

Comparative Metagenomic Analysis of Bacteriophages and Prophages in Gnotobiotic Mouse Models

Oluwaseun A. Ishola,¹ Susanne Kublik,¹ Abilash Chakravarthy Durai Raj,^{1†} Caspar Ohnmacht,² Stefanie Schulz^{1*}, Bärbel U. Foessel^{1††}, Michael Schloter,^{1,3,4}

¹ Research Unit for Comparative Microbiome Analysis, Helmholtz Center Munich, German Research Center for Environmental Health, Neuherberg, Germany.

² Mucosal Immunology Group, Center of Allergy and Environment (ZAUM), Technical University and Helmholtz Center Munich, Munich, Germany.

³ Technical University of Munich, Chair for Environmental Microbiology, Freising, Germany.

⁴ Technical University of Munich, Central Institute for Nutrition and Health, Freising, Germany.

[†] Present address: Max von Pettenkofer Institute of Hygiene and Medical Microbiology, Ludwig-Maximilians-University of Munich, Munich, Germany.

^{††} Present address: Institute of Epidemiology, Research Unit Molecular Epidemiology, Helmholtz Munich, Germany.

Table S1: Gnotobiotic murine models Oligo-MM12 and ASF microflora inoculum

Oligo-MM12	ASF
<i>Clostridium innocuum</i>	<i>Clostridium spp ASF</i>
<i>Bacteroides caecimuris</i>	<i>Lactobacillus murinus</i> <i>ASF</i>
<i>Lactobacillus reuteri</i>	<i>Parabacteriodes</i> <i>goldsteinii</i>
<i>Enterococcus faecalis</i>	
<i>Muribaculum intestinale</i>	
<i>Flavonifractor plautii</i>	
<i>Clostridium clostridioforme</i>	
<i>Akkermansia muciniphila</i>	
<i>Turicimonas muris</i>	
<i>Blautia coccoides</i>	
<i>Acutalibacter muris</i>	
<i>Bifidobacterium animalis</i> <i>subsp. animalis</i>	

Table S2: Read statistics of metagenomic sequencing samples included in this study.

Sample Sequencing name	Sample name	No. of raw reads	No. of reads after adapter removal	No. of reads after trimming	No. of host-mouse reads	No. of non-mouse reads	% of murine reads	No. of 16S rRNA removed	No. of non-rRNA reads
seuntube10_S10_R1_001, pair, clean, fq	SPF ileum content R1	32469279.00	28187328.00	26789345.00	19849360.00	6701229.00	74.09	57003.50	6644225.50
seuntube10_S10_R2_001, pair, clean, fq	SPF ileum content R2	32469279.00	28187328.00	26789345.00	19849360.00	6701229.00	74.09	57003.50	6644225.50
seuntube11_S11_R1_001, pair1, clean, fq	ASF ileum content R1	22518571.00	19158564.00	14528890.00	13775112.00	597319.00	94.81	20252.00	577067.00
seuntube11_S11_R2_001, pair1, clean, fq	ASF ileum content R2	22518571.00	19158564.00	14528890.00	13775112.00	597319.00	94.81	20252.00	577067.00
seuntube12_S12_R1_001, pair1, clean, fq	Oligo-MM ileum content R1	26300108.00	24650174.00	24650174.00	21868625.00	2293007.00	88.72	112982.50	2180024.50
seuntube12_S12_R2_001, pair1, clean, fq	Oligo-MM ileum	26300108.00	24650174.00	24650174.00	21868625.00	2293007.00	88.72	112982.50	2180024.50

	content R2								
seuntube1_S1_ R1_001,pair1_cl ean,fq	SPF colon content R1	33212147.00	29625432.00	22775691.00	1050952.00	21701930.00	4.61	137837.00	21564093.00
seuntube1_S1_ R2_001,pair1_cl ean,fq	SPF colon content R2	33212147.00	29625432.00	22775691.00	1050952.00	21701930.00	4.61	137837.00	21564093.00
seuntube2_S2_ R1_001,pair1_cl ean,fq	ASF colon content R1	24930096.00	23388936.00	22386511.00	3425486.00	18898931.00	15.30	98294.50	18800636.50
seuntube2_S2_ R2_001,pair1_cl ean,fq	ASF colon content R2	24930096.00	23388936.00	22386511.00	3425486.00	18898931.00	15.30	98294.50	18800636.50
seuntube3_S3_ R1_001,pair1_cl ean,fq	Oligo- MM colon content R1	23217211.00	22227299.00	20412986.00	1214256.00	19142525.00	5.95	106352.00	19036173.00
seuntube3_S3_ R2_001,pair1_cl ean,fq	Oligo- MM colon content R2	23217211.00	22227299.00	20412986.00	1214256.00	19142525.00	5.95	106352.00	19036173.00
seuntube4_S4_ R1_001,pair1_cl ean,fq	SPF ileum tissue R1	20201473.00	16104339.00	15024334.00	13479765.00	2346752.00	89.72	114821.50	2231930.50

seuntube4_S4_R2_001,pair1_clean,fq	SPF ileum tissue R2	20201473.00	16104339.00	15024334.00	13479765.00	2346752.00	89.72	114821.50	2231930.50
seuntube5_S5_R1_001,pair1_clean,fq	ASF ileum tissue R1	27893268.00	21613834.00	20208117.00	18010960.00	1996069.00	89.13	33724.50	1962344.50
seuntube5_S5_R2_001,pair1_clean,fq	ASF ileum tissue R2	27893268.00	21613834.00	20208117.00	18010960.00	1996069.00	89.13	33724.50	1962344.50
seuntube6_S6_R1_001,pair1_clean,fq	Oligo-MM ileum tissue R1	31028385.00	26791872.00	21849264.00	17294225.00	4134271.00	79.15	214795.50	3919475.50
seuntube6_S6_R2_001,pair1_clean,fq	Oligo-MM ileum tissue R2	31028385.00	26791872.00	21849264.00	17294225.00	4134271.00	79.15	214795.50	3919475.50
seuntube7_S7_R1_001,pair1_clean	SPF colon tissue R1	21879263.00	20682534.00	19758590.00	16036821.00	2368853.00	81.16	52517.50	2316335.50
seuntube7_S7_R2_001,pair1_clean	SPF colon tissue R2	21879263.00	20682534.00	19758590.00	16036821.00	2368853.00	81.16	52517.50	2316335.50
seuntube8_S8_R1_001,pair1_clean	ASF colon tissue R1	30445992.00	27888628.00	27888628.00	22815114.00	3678338.00	81.81	183416.50	3494921.50

seuntube8_S8_R2_001,pair1_clean	ASF colon tissue R2	30445992.00	27888628.00	27888628.00	22815114.00	3678338.00	81.81	183416.50	3494921.50
seuntube9_S9_R1_001,pair1_clean	Oligo-MM colon tissue R1	10159586.00	8007039.00	6097944.00	5530529.00	497985.00	90.69	12363.50	485621.50
seuntube9_S9_R2_001,pair1_clean	Oligo-MM colon tissue R2	10159586.00	8007039.00	6097944.00	5530529.00	497985.00	90.69	12363.50	485621.50
Total		304255379.00	268325979.00	242370474.00	154351205.00	84357209.00		1144360.50	83212848.50

Table S3: Contig assembly statistics of non-host non-rRNA reads.

Sample names	Total number of contigs	Total contigs length (bp)	Minimum contigs length	Maximum contigs length	Average length (bp)	N50
SPF merged colon content and tissue	304899	279317015	200	420970	916	1250
Oligo-MM12 merged colon content and tissue	12326	27776895	200	290252	2254	32819
ASF merged colon content and tissue	13979	15346287	200	355576	1098	34658
SPF merged ileum content and tissue	51777	59060320	200	147546	1141	2336
Oligo-MM12 merged ileum content and tissue	25536	19102394	200	237544	748	1442
ASF merged ileum content and tissue	5457	4140752	200	104512	759	5099

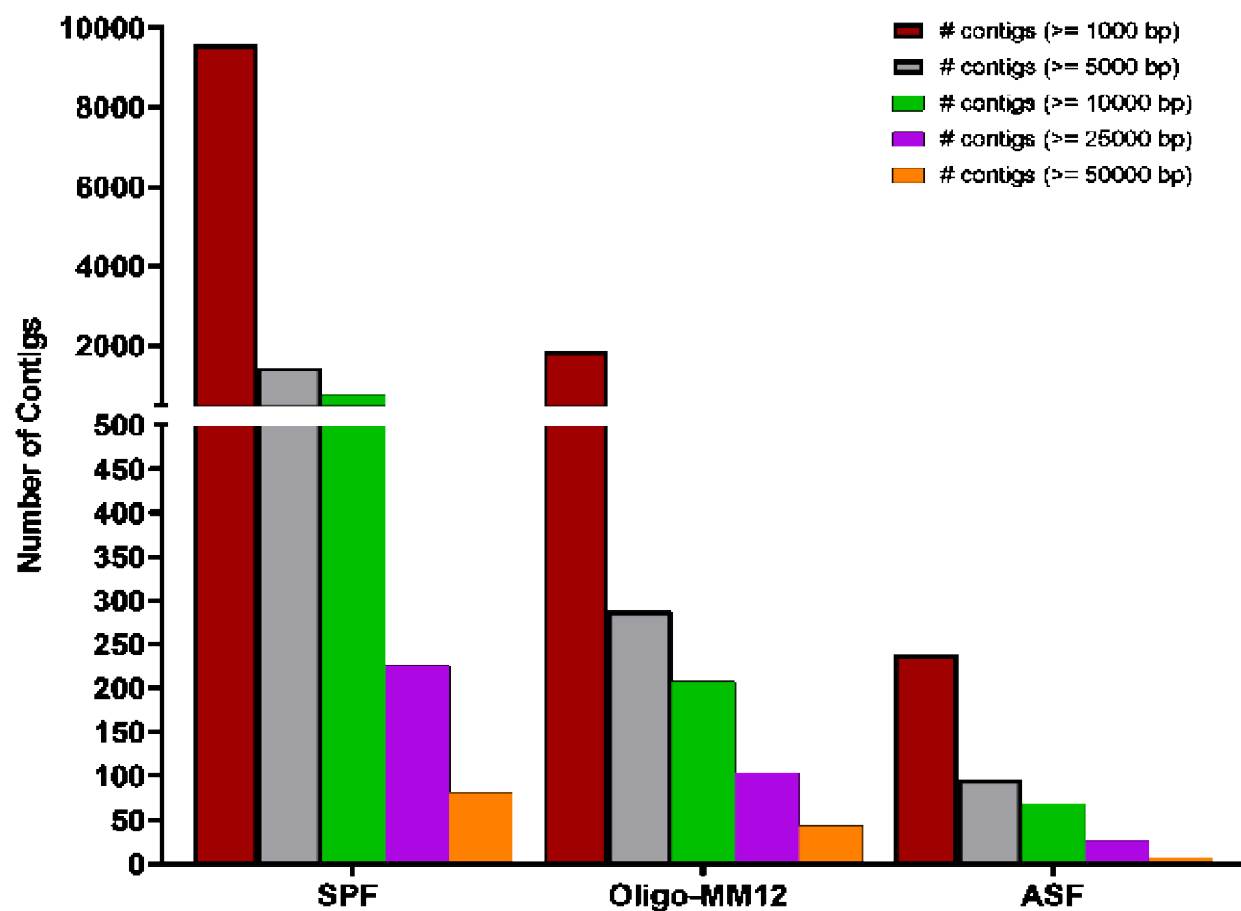


Figure S1: Assembly of murine model reads: Bar chart of paired-end contig assembly distribution in SPF, Oligo-MM12 and ASF.

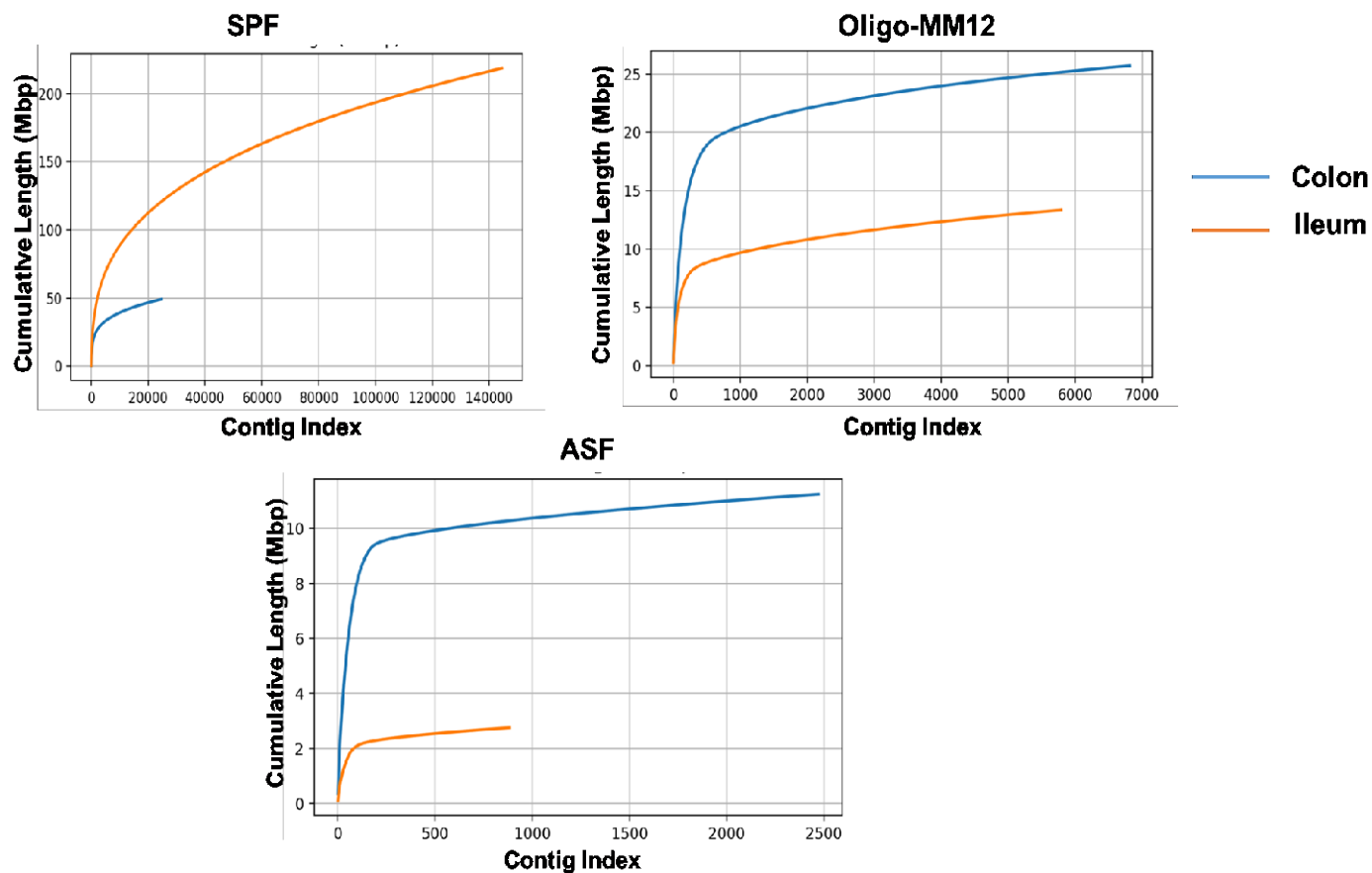


Figure S2: Assembly of murine model reads; frequency of assembled contigs distribution among the murine models. The cumulative length shows the size of an assembly and the number of contigs in it, and the contig index represents the longest to shortest assembly. Orange colour line represents the ileum while blue the colon.

Table S4: Bacterial community structure in ileum and colon samples from the gnotobiotic murine models inoculated with Oligo-MM12 and ASF. Values displayed are relative abundance in % at the species level.

Oligo-MM12			ASF		
Bacterial species	Ileum	Colon	Bacterial species	Ileum	Colon
<i>Clostridium innocuum</i>	0.13	0.07	<i>Clostridium spp</i> <i>ASF</i>	0	6.89
<i>Bacteroides caecimuris</i>	76.19	7.49	<i>Lactobacillus</i> <i>murinus ASF</i>	99.02	0.62
<i>Lactobacillus reuteri</i>	0.01	2.90	<i>Parabacterioidetes</i> <i>goldsteinii</i>	0.98	92.49
<i>Enterococcus faecalis</i>	0.01	0.00			
<i>Muribaculum intestinale</i>	10.62	30.66			
<i>Flavonifractor plautii</i>	0.49	0.32			
<i>Clostridium clostridioforme</i>	6.36	0.97			
<i>Akkermansia muciniphila</i>	3.27	39.67			
<i>Turicimonas muris</i>	2.76	17.62			
<i>Blautia coccoides</i>	0.16	0.30			
Total	100	100		100	100

Table S5: Bacterial community structure in ileum and colon samples from SPF mice. Values displayed are relative abundance in % at the species level.

SPF bacterial species	Ileum	Colon
<i>Acutalibacter muris</i>	0	0.00455
<i>Acutalibacter sp1XD833</i>	0	0.0619
<i>Akkermansia muciniphila</i>	0.15498	0.12654
<i>Alistipes sp</i>	0.02773	3.45665
<i>Anaerotruncus sp1XD4293</i>	0	0.50146
<i>Atopobiaceae bacteriumFL090493</i>	0.0247	0.00568
<i>Bacteria unclassifiedSGB41508</i>	0	0.06453
<i>Bacteria unclassifiedSGB41729</i>	0	0.0288
<i>Bacteria unclassifiedSGB43539</i>	0	0.00414
<i>Bacteria unclassifiedSGB43541</i>	0	0.00386
<i>Bacterium 01xD882</i>	0	0.0103
<i>Bacterium 1XD2113</i>	0	0.03885
<i>Bacterium 1XD421</i>	0	0.52163
<i>Bacterium 1XD4276</i>	0	0.02923
<i>Bacterium 1xD4287</i>	0	0.22607
<i>Bacterium 1xD848</i>	0	0.02486
<i>Bacterium 1xD86</i>	0	0.14364
<i>Bacterium D1629</i>	0	0.05154
<i>Bacterium D1676</i>	0	0.02471
<i>Bacteroidaceae bacterium</i>	0.04505	1.72578
<i>Bacteroidales bacterium</i>	14.99742	4.74278
<i>Bacteroides acidifaciens</i>	0	0.14199
<i>Bacteroides caecimuris</i>	0	0.10552
<i>Bacteroides spL104</i>	0	0.43813
<i>Barnesiella spCU968</i>	3.28986	0.80602
<i>BlautiaSGB43555</i>	0	0.14114
<i>Brevibacterium SGB41697</i>	0	0.02819
<i>Clostridiaceae bacterium</i>	0	0.03219
<i>Clostridiales bacterium</i>	0	0.03974
<i>Clostridium SGB40327</i>	0.68585	0.25611
<i>Desulfovibrio SGB40192</i>	0.31103	10.83932
<i>Desulfovibrio SGB41239</i>	0	0.00324
<i>Dorea sp52</i>	0	0.01006
<i>Duncaniella dubosii</i>	7.6005	2.16354
<i>Duncaniella freteri</i>	1.99252	0.67867
<i>Duncaniella muris</i>	14.7991	4.48316

<i>Emergencia sp1XD2110</i>	0	0.00969
<i>Eubacterium SGB102306 2</i>	0	0.0142
GGB14001 SGB21428	1.0683	0.35265
GGB18827 SGB41440	0	0.0724
GGB20145 SGB41586	0	0.00422
GGB20146 SGB29427	0	0.0496
GGB20149 SGB29430	0	0.06222
GGB23844 SGB35575	0	1.10852
GGB24102 SGB40205	0	0.8953
GGB24132 SGB35935	1.23027	0.43477
GGB24149 SGB35953	2.87501	0.43156
GGB25052 SGB36974	0	0.67076
GGB25107 SGB41514	0	0.21614
GGB261 SGB59900	0	0.02212
GGB27782 SGB40196	0	0.5314
GGB27861 SGB40295	1.5944	0.19307
GGB27866 SGB40300	0.89879	0.43255
GGB27872 SGB40306	0.51612	0.18014
GGB27873 SGB40307	1.46125	0.51149
GGB27885 SGB40319	1.08366	0.38084
GGB27890 SGB40324	1.13688	0.45307
GGB27892 SGB40326	12.21319	4.11916
GGB27929 SGB40368	2.60108	0.878
GGB27929 SGB41624	0	0.00876
GGB28248 SGB40791	0.0543	2.22569
GGB28265 SGB40817	0	1.75288
GGB28308 SGB40878	0.04765	2.00762
GGB28317 SGB40889	0	0.17172
GGB28330 SGB40904	0	0.01785
GGB28357 SGB40935	0	0.15814
GGB28381 SGB40961	0	0.30219
GGB28382 SGB40962	0	0.42572
GGB28383 SGB40963	0.03231	0.18838
GGB28384 SGB40964	0	0.1056
GGB28386 SGB40966	0	0.13723
GGB28392 SGB40972	0	0.13631
GGB28393 SGB40973	0.03231	2.11221
GGB28394 SGB40975	0	0.01379
GGB28401 SGB40983	0	0.60913
GGB28403 SGB40190	0	0.14234
GGB28404 SGB40986	0	0.04308

GGB28409 SGB40991	0	0.01287
GGB28418 SGB41000	0	0.01072
GGB28418 SGB41001	0	0.68208
GGB28430 SGB41013	0	0.00254
GGB28431 SGB41014	0	0.00181
GGB28433 SGB41016	0	0.02539
GGB28437 SGB41020	0	0.02566
GGB28439 SGB41022	0	0.1858
GGB28456 SGB41039	0	0.24674
GGB28632 SGB41253	0	0.01488
GGB28761 SGB41409	0	0.0166
GGB28765 SGB41415	0	0.10759
GGB28769 SGB41421	0	0.00923
GGB28776 SGB41429	0	0.06031
GGB28782 SGB41435	0	0.02816
GGB28783 SGB41436	0	0.00492
GGB28793 SGB41446	0	0.02288
GGB28817 SGB41472	0	0.0245
GGB28822 SGB41478	0	0.00609
GGB28828 SGB41484	0	0.42117
GGB28829 SGB41485	0	0.07246
GGB28835 SGB41494	0	0.33478
GGB28836 SGB41495	0	0.00047
GGB28839 SGB41503	0	0.00146
GGB28841 SGB41505	0	0.01409
GGB28842 SGB41507	0	0.08936
GGB28845 SGB41512	0	0.02214
GGB28849 SGB41516	0	0.10228
GGB28853 SGB41519	0	0.02142
GGB28854 SGB41523	0	0.02539
GGB28855 SGB41524	0	0.03099
GGB28861 SGB41531	0	0.30702
GGB28865 SGB41537	0	0.0118
GGB28865 SGB43001	0	0.00704
GGB28868 SGB41542	0	0.17239
GGB28879 SGB43526	0	0.02334
GGB28880 SGB41560	0	0.06226
GGB28881 SGB41561	0	0.00972
GGB28883 SGB41564	0	0.03677
GGB28885 SGB41566	0	0.53526
GGB28888 SGB41569	0	0.0265

GGB28895 SGB41576	0	0.05296
GGB28901 SGB41592	0	0.06842
GGB28903 SGB41594	0	0.00927
GGB28904 SGB41597	0	0.0624
GGB28905 SGB41598	0	0.0457
GGB28907 SGB41600	0	0.11962
GGB28916 SGB41612	0	0.06896
GGB28927 SGB41625	0	0.0114
GGB28934 SGB41635	0	0.0236
GGB28949 SGB41655	0	0.06175
GGB28958 SGB41667	0	0.00766
GGB28959 SGB41668	0	0.02187
GGB28961 SGB41670	0	0.00247
GGB28967 SGB41417	0	0.0068
GGB28967 SGB41678	0	0.01306
GGB28980 SGB41692	0	0.07409
GGB28981 SGB41693	0	0.02798
GGB28981 SGB41694	0	0.00041
GGB28991 SGB41705	0	0.01749
GGB28996 SGB41712	0	0.50854
GGB29001 SGB41717	0	0.14935
GGB29002 SGB41718	0	0.19764
GGB29003 SGB41719	0	0.10879
GGB29004 SGB41721	0	0.56836
GGB29005 SGB41723	0	1.3658
GGB29008 SGB41728	0	1.04995
GGB29468 SGB42247	0.24007	0.01044
GGB29530 SGB42316	0	0.00513
GGB29531 SGB42317	0	0.22355
GGB29549 SGB42343	0	0.03529
GGB30141 SGB43066	0	0.02761
GGB30142 SGB43067	0	0.05018
GGB30145 SGB43072	0	0.05791
GGB30147 SGB43074	0	0.29976
GGB30290 SGB43252	0	0.46782
GGB30296 SGB43260	0	0.00408
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GGB30301 SGB43265	0	0.00209
GGB30302 SGB43266	0	0.0349
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GGB30311 SGB43288	0	0.68854
GGB30408 SGB43438	0	0.00432
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GGB30450 SGB43507	0	0.53368
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GGB31064 SGB44328	0	0.50223
GGB31109 SGB44380	0	0.44928
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GGB31701 SGB45057	0	0.2236
GGB3171 SGB4185	0	0.13278
GGB31823 SGB45199	0	0.30646
GGB31839 SGB45217	0.03345	1.40112
GGB31850 SGB45228	0	0.61679
GGB31851 SGB45230	0	0.21088
GGB31853 SGB45233	0	0.10812
GGB3583 SGB21441	0	2.13401
GGB3661 SGB41629	0	0.13443
GGB3793 SGB41498	0	0.17019
GGB42328 SGB59496	0	0.04002
GGB42343 SGB59511	0	0.13431
GGB42344 SGB59512	0	0.09735
GGB42586 SGB59781	0	0.02015
GGB42949 SGB43520	0	0.03062
GGB45293 SGB41002	0	0.39775

GGB45514 SGB63186	0	0.01821
GGB45536 SGB63216	0	0.0775
GGB45650 SGB63364	0	0.0103
GGB45977 SGB41021	0	0.01222
GGB47127 SGB65053	0	0.0713
GGB47180 SGB59839	0	0.02132
GGB47462 SGB65425	0	0.02576
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GGB5207 SGB43496	0	0.04238
GGB54153 SGB41631	0	0.46928
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GGB74408 SGB43542	0	0.07777
GGB75036 SGB102224	0	0.01305
GGB75053 SGB43494	0	0.11501
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GGB79848 SGB41595	0	0.05902
GGB79857 SGB42426	0	1.48303
GGB79872 SGB36958	0	0.33777
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GGB79948 SGB41679	0	0.02542
GGB79989 SGB41645	0	0.00182
GGB80042 SGB43554	0	0.86513
GGB80101 SGB21440	4.41276	1.56761
GGB3583 SGB21441	5.6962	0
<i>Hungateiclostridiaceae bacterium KB18</i>	0	0.03345
<i>Lachnospiraceae bacterium</i>	0	0.03026
<i>Lachnospiraceae bacterium MD308</i>	0	0.02835
<i>Lachnospiraceae unclassified SGB41402</i>	0	0.01033
<i>Lachnospiraceae unclassified SGB41424</i>	0	0.02219
<i>Lactobacillus SGB5158</i>	0	0.02068
<i>Lactobacillus taiwanensis</i>	0.53578	0.01862
<i>Lactococcus SGB40208</i>	0	1.31695

<i>Leuconostoc</i> SGB43006	0	0.07949
<i>Ligilactobacillus murinus</i>	0.14169	0
<i>Limosilactobacillus</i> SGB43493	0	0.05189
<i>Limosilactobacillus reuteri</i>	0.14098	0
<i>Methanomethylovoran</i> SGB40959157	0	0.22484
<i>Muribaculaceae</i> bacterium	3.66231	2.52312
<i>Muribaculaceae</i> bacterium Isolate 013 NCI	5.19565	1.82399
<i>Muribaculaceae</i> bacterium Isolate 110 HZI	0.58142	0.22733
<i>Muribaculum intestinale</i>	2.54524	0.95207
<i>Odoribacter</i> spZ80	0	1.08894
<i>Oscillibacter</i> sp13	0	0.01114
<i>Oscillibacter</i> spCU971	0	0.36961
<i>Oscillospiraceae</i> bacterium	0	0.02386
<i>Parabacteroides goldsteinii</i>	0	0.09265
<i>Paramuribaculum intestinale</i>	0.86322	0.34668
<i>Prevotella</i> spPCJ2	0.13709	5.08024
<i>Rikenellaceae</i> bacterium	0	2.26775
<i>Streptococcus</i> SGB45231	0	0.03049
<i>Turicimona muris</i>	5.07825	1.03866
<i>Zoogloeaceae</i> SGB41465	0	0.00438
Total	100	100

Table S6. Bacterial community structure in ileum and colon samples from SPF mice. Values displayed are relative abundance in "%" at the family level.

SPF bacterial families	Ileum	Colon
<i>Aerococcaceae</i>	0.051	2.23
<i>Akkermansiaceae</i>	0.16	0.13
<i>Atopobiaceae</i>	0.02	0.01
<i>Bacteroidaceae</i>	0.05	4.16
<i>Bacteroidetes phylum families</i>	23.18	14.40
<i>Barnesiellaceae</i>	3.29	0
<i>Brevibacteriaceae</i>	0	0.03
<i>Candidatus_Melainabacteria phylum classified families</i>	0	0.45
<i>Candidatus_Saccharibacteria phylum classified families</i>	0	0.09
<i>Christensenellaceae</i>	0	0.17
<i>Clostridiaceae</i>	0.69	0.77
<i>Desulfovibrionaceae</i>	0.35	11.01
<i>Eggerthellaceae</i>	0	0
<i>Eubacteriales_Family_XIII_Incertae_Sedis</i>	0	0.01
<i>Firmicutes phylum classified families</i>	5.71	21
<i>Lachnospiraceae</i>	1.40	1.97
<i>Lactobacillaceae</i>	0.82	0.20
<i>Muribaculaceae</i>	42.63	15.40
<i>Odoribacteraceae</i>	0	1.09
<i>Peptoniphilaceae</i>	0	0.03
<i>Oscillospiraceae</i>	0	6.92
<i>Prevotellaceae</i>	0.14	5.08

<i>Proteobacteria</i>	0	0.32
<i>Rikenellaceae</i>	0.03	6.62
<i>Ruminococcaceae</i>	0	0.01
<i>Selenomonadaceae</i>	13.54	4.57
<i>Staphylococcaceae</i>	2.60	0.89
<i>Streptococcaceae</i>	0	1.35
<i>Sutterellaceae</i>	5.34	1
<i>Tannerellaceae</i>	0	0.09
<i>Zoogloeaceae</i>	0	0
<i>Sum</i>	100	100

Table S7: Percentage of non-mouse reads assigned as prophage and bacteriophage designated fractions.

	Prophages	Bacteriophages
SPF	0.63	4.24
Oligo-MM12	0.45	2.84
ASF	0.80	0.93

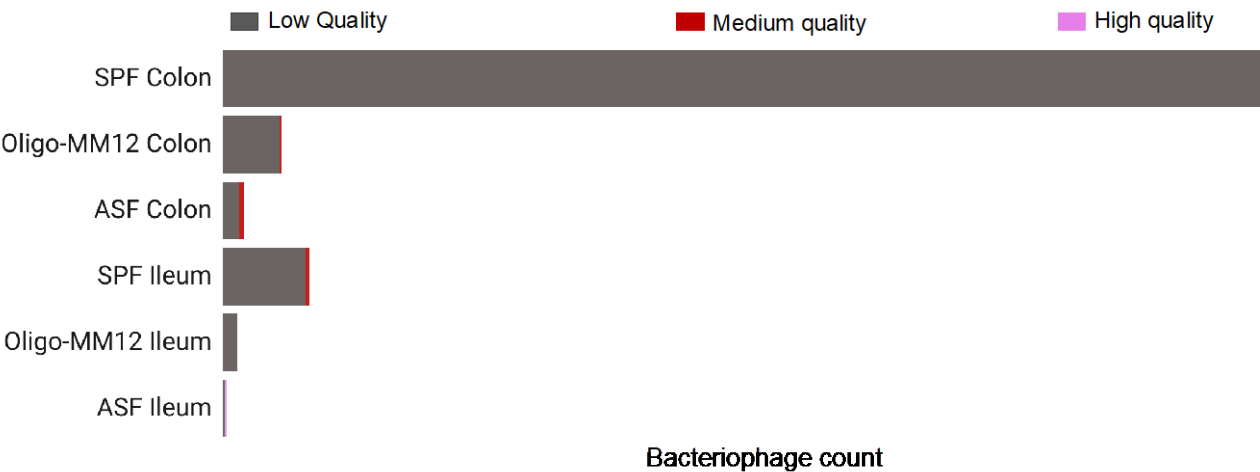


Figure S3: Bacteriophage-designated contigs count in Gnotobiotic Oligo-MM12 and ASF compared to wildtype SPF. Bacteriophage contigs quality was classified based on genome completeness. Red and grey colour bars denote medium and low quality, while pink denotes high quality.

Table S8: List of identified prophages (integrated virus) in SPF and gnotobiotic Oligo-MM12 and ASF mice using PHASTER web tool pipeline (<https://phaster.ca/>) with a default minimum contig length >2000 bp. Complete prophages designated as 100% intact are highlighted in red, > 70% are questionable prophages denoted in black, while prophages with a completeness score of < 70% denoted as green are considered incomplete prophages.

	Viral genome hallmark genes	Length (kb)	Completeness score	NCBI Phage name	GC%
SPF Colon	terminase, tail	50.1	Questionable (70)	<i>Lagaffevirus lagaffe</i>	53.95
	lysine	14.8	Incomplete (20)	<i>Unahavirus uv1H</i>	50.51
	tail	8.7	Incomplete (20)	<i>Caudoviricetes virus</i>	36.69
	Tail, Integrase	7.7	Incomplete (40)	<i>Lullwatervirus</i>	51.42
	Tail, head, portal, terminase	20.3	Questionable (80)	<i>Vedamuthuvirus BM13</i>	45.14
	tail,plate,capsid,port al,terminase,integra se	20.1	Complete (100)	<i>Lilyvirus</i>	38.97
	Coat, head, tail	13.7	Questionable (70)	<i>Yongloolinvirus MMP01</i>	42.86
	Tail, capsid	53	Complete (100)	<i>Brigitvirus</i>	45.05
	NA	5.1	Incomplete (10)	<i>Harrisonvirus</i>	38.69
	Tail, capsid, portal, protease, terminase	16.2	Complete (100)	Trabyvirinae	48.53
	Portal,tail	15.4	Incomplete (50)	<i>Secretariatvirus</i>	51.40
	plate	15.1	Incomplete (20)	<i>Bixzunavirus</i>	49.08

	Lysin, tail, terminase	11.1	Incomplete (50)	<i>Vashvirus lilbooboo</i>	62.41
	Capsid, terminase, head	22	Incomplete (40)	<i>Pippivirus lotta</i>	55.19
	Tail, head, recombinase, terminase	12.5	Incomplete (60)	<i>Caudoviricetes virus</i>	47.85
	Capsid, portal, terminase	11.2	Incomplete (40)	<i>Leicestervirus CD382</i>	45.87
	NA	11.4	Incomplete (10)	<i>Arawnvirus arawn</i>	29.31
	tail	5	Incomplete (20)	<i>Rimavirus rima.</i>	43.47
	Capsid, portal, terminase	14.7	Incomplete (40)	<i>Sherbrookevirus CDHM14</i>	49.01
	Tail	8.9	Incomplete (20)	<i>Oengusvirus oengus</i>	49.34
	Terminase, head	16.3	Incomplete (30)	<i>Pippivirus pippi</i>	56.22
	terminase, portal, protease, head, tail	16	Questionable (70)	<i>Cequinguevirus Ld17</i>	41.21
	portal, terminase, tail	15.4	Incomplete (60)	<i>Caudoviricetes virus</i>	45.22
	Lysin	15.5	Incomplete (20)	<i>Mushuvirus mushu</i>	63.07
	head, tail, portal, capsid, plate	26.4	Complete (100)	<i>Kamchatkavirus AP45</i>	57.77
Oligo-MM12 Colon	tail	9.6	Incomplete (30)	<i>Caudoviricetes virus</i>	48.8
	Lysin	9.3	Incomplete (20)	<i>Mushuvirus mushu</i>	57.51

ASF Colon	NA	17.6	Incomplete (10)	<i>Caudoviricetes virus</i>	31.29
	NA	16.3	Incomplete (10)	<i>Caudoviricetes virus</i>	31.62
	head,plate	12.4	Incomplete (30)	<i>Colneyvirus CD505</i>	23.04
	capsid,tail,head,portal,terminase,reverse transcriptase	25.6	Complete (100)	<i>Sherbrookevirus CD506</i>	29.62
	head,portal,terminase,tail	12.5	Incomplete (60)	<i>Caudoviricetes virus</i>	39.49
SPF Ileum	lysine	14.8	Incomplete (20)	<i>Labanvirus</i>	50.52
	Tail	21.7	Incomplete (20)	<i>Muminivirus filifjonk</i>	42.17
	Reverse transcriptase	16	Incomplete (20)	<i>Baltivirus</i>	50.14
	head,terminase, capsid	22	Incomplete (40)	<i>Pippivirus pippi</i>	55.19
Oligo- MM12 Ileum	Integrase, tail	36.4	Incomplete (50)	<i>Caudoviricetes virus</i>	40.37
	capsid	11.7	Incomplete (20)	<i>Caudoviricetes virus</i>	52.54
ASF Ileum	tail,terminase,portal,head,capsid,lysine	36.2	Complete (100)	<i>Caudoviricetes LfeSau</i>	38.98
	lysine,tail,capsid	18.8	Incomplete (40)	<i>Caudoviricetes virus</i>	41.37

	tail,integrase	5.7	Incomplete (30)	<i>Caudoviricetes</i> <i>virus</i>	37.11
	terminase,capsid	10.2	Incomplete (30)	<i>Caudoviricetes</i> <i>virus</i>	40.73
	integrase,terminase, portal, head	24.7	Questionable (70)	<i>Caudoviricetes</i> <i>virus</i>	39.54

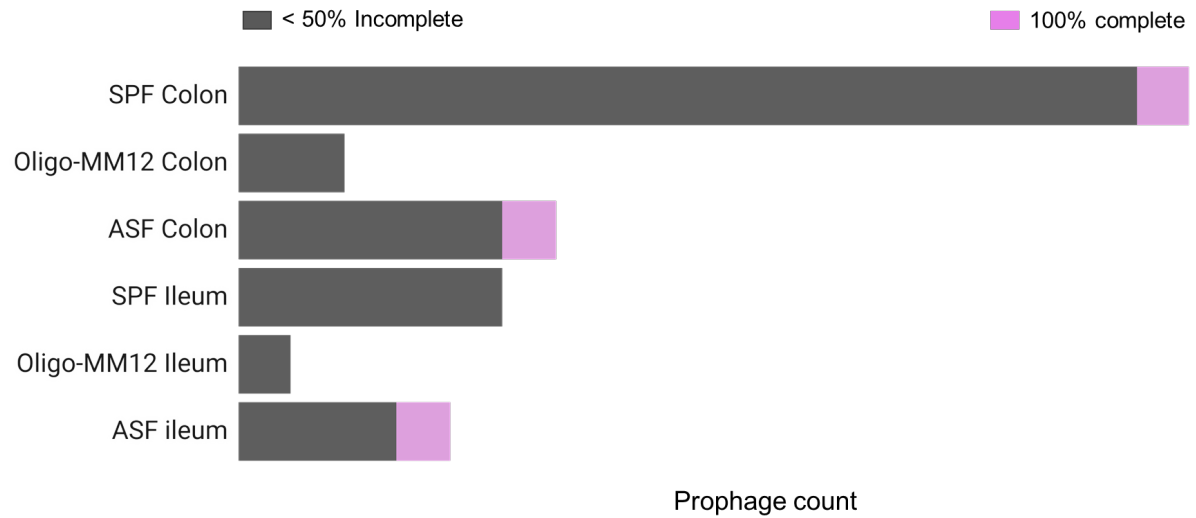


Figure S4: Distribution of prophage contigs according to count and completeness in the colon and ileum of SPF, gnotobiotic Oligo-MM12 and ASF. The identified prophages were classified as complete (100%) and incomplete (< 50%) Grey represents incomplete prophages while pink denotes complete prophages.

Table S9: List of identified prophages (integrated virus) in gnotobiotic Oligo-MM12 and ASF microflora available individual strain sequences (downloaded from NCBI), using PHASTER web tool pipeline (<https://phaster.ca/>) with a default minimum contig length >2000 bp. Complete prophages designated as 100% intact are highlighted in red, > 70% are questionable prophages denoted in black, while prophages with a completeness score of < 70% denoted as green are considered incomplete prophages (1,2).

Oligo-MM12						
Bacteria sequences from NCBI	Family Classification	Viral genome key words	size(kb)	completeness score	NCBI phage name	GC%
<i>Clostridium innocuum</i>	<i>Lachnospraceae</i>	Integrase, tail, terminase, capsid	40.6	questionable (90)	Caudoviricetes phage	41.24
		tail, lysin, transposase	50.2	incomplete(60)	Caudoviricetes phage	24.78
		Integrase, head, terminase, capsid	79.5	questionable (80)	Caudoviricetes phage	
<i>Enterococcus faecalis</i>	<i>Enterococcaceae</i>	tail, capsid	14.6	incomplete(40)	Caudoviricetes phage	38.73
		Integrase	29.9	incomplete(20)	Punavirus RCS47	34.91
<i>Muribaculum intestinale</i>	<i>Muribaculaceae</i>	transposase,head	32.4	incomplete(60)	Gamaleyavirus Bp4	44.87
		Integrase,transposase	31.4	intact(100)	Peduvovirus	46.12
<i>Akkermansia muciniphila</i>	<i>Akkermansiaceae</i>	Integrase	34.9	incomplete(30)	Hollowayvirus F116	55.08
		none	10.4	incomplete(10)	Caudoviricetes phage	51.82
<i>Blautia coccoides</i>	<i>Lachnospraceae</i>	tail, transposase, recombinase, portal, lysis	44.5	intact(140)	Caudoviricetes phage	45.55
		Integrase, terminase, capsid, coat	46	questionable (90)	Leicestervirus CD111.	42.34
		tail, fiber	11.4	incomplete(30)	Caudoviricetes phage	42.5
<i>Acutalibacter muris</i>	<i>Oscillospiraceae</i>	Integrase, tail, recombinase, transposase	38	questionable (80)	Donellivirus	54.1
		Integrase,transposase,plate	18.6	incomplete(60)	Friunavirus	49.44
		coat, lysis	14.9	incomplete(30)	Caudoviricetes phage	59.19
		tail, transposase	21.1	questionable (90)	Leicestervirus CD111.	57.6

<i>Bacteroides caecimuris</i>	<i>Bacteroidaceae</i>	integrase,tail	9.9	incomplete(60)	Caudoviricetes phage	46.78
		tail, transposase	9.5	incomplete(30)	Leicestervirus	42.14
<i>Lactobacillus reuteri</i>	<i>Lactobacillaceae</i>	integrase,transposase	34.8	questionable (70)	Lafunavirus	36.41
<i>Flavonifractor plautii</i>	<i>Oscillospiraceae</i>	recombinase,head	24.6	incomplete(30)	Caudoviricetes phage	50.12
		portal,capsid	16.3	incomplete(30)	Caudoviricetes phage	51.05
		integrase	16.5	incomplete(20)	Caudoviricetes phage	49.28
		tail,plate,terminase,portal,head	34.2	intact(100)	Caudoviricetes phage	60.17
<i>Bifidobacterium animalis subsp. animalis</i>	<i>Bifidobacteriaceae</i>	None				
<i>Turicimonas muris</i>	<i>Sutterellaceae</i>	unknown	14.5	incomplete(10)	Caudoviricetes phage	40.5
		tail,integrase	39.1	incomplete(50)	Caudoviricetes phage	40.57
		head,terminase	8.8	incomplete(30)	Caudoviricetes phage	44.69
<i>Clostridium clostridioforme</i>	<i>Lachnospiraceae</i>	integrase	26.7	incomplete(30)	Caudoviricetes phage	43.42
		integrase, tail	26.9	incomplete(30)	Caudoviricetes phage	46.25
		lysine,tail,plate,capsid,protease,portal,terminase	49.9	intact(150)	caudoviricetes phage; Toutatisvirus	48.09
		transposase	12.8	incomplete(50)	Caudoviricetes phage	45.6
		transposase,integrase	29.4	incomplete(40)	Caudoviricetes; Magadivir	47.34%
		integrase,transposase,tail	8.7	incomplete(50)	Caudoviricetes; Peduovirus	43.28%
		recombinase,transposase	31	questionable(70)	Caudoviricetes Oenococcus phage	46.03%
		transposase,tail	12.9	incomplete(60)	Caudoviricetes phage	44.36%
		recombinase,transposase	24.3	incomplete(40)	Caudoviricetes phage	48.36%
		lysine,transposase,integrase	37.2	questionable(70)	Caudoviricetes phage	42.76%
		tail,head,capsid,portal,terminase,lysine,integrase	42.7	intact(150)	Caudoviricetes phage	47.63%
		lysine	44.2	questionable(77)	Caudoviricetes; Mushuvirus	51.91%
		transposase,tail	17.5	incomplete(40)	unclassified	44.27%
		transposase,tail,integrase	38.3	questionable(80)	Caudoviricetes phage	43.60%

		none	33.6	incomplete(20)	<i>Caudoviricetes; Autographiviridae</i>	45.02%
		none	15.5	incomplete(10)	<i>Caudoviricetes; Kyanoviridae</i>	48.10%
		none	25.3	incomplete(10)	<i>Caudoviricetes; Guelinviridae</i>	50.74%
		tail	9.9	incomplete(20)	<i>Caudoviricetes phage</i>	45.83
		transposase	7	incomplete(40)	<i>Caudoviricetes; Yongloolinvirus</i>	42.78
		integrase	15.7	incomplete(20)	<i>Caudoviricetes phage</i>	50.28
		integrase,transposase	43.7	intact(100)	<i>Caudoviricetes phage</i>	49.21
		none	8	incomplete(10)	<i>Caudoviricetes phage</i>	48.33
		tail,capsid,head,portal	44.2	intact(110)	<i>Caudoviricetes; Yongloolinvirus</i>	49.26
		lysin	45.6	incomplete(30)	<i>Caudoviricetes phage</i>	49.19

ASF						
Bacteria sequences from NCBI	Family taxa	Viral genome key words	Size (kb)	completeness score	NCBI phage name	GC%
<i>Clostridium spp ASF</i>	<i>Clostridiaceae</i>	tail	20.6	incomplete(30)	<i>Abouovirus</i>	28.33
		tail, terminase, capsid, portal, head, plate	22.9	intact(110)	<i>Yongloolinivirus MMP03</i>	30.14
		Integrase	30.2	incomplete(40)	<i>Caudoviricetes phage</i>	31.18
		tail	17.1	incomplete(50)	<i>Caudoviricetes phage</i>	32.16
		integrase,recombinase,terminase,portal,head,tail,capsid	41.1	intact(150)	<i>Sherbrookevirus</i>	29.55
		integrase,tail	9.2	incomplete(30)	<i>Phietavirus</i>	30.34
		tail, capsid	32.1	questionable(70)	<i>Yongloolinivirus</i>	35.38
		none	6.1	incomplete(10)	<i>Saundersvirus</i>	27.72
		integrase	19.6	incomplete(40)	<i>Colneyvirus CD505</i>	29.09
		integrase,head,tail,plate	46.5	intact(100)	<i>Brigitvirus</i>	36.26
		none	12.9	incomplete(10)	<i>Caudoviricetes phage</i>	30.75
		portal,recombinase,integrase,tail	26.9	questionable(70)	<i>Caudoviricetes phage</i>	35.14
		portal,recombinase,tail,integrase	16.2	incomplete(50)	<i>Colneyvirus CD505</i>	29.71
<i>Lactobacillus murinus ASF</i>	<i>Lactobacillaceae</i>	transposase,terminase,portal,tail,capsid,plate,lysin	52	intact(150)	<i>Anamdongvirus</i>	39.89
		Integrase,transposase,tail	17.3	incomplete(60)	<i>Caudoviricetes phage</i>	38.00
		tail, transposase	16	incomplete(40)	<i>Fernvirus</i>	39.94
		capsid, transposase	6.8	questionable(70)	<i>Fernvirus</i>	37.22
<i>Parabacterioidetes goldsteinii</i>	<i>Tannerellaceae</i>	integrase	8.7	incomplete(40)	<i>Oshimavirus</i>	42.82
		head,portal,terminase,tail	12.5	incomplete(60)	<i>Caudoviricetes phage</i>	39.49

Table S10: Similarity percentage (%) of Oligo-MM12 and ASF prophages (integrated virus) to genomes of single bacterial strains used for Oligo-MM12 and ASF to predict their host bacteria using blastn.

	Prophage-designated contig name	Bacteria strains of Gnotobiotic Oligo-MM12 and ASF	Family Taxonomic level	Similarity (%)
Oligo-MM12 Colon	k141_881,flag=1,multi=6.0000,len=10493:671-10493	<i>Clostridium innocuum</i>	<i>Lachnospiraceae</i>	100
	k141_2564,flag=1,multi=29.0000,len=11644:381-11419	<i>Clostridium clostridioforme</i>	<i>Lachnospiraceae</i>	100
Oligo-MM12 Ileum	k141_28455,flag=1,multi=49.9999,len=31210:17020-28738	<i>Akkermansia muciniphila</i>	<i>Akkermansiaceae</i>	92.20
	k141_24561,flag=1,multi=15.0020,len=55382:14360-50825	Unclassified		
ASF Colon	k141_2793,flag=1,multi=61.4261,len=20498:1547-19217	<i>Clostridium sp.</i>	<i>Clostridiaceae</i>	83.81
	k141_4731,flag=1,multi=34.0000,len=42346:6795-23099	<i>Clostridium sp.</i>	<i>Clostridiaceae</i>	84.04
	k141_4731,flag=1,multi=34.0000,len=42346:29024-41515	<i>Clostridium sp.</i>	<i>Clostridiaceae</i>	84.04
	k141_6678,flag=1,multi=35.0119,len=28816:1397-27046	<i>Clostridium sp.</i>	<i>Clostridiaceae</i>	81.91
	k141_7003,flag=0,multi=416.0951,len=67939:2322-14050	Unclassified		
ASF Ileum	k141_2644,flag=1,multi=28.0000,len=44442:4689-40895	<i>Lactobacillus murinus</i>	<i>Lactobacillaceae</i>	81.90
	k141_4358,flag=1,multi=27.0000,len=19627:672-19491	<i>Lactobacillus murinus</i>	<i>Lactobacillaceae</i>	80
	k141_4631,flag=1,multi=15.0000,len=15958:8963-14675	<i>Lactobacillus murinus</i>	<i>Lactobacillaceae</i>	100
	k141_5131,flag=1,multi=26.0720,len=16007:150-10380	<i>Lactobacillus murinus</i>	<i>Lactobacillaceae</i>	100
	k141_6867,flag=1,multi=27.0000,len=24904:167-24904	<i>Lactobacillus murinus</i>	<i>Lactobacillaceae</i>	81.34

a)

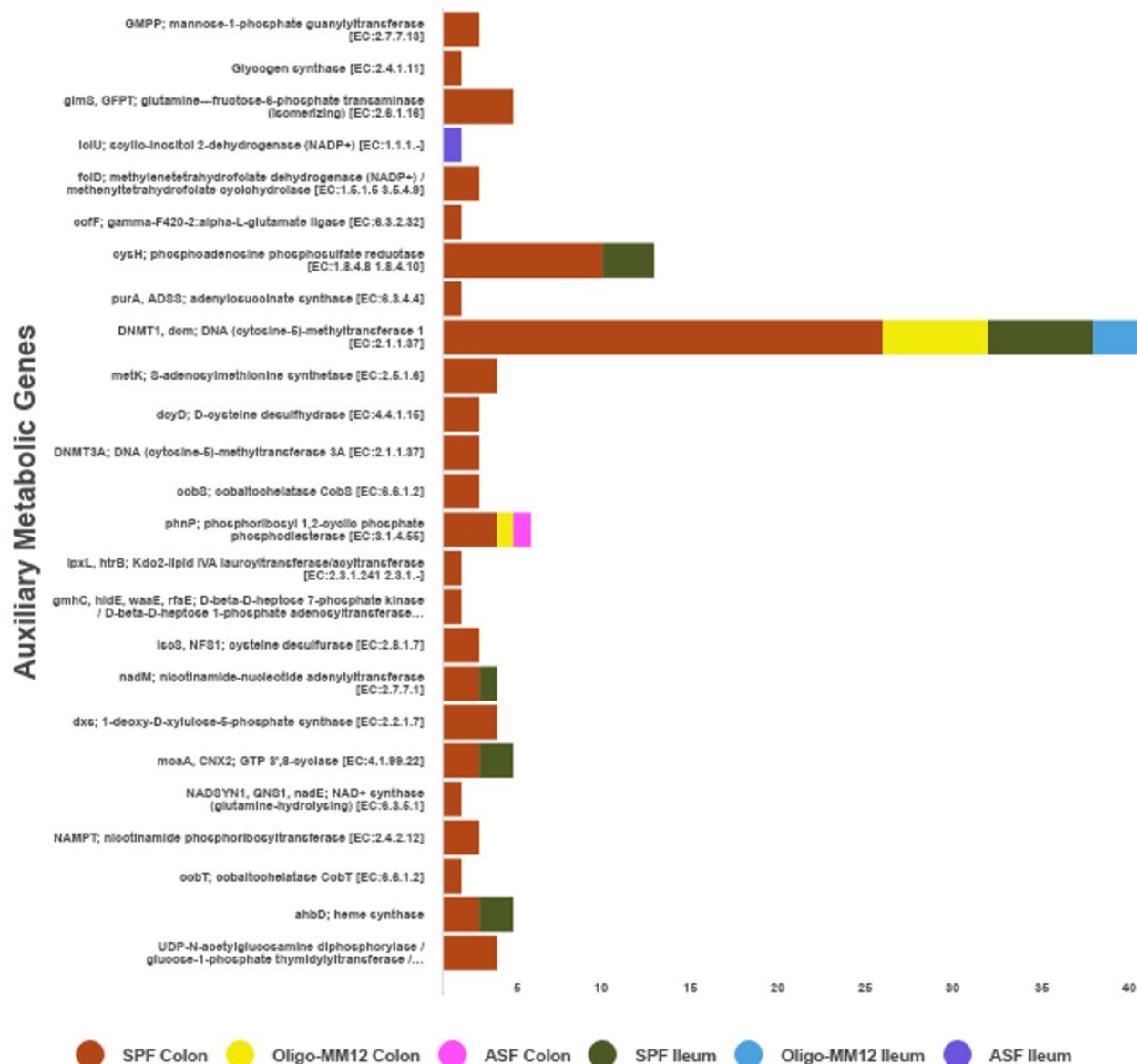


Figure S5: Bacteriophages associated auxiliary metabolic genes copy count in Gnotobiotic Oligo-MM12 and ASF compared to SPF.