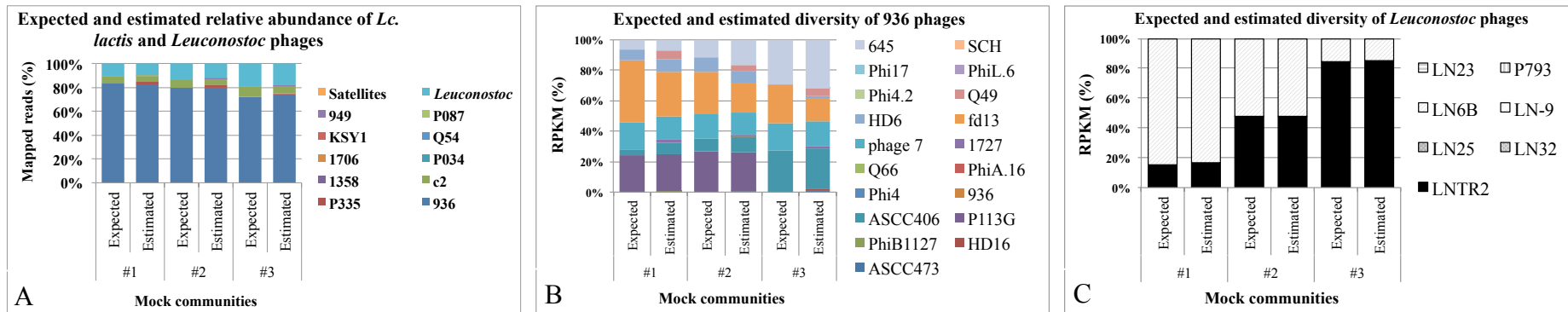
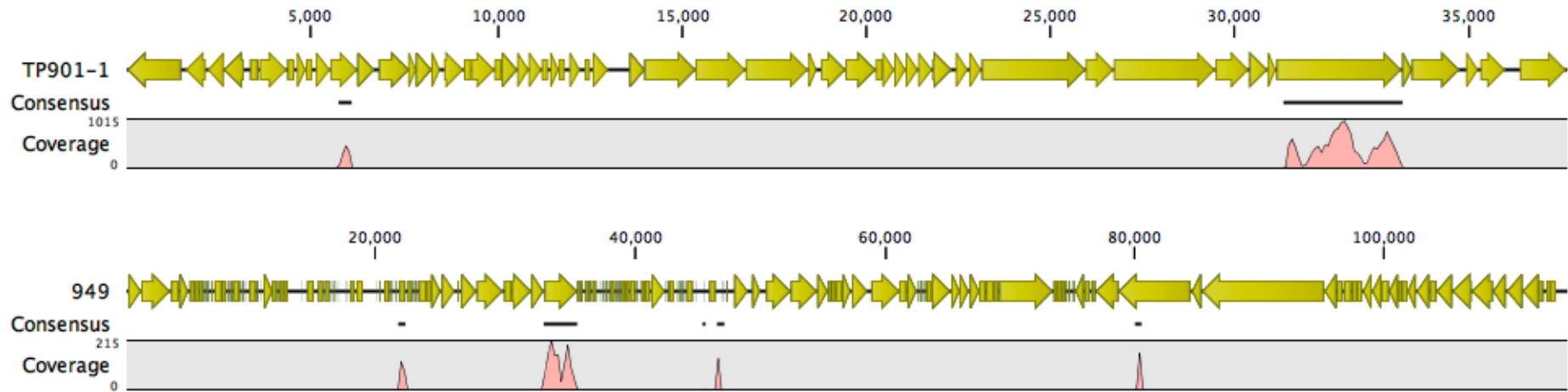


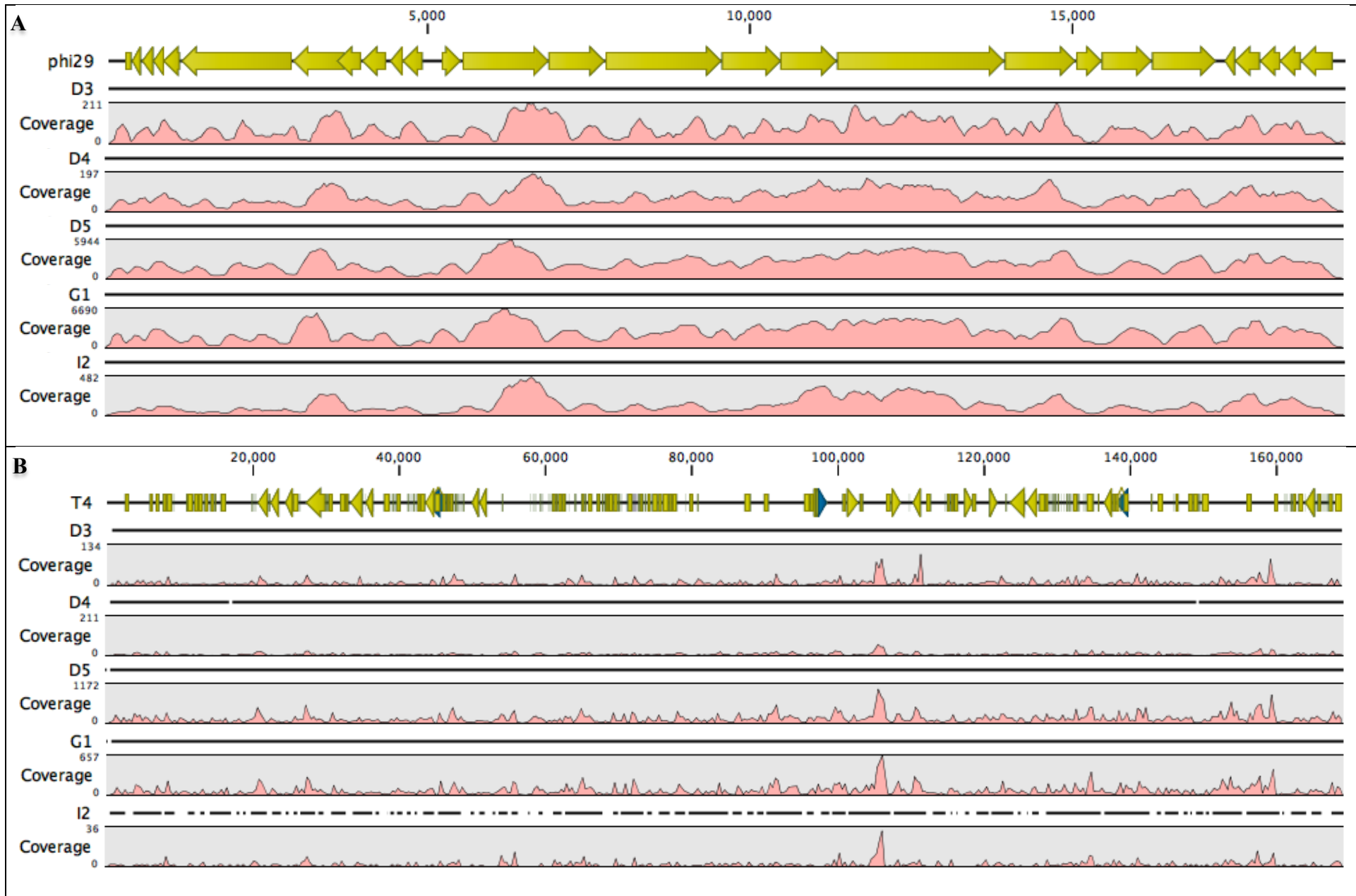
## Supplementary Figures



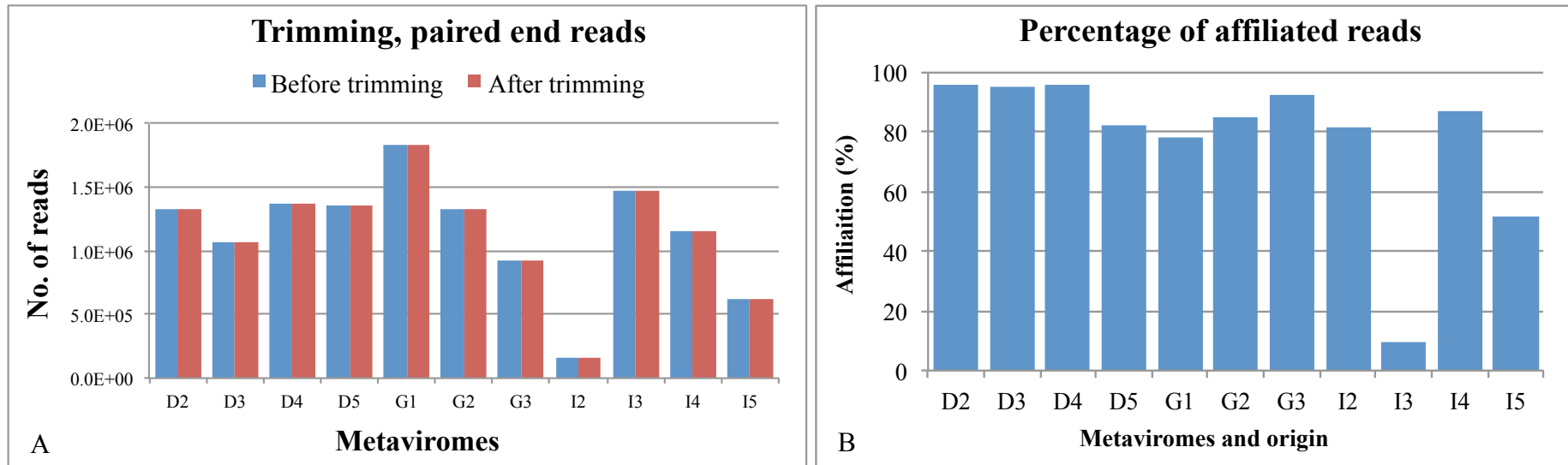
**Fig. S1.** Setting up of parameters for analysis of dairy metaviromes based on synthetic mock communities. The mock communities were intended to have a mixture of one million reads sampled from the genomes of *Lc. Lactis* and *Leuconostoc* phages. The actual or ‘Expected’ distribution of sequences is shown for comparison. (A) Relative abundance estimation of different *Lc. lactis* and *Leuconostoc* phages through mapping to corresponding reference genomes using 50% minimum query length and 80% minimum similarity thresholds. The result is expressed as the ‘Estimated’ percentage of mapped reads. (B) Estimation of the diversity of 936 phages through mapping to 936 phages receptor binding protein (RBP) sequences using 95% minimum query length and similarity thresholds. The result is expressed as reads per kilobase per million reads (RPKM) - the number of mapped reads normalized by the size of the subject RBP sequence. (C) Estimation of the diversity of *Leuconostoc* phages through mapping to *Leuconostoc* phages RBPs (the same threshold as for B).



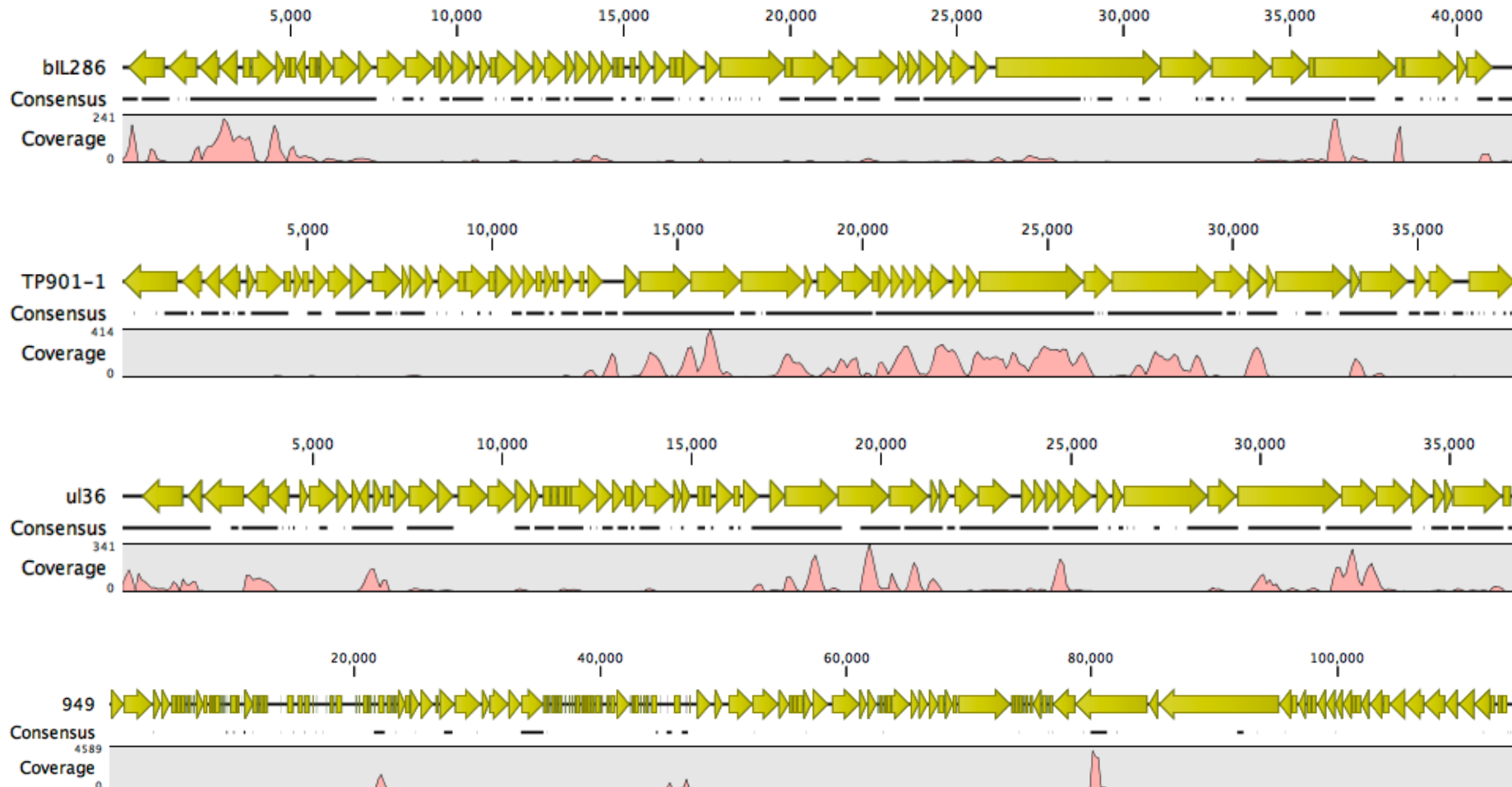
**Fig. S2.** Non-specific mapping of 936 phage sequences to TP901-1 and 949 genomes. A 50% minimum query length and 80% minimum identity thresholds were used for mapping mock communities to reference genomes. X- and Y-axis represent the reference genomes and the coverages, respectively. The regions with read coverage on the TP901-1 genome correspond to *orf11* (left) and *nps* (right), and on the 949 genome to *gp047*, *gp062*, *gt004*, *gt005* (including the upstream intergenic space) and *gp128* (left to right, respectively).



**Fig. S3.** Depth of coverage plots for the mapping of spiked phi29 (panel A) and T4 (panel B) sequences in mock communities. Coverage was assessed by mapping each metavirome dataset against phi29 and T4 reference genomes. X- and Y-axis represent the reference genome and coverage, respectively. Annotated genomes of phi29 and T4 phages are shown with nucleotide positions above the D3 mapping in the corresponding panels. The solid or broken lines above each coverage graph represent consensus sequences. Depth of coverage varies among the different samples, as indicated by the different scales on the Y-axis.



**Fig. S4.** (A) Metavirome sequence trimming prior to analysis. Trimming parameters were set to be as follows: trim Nextera XT adaptors, trim ambiguous nucleotides (limit = 2), trim low quality nucleotides (limit = 0.05), also search on reversed sequence, discard short reads after trimming (<15 nucleotides). (B) The fraction of metavirome sequences corresponding to dairy *Lc. lactis* and *Leuconostoc* phages. Analysis was run using the map-reads-to-reference function of CLC Genomics Workbench 8.5 (Qiagen, Denmark) using 50% minimum query length and 80% minimum identity thresholds, and using as references the genomes of dairy *Lc. lactis* and *Leuconostoc* phages available in GenBank until June 15 2016 and draft genomes obtained from in-house sources.



**Fig. S5.** Representative maps of TP901-1, bIL286, ul36 and 949 genomes with sequences of whey mixture metaviromes. X- and Y-axis represents the reference genome and coverage, respectively. The threshold for mapping in all cases was 50% minimum query length and 80% minimum identity. The regions with read coverage on the 949 genome correspond to *gp047*, *gp062*, *gt004*, *gp089-gt005* intergenic space, *gt005*, *gt006* and *gp128*.

## Supplementary Tables

**Table S1.** Composition of three Illumina NGS sequencing-simulated synthetic metaviromes (mock communities)

Phage strain	Belong to (phage species)	Genome size (bases)	<i>rbp</i> size (bases)	RBP variant	Relative abundance		
					mock 1	mock 2	mock 3
P680	<i>Lc. lactis</i> 936	29631	804	P113G	10.0	6.7	-
P008	<i>Lc. lactis</i> 936	28538	804	P113G	7.5	6.7	-
bIL170	<i>Lc. lactis</i> 936	31754	804	P113G	2.5	6.7	-
712	<i>Lc. lactis</i> 936	30510	759	ASCC406	3.3	6.7	19.4
jm2	<i>Lc. lactis</i> 936	31090	795	phage 7	11.7	6.7	-
phi7	<i>Lc. lactis</i> 936	32382	795	phage 7	4.2	6.7	13.9
sk1	<i>Lc. lactis</i> 936	28451	795	fd13	12.5	6.7	5.6
jj50	<i>Lc. lactis</i> 936	27453	795	fd13	10.8	6.7	11.1
CaseusJM1	<i>Lc. lactis</i> 936	30692	795	fd13	9.2	6.7	-
jm3	<i>Lc. lactis</i> 936	28674	801	HD6	5.8	6.7	-
340	<i>Lc. lactis</i> 936	32337	810	645	5.0	6.7	22.2
bIBB29	<i>Lc. lactis</i> 936	29305	810	645	0.8	6.7	-
c2	<i>Lc. lactis</i> c2	22172	2121	c2	6.7	6.7	8.3
phiLN34	<i>Le. mesenteroides</i>	28022	768	LNTR2	1.7	6.7	16.7
phiLN6B	<i>Le. pseudomesenteroides</i>	25740	933	LN6B	8.3	6.7	2.8

**Table S2.** The impact of varying the amount of input reads on phage relative abundance estimation. Entries are scores representing the percentage of reads mapped to reference genomes and were obtained from statistics generated from mapping of reads to the genome sequences of *Lc. lactis* and *Leuconostoc* phages. The mapping threshold was set to a minimum of 50% query length and 80% identity.

Phage species	Amount of input reads ( $10^2$ to $1.89 \times 10^7$ ), % mapped reads (entries)												
	$10^2$	$5 \times 10^2$	$10^3$	$10^4$	$5 \times 10^4$	$10^5$	$2 \times 10^5$	$5 \times 10^5$	$10^6$	$2 \times 10^6$	$5 \times 10^6$	$10^7$	$1.89 \times 10^7$
936	20.00	35.60	34.40	33.48	34.18	34.07	34.08	33.96	34.00	34.13	34.04	34.07	34.06
P335	-	1.20	2.00	1.80	1.69	1.80	1.71	1.73	1.71	1.71	1.71	1.72	1.72
c2	-	2.20	1.10	1.69	1.48	1.45	1.42	1.50	1.47	1.48	1.48	1.48	1.48
1358	-	-	-	-	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
P034	-	-	-	-	-	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00
1706	-	-	-	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
Q54	-	-	-	0.20	0.09	0.11	0.11	0.10	0.11	0.11	0.10	0.10	0.10
KSY1	-	-	-	-	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
P087	-	-	-	0.02	0.04	0.05	0.04	0.05	0.04	0.04	0.04	0.04	0.04
949	-	0.60	0.40	0.73	0.61	0.63	0.61	0.63	0.62	0.62	0.62	0.62	0.62
<i>Leuconostoc</i>	-	-	-	0.05	0.03	0.04	0.05	0.05	0.05	0.04	0.04	0.04	0.04
Sattelites	-	-	-	0.06	0.03	0.03	0.03	0.02	0.03	0.02	0.02	0.03	0.02



**Table S3.** Summary of *de novo* assembly and BLAST analysis of spiked phages

Meta- genomes	phi29							T4						
	<i>De novo</i> assembly			BLAST analysis				<i>De novo</i> assembly			BLAST analysis			
	Contig length	Reads count	Average coverage	E- value	Identity (%)	HSP length	Bit score	Contig length	Reads count	Average coverage	E- value	Identity (%)	HSP length	Bit score
D3	19226	8769	78.2	0.00	100	19223	34653.0	1737	64	6.1	0.00	100	1750	3133.7
D4	19281	7188	73.8	0.00	100	19258	34716.1	3193	165	10.3	0.00	100	2426	4369.0
D5	19276	212820	2347.9	0.00	100	19273	34743.2	168032	115910	142.7	0.00	100	49334	88501.6
G1	19274	248435	2585.8	0.00	100	19271	34739.6	104664	51199	85.8	0.00	100	26462	47402.8
I2	19265	11670	132.3	0.00	100	19262	34723.3	2793	125	10.7	0.00	100	2156	3887.5

HSP: high-scoring segment pairs

**Table S4.** BLAST comparison of contigs of the highest average read coverage (total reads contigs)

Contigs	Average coverage	Size	Number of HSPs	Lowest E-value	Greatest identity %	Greatest positive %	Greatest HSP length	Greatest bit score	BLAST hit description	Accession
D2_8	7197	371	121	0.0	100	100	272	481	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
D2_85	6290	700	105	0.0	97	97	714	1063	<i>Lactococcus</i> phage ASCC454, complete genome	JQ740802
D2_104	7246	584	111	0.0	100	100	584	1000	<i>Lactococcus</i> phage jm3, complete genome	KC182547
D2_144	13147	608	103	0.0	100	100	609	1035	<i>Lactococcus</i> phage phi145, complete genome	KM091444
D2_156	5805	653	139	0.0	100	100	662	1063	<i>Lactococcus</i> phage phi7, complete genome	KC182552
D2_169	5460	1592	180	0.0	99	99	896	1550	<i>Lactococcus</i> phage CB20, complete genome	FJ848885
D2_170	9123	692	124	0.0	100	100	702	1177	<i>Lactococcus</i> phage ASCC544, complete genome	JQ740814
D2_261	8330	1061	107	0.0	100	100	1061	1779	<i>Lactococcus</i> phage CB14, complete genome	FJ848883
D2_271	13080	274	105	0.0	100	100	274	477	<i>Lactococcus</i> phage P680, complete genome	KC182551
D2_319	5416	567	104	0.0	100	100	567	982	<i>Lactococcus</i> phage SL4, complete genome	FJ848881
D3_7	4259	3437	179	0.0	100	100	3424	5025	<i>Lactococcus</i> phage bIBB29, complete genome	EU221285
D3_10	4014	712	171	0.0	95	95	710	885	<i>Lactococcus</i> phage ASCC191, complete genome	JQ740787
D3_12	3202	6696	367	0.0	100	100	2907	4145	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
D3_13	2774	2384	142	0.0	100	100	2385	3709	<i>Lactococcus</i> phage phi15, complete genome	KM091442
D3_18	4508	1616	96	0.0	100	100	1630	2629	<i>Lactococcus</i> phage CB20, complete genome	FJ848885
D3_19	3465	2177	142	0.0	100	100	2190	3453	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
D3_20	2779	2497	150	0.0	100	100	2511	4021	<i>Lactococcus</i> phage P680, complete genome	KC182551
D3_23	3180	760	101	0.0	100	100	760	1267	<i>Lactococcus</i> phage phi15, complete genome	KM091442
D3_53	3515	2291	285	0.0	100	100	1704	2416	<i>Lactococcus</i> phage CB13, complete genome	FJ848882
D3_116	2751	797	101	0.0	98	98	797	1307	<i>Lactococcus</i> phage fd13, complete genome	KC182545
D4_5	4271	5330	427	0.0	100	100	2622	3549	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
D4_7	5050	7845	367	0.0	100	100	4103	6019	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
D4_9	7886	4258	329	0.0	100	100	4258	6374	Bacteriophage bIL170, complete genome	AF009630
D4_22	4108	1543	154	0.0	100	100	1541	2358	<i>Lactococcus</i> phage bIBB29, complete genome	EU221285
D4_33	3981	2322	142	0.0	100	100	2360	3702	Phage 645, complete genome	KC182543
D4_55	4229	3184	307	0.0	100	100	1909	2580	<i>Lactococcus</i> phage CB13, complete genome	FJ848882
D4_89	4376	1377	105	0.0	100	100	1380	2095	Phage P475, complete genome	KC182550
D4_91	7932	754	102	0.0	100	100	754	1280	<i>Lactococcus</i> phage jm3, complete genome	KC182547
D4_92	5730	909	108	0.0	100	100	909	1532	<i>Lactococcus</i> phage phi15, complete genome	KM091442
D4_96	4155	863	147	0.0	100	100	708	1121	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
D5_17	7032	511	158	0.0	100	100	511	872	<i>Lactococcus</i> phage P008, complete genome	DQ054536

D5_51	9341	440	105	0.0	100	100	441	759	<i>Lactococcus</i> phage phi7, complete genome	KC182552
D5_52	6271	356	105	0.0	100	100	357	616	Phage p272, complete genome	KC182549
D5_62	8748	815	104	0.0	100	100	815	1412	<i>Lactococcus</i> phage CB14, complete genome	FJ848883
D5_108	4827	506	141	0.0	100	100	509	800	<i>Lactococcus</i> phage ASCC506, complete genome	JQ740810
D5_186	7322	492	128	0.0	100	100	492	829	<i>Lactococcus</i> phage CB14, complete genome	FJ848883
D5_187	6722	474	101	0.0	100	100	471	827	<i>Lactococcus</i> phage SL4, complete genome	FJ848881
D5_194	5241	632	100	0.0	100	100	632	1082	<i>Lactococcus</i> phage ASCC544, complete genome	JQ740814
D5_204	7303	447	107	0.0	100	100	457	733	<i>Lactococcus</i> phage phi145, complete genome	KM091444
D5_378	8062	420	105	0.0	100	100	420	710	<i>Lactococcus</i> phage SL4, complete genome	FJ848881
G1_1	16145	30652	1836	0.0	100	100	11135	14302	<i>Lactococcus</i> phage CB20, complete genome	FJ848885
G1_9	2586	19274	161	0.0	100	100	19271	34740	<i>Bacillus</i> phage phi29, complete genome	EU771092
G1_12	1101	438	122	0.0	97	97	438	705	<i>Lactococcus</i> phage bIBB29, complete genome	EU221285
G1_19	1297	397	100	0.0	100	100	395	618	Bacteriophage US3 lytA gene, complete cds	M90423
G1_21	2210	743	103	0.0	100	100	743	1192	Phage 645, complete genome	KC182543
G1_22	944	25715	284	0.0	100	100	20711	31605	<i>Leuconostoc</i> phage phiLN04, complete genome	KC013023
G1_31	879	455	240	0.0	100	100	455	528	<i>Lactococcus</i> phage ASCC532, complete genome	JQ740813
G1_52	753	437	111	0.0	100	100	435	705	Phage p272, complete genome	KC182549
G1_115	686	549	243	0.0	100	100	549	638	<i>Lactococcus</i> phage ASCC191, complete genome	JQ740787
G1_124	1072	508	105	0.0	100	100	506	809	<i>Lactococcus</i> phage jm3, complete genome	KC182547
G2_5	3839	19878	1222	0.0	100	100	15284	21456	<i>Lactococcus</i> phage CB19, complete genome	FJ848884
G2_9	5875	6935	392	0.0	100	100	6198	7960	<i>Lactococcus</i> phage SL4, complete genome	FJ848881
G2_48	4815	2996	172	0.0	100	100	1630	2463	<i>Lactococcus</i> phage ASCC544, complete genome	JQ740814
G2_52	5783	2268	139	0.0	97	97	2187	3466	<i>Lactococcus lactis</i> phage 645, complete genome	KC182543
G2_53	5024	4079	155	0.0	100	100	4097	6284	<i>Lactococcus</i> phage jm3, complete genome	KC182547
G2_54	6042	2546	142	0.0	100	100	2546	4021	<i>Lactococcus</i> phage CB20, complete genome	FJ848885
G2_60	4271	1698	106	0.0	100	100	1716	2802	<i>Lactococcus</i> phage jm3, complete genome	KC182547
G2_97	3949	1248	101	0.0	96	96	1248	2003	<i>Lactococcus</i> phage jm3, complete genome	KC182547
G2_111	5244	731	75	0.0	91	91	712	852	<i>Lactococcus</i> phage fd13, complete genome	KC182545
G2_123	4113	1062	104	0.0	100	100	1062	1763	<i>Lactococcus</i> phage P680, complete genome	KC182551
G3_3	7894	21898	2457	0.0	100	100	4081	5262	<i>Lactococcus</i> phage ASCC544, complete genome	JQ740814
G3_5	6707	5786	0						NA	NA
G3_8	3695	3904	0						NA	NA
G3_9	3062	1750	0						NA	NA
G3_10	2607	7095	561	0.0	96	96	4648	6055	<i>Lactococcus</i> phage PhiLj, complete genome	KP793133

G3_21	2142	7267	950	0.0	100	100	2563	3240	<i>Lactococcus</i> phage ASCC365, complete genome	JQ740797
G3_23	9309	1051	196	0.0	100	100	1061	1628	<i>Lactococcus</i> phage PhiL.6, complete genome	KP793122
G3_27	2426	4194	475	0.0	99	99	4201	6784	<i>Lactococcus</i> phage ASCC397, complete genome	JQ740800
G3_32	2025	2129	286	0.0	97	97	1271	1815	<i>Lactococcus</i> phage PhiS0139, complete genome	KP793134
G3_49	15681	1303	100	0.0	97	97	1302	2118	<i>Lactococcus</i> phage ASCC544, complete genome	JQ740814
I2_1	1712	30122	1614	0.0	100	100	12707	21582	<i>Lactococcus</i> phage jm2, complete genome	KC182546
I2_2	291	3765	109	0.0	100	100	3781	6737	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
I2_3	643	8132	590	0.0	100	100	8132	14275	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
I2_5	224	5826	656	0.0	100	100	2779	4809	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
I2_6	283	7790	688	0.0	100	100	3881	6975	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
I2_7	132	19265	161	0.0	100	100	19262	34723	<i>Bacillus</i> phage phi29, complete genome	EU771092
I2_9	135	400	110	0.0	100	100	414	679	<i>Lactococcus</i> phage jm2, complete genome	KC182546
I2_12	217	2549	146	0.0	100	100	2564	4598	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
I2_425	113	702	104	0.0	98	98	716	1170	<i>Lactococcus</i> phage jm2, complete genome	KC182546
I2_426	414	472	113	0.0	100	100	472	852	<i>Lactococcus</i> phage jm2, complete genome	KC182546
I3_58	1681	626	0						NA	NA
I3_79	1822	594	0						NA	NA
I3_82	1874	5344	973	0.0	100	100	4973	6030	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
I3_107	4576	1451	176	0.0	100	100	476	425	<i>Strep. pyogenes</i> MGAS315, complete genome	AE014074
I3_115	4347	904	125	0.0	100	100	836	201	<i>Strep. pyogenes</i> MGAS2096, complete genome	CP000261
I3_147	5315	2396	103	0.0	100	100	2162	3875	<i>Lactococcus</i> phage TP712, complete sequence	AY766464
I3_148	999	648	105	0.0	100	100	375	124	<i>Strep. epidermidis</i> RP62A, complete genome	CP000029
I3_151	1937	872	116	0.0	100	100	795	236	<i>Strep. pyogenes</i> NZ131, complete genome	CP000829
I3_191	987	1341	91	0.0	100	100	153	55	<i>Strep. pyogenes</i> M1 GAS, complete genome	AE004092
I3_21166	1345	619	59	0.0	95	95	600	364	<i>Strep. pyogenes</i> MGAS2096, complete genome	CP000261
I4_1	16184	3056	120	0.0	100	100	3069	4301	Bacteriophage c2 complete genome	L48605
I4_2	5797	3083	106	0.0	100	100	3088	4221	<i>Lactococcus</i> phage bIL67, complete genome	L33769
I4_4	15581	2310	67	0.0	100	100	2306	3018	Bacteriophage c2 complete genome	L48605
I4_5	11369	1285	52	0.0	100	100	1285	1612	Bacteriophage c2 complete genome	L48605
I4_6	18480	5516	117	0.0	100	100	4012	5722	Bacteriophage c2 complete genome	L48605
I4_7	15697	4902	143	0.0	100	100	1749	2091	Bacteriophage c2 complete genome	L48605
I4_9	13558	6482	175	0.0	100	100	1708	2614	Bacteriophage c2 complete genome	L48605
I4_13	5721	1615	109	0.0	100	100	1615	2301	<i>Lactococcus</i> phage Rc16 genes, complete cds	AY570987
I4_19	8125	880	104	0.0	100	100	880	1255	Bacteriophage c2 complete genome	L48605

I4_25	4768	648	103	0.0	95	95	648	871	Bacteriophage c2 complete genome	L48605
I5_9	1142	1188	133	0.0	100	100	717	901	Bacteriophage c2 complete genome	L48605
I5_10	5284	21527	187	0.0	100	100	7326	10235	<i>Lactococcus</i> phage bIL67, complete genome	L33769
I5_12	2248	1215	103	0.0	100	100	1215	1657	<i>Lactococcus</i> phage Rc16 genes, complete cds	AY570987
I5_13	1630	5622	171	0.0	100	100	1708	2614	Bacteriophage c2 complete genome	L48605
I5_14	2529	1640	112	0.0	100	100	1639	2337	Bacteriophage c2 complete genome	L48605
I5_16	1478	1627	111	0.0	100	100	1625	2358	<i>Lactococcus</i> phage Rc16 genes, complete cds	AY570987
I5_25	2691	4014	128	0.0	100	100	2028	2760	Bacteriophage c2 complete genome	L48605
I5_36	1148	1050	0						NA	NA
I5_39	2061	3236	120	0.0	100	100	3248	4457	Bacteriophage c2 complete genome	L48605
I5_40	1445	5039	109	0.0	100	100	5009	6804	Bacteriophage c2 complete genome	L48605

HSP: high-scoring segment pairs, D: Denmark, G: Germany, I: Ireland, NA: Not available

**Table S5.** BLAST comparison of contigs of the longest sizes (total reads contigs)

Contigs	Average coverage	Size	Number of HSPs	Lowest E-value	Greatest identity %	Greatest positive %	Greatest HSP length	Greatest bit score	BLAST hit description	Accession
D2_7	4181	5283	554	0	100	100	2551	3532	<i>Lactococcus</i> phage phi15, complete genome	KM091442
D2_10	2229	10734	763	0	99	99	3186	2989	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
D2_17	1704	11070	1251	0	100	100	2582	3296	<i>Lactococcus</i> phage CB13, complete genome	FJ848882
D2_18	3689	6263	700	0	100	100	2760	3316	<i>Lactococcus lactis</i> phage p272, complete genome	KC182549
D2_22	4193	6225	410	0	100	100	5166	6428	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
D2_229	314	27483	306	0	98	98	9357	12796	<i>Lactococcus</i> phage bIL67, complete genome	L33769
D2_341	69	15126	149	0	100	100	10108	11680	<i>Lactococcus</i> phage bIL67, complete genome	L33769
D2_412	60	33441	768	0	100	100	21930	38415	<i>Lactobacillus</i> phage Ld25A, complete genome	KJ564036
D2_717	8	8060	136	0	100	100	57	54	<i>Staphylococcus aureus</i> 04-02981, complete genome	CP001844
D2_762	4	5487	220	0	97	97	2118	1931	<i>Streptococcus</i> phage TP-J34 complete genome	HE861935
D3_2	736	4816	267	0	100	100	3405	4973	<i>Lactococcus</i> phage ASCC324, complete genome	JQ740793
D3_4	1572	6001	355	0	98	98	2788	3707	<i>Lactococcus lactis</i> phage p2, complete genome	GQ979703
D3_11	2747	20699	1563	0	100	100	12255	19276	<i>Lactococcus lactis</i> phage P475, complete genome	KC182550
D3_12	3202	6696	367	0	100	100	2907	4145	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
D3_14	2639	17770	1334	0	100	100	5167	5895	<i>Lactococcus</i> phage SL4, complete genome	FJ848881
D3_28	650	11167	1039	0	100	100	2900	4656	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
D3_40	574	5423	511	0	100	100	3838	4872	<i>Lactococcus</i> phage P680, complete genome	KC182551
D3_75	1369	6270	601	0	100	100	2427	3173	<i>Lactococcus</i> phage ASCC544, complete genome	JQ740814
D3_137	78	19226	161	0	100	100	19223	34653	<i>Bacillus</i> phage phi29, complete genome	EU771092
D3_191	8	5421	200	0	100	100	4464	7630	Bacteriophage S13 circular DNA, complete genome	M14428
D4_1	2098	11364	822	0	98	98	4329	4988	<i>Lactococcus</i> phage SL4, complete genome	FJ848881
D4_2	2752	8147	712	0	100	100	5744	9285	<i>Lactococcus lactis</i> phage P475, complete genome	KC182550
D4_6	2730	11682	559	0	97	97	8513	11824	<i>Lactococcus</i> phage SL4, complete genome	FJ848881
D4_7	5050	7845	367	0	100	100	4103	6019	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
D4_10	1123	8871	429	0	100	100	7490	10295	<i>Lactococcus</i> phage ASCC287, complete genome	JQ740791
D4_11	1911	11507	859	0	98	98	2447	3150	<i>Lactococcus lactis</i> phage p2, complete genome	GQ979703
D4_12	717	9050	764	0	100	100	3004	4759	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
D4_16	1035	9383	784	0	100	100	3797	4549	<i>Lactococcus</i> phage ASCC497, complete genome	JQ740808
D4_17	1699	9150	810	0	100	100	3921	4654	<i>Lactococcus</i> phage phi7, complete genome	KC182552
D4_118	74	19281	161	0	100	100	19258	34716	<i>Bacillus</i> phage phi29, complete genome	EU771092
D5_3	849	13293	795	0	99	99	3723	4466	<i>Lactococcus</i> phage CB20, complete genome	FJ848885

D5_24	168	25687	288	0	100	100	23947	40673	<i>Leuconostoc</i> phage phiLN6B, complete genome	KC013024
D5_47	143	168032	7561	0	100	100	49334	88502	<i>Enterobacteria</i> phage RB59, complete genome	KM607003
D5_53	48	18647	511	0	100	100	3204	5350	<i>Lactococcus</i> bacteriophage phi31	AJ292531
D5_77	2348	19276	161	0	100	100	19273	34743	<i>Bacillus</i> phage phi29, complete genome	EU771092
D5_230	41	31258	131	0	100	100	87	64	<i>Shewanella piezotolerans</i> WP3, complete genome	CP000472
D5_357	136	21902	213	0	100	100	7565	9437	Bacteriophage c2 complete genome	L48605
D5_419	60	17840	440	0	96	96	7725	9494	Bacteriophage 187, complete genome	AY954950
D5_523	27	9222	149	0	97	97	587	173	<i>Lactobacillus</i> phage PL-1, complete genome	KC171647
D5_622	18	9016	86	0	100	100	43	46	<i>Pseudoplusia includens</i> SNPV IE, complete genome	KJ631622
G1_1	16145	30652	0						NA	NA
G1_9	2586	19274	161	0	100	100	19271	34740	<i>Bacillus</i> phage phi29, complete genome	EU771092
G1_12	1101	438	285	0	100	100	20711	31605	<i>Leuconostoc</i> phage phiLN04, complete genome	KC013023
G1_19	1297	397	0						NA	NA
G1_21	2210	743	985	0	100	100	5015	7612	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
G1_22	944	25715	4124	0	100	100	24041	43351	<i>Enterobacteria</i> phage RB59, complete genome	KM607003
G1_31	879	455	1507	0	100	100	26462	47403	<i>Enterobacteria</i> phage RB59, complete genome	KM607003
G1_52	753	437	443	0	100	100	3503	1606	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
G1_115	686	549	0						NA	NA
G1_124	1072	508	0						NA	NA
G2_5	3839	19878	1222	0	100	100	15284	21456	<i>Lactococcus</i> phage CB19, complete genome	FJ848884
G2_76	27	13116	247	0	100	100	3492	1558	<i>Strep. pyogenes</i> M1 GAS, complete genome	AE004092
G2_90	29	20611	551	0	100	100	5191	3386	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
G2_125	27	12988	245	0	100	100	1810	854	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
G2_135	27	13598	262	0	100	100	5444	2297	<i>Strep. pyogenes</i> MGAS6180, complete genome	CP000056
G2_155	26	14462	538	0	100	100	2848	1660	<i>Strep. pyogenes</i> MGAS10270, complete genome	CP000260
G2_177	29	13046	305	0	100	100	2371	1276	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
G2_200	29	18409	458	0	100	100	4808	2203	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
G2_226	32	13086	260	0	100	100	2523	1705	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
G2_235	25	12907	340	0	100	100	2336	1848	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
G3_3	7894	21898	0						NA	NA
G3_18	206	25637	278	0	100	100	20711	31605	<i>Leuconostoc</i> phage phiLN04, complete genome	KC013023
G3_19	17	12615	273	0	100	100	2260	977	<i>Strep. pyogenes</i> MGAS6180, complete genome	CP000056
G3_79	18	27753	319	0	100	100	2976	1502	<i>Strep. pyogenes</i> MGAS6180, complete genome	CP000056
G3_107	20	13452	238	0	100	100	2371	1276	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121

G3_126	24	17128	0						NA	NA
G3_139	23	16000	0						NA	NA
G3_143	22	14787	444	0	100	100	2091	2295	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
G3_160	20	13326	0						NA	NA
G3_210	23	16762	0						NA	NA
I2_1	1712	30122	1614	0	100	100	12707	21582	<i>Lactococcus</i> phage jm2, complete genome	KC182546
I2_3	643	8132	590	0	100	100	8132	14275	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
I2_5	224	5826	615	0	100	100	2779	4809	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
I2_6	283	7790	688	0	100	100	3881	6975	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
I2_7	132	19265	161	0	100	100	19262	34723	<i>Bacillus</i> phage phi29, complete genome	EU771092
I2_10	40	8081	236	0	90	90	3951	5125	Bacteriophage 187, complete genome	AY954950
I2_18	7	5678	207	0	96	96	4670	5222	Bacteriophage 187, complete genome	AY954950
I2_22	9	4341	114	0	100	100	1452	2254	Bacteriophage bIL285, complete genome	AF323668
I2_25	7	4037	139	0	100	100	3144	4688	Bacteriophage TP901-1, complete sequence	AF304433
I2_38	8	4563	123	0	100	100	4648	8068	<i>Strep. thermophilus</i> phage 2972, complete genome	AY699705
I3_5	226	98658	1031	0	100	100	1815	1563	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
I3_10	200	96714	1273	0	100	100	2823	1513	<i>Strep. pyogenes</i> M1 GAS, complete genome	AE004092
I3_12	179	117729	1317	0	100	100	2493	1678	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
I3_25	215	80678	1273	0	100	100	1994	863	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
I3_26	178	140859	1559	0	100	100	1926	962	<i>Strep. pyogenes</i> MGAS10270, complete genome	CP000260
I3_27	154	141287	1650	0	100	100	2403	1240	<i>Strep. pyogenes</i> NZ131, complete genome	CP000829
I3_30	225	138640	1655	0	100	100	2786	1233	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
I3_46	183	74592	656	0	100	100	1519	596	<i>Strep. pyogenes</i> M1 GAS, complete genome	AE004092
I3_48	184	73022	1217	0	100	100	3970	2663	<i>Strep. pyogenes</i> MGAS10270, complete genome	CP000260
I3_65	200	83179	1151	0	100	100	1597	1074	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
I4_35	21	14746	423	0	100	100	2386	1480	<i>Strep. pyogenes</i> MGAS10270, complete genome	CP000260
I4_88	16	13532	307	0	100	100	2394	798	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
I4_101	23	12789	394	0	100	100	1726	2191	Bacteriophage bIL311, complete genome	AF323672
I4_133	12	13631	0						NA	NA
I4_145	17	22637	278	0	100	100	7509	11581	Bacteriophage TP901-1, complete sequence	AF304433
I4_G3	18	12874	277	0	100	100	3382	1202	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
I4_229	28	14408	423	0	100	100	2877	2443	<i>Strep. pyogenes</i> M1 GAS, complete genome	AE004092
I4_267	15	13171	180	0	100	100	1298	490	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
I4_311	21	12518	177	0	100	100	650	218	<i>Lactobacillus</i> salivarius UCC118, complete genome	CP000233



I4_788	14	13517	342	0	100	100	2162	959	<i>Lactobacillus johnsonii</i> NCC 533, complete genome	AE017198
I5_21	23	38367	379	0	100	100	1314	896	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
I5_31	30	75448	813	0	100	100	2605	3031	Bacteriophage bIL310, complete genome	AF323671
I5_59	27	34685	576	0	100	100	1606	1049	<i>Strep. pyogenes</i> M1 GAS, complete genome	AE004092
I5_89	29	35390	544	0	100	100	1717	786	<i>Strep. pyogenes</i> MGAS10270, complete genome	CP000260
I5_90	28	32645	582	0	100	100	2386	1466	<i>Strep. pyogenes</i> MGAS10270, complete genome	CP000260
I5_105	26	33213	451	0	100	100	1926	813	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
I5_135	27	37176	724	0	100	100	3349	1864	<i>Strep. pyogenes</i> MGAS2096, complete genome	CP000261
I5_182	29	51814	792	0	100	100	2653	1274	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
I5_241	23	46659	572	0	100	100	1255	613	<i>Strep. pyogenes</i> MGAS10750, complete genome	CP000262
I5_273	30	51672	909	0	100	100	1877	966	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121

HSP: high-scoring segment pairs, D: Denmark, G: Germany, I: Ireland, NA: Not available

**Table S6.** BLAST comparison of contigs of the highest average read coverage (unclassified reads contigs)

Contigs	Average coverage	Size	Number of HSPs	Lowest E-value	Greatest identity %	Greatest positive %	Greatest HSP length	Greatest bit score	BLAST hit description	Accession
D2_4	529	4197	411	0	100	100	710	274	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
D2_13	1114	1762	177	0	100	100	181	238	<i>Lactococcus lactis</i> phage 645, complete genome	KC182543
D2_14	444	536	74	0	96	96	536	701	Bacteriophage phi-41 orfs L1-12, complete cds's, orf 13, 5' end	L35061
D2_15	529	535	119	0	100	100	98	129	Bacteriophage bIL191 putative fiber protein gene, partial cds	AY054977
D2_16	227	609	122	0	96	96	609	802	Bacteriophage phi-41 orfs L1-12, complete cds's, orf 13, 5' end	L35061
D2_20	284	214	47	0	97	97	189	153	<i>Lactococcus</i> phage 949, complete genome	HM029250
D2_22	316	390	64	0	96	96	349	176	<i>Lactococcus</i> phage P335, complete genome	DQ838728
D2_29	287	369	82	0	96	96	365	283	Bacteriophage Tuc2009, complete genome	AF109874
D2_37	335	486	191	0	100	100	485	726	<i>Lactococcus</i> phage phi15, complete genome	KM091442
D2_39	234	524	80	0	96	96	519	676	Bacteriophage phi-41 orfs L1-12, complete cds's, orf 13, 5' end	L35061
D3_1	323	407	105	0	100	100	331	295	<i>Lactococcus</i> phage 949, complete genome	HM029250
D3_3	129	325	105	0	100	100	57	41	HIV-1 isolate BJOX010000.e34 from China	KM217737
D3_4	2221	1580	94	0	100	100	102	173	<i>Lactococcus</i> phage P008, complete genome	DQ054536
D3_5	149	653	229	0	100	100	253	171	<i>Lactococcus</i> phage P680, complete genome	KC182551
D3_6	143	1471	148	0	100	100	135	182	<i>Lactococcus</i> phage phi15, complete genome	KM091442
D3_7	135	547	174	0	100	100	473	425	Bacteriophage bIL309, complete genome	AF323670
D3_9	241	560	159	0	100	100	531	544	Bacteriophage bIL15 putative fiber protein gene, partial cds	AY054976
D3_22	217	398	114	0	100	100	175	281	<i>Lactococcus</i> phage phi15, complete genome	KM091442
D3_30	115	291	101	0	100	100	184	142	<i>Lactococcus</i> phage phi145, complete genome	KM091444
D3_31	111	247	176	0	100	100	128	200	<i>Bacteriophage</i> US3 lytic-enzyme (lytA) gene, complete cds	M90423
D4_1	2660	1586	95	0	100	100	103	174	<i>Lactococcus</i> phage P008, complete genome	DQ054536
D4_3	403	774	144	0	100	100	693	881	Bacteriophage phi-41 orfs L1-12, complete cds's, orf 13, 5' end	L35061
D4_9	368	400	69	0	100	100	324	292	<i>Lactococcus</i> phage 949, complete genome	HM029250
D4_10	169	1477	148	0	100	100	136	183	<i>Lactococcus</i> phage phi15, complete genome	KM091442
D4_17	199	434	108	0	100	100	211	320	<i>Lactococcus</i> phage phi15, complete genome	KM091442
D4_20	104	431	100	0	100	100	241	295	<i>Lactococcus</i> phage phi145, complete genome	KM091444
D4_32	107	547	149	0	100	100	473	425	Bacteriophage bIL309, complete genome	AF323670
D4_36	132	603	129	0	98	98	111	162	<i>Bacteriophage</i> US3 lytic-enzyme (lytA) gene, complete cds	M90423
D4_40	161	999	164	0	97	97	812	1072	<i>Lactococcus</i> phage phi145, complete genome	KM091444
D4_51	128	205	58	0	100	100	177	207	<i>Lactococcus</i> phage ASCC532, complete genome	JQ740813
D5_1	794	19272	161	0	100	100	19269	34736	<i>Bacillus</i> phage phi29, complete genome	EU771092

D5_3	468	1193	133	0	94	94	522	182	<i>Lactococcus</i> phage ASCC454, complete genome	JQ740802
D5_9	212	3481	319	0	100	100	737	277	<i>Lactococcus</i> phage jm2, complete genome	KC182546
D5_10	744	1502	198	0	100	100	146	192	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
D5_20	318	1649	154	0	100	100	124	178	<i>Lactococcus</i> phage phi15, complete genome	KM091442
D5_24	255	568	134	0	96	96	550	351	<i>Lactococcus</i> phage fd13, complete genome	KC182545
D5_53	226	227	63	0	100	100	257	205	<i>Lactococcus</i> phage WRP3, complete genome	KM677185
D5_55	276	608	125	0	96	96	606	806	Bacteriophage phi-41 orfs L1-12, complete cds's, orf 13, 5' end	L35061
D5_56	193	536	108	0	100	100	536	701	Bacteriophage phi-41 orfs L1-12, complete cds's, orf 13, 5' end	L35061
D5_75	178	507	110	0	100	100	506	688	Bacteriophage phi-41 orfs L1-12, complete cds's, orf 13, 5' end	L35061
G1_8	2066	364	114	0	100	100	113	176	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
G1_9	152	9734	174	0	100	100	871	852	<i>Streptococcus</i> phage TP-778L complete genome	HG380752
G1_14	627	19273	161	0	100	100	19270	34738	<i>Bacillus</i> phage phi29, complete genome	EU771092
G1_26	122	5837	2349	0	100	100	5170	7862	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
G1_46	49	1198	36	0	100	100	444	360	<i>Streptococcus pyogenes</i> MGAS315, complete genome	AE014074
G1_78	1692	551	111	0	100	100	540	292	<i>Lactococcus</i> phage P335, complete genome	DQ838728
G1_239	94	352	72	0	100	100	288	396	<i>Bacteriophage</i> US3 lytic-enzyme (lytA) gene, complete cds	M90423
G1_416	52	704	103	0	98	98	276	201	<i>Lactococcus</i> bacteriophage Q65 putative <i>rbp</i> gene, complete cds	AY576320
G1_455	60	915	57	0	100	100	64	55	<i>Lactobacillus johnsonii</i> NCC 533, complete genome	AE017198
G1_481	76	570	21	0	92	92	568	144	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
G2_36	227	2079	137	0	98	98	150	241	Bacteriophage Tuc2009, complete genome	AF109874
G2_47	262	493	221	0	100	100	431	328	<i>Lactococcus</i> phage jm3, complete genome	KC182547
G2_74	836	314	100	0	98	98	43	70	<i>Lactococcus</i> phage CB13, complete genome	FJ848882
G2_111	288	232	74	0	100	100	47	72	<i>Lactococcus</i> phage phi7, complete genome	KC182552
G2_143	171	504	69	0	100	100	486	290	<i>Lactococcus</i> phage SL4, complete genome	FJ848881
G2_186	272	570	76	0	100	100	569	393	<i>Lactococcus</i> phage phi7, complete genome	KC182552
G2_217	154	377	83	0	100	100	182	153	<i>Lactococcus lactis</i> phage p272, complete genome	KC182549
G2_279	310	205	40	0	100	100	203	156	<i>Lactococcus</i> phage phi145, complete genome	KM091444
G2_295	156	273	98	0	95	95	87	106	<i>Lactococcus lactis</i> phage P475, complete genome	KC182550
G2_296	369	419	208	0	100	100	105	174	<i>Lactococcus lactis</i> phage p272, complete genome	KC182549
G3_6	83	910	295	0	95	95	400	274	<i>Lactococcus</i> phage 936, complete genome	KC182544
G3_34	87	5807	2388	0	100	100	4821	7397	<i>Strep. pneumoniae</i> AP200, complete genome	CP002121
G3_63	78	558	127	0	96	96	119	189	<i>Lactococcus</i> bacteriophage Q66 putative <i>rbp</i> gene, complete cds	AY576319
G3_116	159	469	126	0	100	100	184	164	<i>Lactococcus</i> phage ASCC544, complete genome	JQ740814
G3_130	454	592	189	0	100	100	389	589	<i>Lactococcus</i> phage phi15, complete genome	KM091442

G3_135	59	315	158	0	100	100	345	265	<i>Lactococcus</i> phage fd13, complete genome	KC182545
G3_191	320	275	96	0	100	100	275	234	<i>Lactococcus</i> phage phi145, complete genome	KM091444
G3_219	79	512	103	0	100	100	518	351	<i>Lactococcus</i> phage ASCC532, complete genome	JQ740813
G3_425	107	281	177	0	100	100	281	430	<i>Lactococcus</i> phage P008, complete genome	DQ054536
G3_471	60	628	269	0	100	100	574	230	<i>Bacteriophage</i> US3 lytic-enzyme (lytA) gene, complete cds	M90423
I2_1	126	19430	162	0	100	100	19250	34702	<i>Bacillus</i> phage phi29, complete genome	EU771092
I2_3	50	1324	414	0	96	96	490	503	<i>Lactococcus</i> phage phi15, complete genome	KM091442
I2_9	37	8165	236	0	90	90	3951	5125	Bacteriophage 187, complete genome	AY954950
I2_15	16	1640	125	0	100	100	1619	2201	Bacteriophage 187, complete genome	AY954950
I2_16	28	375	235	0	100	100	116	137	<i>Lactococcus lactis</i> bacteriophage sk1 sequences	U01068
I2_17	26	3789	141	0	100	100	1950	2586	Bacteriophage 187, complete genome	AY954950
I2_22	11	2793	200	0	100	100	2156	3888	<i>Enterobacteria</i> phage RB55, complete genome	KM607002
I2_28	11	1701	134	0	100	100	1490	1702	Bacteriophage 187, complete genome	AY954950
I2_30	9	772	178	0	100	100	772	1388	<i>Enterobacteria</i> phage T4 isolate R4 and R8 gp37 and gp38 genes	KP162265
I2_130	10	461	93	0	100	100	267	476	<i>Enterobacteria</i> phage RB59, complete genome	KM607003
I3_7	608	984	85						NA	NA
I3_19	487	3598	125	0	100	100	81	52	<i>Lactococcus</i> phage WRP3, complete genome	KM677185
I3_23	390	1033	120	0	97	97	512	129	<i>Staphylococcus aureus</i> 04-02981, complete genome	CP001844
I3_38	505	5473	1752	0	100	100	4703	5844	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
I3_41	450	248	132	0	100	100	217	95	<i>Streptococcus pyogenes</i> MGAS6180, complete genome	CP000056
I3_53	1456	751	0						NA	NA
I3_57	1590	1313	176	0	100	100	476	425	<i>Streptococcus pyogenes</i> MGAS315, complete genome	AE014074
I3_58	1322	1168	116	0	100	100	1081	304	<i>Streptococcus pyogenes</i> NZ131, complete genome	CP000829
I3_63	629	834	102	0	100	100	470	131	<i>Staphylococcus epidermidis</i> RP62A, complete genome	CP000029
I3_90	972	459	0						NA	NA
I4_2	1433	438	112	0	100	100	386	218	Bacteriophage c2 complete genome	L48605
I4_5	149	499	0						NA	NA
I4_8	4779	709	82	0	100	100	643	393	<i>Lactococcus</i> phage bIL67 ORF35 gene, complete cds	AY180212
I4_14	54	234	0						NA	NA
I4_16	67	419	0						NA	NA
I4_37	109	5173	793	0	100	100	4889	5916	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
I4_136	55	1245	116	0	100	100	1228	371	<i>Streptococcus pyogenes</i> NZ131, complete genome	CP000829
I4_177	52	2319	107	0	100	100	59	43	<i>Mikumi yellow baboon virus 1</i> MYBV_M100 genome	KM110939
I4_320	259	407	114	0	100	100	327	284	Bacteriophage c2 complete genome	L48605

I4_928	60	255	88	0	100	100	92	117	<i>Lactococcus</i> phage bIL67, complete genome	L33769
I5_29	923	450	0						NA	NA
I5_61	791	384	139	0	100	100	267	384	<i>Orf virus</i> strain D1701, complete genome	HM133903
I5_116	1078	705	81	0	100	100	643	393	<i>Lactococcus</i> phage bIL67 ORF35 gene, complete cds	AY180212
I5_127	842	680	0						NA	NA
I5_172	730	1814	0						NA	NA
I5_510	617	434	135	0	100	100	123	196	<i>Lactococcus</i> phage bIL67, complete genome	L33769
I5_720	477	442	0						NA	NA
I5_2254	504	481	103	0	100	100	300	337	<i>Orf virus</i> strain D1701, complete genome	HM133903
I5_3911	598	442	0						NA	NA
I5_4483	418	415	101	0	100	100	86	120	<i>Jaagsiekte sheep retrovirus</i> , complete genome	DQ838494

HSP: high-scoring segment pairs, D: Denmark, G: Germany, I: Ireland, NA: Not available

**Table S7.** BLAST comparison of contigs of the longest sizes (unclassified reads contigs)

Contigs	Average coverage	Size	Number of HSPs	Lowest E-value	Greatest identity %	Greatest positive %	Greatest HSP length	Greatest bit score	BLAST hit description	Accession
D2_3	18	27048	972	0	100	100	21930	38415	<i>Lactobacillus</i> phage Ld25A, complete genome	KJ564036
D2_4	529	4197	411	0	100	100	710	274	<i>Lactococcus</i> phage CaseusJM1, complete genome	KC522412
D2_12	63	1573	63	0	100	100	102	138	<i>Lactococcus</i> phage P008, complete genome	DQ054536
D2_13	1114	1762	177	0	100	100	181	238	<i>Lactococcus lactis</i> phage 645, complete genome	KC182543
D2_28	15	5437	149	0	100	100	4996	8735	<i>Lactobacillus</i> phage Ld25A, complete genome	KJ564036
D2_30	3	1634	102	0	100	100	1634	2858	<i>Streptococcus</i> phage 5093, complete genome	FJ965538
D2_49	4	2165	66	0	100	100	2165	3879	<i>Streptococcus</i> phage 5093, complete genome	FJ965538
D2_70	3	1431	205	0	100	100	105	45	<i>Choristoneura rosaceana entomopoxvirus</i> 'L', complete genome	HF679133
D2_82	3	2149	87	0	100	100	2149	3859	<i>Streptococcus</i> phage 5093, complete genome	FJ965538
D2_83	5	1676	107	0	100	100	53	70	Bacteriophage Tuc2009, complete genome	AF109874
D3_4	2221	1580	94	0	100	100	102	173	<i>Lactococcus</i> phage P008, complete genome	DQ054536
D3_11	39	9481	124	0	100	100	9484	17068	<i>Bacillus</i> phage phi29, complete genome	EU771092
D3_12	28	3868	123	0	100	100	3892	6977	<i>Bacillus</i> phage phi29, complete genome	EU771092
D3_15	29	5172	118	0	100	100	5187	9323	<i>Bacillus</i> phage phi29, complete genome	EU771092
D3_19	22	1661	124	0	100	100	1666	2997	<i>Enterobacteria</i> phage RB59, complete genome	KM607003
D3_67	12	1625	182	0	100	100	1625	2926	<i>Enterobacteria</i> phage RB59, complete genome	KM607003
D3_74	6	1737	262	0	100	100	1750	3134	<i>Enterobacteria</i> phage RB59, complete genome	KM607003
D3_92	6	1614	223	0	100	100	1614	2912	<i>Enterobacteria</i> phage RB59, complete genome	KM607003
D3_121	6	1615	802	0	100	100	1615	2908	<i>Enterobacteria</i> phage RB59, complete genome	KM607003
D3_129	6	1521	144	0	100	100	1521	2735	<i>Enterobacteria</i> phage RB59, complete genome	KM607003
D4_1	2660	1586	95	0	100	100	103	174	<i>Lactococcus</i> phage P008, complete genome	DQ054536
D4_6	26	19151	162	0	100	100	19148	34521	<i>Bacillus</i> phage phi29, complete genome	EU771092
D4_12	4	1819	247	0	100	100	1839	3256	<i>Enterobacteria</i> phage T4T, complete genome	HM137666
D4_18	29	1641	113	0	100	100	95	128	Bacteriophage phi LC3, complete genome	AF242738
D4_61	10	3193	258	0	100	100	2426	4369	<i>Enterobacteria</i> phage RB55, complete genome	KM607002
D4_63	4	1616	825	0	100	100	1625	2916	<i>Enterobacteria</i> phage RB59, complete genome	KM607003
D4_64	7	1764	500	0	100	100	1764	3182	<i>Enterobacteria</i> phage RB59, complete genome	KM607003
D4_106	6	1940	116	0	100	100	1940	3469	<i>Enterobacteria</i> phage T4 isolate R4 or R8 gp37 and gp38 genes	KP162265
D4_122	4	1569	167	0	100	100	1580	2831	<i>Enterobacteria</i> phage RB59, complete genome	KM607003
D4_130	5	1844	557	0	100	100	1900	3321	<i>Enterobacteria</i> phage RB55, complete genome	KM607002
D5_1	794	19272	161	0	100	100	19269	34736	<i>Bacillus</i> phage phi29, complete genome	EU771092

D5_4	55	30429	2726	0	100	100	15288	27310	<i>Enterobacteria</i> phage T4T, complete genome	HM137666
D5_6	40	66116	4766	0	100	100	49334	88498	<i>Enterobacteria</i> phage RB59, complete genome	KM607003
D5_7	51	18169	689	0	100	100	18169	32741	<i>Enterobacteria</i> phage RB59, complete genome	KM607003
D5_11	59	53589	2555	0	100	100	23327	41876	<i>Enterobacteria</i> phage T4 strain wild, complete genome	KJ477684
D5_25	12	10017	123	0	100	100	68	48	<i>Rhodococcus</i> phage REQ3, complete genome	JN116824
D5_33	9	5112	0						NA	NA
D5_35	31	5518	156	0	100	100	5274	6544	Bacteriophage 187, complete genome	AY954950
D5_50	12	5200	111	0	100	100	71	46	<i>Mycobacterium</i> phage Squirty, complete genome	KM101124
D5_103	13	5899	114	0	100	100	87	52	<i>Mycobacterium</i> phage Dori, complete genome	JN698995
G1_3	12	6517	199	0	100	100	3503	1606	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
G1_9	152	9734	174	0	100	100	871	852	<i>Streptococcus</i> phage TP-778L complete genome	HG380752
G1_14	627	19273	161	0	100	100	19270	34738	<i>Bacillus</i> phage phi29, complete genome	EU771092
G1_17	16	6278	173	0	100	100	1334	239	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
G1_18	13	6567	686	0	100	100	3881	6921	<i>Enterobacteria</i> phage RB59, complete genome	KM607003
G1_21	22	7611	533	0	100	100	6080	10886	<i>Enterobacteria</i> phage RB59, complete genome	KM607003
G1_23	21	6030	477	0	100	100	6032	10876	<i>Enterobacteria</i> phage RB59, complete genome	KM607003
G1_70	22	6376	199	0	100	100	6249	7233	<i>Streptococcus pyogenes</i> MGAS6180, complete genome	CP000056
G1_99	16	9750	46	0	100	100	1945	524	<i>Streptococcus pyogenes</i> MGAS10270, complete genome	CP000260
G1_206	14	6050	197	0	100	100	3470	2504	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
G2_8	81	5076	826	0	100	100	5015	7608	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
G2_21	12	4123	100	0	100	100	1396	728	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
G2_80	10	4927	388	0	100	100	2702	1550	<i>Streptococcus pyogenes</i> MGAS10270, complete genome	CP000260
G2_124	17	6082	198	0	100	100	6089	7126	<i>Streptococcus pyogenes</i> M1 GAS, complete genome	AE004092
G2_232	12	4297	147	0	100	100	1688	1347	<i>Streptococcus pyogenes</i> MGAS10750, complete genome	CP000262
G2_415	19	4859	174	0	93	93	3046	2746	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
G2_447	11	3977	167	0	100	100	3470	2459	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
G2_471	10	4306	139	0	100	100	1810	854	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
G2_483	9	4748	280	0	100	100	2243	795	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
G2_484	14	4313	97	0	100	100	2282	472	<i>Streptococcus pyogenes</i> MGAS2096, complete genome	CP000261
G3_1	14	9246	190	0	100	100	1905	1384	<i>Streptococcus pyogenes</i> MGAS6180, complete genome	CP000056
G3_41	17	11109	216	0	100	100	4507	4284	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
G3_53	11	7813	191	0	97	97	2091	1491	<i>Streptococcus pyogenes</i> MGAS10270, complete genome	CP000260
G3_74	18	7620	187	0	100	100	7296	8488	<i>Streptococcus pyogenes</i> M1 GAS, complete genome	AE004092
G3_83	12	6777	121	0	100	100	1334	239	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121

G3_114	8	18448	458	0	100	100	2260	977	<i>Streptococcus pyogenes</i> MGAS6180, complete genome	CP000056
G3_127	13	13131	77	0	100	100	1945	524	<i>Streptococcus pyogenes</i> MGAS10270, complete genome	CP000260
G3_143	8	7236	158	0	100	100	1073	573	<i>Streptococcus pyogenes</i> MGAS2096, complete genome	CP000261
G3_232	12	8632	226	0	100	100	2690	3458	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
G3_234	13	6912	159	0	100	100	5191	3384	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
I2_1	126	19430	162	0	100	100	19250	34702	<i>Bacillus</i> phage phi29, complete genome	EU771092
I2_5	9	3846	108	0	100	100	3926	6775	<i>Streptococcus</i> phage 858, complete genome	EF529515
I2_7	6	1949	91	0	100	100	1766	2773	<i>Streptococcus</i> phage Abc2, complete genome	FJ236310
I2_9	37	8165	236	0	90	90	3951	5125	Bacteriophage 187, complete genome	AY954950
I2_13	5	3399	138	0	100	100	3392	5047	<i>Streptococcus thermophilus</i> bacteriophage 2972, complete genome	AY699705
I2_17	26	3789	141	0	100	100	1950	2586	Bacteriophage 187, complete genome	AY954950
I2_20	6	2246	107	0	96	96	2242	2185	Bacteriophage 187, complete genome	AY954950
I2_22	11	2793	200	0	100	100	2156	3888	<i>Enterobacteria</i> phage RB55, complete genome	KM607002
I2_24	5	2000	124	0	100	100	1098	643	<i>Staphylococcus</i> phage vB_SepiS-phiIPLA7, complete genome	JN192401
I2_42	6	2501	149	0	96	96	2400	3058	Bacteriophage 187, complete genome	AY954950
I3_3	70	137688	1649	0	100	100	2786	1233	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
I3_4	55	117628	1317	0	100	100	2493	1678	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
I3_14	67	80420	1253	0	100	100	1994	863	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
I3_15	48	79278	1240	0	100	100	2403	1240	<i>Streptococcus pyogenes</i> NZ131, complete genome	CP000829
I3_18	63	88786	1197	0	100	100	2823	1513	<i>Streptococcus pyogenes</i> M1 GAS, complete genome	AE004092
I3_31	61	141086	1857	0	100	100	1678	1074	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
I3_35	51	77196	970	0	100	100	1630	631	<i>Streptococcus pyogenes</i> MGAS10750, complete genome	CP000262
I3_49	68	112858	1328	0	100	100	5202	4250	<i>Streptococcus pyogenes</i> MGAS5005, complete genome	CP000017
I3_87	58	73756	1042	0	100	100	1810	878	<i>Lactobacillus johnsonii</i> NCC 533, complete genome	AE017198
I3_129	48	73702	655	0	100	100	1519	596	<i>Streptococcus pyogenes</i> M1 GAS, complete genome	AE004092
I4_6	23	8376	122	0	100	100	380	146	<i>Staphylococcus aureus</i> 04-02981, complete genome	CP001844
I4_26	15	6288	215	0	100	100	2667	2448	<i>Streptococcus pyogenes</i> M1 GAS, complete genome	AE004092
I4_37	109	5173	789	0	100	100	4889	5916	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
I4_217	24	5107	80	0	100	100	1656	306	<i>Lactobacillus johnsonii</i> NCC 533, complete genome	AE017198
I4_256	25	7709	182	0	100	100	6576	3873	<i>Streptococcus pyogenes</i> MGAS2096, complete genome	CP000261
I4_303	7	4593	132	0	100	100	556	275	<i>Streptococcus pyogenes</i> NZ131, complete genome	CP000829
I4_305	7	5455	241	0	100	100	1325	378	<i>Streptococcus pyogenes</i> NZ131, complete genome	CP000829
I4_319	8	4479	200	0	100	100	1033	371	<i>Streptococcus pyogenes</i> NZ131, complete genome	CP000829
I4_514	10	4713	292	0	100	100	1586	1058	<i>Streptococcus pyogenes</i> M1 GAS, complete genome	AE004092



14_584	8	5251	0						NA	NA
15_89	21	23390	459	0	100	100	2386	1466	<i>Streptococcus pyogenes</i> MGAS10270, complete genome	CP000260
15_100	19	29403	453	0	100	100	2135	1045	<i>Lactobacillus salivarius</i> UCC118, complete genome	CP000233
15_104	29	22849	586	0	100	100	1916	553	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
15_125	23	31339	343	0	100	100	2093	797	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
15_217	23	22185	356	0	100	100	1508	999	<i>Streptococcus pyogenes</i> NZ131, complete genome	CP000829
15_311	20	22484	389	0	100	100	2338	609	<i>Streptococcus pneumoniae</i> AP200, complete genome	CP002121
15_330	20	35138	531	0	100	100	1970	800	<i>Lactobacillus salivarius</i> UCC118, complete genome	CP000233
15_372	22	23787	480	0	100	100	1803	1249	<i>Streptococcus pyogenes</i> NZ131, complete genome	CP000829
15_375	27	29703	553	0	100	100	5202	4216	<i>Streptococcus pyogenes</i> MGAS5005, complete genome	CP000017
15_640	18	21933	447	0	100	100	1451	573	<i>Streptococcus pyogenes</i> MGAS315, complete genome	AE014074

HSP: high-scoring segment pairs, D: Denmark, G: Germany, I: Ireland, NA: Not available

**Table S8.** Diversity of 936 phages in whey mixture metavirome sequences. Reads per kilobase per million mapped reads (RPKM) values were derived from the number of reads that showed a minimum of 95% identity over 95% of the query length upon Ublast against 936 phages RBP sequences. Obtained numbers were normalized by the size of the subject RBP sequence, followed by the size of the metavirome.

RBP variant	RPKM values										
	D2	D3	D4	D5	G1	G2	G3	I2	I3	I4	I5
ASCC473	251	347	412	123	49	658	202	4	0	0	0
HD16	101	454	436	43	17	28	122	0	0	0	0
PhiB1127	168	60	73	40	48	64	352	4	0	0	0
P113G	146	189	76	95	4	58	79	349	1	0	0
ASCC406	1639	1050	814	1489	8	32	2456	3565	0	1	0
936	146	47	31	87	120	28	4	198	0	0	0
Phi4	245	6	1	127	118	7209	388	15	0	0	0
PhiA16	69	0	0	0	24	1428	71	4	0	0	0
Q66	397	0	0	217	30	247	146	10	0	0	0
1727	898	792	5215	1478	49	4499	2019	34	0	8	1
phage 7	9130	5004	3732	9070	40	1271	15616	14718	3	4	2
fd13	1061	565	460	445	2	6	426	4083	0	1	0
HD6	333	13	3	137	0	25	1	230	0	0	0
Q49	392	417	267	178	0	2	36	0	0	0	0
Phi42	1154	19	3	1218	0	22	285	0	0	0	0
PhiL6	6474	23	10	3274	4	8	5	0	0	3	1
Phi17	0	0	0	0	0	0	0	0	0	0	0
SCH	5594	4069	4293	2867	13307	2051	0	0	0	3	2
645	1383	8258	6478	279	10	0	1012	0	2	1	2

D: Denmark, G: Germany, I: Ireland

Table S9

Diversity of *Leuconostoc* phages in whey mixture metavirome sequences. Reads per kilobase per million mapped (RPKM) values were derived from the number of reads that showed a minimum of 95% identity over 95% of the query length upon Ublast against *Leuconostoc* phages RBP sequences. Obtained numbers were normalized by the size of the subject RBP sequence, followed by the size of the metavirome.

RBP variant	RPKM values										
	D2	D3	D4	D5	G1	G2	G3	I2	I3	I4	I5
LNTR2	0	0	0	2	0	0	0	0	0	0	0
LN32	0	0	0	0	0	0	0	0	0	0	0
LN25	0	0	0	0	0	0	0	0	0	0	0
LN-9	0	0	0	0	0	0	0	0	0	0	0
LN6B	1	2	0	185	875	0	265	0	0	0	0
P793	0	0	0	0	65	0	22	0	0	0	0
LN23	0	0	0	0	0	0	3	0	0	0	0

D: Denmark, G: Germany, I: Ireland