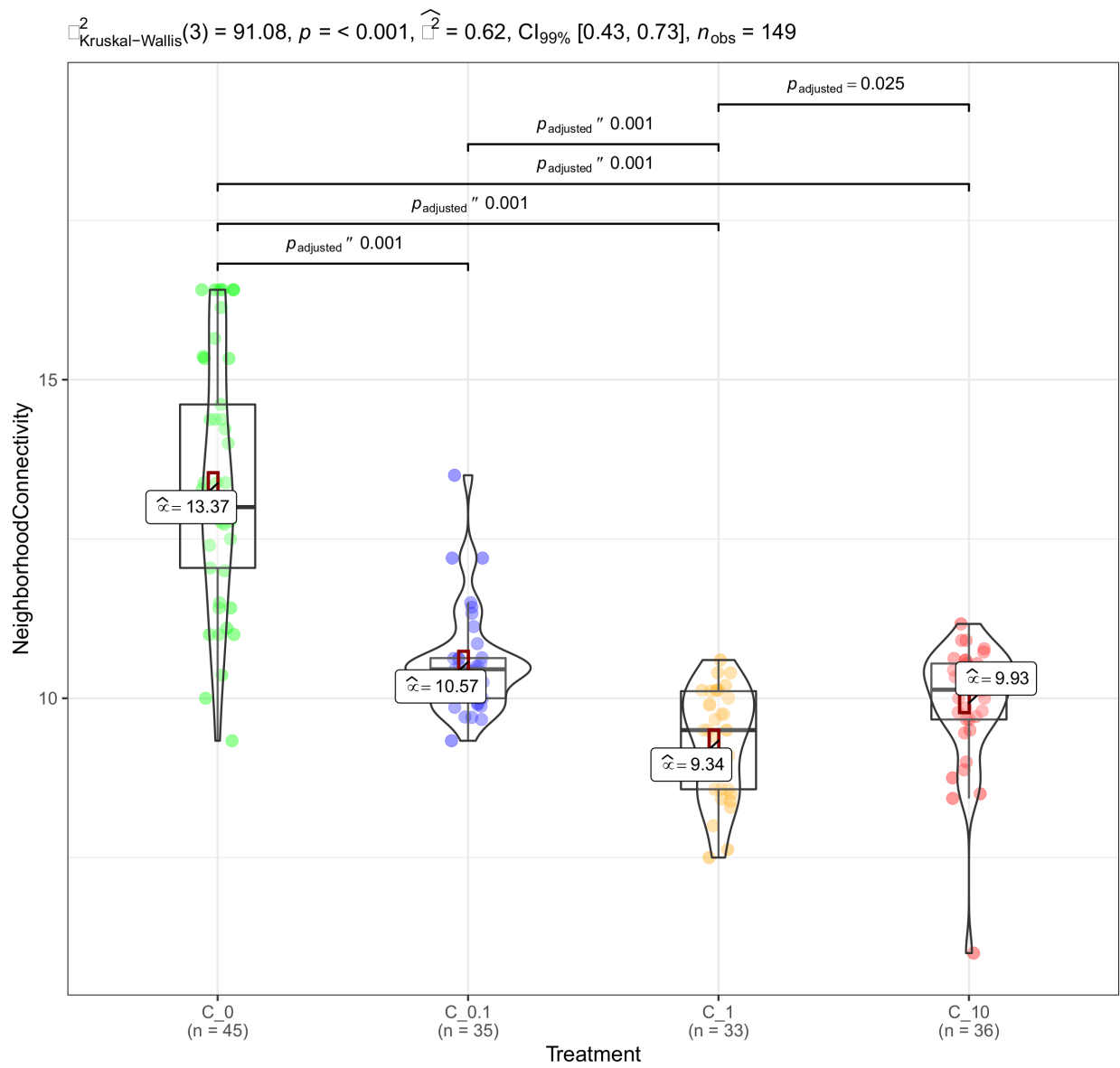


Figure S2 : Violin plot of Closeness Centrality from taxa in midgut microbial networks



Pairwise comparisons: **Dunn test**; Adjustment (p-value): **Benjamini & Hochberg**

Figure S3 : Violin plot of Neighborhood Connectivity from taxa in midgut microbial networks



Pairwise comparisons: **Dunn test**; Adjustment (p-value): **Benjamini & Hochberg**

Figure S4 : Violin plot of Degree from taxa in ileum microbial networks

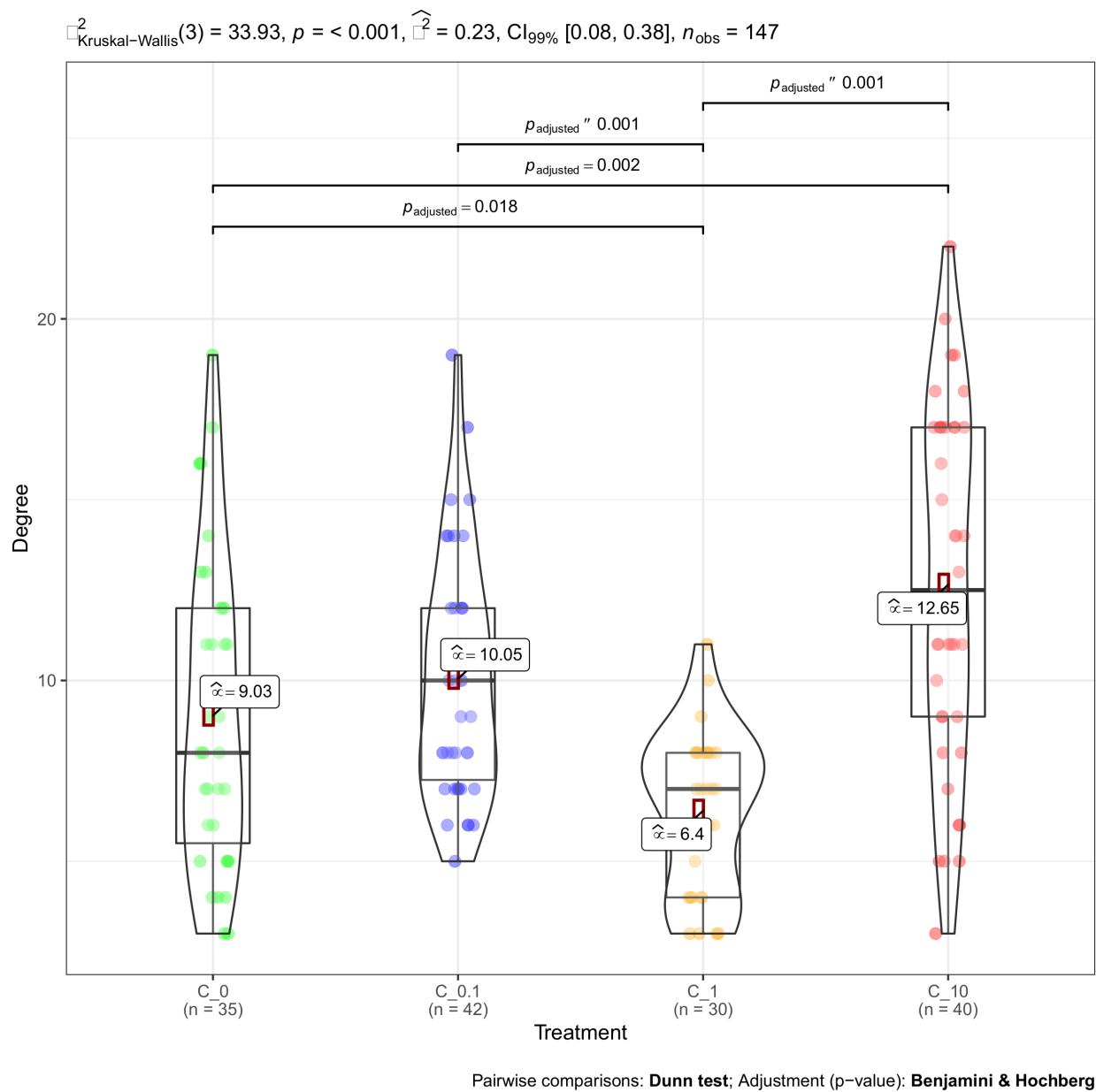
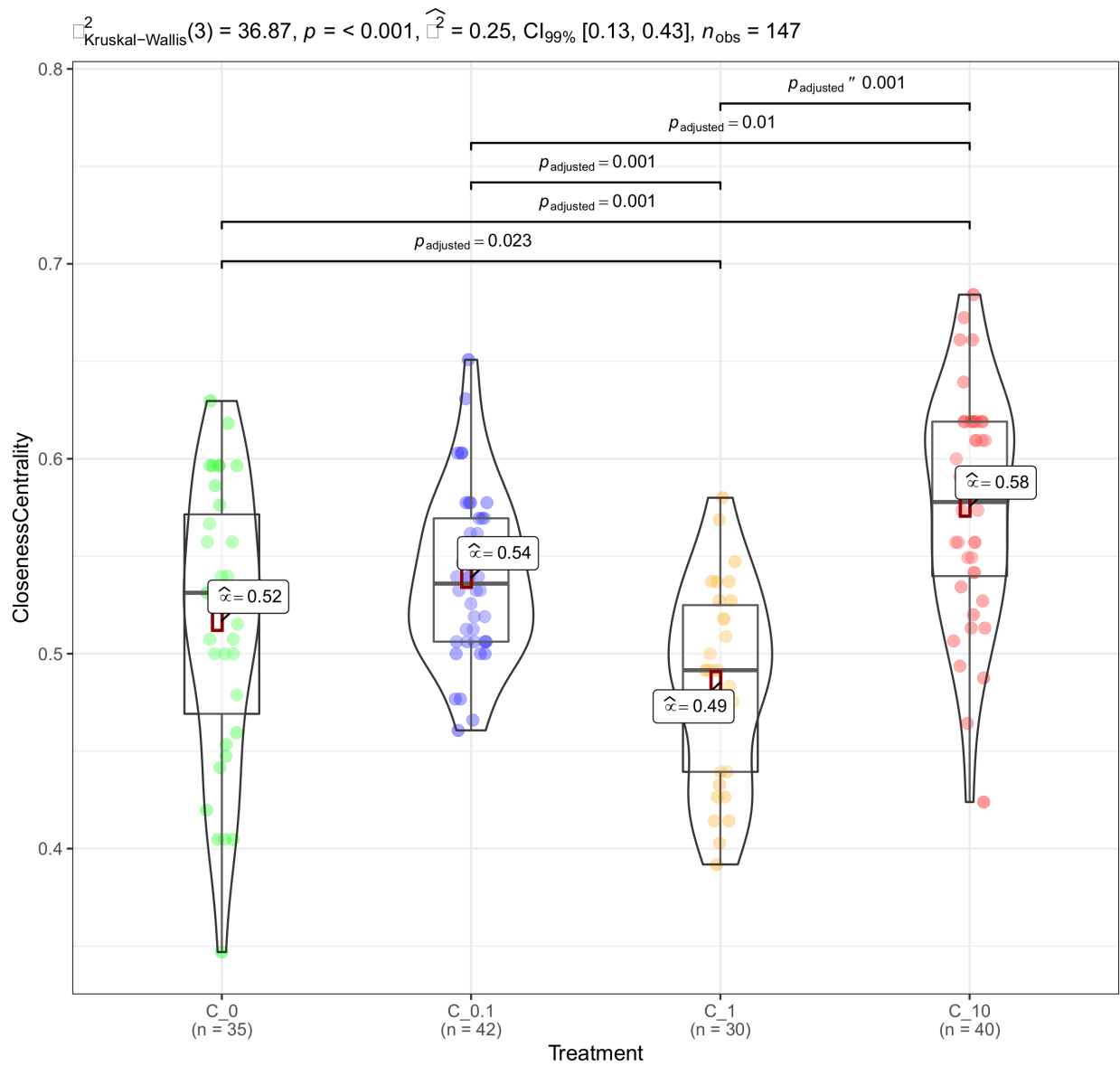


Figure S5 : Violin plot of Closeness Centrality from taxa in ileum microbial networks



Pairwise comparisons: **Dunn test**; Adjustment (p-value): **Benjamini & Hochberg**

Figure S6 : Violin plot of Neighborhood Connectivity from taxa in ileum microbial networks

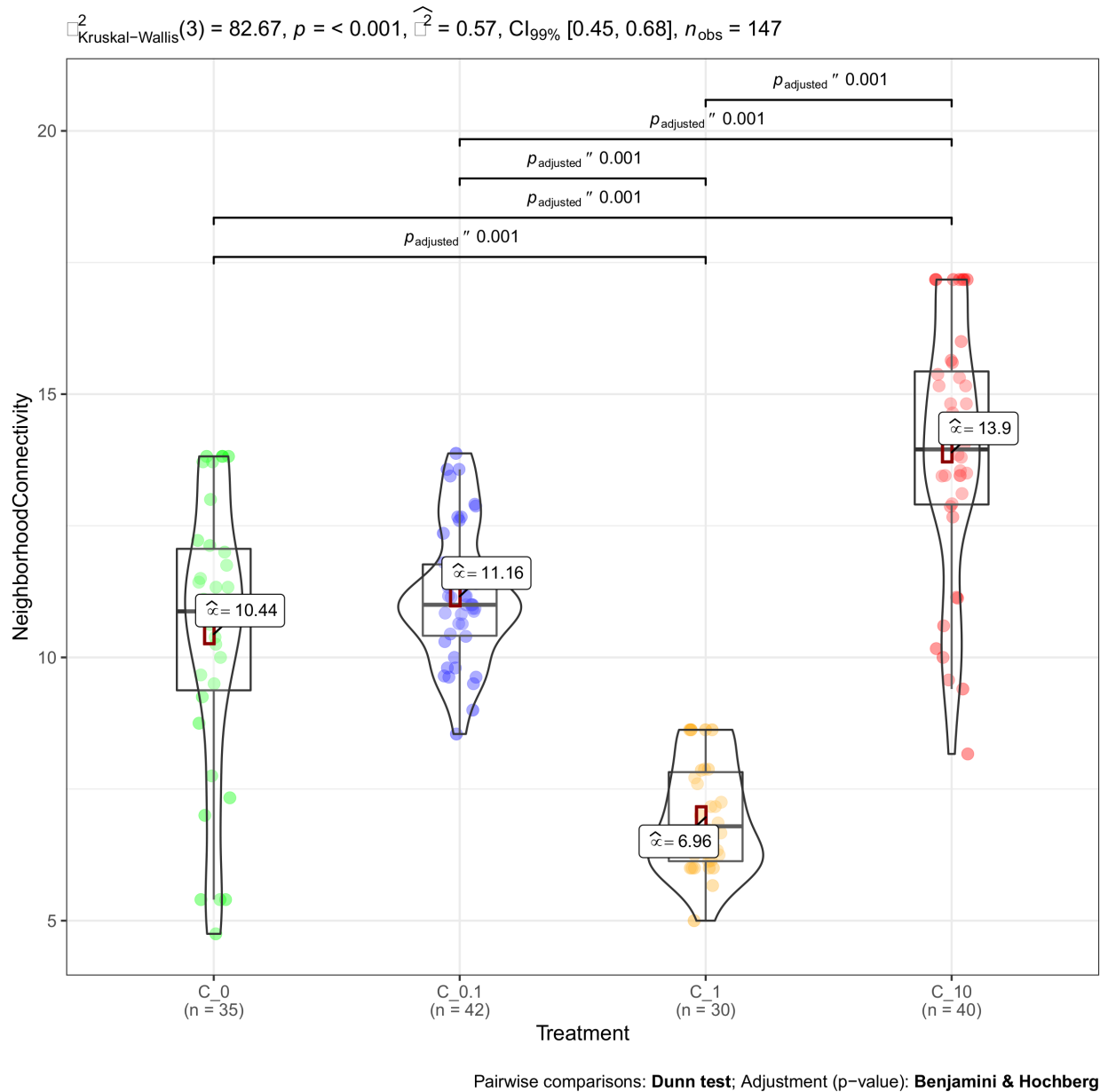


Figure S7 : Violin plot of Degree from taxa in rectum microbial networks

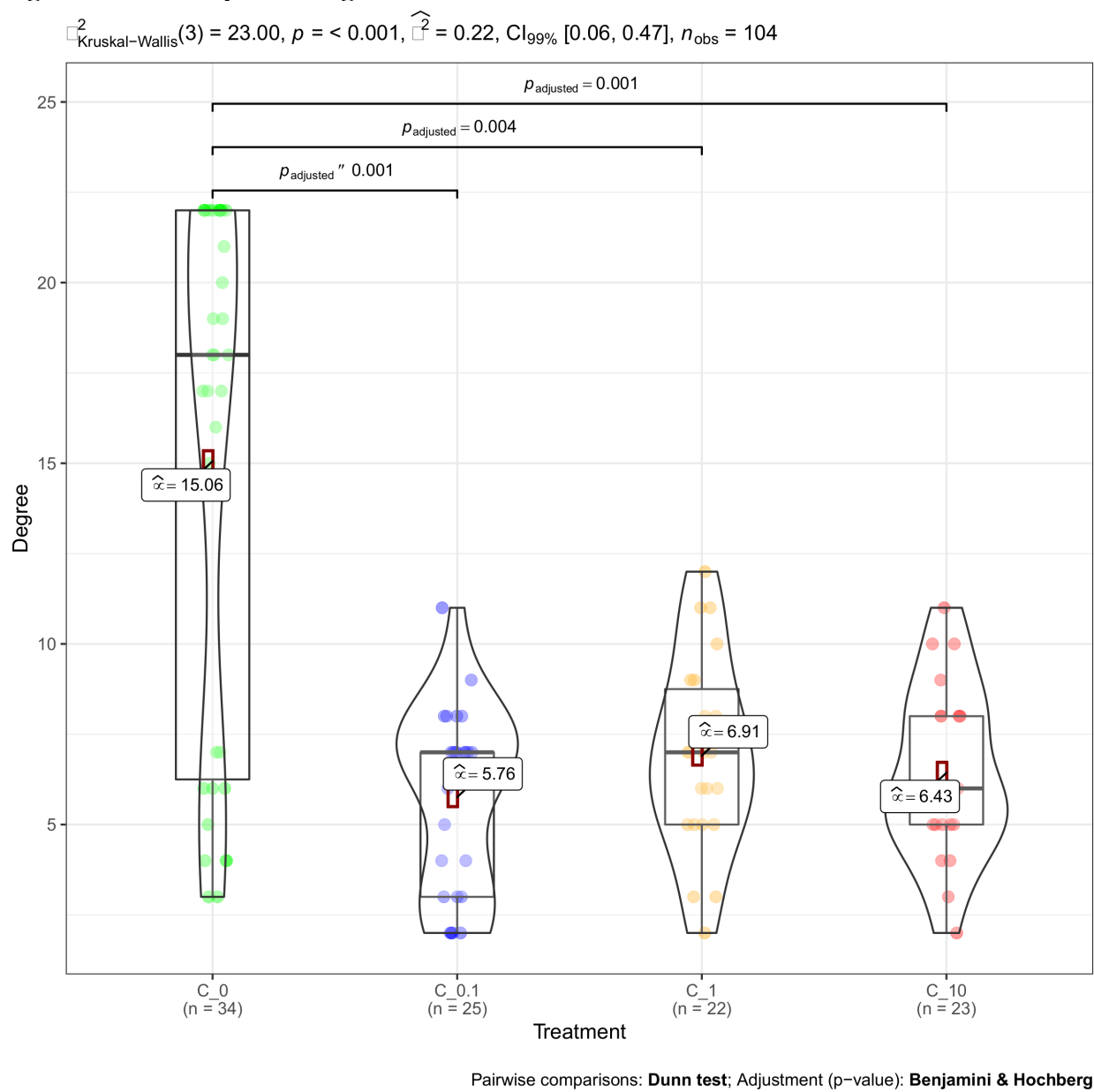


Figure S8 : Violin plot of Closeness Centrality from taxa in rectum microbial networks

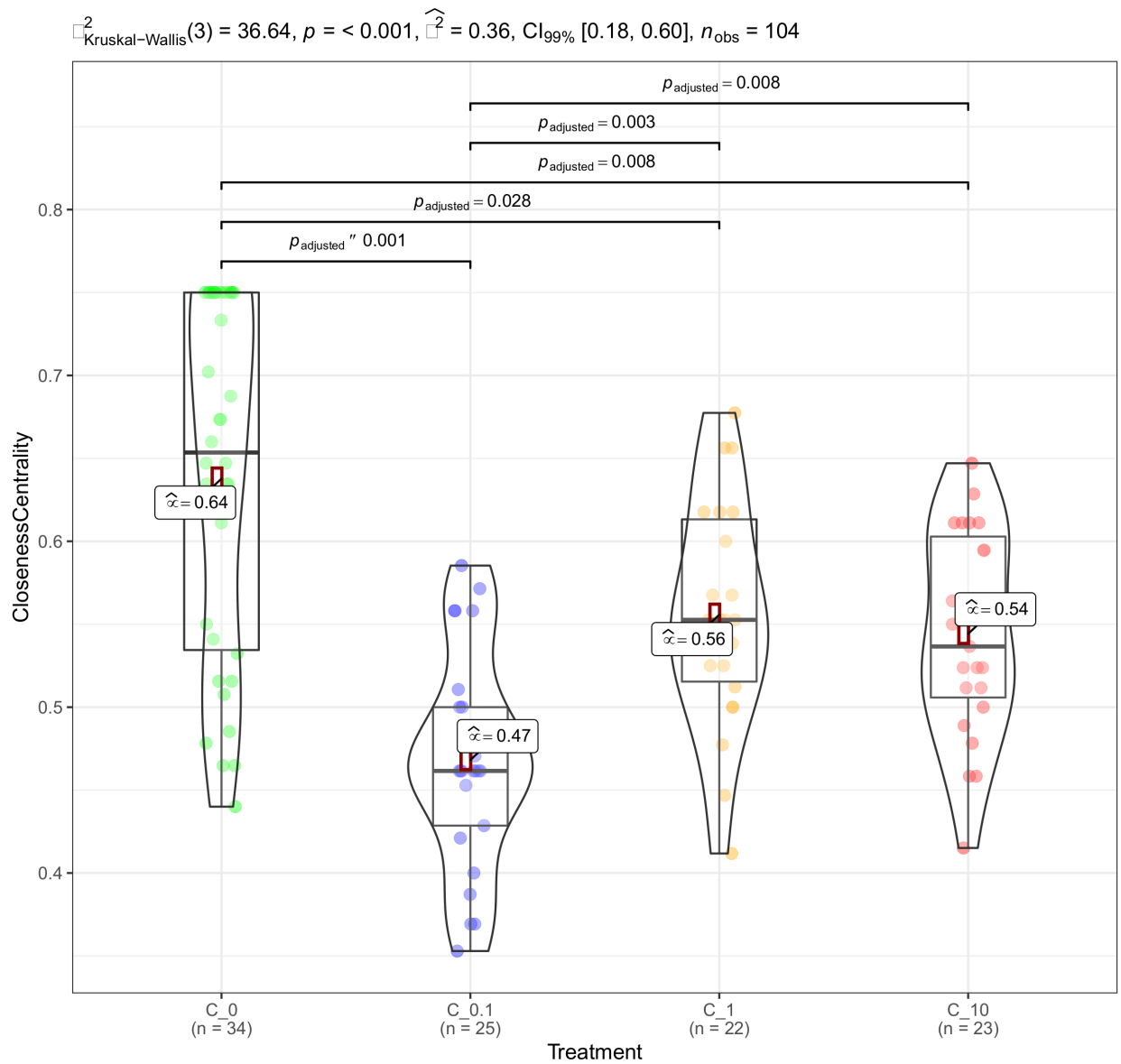


Figure S9 : Violin plot of Neighborhood Connectivity from taxa in rectum microbial networks

