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use of phages for Campylobacter reduction

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AgriFutures®
Chicken Meat

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Foreword

Camplyobacter is a high priority food-born pathogen, as a low number of organisms can cause human illness. Poultry are a major source of *Camplyobacter* as it routinely colonises the chicken gut, where it can reach high numbers. Without effective on-farm control, there is potential for *Camplyobacter* to persist throughout the supply chain to contaminate the final product. This project builds on previously funded AgriFutures that seeks to develop an environmentally friendly biological control based on bacteriophages commonly found in commercial broiler farms that infect and kill *Camplyobacter*.

This project demonstrated that a two-log reduction in *Camplyobacter* levels was achieved in both on-farm and in-vitro experiments and created a broad understanding of potential phage candidates to target for future commercialisation. This will benefit the entire chicken meat supply chain from breeder flocks to the consumer through exploitation of a naturally occurring predator-prey relationship between bacteriophages (viruses) that infect and kill *Camplyobacter*. A 2-log reduction in *Camplyobacter* levels could reduce human infections by 90%.

This project identified phage candidates with commercialisation potential by demonstrating their effectiveness on-farm with low levels (7%) of resistance as well as reducing surface contamination of chicken carcass during processing. Genomic sequencing of these candidate phages revealed no recognisable antibiotic or pathogenicity related genes, confirming their suitability for biocontrol applications. Importantly, this project generated the required data to facilitate regulatory of approval of these phages for biocontrol of *Campylobacter* in the Australian chicken meat industry.

This project was funded by AgriFutures Chicken Meat Program, with co-funding provided by the Queensland Department of Agriculture and Fisheries, as part of the Objective 1 of the Chicken Meat Program RD&E Plan 2019-22 *Improving the Food Safety of Australian chicken meat*.

This report is an addition to AgriFutures Australia's diverse range of research publications and it forms part of our growing profitability arena, which aims to enhance the profitability and sustainability of our levied rural industries. The AgriFutures Chicken Meat Program seeks to grow the long-term prosperity of the Australian chicken meat industry.

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Mr John Smith

General Manager, Research
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About the Authors

Dr Nalini Chinivasagam – Principal Research Scientist, Department of Agriculture and Fisheries, Queensland, is a food microbiologist worked in the area of food-safety for more than 30 years and has extensive experience working with food-borne pathogens, including *Salmonella* and *Campylobacter,* in the poultry, pig and seafood industries. Dr Chinivasagam has led a series of RIRDC and Poultry CRC funded projects that all delivered practical focused outcomes that have proven of value to the poultry industry. The projects include " A proof of concept study for *Campylobacter* control", "assessing *Campylobacter* dynamics in free-range and other farming systems" (RIRDC), "Evaluating food-borne pathogen transfer associated with partial and full re-use litter" (RIRDC), "Aerobiology around broiler sheds" (RIRDC), "Re-use of litter across farming systems" (CRC), Survey of Australian litter, (RIRDC) and a research summary that encompasses most of the above work titled "Food Safety Pathogens, Litter, and Aerosols – Summarising a Decade (2004 – 2014) of Research". Dr Chinivasagam has also carried out work on composting of layer industry waste (AECL) as well as work on piggery effluent, composts, aerosols (APL) and seafood quality (FRDC).

Professor Ian Connerton - Chair of Food Safety, Head of Division of Microbiology, Brewing and Biotechnology, School of Biosciences, University of Nottingham is the 2 Sisters Food Group Chair of Food Safety at the University of Nottingham where he leads the Food Microbiology and Safety Section. He has been involved in molecular biology research for more than 30 years which includes food-borne zoonotic pathogens. He is also involved in research on the influence and therapeutic use of bacteriophage against zoonotic pathogens in the human food chain, the synthesis and delivery pathogen products to host cells and their molecular responses, host protein interactions, enzyme technology in partnership with agri-food industries as well as making use of the traditional benefits of biological catalysts (chemical specificity, mild reaction conditions and low environmental loads) for food application. He is actively engaged in research on *Campylobacter* phages and has extensively published in this area of work. These include isolation, classification and genomics of *Campylobacter* bacteriophages. He has several publications and contributes to strategies in controlling *Campylobacter* in poultry in the UK.

Dr. Craig Billington - Science Leader in the Risk and Response Group at the Institute for Environmental Science and Research (ESR), Christchurch, New Zealand, has more than 19-year's research experience in food safety. The focus of his research has been the control of pathogenic and spoilage organisms in foods, food processing environments and on livestock. Craig is an internationally recognised expert in bacteriophages (phages; viruses of bacteria) and developed New Zealand's first registered phage product, STECleanz®, released in 2014 for the control of *E. coli* O157. This product was approved for use in both New Zealand and the USA. Craig's other interests include active packaging, new methods for pathogen detection, metagenomics, antimicrobial resistance, food traceability/authenticity and the development of pathogen mimics. He is a regular peer reviewer for international journals and overseas funding agencies. He is a founding member of the International Phage Research Centre based in Nanjing, currently sitting on its academic committee, and is a member of the Science Leadership Team for the New Zealand China Food Protection Network.

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- Dr Margaret A MacKenzie, (former Group Executive General Manager Technical Services, Ingham's Enterprises Pty Ltd.) for her support across studies including access to farms and plant
- Ms Kelly McTavish, Ingham's Enterprises Pty Ltd. for assistance with all farm work
- The farmers who allowed free access and provided samples that supported both original studies that made the current study possible
- Agrifutures for providing the funding for the current study that facilitated a detailed understanding of the phages via international collaboration with both the University of Nottingham and Environmental Sciences Research, New Zealand
- The Poultry CRC for funding the "proof of concept study" that provided the opportunities to narrow down these phages to cocktail candidates that enabled the progression of two on-farm trials in collaboration with the University of Nottingham
- The RIRDC (AgriFutures) for funding the "*Campylobacter* dynamics…" study that resulted in acquiring a large collection of *Campylobacter* bacteriophages to progress to phage biocontrol
- Department of Agriculture and Fisheries (Queensland) for co-funding this study and all previous studies

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Executive Summary

Poultry are a major source of *Campylobacter* with the organism having no impact on the bird. Irrespective of this situation, the important single source of campylobacteriosis is considered to be broiler meat (European Food Safety Authority 2016). The reported number of cases of campylobacteriosis in Australia in 2015 was 22,573 (Communicable Disease Intelligence 2019). Studies have suggested that a reduction in *Campylobacter* levels by greater than 2-$\log_{10}$ units would contribute to the reduction of the public health risk by more than 90% (European Food Safety Authority 2011). Overseas models have suggested that bacteriophage treatment has the greatest potential of all known/potential methods to reduce *Campylobacter* levels in the live chicken (Havelaar et al. 2007).

Campylobacter naturally colonises the chicken gut, where it can reach high numbers and potentially contaminate the marketed product. A low number of organisms can cause human illness. This study is exploring a biocontrol option using bacteriophages (phages) to reduce *Campylobacter* numbers in chickens. Bacteriophages are viruses that infect and kill the target bacteria. These specific, *Campylobacter*-killing phages occur naturally in farm chickens, where they are already in a 'predator–prey relationship' with *Campylobacter*. The aim of this study is to better the outcome of this natural phenomenon. The study builds upon data from previous studies to progress the option of using *Campylobacter* bacteriophages to control *Campylobacter* levels in poultry.

The report is targeted at the Australian Poultry Industry, those with a role of food-safety at an industry level and also have a regulatory role.

Background

Risk assessment studies predict that a reduction of *Campylobacter* levels on chicken meat can contribute to significantly less human illness (Rosenquist et al. 2006). A 1.0-log reduction in faecal count supported by a 1.0-log reduction in contamination of the exterior of chickens, during processing would result in a 90% reduction of human infections (Havelaar et al. 2007). Hence, the development and validation of on-farm control options for reducing *Campylobacter* levels by 1.0 to 2.0 logs can realistically result in a lowering of human infections from 50,000 to 5,000 cases per year.

Australian on-farm studies have addressed *Campylobacter* levels in the caeca of the bird across litter practices, including free-range across four years (Chinivasagam et al. 2015, Chinivasagam et al. 2016) compared three litter practices (including re-use) over a two year period on two farms and across six sequential farming cycles (Chinivasagam et al. 2016). During this extensive study, *Campylobacter* levels varied little across litter practices and were high and in the range of log 8.0–9.0 CFU/g in caeca (Chinivasagam et al. 2016). These factors highlight the need for options to reduce *Campylobacter* levels on-farm. The bacteriophage – bacteria (*Campylobacter*) interaction is a natural and on-going interaction that occurs in the gut of the bird and are found in commercial broiler farm environments and the bird. A study assessing UK broiler chicken flock (n=205) have demonstrated a significant reduction ($P < 0.001$) of *Campylobacter jejuni* counts in caeca in the chickens with a presence of *Campylobacter*-specific bacteriophages, with mean counts of $\log_{10}$ 5.1 CFU/g Vs 6.9 CFU/g in chickens in the absence of *Campylobacter* phages (Atterbury et al. 2005). The ability to harness this natural reaction offers opportunities for a natural bio-control option.

A range of phage products are currently available against other food-borne pathogens such as *Salmonella*, *Listeria* and *E. coli* (EHEC), but there are none against *Campylobacter*, to date. The use of phages as bio-control agents (or processing aids) is fast gaining interest internationally, driven by consumer demands for natural alternatives. The bio-control of *Campylobacter* using phages is an environmentally friendly option, with potential for positive market acceptance and the delivery of a safer product to the consumer.

This study is built upon and continues from two prior studies on *Campylobacter*. A previous study on on-farm *Campylobacter* dynamics in 2011 – 2015, comparing four litter practices, (Chinivasagam et al. 2015) provided the opportunity to isolate *Campylobacter* phages from Australian farming environments, which formed a large collection. A second short 1.5 year study 2015 – 2016 (Chinivasagam et al. 2017), via addressing a "proof of concept" provided the opportunity to create a panel of phages and carry-out two targeted trials on a small number of farmed birds, within the commercial farming framework. More specifically, this study created a broad understanding of the phage candidates to enable progression to the next stage.

Aims/objectives

- Assess the relationship between the phages and farm *Campylobacter* isolates via a series of logical and targeted laboratory-based studies
- Evaluate selected phages that may form a cocktail for their suitability based on simple lytic profiles and detailed molecular studies
- Achieve a suitable log reduction of *Campylobacter* with the possible inclusion of either "active" or "passive" phage therapy strategy, which is assessed in-vitro (micro titre plates)
- Based on the knowledge of all the above develop a cocktail of phages
- Carry out trials on farm raised birds (farm) and on processed carcasses (lab) (not undertaken due to variation) – Appendix 1
- Generate data to support necessary Australian regulatory framework for the use of phages as bio-control agents by the Australian Poultry Industry
- Provide the Australian Poultry Industry an efficacious environmentally friendly option to control *Campylobacter* that will benefit the poultry industry and the consumer

Methods used

- A logical representation of *Campylobacter* hosts were used to expand a previously available *Campylobacter* phage candidate panel from 19 - 23 candidates. This included backyard and NSW source material (in addition to Queensland). This included both *C. jejuni* and *C. coli*
- The activity of the candidate panel was assessed on a farm by farm basis based on previously available screening data and the overall candidate panel performance was statistically analysed
- The expanded candidate panel was assessed against a broader group of *Campylobacter* isolates based on year sourced, origin on farm, litter practice and species
- *In-vitro* log reduction studies were undertaken to assess efficiency of reduction afforded by host and phage via in-vitro studies and compared with on-farm reductions (former CRC study)
- *In-vitro* resistance studies were undertaken to assess the potential development of resistance during application. The outcomes were compared with the outcomes from the CRC farm trial
- Cocktail formulation was undertaken using both Australian and New Zealand *Campylobacter* hosts and the resultant outcomes were compared as to best performers

- Detailed molecular studies on a small number of candidate phages were undertaken to demonstrate the use of this approach as a pathway to intelligent cocktail formulation, address safety and required regulatory needs

- Finally, all outcomes across the present and previous studies were summarised to demonstrate phage bio-control as a safe option that can be adopted by the industry within a framework of regulatory requirements as generated across all relevant studies

Results/key findings

- The original phage candidate panel was found to be optimum by analysing previously generated farm *Campylobacter* and phage data. An additional four candidates made up the panel to 23 phages, which followed the use of diverse source samples for screening

- Selected phage candidates (PH 16, 17, 18, 19) that showed better activity over others were apparent when analysing individual farm data (241 isolates across various farms) or when comparing species. The phage activity pattern against *Campylobacter* isolates present at the time naturally varied on the same farm when comparing sequential years (due to different populations). In general, the sheds across a single farm at a particular time had a similar *Campylobacter* – cocktail candidate activity

- Lytic profiles using a panel of 19 phage cocktail candidates was carried across a random selection of *Campylobacter* (241) isolates sourced from 2012 – 2016 from 11 Queensland farms. The outcomes were statistically analysed and involved using 23 shed/year combinations which commonly had *C. jejuni* or *C. coli* on a single farm. For the initial screening of activity scores across farms, generalised linear mixed models (GLMM) were used with restricted maximum likelihood (REML) in GenStat (2016). From an overall perspective representative phage activity of phage cocktail candidates was observed across both *C. jejuni* and *C. coli* (241 farm isolates were analysed)

- The 23-panel candidate panel was re-analysed against an expanded group of *Campylobacter* isolates (74) that considered year of isolation (2003 – 2016), litter practice, species and source of isolation. From an overall perspective phages PH 4, 5, 11, 16, 17, 18 and 19 dominated compared to the rest of the panel members. Generally, over five farms showed sensitivity to each individual phage cocktail candidate. The total number of *Campylobacter* isolates lysed by each phage (PH 1 – 23) is also presented in showing an overall good representation of the 23 member phage cocktail candidate panel with phages PH 18 and 19 lysing around 50 *Campylobacter* isolates among the total of 74 *Campylobacter* isolates that formed this special group. The other lysed around 15 *Campylobacter* isolates (and some over that number)

- *In-vitro* studies using the universal international host *C. jejuni* PT 14 and PH 19, demonstrated a 2-log reduction, this was compared with the log reductions achieved during the CRC farm trials

- *In-vitro* studies using farm campylobacters and selected phage candidates demonstrated only a 7% resistance, which is comparable to published work. This aspect is discussed in detail along with the inconsistencies that prevail over extrapolating in-vitro resistance outcomes with what occurs within the bird. (i.e. the resistant form is non-motile and cannot prevail for long in the chicken gut the flagella is required for colonisation)

- The application of phages isolated in this study can reduce the contamination of surface deposited campylobacters and those on chicken carcass surfaces at refrigeration temperatures by 1-2 $\log_{10}$ CFU (passive therapy application)

- Phage isolated in the course of this project from farm sources in Australia are typical of group 3 phage isolated from farm environments elsewhere in the world. Phage treatment of host bacteria at or over the phage proliferation threshold of 7 $\log_{10}$ CFU /ml achieved a reduction of 2 $\log_{10}$ CFU/ml (active therapy application)

- Genomic DNA sequences of phage isolated in Australia and included in the phage cocktails contain no recognisable antibiotic or pathogenicity related genes making them suitable for biocontrol applications

- Demonstrated how detailed genomic analysis can provide a greater understanding of phage – *Campylobacter* binding (in addition to other factors assessed within the project) to enable intelligence-based refinement of the phage cocktails, which address both safety and efficiency.

- Based on the knowledge of the above, phage cocktails were formulated in New Zealand where there exists previous expertise for the phages to move to commercialisation. Both Australian and New Zealand hosts were used for the purpose

- A total of eleven cocktails were created using Australian phages. Some of the Australian phage cocktails were further tested by addition of New Zealand isolated phages to determine if there was any added benefit. The combined formulations performed the best and are active against AU and NZ *Campylobacter* isolates

- Work to optimise phage cocktail formulations will be guided by this data

- Finally, all outcomes across the present and previous studies were combined to address the final objective i.e. generate data necessary to support Australian regulatory frame work for bio-control and provide the Australian poultry industry an officious environmentally friendly option to control *Campylobacter* was addressed drawing the key elements across the previous Poultry CRC and current study

- This included the demonstration of the achieved 2-log reduction (both on-farm and in-vitro), the identification of the future need to exploit the co-contribution of the natural phage population that became apparent during the Poultry CRC farm trials, the demonstration that resistance being not deterrent to phage bio-control, as demonstrated, which also can be managed by targeting the treatment period, the demonstration of phage free-carcasses based on the previously performed farm trials (for consumer acceptance), the existence of phages in litter only in the presence of phage positive birds when assessed across 2 –years and 24 farms (outcomes from a previous study on *Campylobacter* dynamics), and the optimum survival of phage candidates in tap water that ensures a simple and easy delivery option on-farm

- This work has been presented as an invited presentation at the international conference "Tropical Agriculture" held in Brisbane 11th – 13th November 2019 (Appendix 3)

Implications for relevant stakeholders

Poultry are a major source of *Campylobacter*, although a zoonotic pathogen the organism has minimal impact on birds. Campylobacteriosis is the most common form of bacterial foodborne disease worldwide, and the single most important source of *Campylobacter* is broiler meat (European Food Safety Authority 2016). European studies indicate that on-farm interventions can exert effective control, with a 2.0 log reduction in faecal *Campylobacter* counts predicted to reduce human infections by 75% or a 1.0 log reduction in faecal count supported by a 1.0 log reduction in contamination of the exterior of processed chicken meat a 90% reduction of human infection (Havelaar et al. 2007). Hence, the development of an on-farm intervention to control *Campylobacter* levels by 1.0 to 2.0 logs is of

significance to industry and policymakers to bring about reductions in human infections from 50,000 to 5,000 case per year.

This study represents progress towards delivering a sustainable and low environmental impact option, which is likely to gain consumer acceptance for the control of one the key foodborne pathogens responsible for human illness.

In summary:

- Poultry are a major source of *Campylobacter*, with the most important single source of campylobacteriosis considered to be broiler meat
- Modelling indicates that on-farm poultry interventions can be very effective in reducing human infections
- Development and validation of on-farm control options for reducing *Campylobacter* levels by 1.0 to 2.0 logs can realistically result in a 90% reduction of human infections
- This study is progressing towards delivering an environmentally compatible option for the industry to achieve these reductions in *Campylobacter* on-farm

Recommendations

The research undertaken to date developing a *Campylobacter* bio-control solution for the poultry industry has been significantly advanced in this work. This work now needs to be capitalised upon to bring this closer to a commercial reality.

Based on these outcomes there is need for future work with respect to the following:

There is a need to continue sequence annotation for the rest of the cocktail candidates as demonstrated in this section

Co-contribution of the natural phage – *Campylobacter* interaction which can be harnessed to enhance cocktail contribution

There is need to formulate and address selection of cocktails from a scale up perspective to ensure a viable commercialisation pathway to market

There is need to seek potential commercial entities to understand the way forward in providing a Australian regulatory frame work for the use of phages as bio-control agents by the Australian Poultry Industry

Introduction

Poultry are a major source of *Campylobacter* with the organism having no impact on the bird. Irrespective of this situation, the important single source of campylobacteriosis is considered to be broiler meat (European Food Safety Authority 2016). Risk assessment studies predict that a reduction of *Campylobacter* levels on chicken meat can contribute to significantly less human illness (Rosenquist et al. 2006). European studies indicate that on-farm interventions can be very effective, i.e. a 2.0 log reduction in faecal *Campylobacter* counts will reduce human infections by 75%. Similarly, a 1.0 log reduction in faecal count supported by a 1.0 log reduction in contamination of the exterior of chickens, during processing would result in a 90% reduction of human infections (Havelaar et al. 2007). Hence, the development and validation of on-farm control options for reducing *Campylobacter* levels by 1.0 to 2.0 logs can realistically result in a lowering of human infections from 50,000 to 5,000 case per year.

There are limited options to control *Campylobacter* in farmed poultry. In the UK, due to both the disease and economic burden attributed to infectious intestinal diseases, *Campylobacter* (along with norovirus and rotavirus) have been classified as a high priority pathogen by the food standard agency's food-borne disease strategy (Tam and O'Brien 2016). A recent review on the global epidemiology of *Campylobacter*, places focus on the poultry sector and highlights the need for a worldwide campaign to encourage interventions within the sector (Kaakoush et al. 2015). Overseas models have suggested that phage treatment has the greatest potential of all known/potential methods to reduce *Campylobacter* levels in the live chicken (Havelaar et al. 2007). The proposed study is a step in that direction and is designed to develop a biological process to control *Campylobacter* using phages.

The use of phages as bio-control agents (or processing aids) is fast gaining interest internationally, driven by consumer demands for natural alternatives. The bio-control of *Campylobacter* using phages is an environmentally friendly option, with potential for positive market acceptance and the delivery of a safer product to the consumer. Though well used in Eastern Europe where there is a history of active research and use, the concerns on the use of phages elsewhere are mostly driven due to the scarcity of strong scientific evidence generated through fully controlled trials, supported by ethical standards of the West (Sillankorva et al. 2012). Further when compared to other treatments such as the used of electrolysed oxidizing water, phage therapy has been shown to have a higher cost benefit effect (Gellynck et al. 2008). The first phage-based pesticide on the market was against *Erwinia amylovora*, which causes fire blight in apples (Meczker et al. 2014). The Environmental Protection Agency (in 2002) approved the use of phages to control bacterial spot (rot) of tomatoes and peppers i.e. plant pathogens *Xanthomonas campestris* subsp *vesicatoria* and *Pseudomonas syringae* (Goodridge and Bisha 2011). The United States Food and Drug Administration (USDA) has supported the use of *E. coli* 0157 and *Salmonella* based "hide sprays" on cattle prior to slaughter plus approved products are available for red-meat parts and trims (Goodridge and Bisha 2011). Phage-preparations are also being used on 'post-harvest' product with Food and Drug Administration, USA (FDA) and USDA approval against *Listeria* (Goodridge and Bisha 2011).

Phages have potential to reduce on-farm *Campylobacter* in poultry (Connerton et al. 2011). The phage – bacteria (*Campylobacter*) interaction is a natural and on-going interaction that occurs in the gut of the bird. Phages isolated from commercial broiler house environments between successive flocks have shown relationships/variations across successive flocks reflecting the diversity that occurs across poultry farming environments, (Connerton et al. 2004). Phages have also been isolated across Australian broiler farming environments (Estella et al. 2015). A study assessing UK broiler chicken flock (n=205) have demonstrated a significant reduction ($P < 0.001$) of *Campylobacter jejuni* counts in caeca in the chickens with a presence of *Campylobacter*-specific phages, with mean counts of $\log_{10}$ 5.1 CFU/g Vs 6.9 CFU/g in chickens in the absence of *Campylobacter* Phages (Atterbury et al. 2005). The ability to harness this natural reaction offers opportunities for a natural bio-control option. Studies have also demonstrated that *Campylobacter* levels decreased between 0.5 and 5 log CFU/g in the

caeca of *C. jejuni*-colonised birds compared to untreated birds over 5-days, with such reductions depending on the phage-*Campylobacter* combinations, doses administered and post treatment time, (Carrillo et al. 2005).

A range of products are already available against food-safety pathogens. The availability of such products has demonstrated the economic viability of phage-based options with no limitations in uptake mainly for food-safety organism such as *Listeria*, *Salmonella* and *Escherichia coli* 0157. Commercial phage products are already marketed against these organisms by various companies in Europe and USA. These phage products are largely marketed as "processing aids". Listed below are some examples of products from selected companies. New Zealand has commercialised the countries first phage product against EHEC to be used for cattle hides (Dr. Billington, personal communication).

Listeria - Listex P100 produced by Micreos (Netherlands). This is the first phage product to be permitted to be used in Australasia as a food processing aid and has Food Standards Australia New Zealand (FSANZ) approval to be used in Australia (http://www.foodproductiondaily.com/Safety-Regulation/Listeria-killing-phage-product-gets-FSANZ-approval). This product has organic and halal certification.

Listeria, (Listshield), E. coli 0157 (Ecoshield) and *Salmonella* (Salmofresh) are all products registered for use by "Intralytix (http://www.intralytix.com/Intral_Food.htm.

Salmonella (Salmonellex) is approved for use by the FDA and USDA as a GRAS (Generally Recognised As Safe), and produced by Micreos. This company is going further to seek approval by the Organic Material Review Institute (OMRI) to enable the product to be used in organic products

These few examples of companies are listed here to reiterate the fact that international companies are actively producing and marketing products. This activity in the market clearly indicates there is uptake and active use of phage-based products due to the nature of such products and their ability to control food-safety pathogens. To date, there are no commercial phage products against *Campylobacter*. Australian on-farm studies (Chinivasagam et al. 2016, Chinivasagam et al. 2015) have addressed *Campylobacter* levels in the caeca of the bird, from varying litter practices including free-range. The 2016 study (Chinivasagam et al. 2016) compared three litter practices (including re-use) over a two-year period on two farms and across six sequential farming cycles. During this extensive study, *Campylobacter* levels varied little across litter practices and were high and in the range of log 8.0–9.0 CFU/g in caeca (Chinivasagam et al. 2016). These factors point to the need for an option to reduce *Campylobacter* levels on-farm.

The current study is built upon and continues from two prior studies on *Campylobacter* (Chinivasagam et al. 2015, Chinivasagam et al. 2017). A previous study (Chinivasagam et al. 2015) on on-farm *Campylobacter* dynamics (when comparing four litter practices) provided the opportunity isolate *Campylobacter* phages from Australian farming environments, which formed a large collection. A second short 1.5 year study (Chinivasagam 2017, Chinivasagam 2020), via addressing a "proof of concept" provided the opportunity to create a panel of phages and carry-out two targeted trials on a small number of farmed birds, within the commercial farming framework. The sequence and previous contributions from which the current study follows are presented in Table 1.

Table 1 Initial and supporting studies to current study

	Study details	**Key contributions of relevant studies**
1	**RIRDC (Agrifutures)** *"Campylobacter* dynamics in free-range and conventional farming systems". 2011-2014; - PRJ-006238 (Chinivasagam et al. 2015) – 3 years	(1) A collection of 500 phages isolated across diverse broiler farming environments (and litter practices) in Queensland over a two-year period (2) An understanding phage isolation pattern across farms (including caeca and litter) that supports necessary Australian regulatory framework for the use of phages as bio-control agents. (3) Invited peer review publication in progress
2	**Poultry CRC** "A "proof of concept" study to control *Campylobacter* using phages". Sub-Project No: 3.1.6; - 2015 -2016; (Chinivasagam 2017) – 1.5 years Collaboration: **University of Nottingham, UK**	(1) A well screened 19-member phage cocktail candidate panel for cocktail preparation, following extensive screening against a range of farm *Campylobacter* isolates (2) Targeted farm trial based on: that a week before final pick-up (time of treatment) (a) the flock be phage negative (b) have a high *Campylobacter* levels (c) be sensitive to two or more candidates (3) Testing was done on-farm, during transport and at the plant (4) On Farm A, a 2-log reduction was achieved on-farm (5) On Farm B, log reductions were achieved in both test and controls but a phage inherent in the system interfered with assessing the cocktail phage outcome (6) This study provided the main candidate panel, demonstrated log reduction and the need for future work on including the co-contribution of inherent phages to cocktails (not addressed in the current study) (7) Publication and presentation: Chinivasagam, H.N., Estella, W., Maddock, L., Mayer, D.G., Weyand, C., Connerton, P.L. and Connerton, I.F. (2020) Bacteriophages to Control Campylobacter in Commercially Farmed Broiler Chickens, in Australia. Frontiers in Microbiology 11. https://www.frontiersin.org/article/10.3389/fmicb.2020.00632
3	**Agrifutures** Concept to control ….(Chinivasagam et al. 2020, current study), PRJ-010208; - 2016 - 2019 Collaboration: (1) **University of Nottingham, UK** **(2) Environmental Sciences Research, NZ**	(1) Analysed previously unanalysed CRC data to have a better understanding of cocktail performance (2) Increased the panel form 19 – 23 candidates (3) Created a detailed understanding of candidate phages (including demonstration of selected cocktail performance) to supports necessary Australian regulatory framework for the use of phages as bio-control agents. (4) Peer review publications, planned

Thus, the relevant outcomes of previous studies have been combined to address selected objectives of the current study as is relevant.

More specifically the current study progressed to expand and analyse the candidate panel for performance against farm campylobacters, undertook in-vitro log reduction and resistance studies include cocktail formulation and analysis against collective set of isolates to address performance and detailed molecular studies to gain an overall perspective. The outcomes were targeted at delivering a safe biocontrol option that has a marketable potential and backed by data to advance regulatory support. All these options leading to providing an environmentally friendly biocontrol option to control on-farm *Campylobacter*.

Objectives

- Assess the relationship between the phages and farm *Campylobacter* isolates via a series of logical and targeted laboratory-based studies
- Evaluate selected phages that may form a cocktail for their suitability based on simple lytic profiles and detailed molecular studies
- Achieve a suitable log reduction of *Campylobacter* with the possible inclusion of either “active” or “passive” phage therapy strategy, which is assessed in-vitro (micro titre plates)
- Based on the knowledge of all the above develop a cocktail of phages
- Carryout trials on farm raised birds (farm) and on processed carcasses (lab) (not undertaken due to variation) – Appendix 1
- Generate data to support necessary Australian regulatory framework for the use of phages as bio-control agents by the Australian Poultry Industry
- Provide the Australian Poultry Industry an efficacious environmentally friendly option to control *Campylobacter* that will benefit the poultry industry and the consumer.

Chapter 1: Assessing the relationship between the phages and farm *Campylobacter* isolates via a series of logical and targeted laboratory based studies

1.0 Background

This section reports the methodologies adopted for phage isolation and diversification using farm samples and farm *Campylobacter* hosts. Additional phages were isolated to expand the original CRC candidate panel of 19 candidates. Since that panel was created for the purpose of fulfilling the requirements of the farm trials required for the proof of concept and the overall study period was short (1.5 year) time spent on the panel work was limited. This section of work used previously unused approaches to try to diversify phages that may have potential to be included in the original panel. For this purpose the following were undertaken;

- Use of NSW samples to diversify the source of phage isolation
- Sourcing of new *Campylobacter* (2016) isolates from six Queensland farms to use additional screening and use of samples from those farms
- Expanding candidate panel based on outcomes

1.2 Methodologies

This section reports phage isolation (with the inclusion of enrichment), phage purification and phage spotting technique used for screening of isolates.

1.2.1 *Campylobacter* isolation

This is described in (Chinivasagam et al. 2016).

1.2.2 *Campylobacter* phage isolation

This following was carried as per methodology of Atterbury et al. (2003) with slight modifications to the original methodology. The methodologies for *Campylobacter* phage isolation (and purification) was also based on the published methodologies of Frost et al. (1999), El-Shibiny et al. (2005) and Sambrook et al. (1989).

Ten grams of litter and caeca were weighed into ninety millilitre of SM buffer then stomached using a stomacher for one minute for caeca. Litter and soil samples were shaken for 15 minutes. Following this initial preparation all samples were gently shaken at 4^{o}C overnight on a platform shaker. The samples were distributed into micro centrifuge tubes and centrifuged at 15,000g for 5 minutes, chilled for 5 minutes then centrifuge again at 15,000g for 5 minutes. The supernatant was removed to a new

tube and filtered using membrane filtration with a 0.22 micrometre pore size filter (low DNA binding). The levels of phage were enumerated using direct plating. For this a mixture of 100 µl sample plus 200 µl of 10^8 cfu/ml *C. jejuni* PT 14 host was incubated aerobically at 42ºC for 30 min. This mixture was then added to 5 ml of 0.6% overlay agar, which was poured on top of a 1% agar base plate and allowed to settle for around 30 minutes. The plates were incubated at 42ºC for 24 hours under micro anaerobic condition. Plaques were observed and counted. A representative single plaque was punched and stored in SM buffer for purification.

1.2.3 Enrichment for phage isolation

Hosts used were the universal international strain C. *jejuni* PT14 QC Strain (NC3163) or strain /strains relevant to this study (i.e. hosts from farms PU, PT and SH) based on the three farms that were part of this work.

The relevant samples (caeca, litter or soil) were prepared for enrichment and sampled as listed.in Table 2.

Table 2 Sample preparation for enrichment

Sample	Weight/Volume	Preston Broth Supplemented with Mg2+, Ca2+
Caeca	10g	40 ml (1:4)
Litter	17.5g	105 ml (1:6)
Soil	35g	105 ml (1:3)

The samples were mixed for 60 seconds in a stomacher and 100 µl of each culture of each overnight culture was added and incubated at 42ºC under micro aerobic conditions overnight. Following incubation 10ml of the supernatant was dispensed into 15 ml centrifuge tubes and centrifuged at 4,000xg for 10 minutes. The supernatant was centrifuged at 13,000xg for 5 minutes twice after brief storage on ice and filtered through a 0.22 µm membrane filter, following which it was tested for phages.

1.2.4 Phage purification and plate lysate stocks

This was carried out based on the method of Sambrook et al. (1989). The selected phage was grown at an appropriate dilution after which a single selected plaque was punched and plated again. This was carried two more times leading to a plaque being purified three times to ensure purity. After this the purified phage was grown as a confluent plate by adding 100ul of serial dilution of pure phage into 200ul PT14 incubate aerobically at 42ºC for 30 min, then mixed with 5 ml of 0.5% overlay agar and poured on top of a 1% agar base plate. Incubation was carried out at 42ºC for 24 hours under micro anaerobic condition. From this plating, a suitable plate was selected where the plaques just touched one another with bacterial growth webbing that marked the junction between adjacent plaques. The top agar layer was gently crushed using a sterile spreader to which 5 ml SM buffer was added and allowed to stand for 30 min. Then the agar was scraped with liquid into sterile centrifuge tube. The base plate was washed a few times with SM buffer and all the liquid was collected into a tube. The mixture was centrifuge at 15,000g for 5 minutes at 4ºC. The supernatant was recovered by filtering using a 0.22µm pore size filter membrane. The phage stock was stored in SM buffer with 25% glycerol at 4ºC and -80ºC.

1.2.5 Determination of lytic profiles

The determination of *Campylobacter* host range was carried out as per Connerton and Timms (2015). Briefly *Campylobacter* overlays were prepared as previously described and the relevant phage was spotted in 10 µl aliquots (at log 10^7 PFU/ml) on the surface of the overlay. The well dried plates were incubated overnight at 42^{o}C and scored as 0 = no lysis; 1 = poor lysis; 2 = medium lysis; 3 = very good lysis. The activity of a phage against a particular strain was assessed in this manner.

1.2.6 Examples of screening of host *Campylobacter* against phage (filtrate)

The following is an example of screening isolate NC 4096 against 16 phages (done in triplicate). The clear areas on the host depict areas of lysis, which were also scored as previously described.

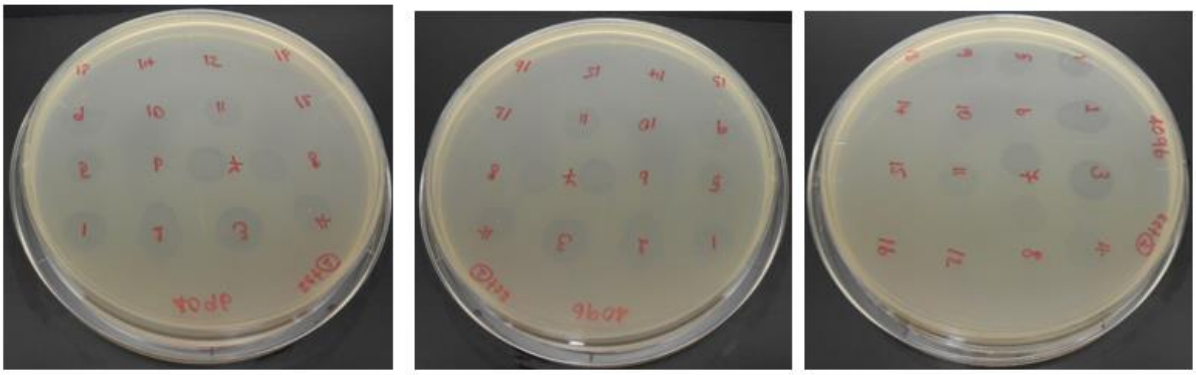


Figure 1 Examples of screening done (in triplicate) for a single culture

1.3 Results

The sequential steps that resulted in increasing the original candidate panel of 19 members to 23 members to diversify phage isolation is described. This was largely based on adopting multi-culture enrichment. This is followed by describing the "*Campylobacter* panel" created previously to accelerate screening. The original *Campylobacter* screening panel was expanded with new *Campylobacter* isolates (as a separate group) that were sensitive to NSW phages. Finally, four new candidates were added to the original panel of 19 to form a 23-member phage candidate panel. This panel was a focus of the rest of the reported studies.

1.3.1 Increased numbers and diversity of *Campylobacter* isolates

A total of 162 *Campylobacter* isolates (Table 3) that were isolated in 2016 (during the CRC study) were included to create hosts diversity. They were sourced across six farms. The farms were Farms R (sampled twice), SN, PU, CH and GH with isolates coming across multiple sheds during a single cycle, Table 3. The majority were *C. jejuni* with the rest *C. coli* as is normally seen on-farm.

Table 3 Campylobacter isolation from chicken ileum and caeca

Date	Farm	No. of culture	Culture No.	Strain
12/07/2016	Farm R Shed 5	5	NC4059-4063	*C. coli*
12/07/2016	Farm R Shed 6	5	NC4064-4068	*C. coli*
12/07/2016	Farm R Shed 7	5	NC4069-4073	*C. coli*
12/07/2016	Farm SN Shed 1	5	NC4074-4079	*C. jejuni*
12/07/2016	Farm SN Shed 5	5	NC4080-4083	*C. jejuni*
12/07/2016	Farm SN Shed 9	5	NC4084-4088	*C. jejuni*
12/07/2016	Farm SN Shed 14	5	NC4089-4093	*C. jejuni*
4/09/2016	Farm PU Shed 1	8	NC4094-4101	*C. jejuni*
4/09/2016	Farm PU Shed 3	14	NC4102-4115	*C. jejuni*
4/09/2016	Farm PU Shed 5	10	NC4116-4125	*C. jejuni*
7/09/2016	Farm P Shed 1	15	NC4126-4140	*C. jejuni*
31/10/2016	Farm R Shed 1	10	NC4144-4153	*C. jejuni*
31/10/2016	Farm R Shed 2	10	NC4154-4163	*C. jejuni*
31/10/2016	Farm R Shed 7	10	NC4164-4173	*C. jejuni*
31/10/2016	Farm CH shed 1	10	NC4174-4183	*C. jejuni*
31/10/2016	Farm CH shed 2	10	NC4184-4193	*C. jejuni*
31/10/2016	Farm GH Shed 3	10	NC4194-4203	*C. jejuni*
31/10/2016	Farm GH Shed 7	10	NC4204-4213	*C. jejuni*
31/10/2016	Farm GH Shed 8	10	NC4214-4223	*C. jejuni*

1.3.2 Isolation of phages by spot testing from NSW poultry environments using host *Campylobacter jejuni* PT14

A diverse set of samples, that included both backyard and commercial chicken farming facilities were sourced from Armidale and Northern NSW. Table 3 presents the diverse environments sampled, which for the first time included backyard chickens with the aim for phage diversity. However, phages were only isolated from environment C (i.e. C1, C2, C3, C4, C5 and C6) and B which were commercial free-range broiler farms. Eighteen phages (PH761-778) were isolated using the

Campylobacter PT14 as host (the commonly used host to isolate phages). These phages were isolated from the caeca. It is also worth noting that the non-commercial farm environments (backyard farming) all litter and soil along with the single farm environment B soil did not yield phages (in comparison for caeca, commercial farm) which was positive for *Campylobacter* phages.

Table 4 Source of phage isolation from NSW samples (using Campylobacter jejuni PT14 as host)

Code	Source	Type	Phage +/-
B1	back yard hens location A	Shed litter	-
B2	back yard hens location A	Shed soil	-
B3	back yard hens location A	Shed litter	-
B4	back yard hens location A	Hen faeces	-
B5	back yard hens location B	Outer shed litter	-
B6	back yard hens location B	Outer shed soil 15cm deep	-
B7	back yard hens location B	Inner shed dry litter	-
B8	back yard hens location B	Inner shed dry litter	-
B9	back yard hens location B	Hen faeces + soil	-
B10	back yard hens location B	Outdoor Moist soil	-
B11	back yard hens location B	Back hen shed bedding litter	-
B12	back yard hens location B	Litter composite	-
B13	back yard hens location B	Litter composite	-
B14	back yard hens location A	Soil inner shed 15cm	-
B15	back yard hens location A	Surface litter outer shed	-
B16	back yard hens location A	Outdoor 15cm deep	-
B17	back yard hens location A	Surface litter inner shed	-
B30	free range hens location C1	Soil inner shed 15cm	-
B31	free range hens location C1	Soil inner shed 15cm	-
B32	broiler shed location D	Soil outside shed 15cm	-
B33	broiler shed location D	Soil outside shed 15cm	-
B34	broiler farm location E	Soil outside shed 15cm	-
B35	broiler farm location E	Soil outside shed 15cm	-
B36	broiler facility location F	Caecum samples	-
C1	free range hens location C2	Caecum samples	+
C2	free range hens location C3	Caecum samples	+
C3	free range hens location C4	Caecum samples	+
C4	free range hens location C5	Caecum samples	+
C5	free range hens location C6	Caecum samples	+
C6	free range hens location C7	Caecum samples	+

1.3.3 Isolation of phages by spot testing from NSW poultry environments using Queensland hosts

A total of 79 *Campylobacter* farm isolates (from Table 3) were used to screen 42 NSW phage filtrates by spot testing as this method enables the easy screening to a larger number of samples. A total of 95 phages were isolated. Figure 2 illustrates the outcome of the extensive screening. The "shaded areas" represent phage positive isolations for a given *Campylobacter* isolate (left) and the various NSW sample filtrates (top). In summary, higher numbers of phages were isolated from the NSW samples using Queensland farm hosts rather than the routinely used international strain, *Campylobacter jejuni* PT14 as host (as reported in section 1.3.2).

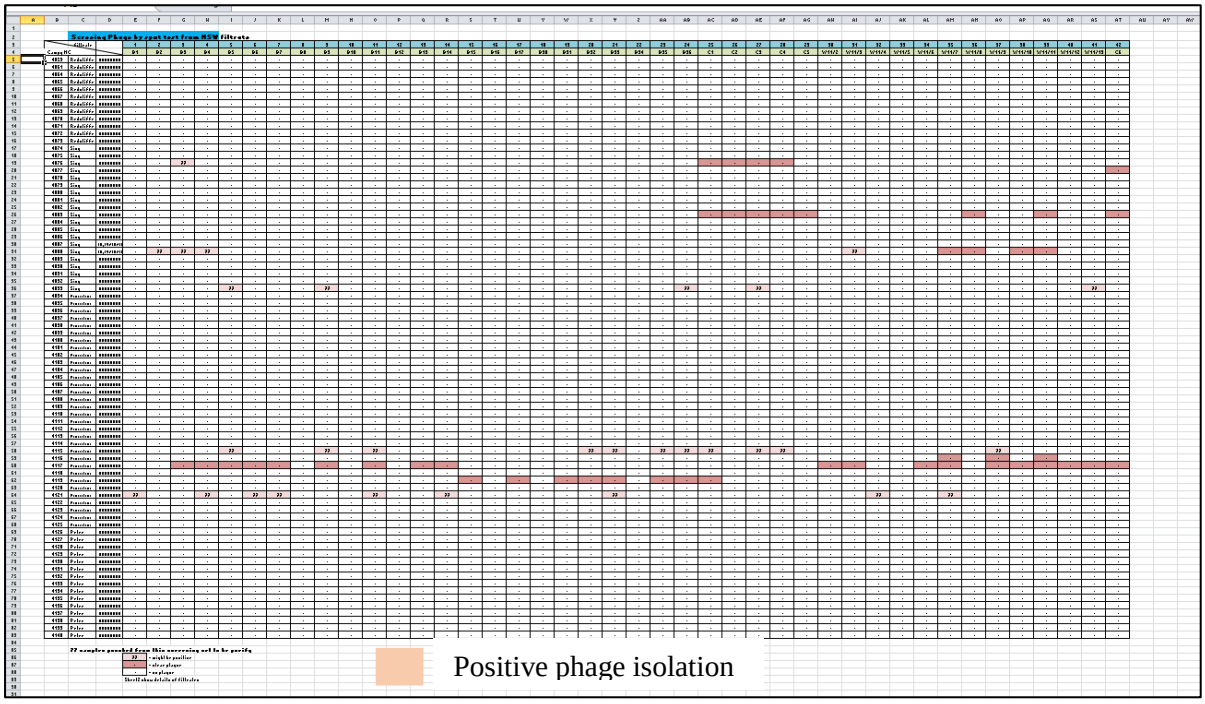


Figure 2 Screening of Queensland farm Campylobacter isolates against NSW farm filtrates

In summary, a total of 101 phages were isolated using both the above approaches (i.e. using either *Campylobacter jejuni* PT14 (international host) or Queensland farm hosts from the diverse range of NSW samples. This approach ensured phage diversity with potential to enhance the candidate panel.

1.3.4 Using *Campylobacter jejuni* PT14 host for farm PU filtrates

Farm PU was a Queensland farm sampled in 2016 and the approach adopted for Farm PU is reported in this section.

Both caeca and ileum samples sourced from three sheds were used. *Campylobacter jejuni* PT14 was used as host. A total of 37 phages (PH779 - 815) were isolated, Table 5.

Table 5 Purified phages (and phage collection numbers) sourced from caeca and ileum from Farm PU

Date	Phage no.	Sample	Date	Phage no.	Sample
4.10.16	779	caeca shed 5	4.10.16	798	Ileum shed 5
4.10.16	780	caeca shed 5	4.10.16	799	Ileum shed 5
4.10.16	781	caeca shed 5	4.10.16	800	Ileum shed 5
4.10.16	782	caeca shed 5	4.10.16	801	Ileum shed 5
4.10.16	783	caeca shed 5	4.10.16	802	Ileum shed 5
4.10.16	784	caeca shed 5	4.10.16	803	Ileum shed 5
4.10.16	785	caeca shed 5	4.10.16	804	caeca shed 1
4.10.16	786	caeca shed 5	4.10.16	805	caeca shed 1
4.10.16	787	caeca shed 5	4.10.16	806	caeca shed 3
4.10.16	788	caeca shed 5	4.10.16	807	caeca shed 3
4.10.16	789	caeca shed 5	4.10.16	808	caeca shed 5
4.10.16	790	caeca shed 5	4.10.16	809	caeca shed 5
4.10.16	791	caeca shed 5	4.10.16	810	Ileum shed 1
4.10.16	792	Ileum shed 5	4.10.16	811	Ileum shed 1
4.10.16	793	Ileum shed 5	4.10.16	812	Ileum shed 3
4.10.16	794	Ileum shed 5	4.10.16	813	Ileum shed 3
4.10.16	795	Ileum shed 5	4.10.16	814	Ileum shed 5
4.10.16	796	Ileum shed 5	4.10.16	815	Ileum shed 5
4.10.16	797	Ileum shed 5			

1.3.5 Phage isolation from Farm PU caeca using both multi-host enrichment and isolation

Farm PU caeca was used as source sample. Multi-host enrichment was adopted here. In this instance Farm PU isolates, NC 4094 – NC 4125 were used together in the enrichment process following which testing was done on individual Farm PU isolates, NC 4094 – NC 4125, Table 6.

Table 6 Isolation of phages from Farm PU caeca following "multi- host enrichment and isolation"

Isolate No	Shed	Caeca Shed 1 (C1)	Caeca Shed 3 (C3)	Caeca Shed C5(C5)
NC4094	*1*	-	-	-
NC4095	*1*	-	-	+++
NC4096	*1*	-	-	+++
NC4097	*1*	-	-	-
NC4098	*1*	-	-	+++
NC4099	*1*	-	-	-
NC4100	*1*	-	-	+++
NC4101	*1*	-	-	-
NC4102	*3*	-	-	-
NC4103	*3*	-	+++	+++
NC4104	*3*	-	-	+++
NC4105	*3*	-	-	-
NC4106	*3*	+++	+++	+++
NC4107	*3*	-	-	+++
NC4108	*3*	+++	+++	+++
NC4109	*3*	+++	+++	+++
NC4110	*3*	+++	-	-
NC4111	*3*	+++	+++	+++
NC4112	*3*	+++	+++	+++
NC4113	*3*	+++	+++	+++
NC4114	*3*	+++	+++	+++
NC4115	*3*	+++	+++	+++
NC4116	*5*	+++	+++	+++
NC4117	*5*	+++	+++	+++
NC4118	*5*	-	-	-
NC4119	*5*	+++	+++	+++
NC4120	*5*	-	-	-
NC4121	*5*	+++	+++	+++
NC4122	*5*	+++	+++	+++
NC4123	*5*	+++	+++	+++
NC4124	*5*	+++	+++	+++
NC4125	*5*	+++	+++	+++

1.3.6 Phage isolation from Farm PT caeca using multi-host for both enrichment and isolation

In this instance phages were isolated from Farm PT caeca using multi-host enrichment with Farm PU isolates NC 4094 – NC 4125 plus Farm PT isolates NC 4126 – 4140. Following enrichment testing was carried out on individual host isolates from Farm PU (NC4094 – NC 4125) and individual host isolates form Farm PT (NC 4126 – 4140), Table 7.

Table 7 Isolation of phages from Farm PT caeca, following both multi-host enrichment and isolation

Isolate No.	Shed	Caeca shed 1 (C1)	Caeca shed 5 (C5)	Caeca shed 6 (C6)	Caeca shed 7 (C7)
NC4094	*1*	FL	FL	FL	FL
NC4095	*1*	FL	FL	FL	FL
NC4096	*1*	FL	FL	FL	FL
NC4097	*1*	FL	FL	FL	FL
NC4098	*1*	FL	FL	FL	FL
NC4099	*1*	FL	FL	FL	FL
NC4100	*1*	-	-	+++	-
NC4101	*1*	FL	-	-	-
NC4102	*3*	-	-	+++	+++
NC4103	*3*	?	?	+++	+++
NC4104	*3*	+++	+++	+++	+++
NC4105	*3*	FL	-	-	-
NC4106	*3*	?	?	?	?
NC4107	*3*	+++	+++	+++	+++
NC4108	*3*	-	-	-	-
NC4109	*5*	+++	+++	+++	+++
NC4110	*5*	+++	+++	+++	+++
NC4111	*5*	??	-	+++	+++
NC4112	*5*	+++	+++	+++	+++
NC4113	*5*	+++	+++	+++	+++
NC4114	*5*	+++	+++	+++	+++
NC4115	*5*	+++	+++	+++	+++
NC4116	*5*	+++	+++	+++	+++
NC4117	*5*	+++	+++	+++	+++
NC4118	*5*	-	-	-	-
NC4119	*5*	+++	+++	+++	+++
NC4120	*5*	-	-	+++	-
NC4121	*5*	+++	+++	+++	+++
NC4122	*5*	+++	+++	+++	+++
NC4123	*5*	+++	+++	+++	+++
NC4124	*5*	+++	+++	+++	+++
NC4125	*5*	+++	+++	+++	+++

FL – Fully lysed +++ Clear lysis ? Uncertain (NC 4126 – NC 4140 negative)

1.3.7 Phage isolation from Farm SH farm caeca following both multi-host enrichment and isolation

Screening for phages was done via "multi- host enrichment" using *Campylobacter* isolates from Farm SH (NC 4074-4093) and phage sensitive *Campylobacter*, from Farm PU (NC4096, 4098, 4100, 4102, 4110, 4116, 4125 & PT14). This was followed by screening Farm SH against individual Farm SH isolates and Farm PU isolates (NC4096, 4098, 4100, 4102, 4110, 4116, 4125 & PT14)

No phages were isolated from Farm SH caeca.

1.3.8 Summary of phages isolated to progress candidate selection

A total of 215 additional phages were isolated (Table 8) to enable progress phage candidate selection. There was a need to use both *C. jejuni* PT14 the universal host and Queensland farm hosts to isolate phages from both NSW samples and Queensland farms PU and PT. Thus, host diversity was used to ensure phage diversity.

Table 8 A breakdown of purified Campylobacter phages (with allocated phage numbers) and phage punches

Source	Phage number.	Number of phage	Punched
NSW (PT14)	PH761-778	18	
NSW (using farm host)	-	-	77
Farm PU(Using PT14)	PH779-815	37	
Farm PU and Farm PT (using farm host)	-	-	138
Total		55	215

1.4 Lytic profile for phages isolated

A total of 38 purified phages (from Table 7) were screened against the 39 *Campylobacter* screening panel (created during the Poultry CRC study). The phages we used were from NSW (18 phages) and Farm PU, (20 phages). The *Campylobacter* screening panel contains “hard”, “medium” and “easy” to lyse phages and was the basis for the selection of the 19-member candidate panel (Poultry CRC)

Based on this screening, 17 phages from NSW and 1 phage from Farm PU are able to lyse 5 *Campylobacter* reference panel isolates (NC3209, 3210, 3217, 3223, and 3234), as illustrated by the yellow shading (very good lysis, Figure 3) and pink (medium lysis, Figure 3). This approach was using to narrow down potential candidate phages.

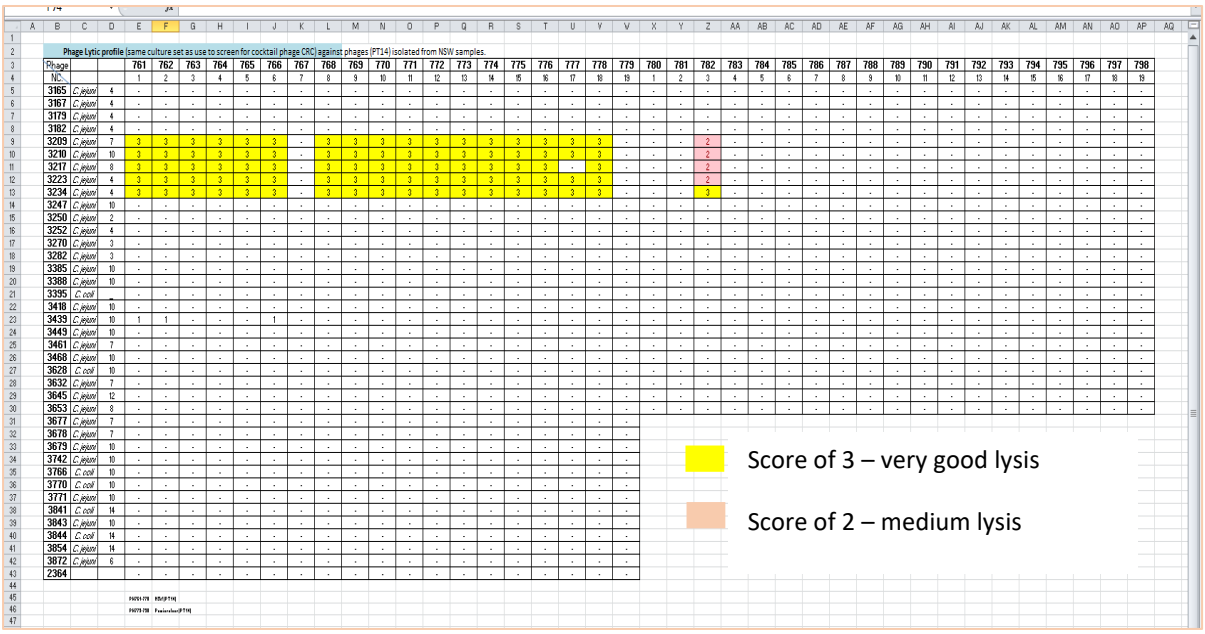


Figure 3 Lytic profile of a select group of Campylobacter phages screened against a select panel of Campylobacter isolates (as used to develop cocktail for the CRC phage study)

1.5 Narrowing down isolated phages from Queensland and NSW

During the CRC study a 19-member phage cocktail candidate panel was created in a manner similar to that reported. The aim with this study was to further diversify this panel with phages sourced from farms that were potential candidate farms for the Poultry CRC farm trials along with those isolated from NSW poultry environments (including broiler chicken caeca).

The following path was undertaken to select the optimum candidates, which ultimately all came from Queensland farm environments.

1.5.1 The *Campylobacter* screening panel

As previously described the *Campylobacter* screening panel made of hard to lyse, medium and easy candidates is illustrated in Figure 4.

Resistance	lysed 4,5 campy	More sntv +nsw sntv	Varity RCptr	sensitive
3165	3449	3209	3346	2480
3167	3461	3210	3351	2482
3179	3632	3217		2485
3182	3653	3223		2975
3247	3677	3234		2981
3250	3678	3330		2985
3252	3679	3332		2988
3270	3771			2990
3282	3333			2992
3385	3361			2993
3388	3366			3034
3395	3527			3037
3418	3795			3042
3468	3796			3109
3628				
3645				
3742				
3766				
3770				
3841				
3843				
3844				
3854				
3872				
2364				
3331				
3335				
3359				
3517				
3528				
3531				
3558				
3816				

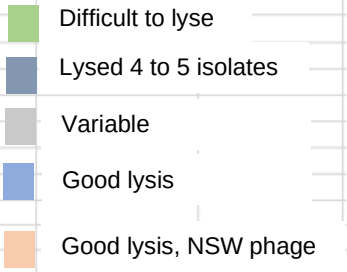


Figure 4 Campylobacter screening panel (inclusive of isolates that demonstrated good lysis to NSW phages)

The difficult to lyse isolates (orange), those that lysed 4 – 5 isolates (blue) are followed by those isolates that were able to lyse NSW phages (pink) and the overall isolates with good lysis (Queensland in light blue) are displayed in Figure 4.

1.5.2 The two-step screening process

A two-step screening process was adopted to identify the optimum candidates as follows:

– The phages described in this section were initially screened against the sensitive *Campylobacter* isolates from the original *Campylobacter* screening panel, Figure 5.

– The phages described in this section were then screened against the *Campylobacter* isolates that were more sensitive to NSW phages, Figure 6.

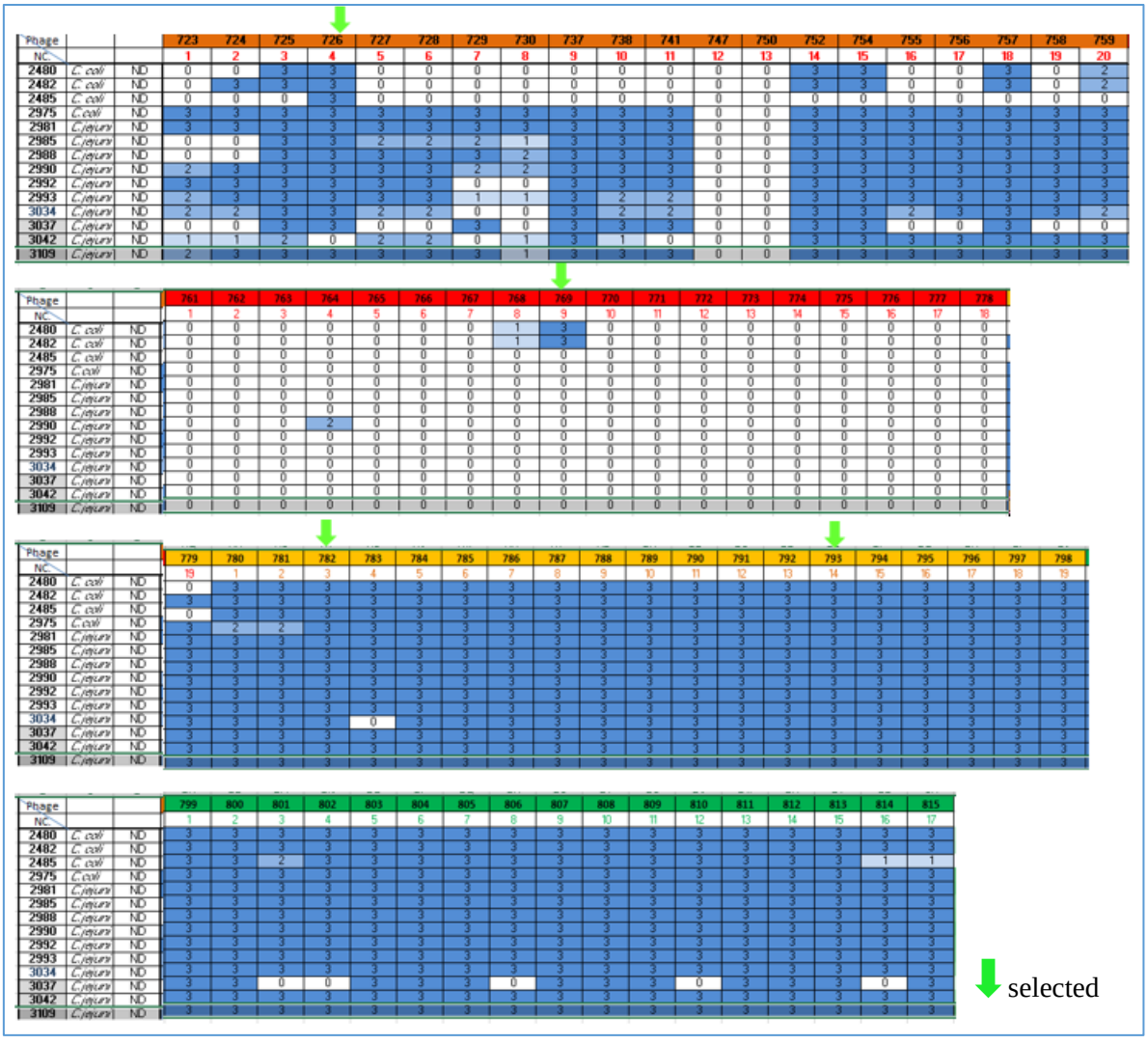


Figure 5 Lytic profile of phages against most sensitive isolates from original Campylobacter panel

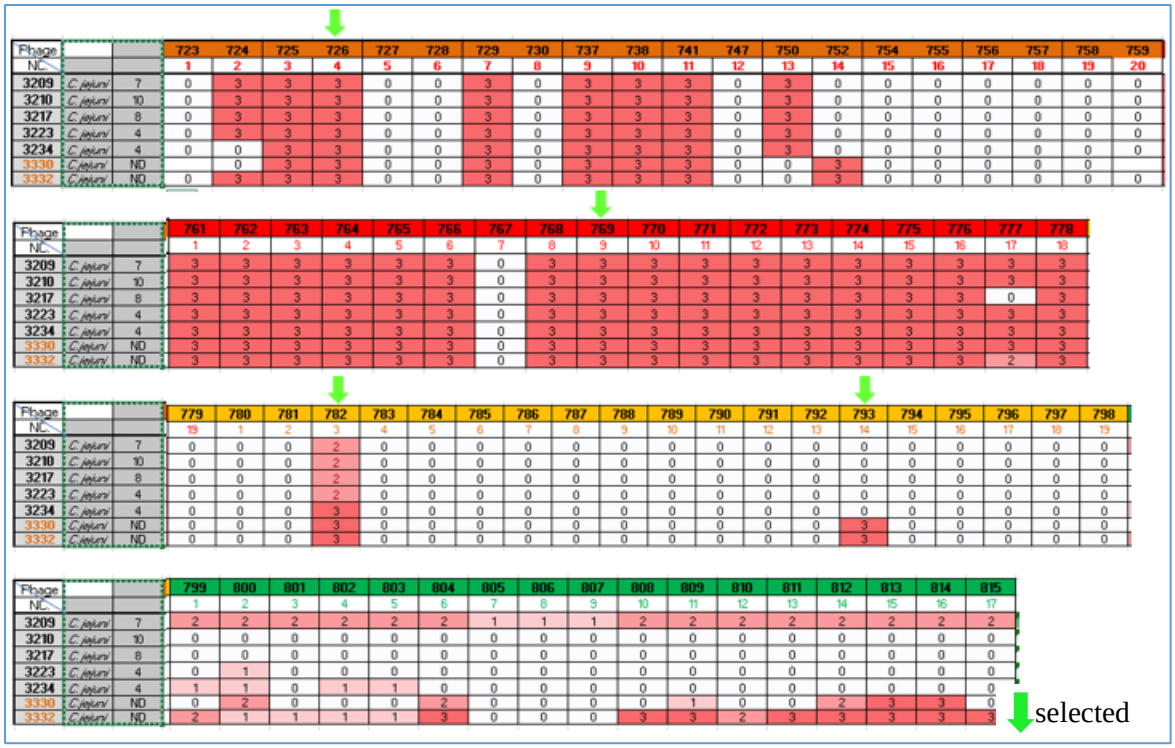


Figure 6 Lytic profile of isolates screened against Campylobacter isolates most sensitive to NSW phages

1.5.3 The final selection to be added to the candidate panel

Following analysis of the overall screening, four additional candidates were selected and added to the panel of 19 candidates. The diversification work carried out as reported resulted in the recently isolated phages PH 726, 769, 782, and 793 being added to the panel to final phage cocktail candidate panel of 23 members. From this point onwards the phages would be coded from 1 - 23 as PH 1 – 23 (which are also inclusive of these four phages which formed the 23-member phage cocktail panel).

1.6 Summary, phage isolations and *Campylobacter* farm hosts

A diverse set of samples (previously not tested) from both NSW and QLD poultry/poultry environments were used for both *Campylobacter* and phage isolation. A total of 160 diverse *Campylobacter* isolates from poultry ileum (never tested before) and caeca collected from a cluster of QLD farms were used. Phage diversity was achieved by using these this set of new *Campylobacter* isolates for screening both via direct and enrichment techniques (as described in this section).

A lytic profile using the Poultry CRC - 39 member *Campylobacter* screening panel isolates and a selection of *Campylobacter* isolates that were sensitive to NSW screening were used to narrow down candidates as panel members. Based on the outcomes and analysis an additional 4 candidates were added to the panel making it a total of 23 phage cocktail candidate panel to allow for cocktail formulation.

Chapter 2: Evaluate selected phages that may form a cocktail for their suitability based on simple lytic profiles and detailed molecular studies

2.1 Background

This section combines outcomes of the work undertaken under the current study and previously unanalysed Poultry CRC study data. Thus, this section provides comprehensive analysis of phages (including host – phage relationships). It summarises the host and phage sources, their lytic spectra against selected farm *Campylobacter* isolates, resistant profiles including Pulse Field Gel Electrophoresis along with DNA sequencing of phages.

Whilst the Poultry CRC study undertook extensive screening to narrow down to cocktail candidates to enable the facilitation of the proof of concept farm trials, detailed analysis of the phage-host data remained un-analysed due to the short duration of that project (i.e. 1.5 years). This was undertaken during the current study. In summary the following are described in this section:

- Analysed the extensive screening data generated by the poultry CRC to gain a broader understanding in relation to the 19-phage cocktail candidate panel and farm *Campylobacter* isolates on a farm to farm basis and subsequent overall summary of panel activity
- The activity of the 23-member cocktail panel against an expanded set of host *Campylobacter* sourced from 2004 – 2016 to understand broader activity
- One-step log reductions to understand performance of selected phage cocktail candidates
- In-vitro resistance studies to support the in-vivo resistance observations (no resistance during the poultry CRC farm trials following phage introduction to birds)
- Detailed analysis of phages via both PFGE and DNA analysis

2.2 Methodologies adopted

The Phage screening methodologies are as described in Chapter 1.

2.2.1 Phage genome size determination using Pulse Field Gel Electrophoresis (PFGE)

This method was based on Atterbury et al. (2003) and Loc Carrillo et al.(2007).

2.2.2 Restriction endonuclease digests

This method was based on Loc Carrillo et al. (2007).

2.2.3 Phage morphology (Transmission Electron Microscopy)

This was undertaken as per Atterbury et al. (2003).

2.2.4 Genome sequencing

High titer phage stocks (>10^9 PFU/ml) were prepared as described previously using *C. jejuni* PT14 as the host. Phage preparations were treated with proteinase K (100 µg/ml in 10 mM EDTA [pH 8]) to remove the capsid and DNA extracted using the DNA Wizard Kit (Promega, UK) according to the manufacturer's instructions. Library preparations of genomic DNAs followed the Illumina NexteraTM tagmentation protocol (Illumina, Cambridge, UK) and the library sequenced using the Illumina v3 sequence cassette for 600 cycles on the MiSeq platform to produce paired-end sequence reads of 250 bp. De novo assembly of sequence reads was performed using CLC Genomics Workbench version 11.0.1 (Qiagen, Aarhus, Denmark). Assembled reads yielded a complete dsDNA genomes. Gene predictions were made using PHASTER (Arndt et al. 2016) to identify putative open reading frames (ORFs), followed by manual curation using BLAST (non-reductive databases) with the genome sequence browser Artemis.

2.3 Distribution of phages

The bacteriophages that formed the basis of the candidate panel were all isolated across Queensland farms from widely distributed locations across the north and south of the areas around Brisbane (Figure 6). This included commercial 21 farms and two commercial piggeries.

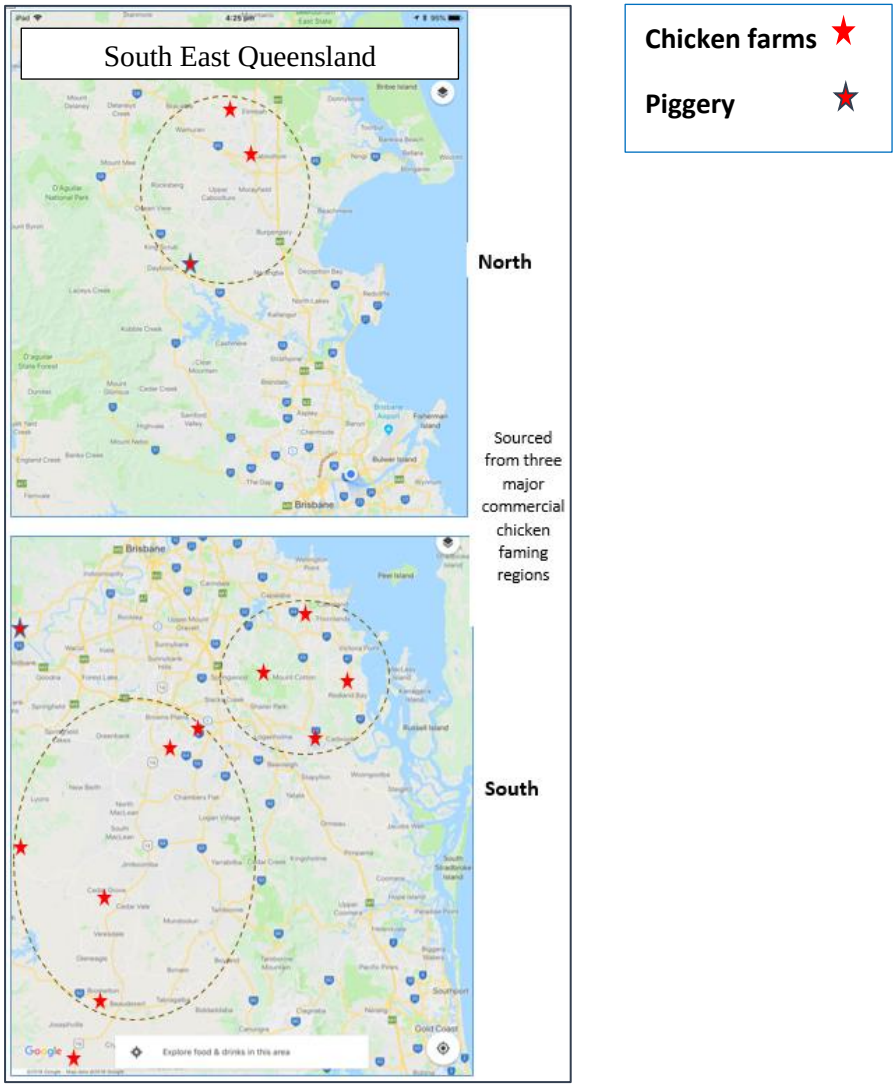


Figure 7 Source of phages from Queensland farms

The phage cocktail candidates originated from Queensland meat chicken farms from two integrator companies and two commercial piggeries. The details of the phage cocktail candidates and their method of isolation (direct isolation or enrichment) and source sample (caeca, litter or soil) and hosts used (universal host *C. jejuni* PT 14 with or without farm hosts) and year isolated is presented in Table 9.

Table 9 Details of phage final panel of 23 phage cocktail candidates

Phage Number	Date	Farm, location	Source and isolation; Direct – (with *C. jejuni* PT 14 only) or Enriched with farm hosts *C. coli* (NC2934), *C. jejuni* (NC3142) and *C. jejuni* PT 14)
1	2012	Redland bay area- free-range re-use	Farm Soil - Enriched
2	2012	Beaudesert area, free-range full clean-out	Farm Soil - Enriched
3	2012	Redland bay, re-use	Carcass rinse - Enriched
4	2012	Caboolture area, re-use	Litter No re-use - Enriched
5	2012	Caboolture area, re-use	Litter No re-use - Enriched
6	2012	Carbrook area, free-range litter re-use	Caeca, free range - Enriched
7	2012	Carbrook area, free-range litter re-use	Farm Soil - Enriched
8	2013	Carbrook area, free-range litter re-use	Caeca, free-range – Direct
9	2013	Carbrook area, free-range litter re-use	Re-used Litter practice - Direct
10	2013	Carbrook area, free-range litter re-use	Farm Soil, free-range - Direct
11	2013	Carbrook area, free-range litter re-use	Carcass rinse, free-range - Direct
12	2013	Ipswich, full-cleanout	Litter, No re-use - Direct
13	2013	Redland bay area, litter re-use	Caeca - Direct
14	2013	Redland bay area, litter re-use	Litter, - Direct
15	2013	Redland bay area, litter re-use	Caeca, - Direct
16	2013	Redland bay area, full clean-out	Caeca, - Direct
17	2013	Redland bay area full clean-out	Caeca, - Direct
18	2015	Piggery, commercial	Pig Effluent, enrich *C. jejuni* PT14 only
19	2015	Piggery, commercial	Pig Effluent, enrich *C. jejuni* PT14 only
20	2015	Redland bay area, full clean-out	Litter, Direct
21	2016	Beaudesert area, re-use	Caeca, - Direct
22	2016	Caboolture area, litter re-use	Caeca, - Direct
23	2016	Caboolture area, litter re-use	Ileum, - Direct

2.4 Analysis of farm screening data

The phage – farm activity screening data was part of the cocktail candidate selection process during the CRC study to enable progression to farm trials. This was a short 1.5-year study hence detailed analysis of that data remained unanalysed on progression to the current study. This data was analysed to enable a better understanding of farm – *Campylobacter* activity. The available screening data on farm by farm basis has been addressed in this section. In summary, the then available 19-candidates were screened against the *Campylobacter* hosts and based on the lytic profile were scores as illustrated in Figure 8.

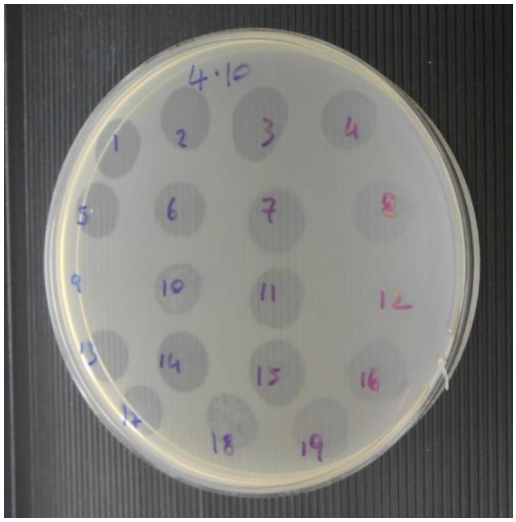


Figure 8 An example of a lytic profile of the 19 phage cocktail candidates' against a single farm Campylobacter isolate (scored from 0 -3 based on activity)

2.4.1 Farm PG against – 19-member panel

The isolates from this farm was sourced in 2012 and were linked to Company 1. The farm was a conventional litter re-use farm, the isolates were sourced on day 41 (pick-up day 51). A total of three isolates were tested against the panel, they were all *C. jejuni*. The best phages (score 3) are PH 5, 9, 12, 16, 17, Figure 9.

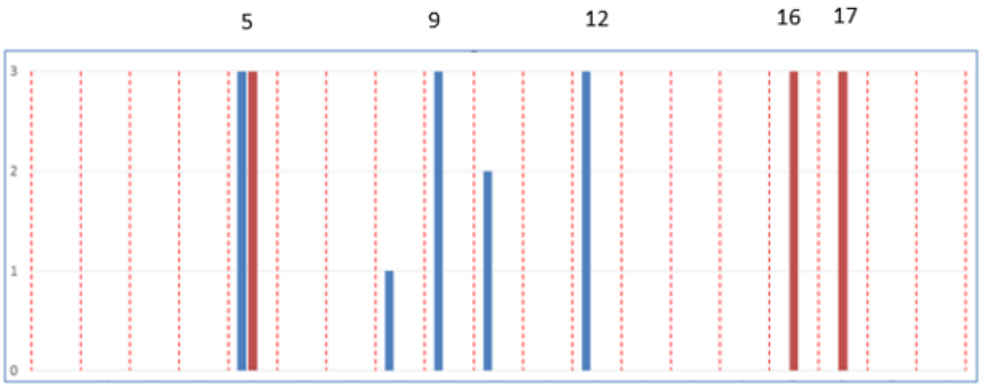


Figure 9 Activity of candidate phage panel (PH 1- 19) against selected isolates from Farm PG

2.4.2 Farm AK against – 19-member panel

The isolates for this farm were sourced over two years (2012 and 2013) and were linked to Company 1. The farm was a free-range litter re-use farm. The isolates were sourced on day 43 (pick-up day 48 in 2012) and day 39 (pick-up day 41 in 2013). A total of 25 isolates were sourced in 2012 and three in 2013. In 2012, the overall best phages (score 3) are PH 6, 9, 12, 18, 19. In 2012 there was a mix of *C. jejuni* and *C. coli* among the 25 isolates tested and all these isolates were sensitive to the latter two phages PH 18 and 19. The others had a score of 2 against select candidates, Figure 10.

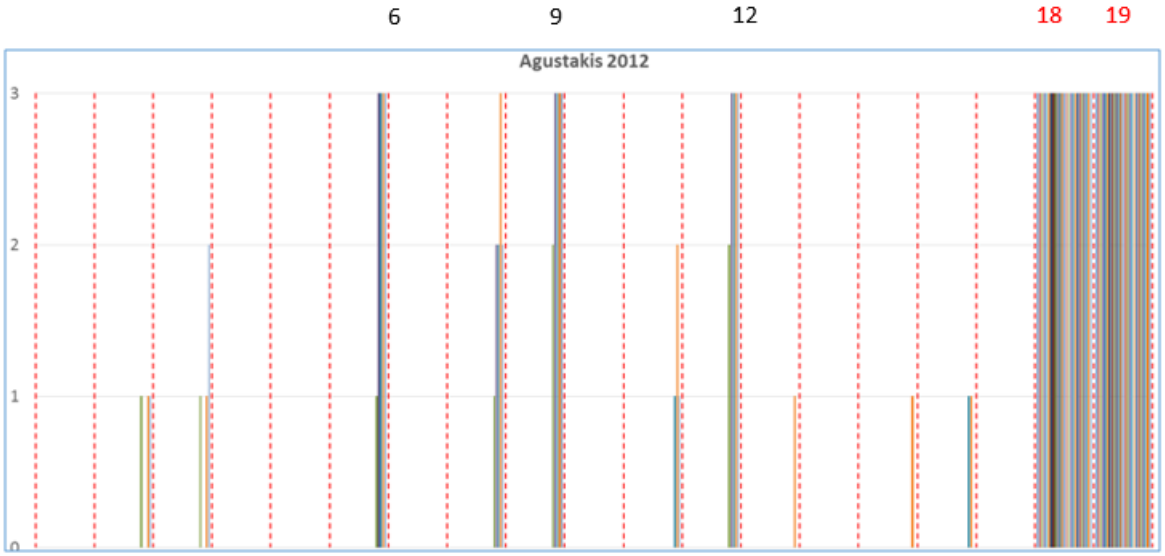


Figure 10 Activity of candidate phage panel (PH 1- 19) against selected isolates from Farm AK (2012)

Three isolates sourced in 2013 presented a different picture as illustrated in Figure 11. Phages PH 5, 16 and 17 gave a lytic score of 3 against these isolates. All these three isolates were *C. jejuni*.

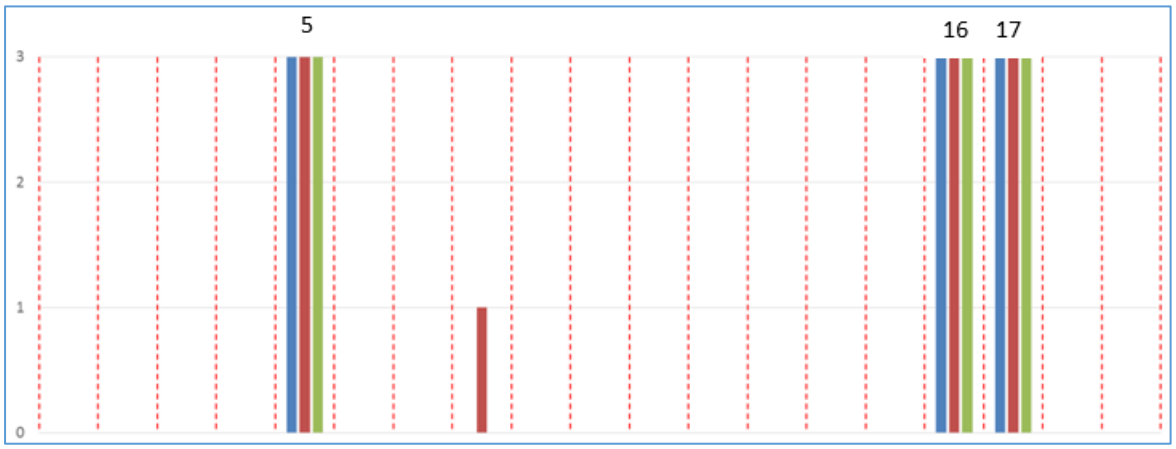


Figure 11 Activity of candidate phage panel (PH 1- 19) against selected isolates from Farm AK (2013)

2.4.3 Farm QN against – 19-member panel

This farm was tested in 2013 only and three isolates were chosen to carry out lytic profile. The farm was a conventional litter re-use farm and the isolates were sourced on day 48 (final pick-up day 54). The farm was linked to company 1. Two of the isolates were *C. coli* and the other *C. jejuni*. Both *C. coli* isolates presented a lytic score of 3 against phages PH 18 and 19 (but not the *C. jejuni* isolate, lytic against PH 5), Figure 12.

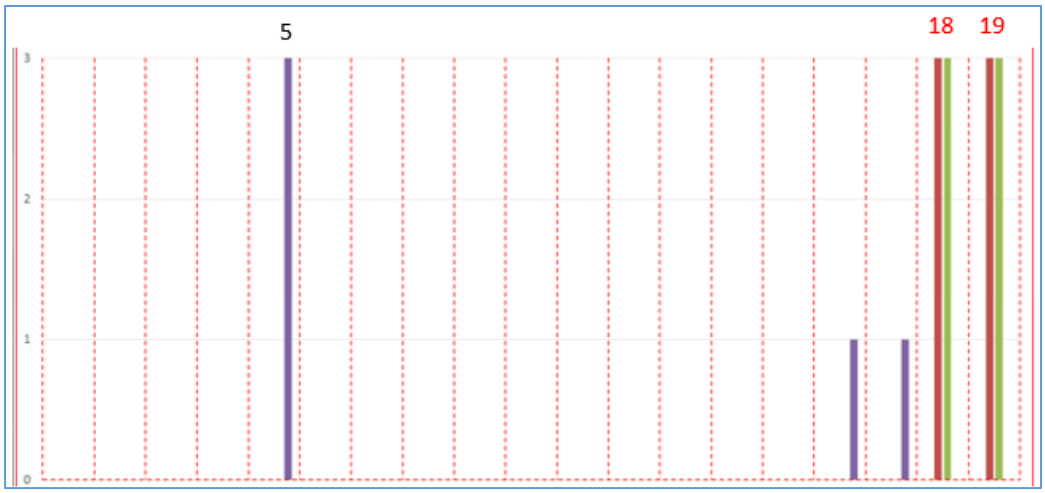


Figure 12 Activity of candidate phage panel (PH 1- 19) against selected isolates from Farm QN

2.4.4 Farm SN against – 19-member panel

This farm was tested in 2013 and was linked to Company 2. This was a conventional full clean-out farm. The isolates were sourced on day 53 (pick-up day 54). There was a mix of two *C. jejuni* and two *C. coli* isolates. Both *C. coli* isolates had a lytic score of 3, against phages PH 18 and 19, Figure 13.

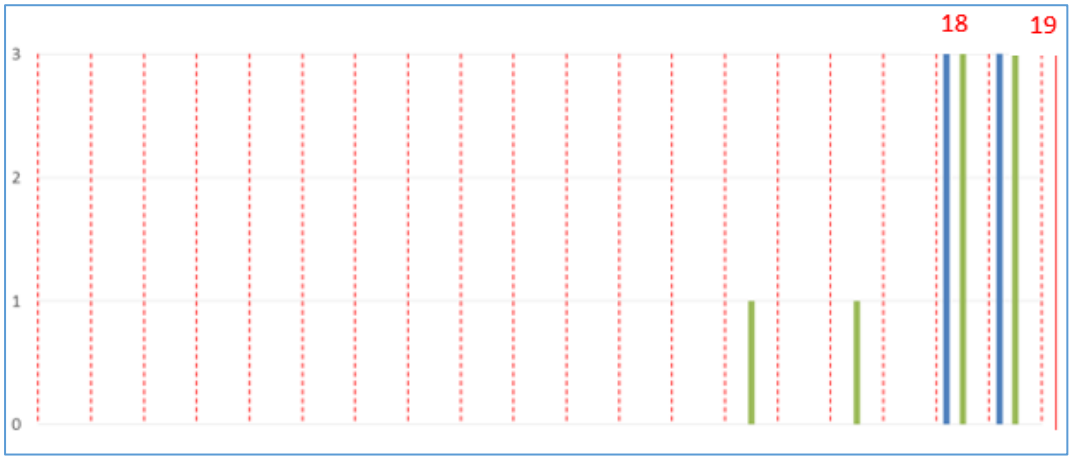


Figure 13 Activity of candidate phage panel (PH 1- 19) against selected isolates from Farm SN

2.4.5 Farm PT against – 19-member panel

This farm was tested both in 2012 and 2013 and was linked to company 1. This was a farm that phages were not isolated originally, thus a large number of isolates were tested.

The farm was a conventional litter re-use farm. The isolates were sourced on day 48 (pick-up day 49) in 2012 and day 47 (pick-up day 50) in 2013. A total of 39 isolates were sourced in 2012 and a total of 19 isolates were sourced in 2013. Among the isolates sourced in 2012, eight were *C. coli* and the *C. jejuni* with one having no species identity. In 2012, seven isolates sourced were *C. coli* and nine *C. jejuni*.

In this instance a "cluster of *C. jejuni* isolates, had a score of 3 only reacting against PH 19. None of the *C. coli* isolates in this instance presented a score of 3 against PH 19 (as in some previous instances. Overall, the representation of isolates lysing the 2012 *Campylobacter* were low, Figure 14.

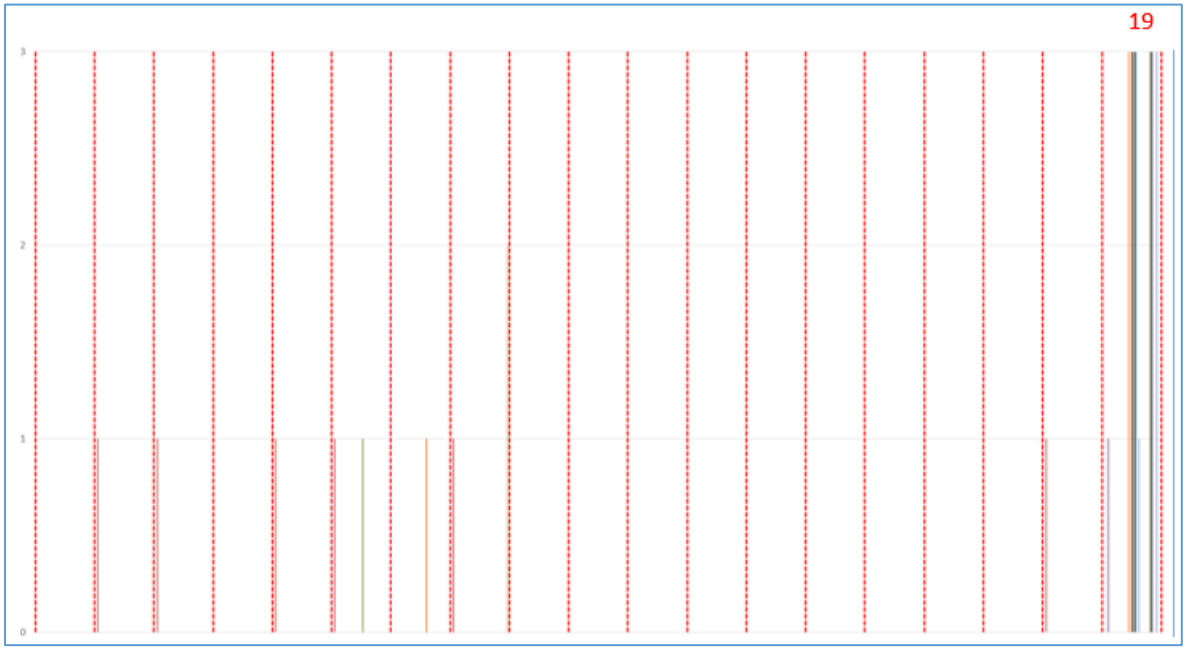


Figure 14 Activity of candidate phage panel (PH 1- 19) against selected isolates from Farm PT (2012)

In 2013, there was a different pattern of phage lysis based on the isolates at the time. Majority of 2013 Farm PT isolates reacted against many of the cocktail candidates. A better lysis pattern in general was obtained in 2013 compared to 2012 (also being a farm with poor phage isolation). *C. coli* (as in most cases) presented a score of 3 for phages PH 18, 19 and *C. jejuni* a score of 3 against phages PH 16, 7 (in addition to 5) and a few reacted against PH 6 and 8, Figure 15.

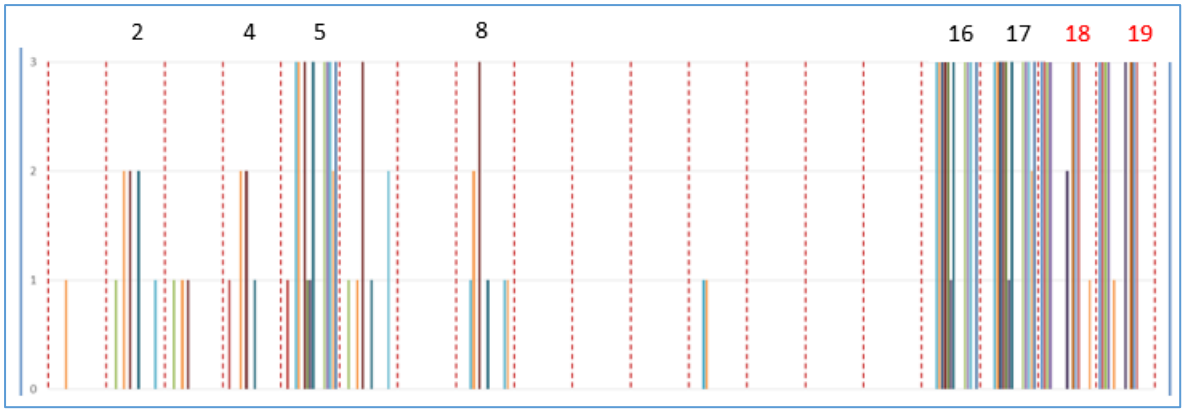


Figure 15 Activity of candidate phage panel (PH 1- 19) against selected isolates from Farm PT (2013)

2.4.6 Farm CW against – 19-member panel

Isolates from this farm were tested both in 2012 and 2013. This was a conventional full clean-out farm and was linked to Company 1. The isolates were sourced on day 46 (pick-up 49) in 2012 and on day 53 (pick up not available) in 2013. A total of 20 isolates were tested in 2012 (all isolates were *C. jejuni*). A wide lysis profile against a range of candidates was apparent across all candidates except phage PH 7, Figure 16. This was in contrast to the rest of the farms tested. More specifically, all candidates had a score of 3, with the exceptions of phages PH 7, 13 and 14, Figure 17.

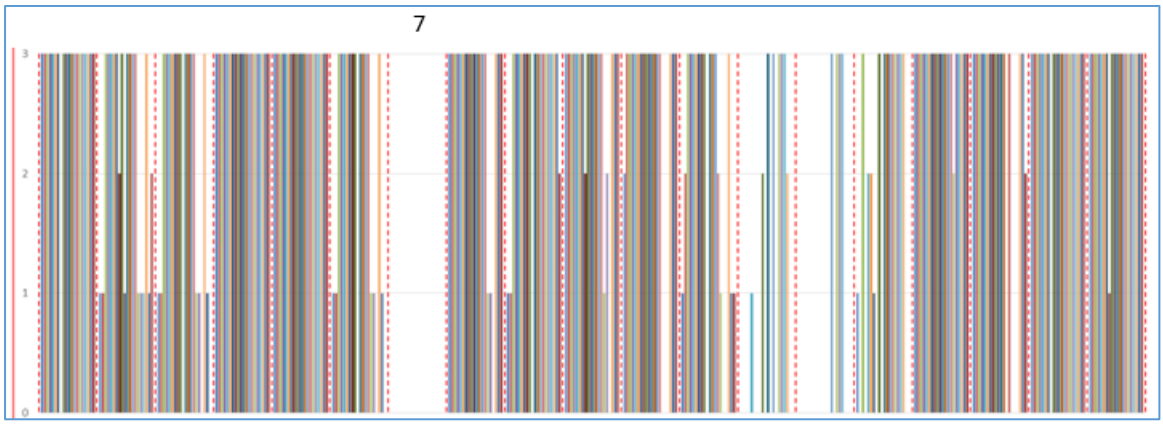


Figure 16 Activity of candidate phage panel (PH 1- 19) against selected isolates from Farm CW (2012)

During 2013, as in 2012, a broad lytic profile was presented with good activity across isolates sourced during both sequential years. All isolates in 2013 were also *C. jejuni* as was in 2012. Due to the optimum activity across these set of isolates Figure 17 is presented only on the basis of those isolates that scored 3.

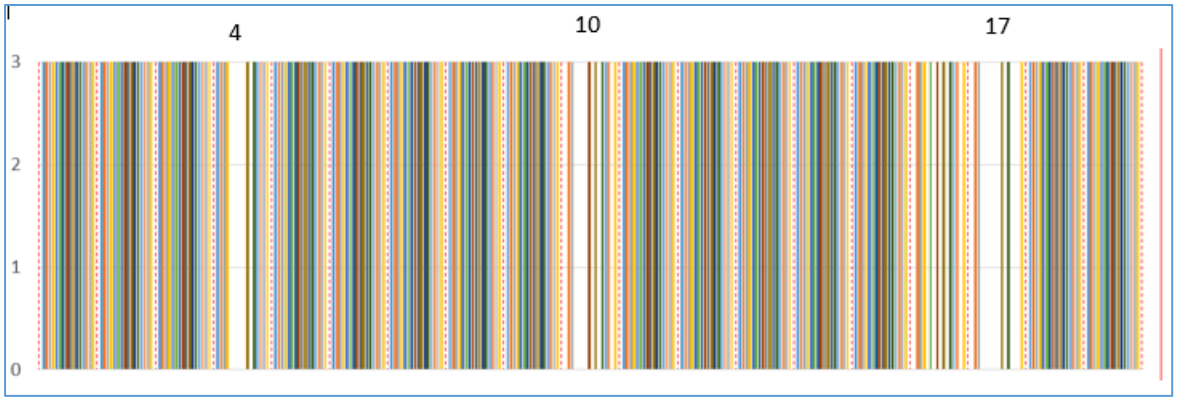


Figure 17 Activity of candidate phage panel (PH 1- 19) against selected isolates from Farm CW, score - 3 only (2013)

2.4.7 Farm SH against – 19-member panel

This farm is linked to Company 1 and four sheds were sampled on the same day. In total a random selection of eights isolates were drawn from shed 1, six each from sheds 5 and 9 and five from shed 14. Selected *C. jejuni* isolates presented a score of three for all candidates (Figure 18).

There seems to be a common *C. jejuni* strain across all sheds (except Shed 9) that that had good lysis (score 3) across all cocktail candidates.

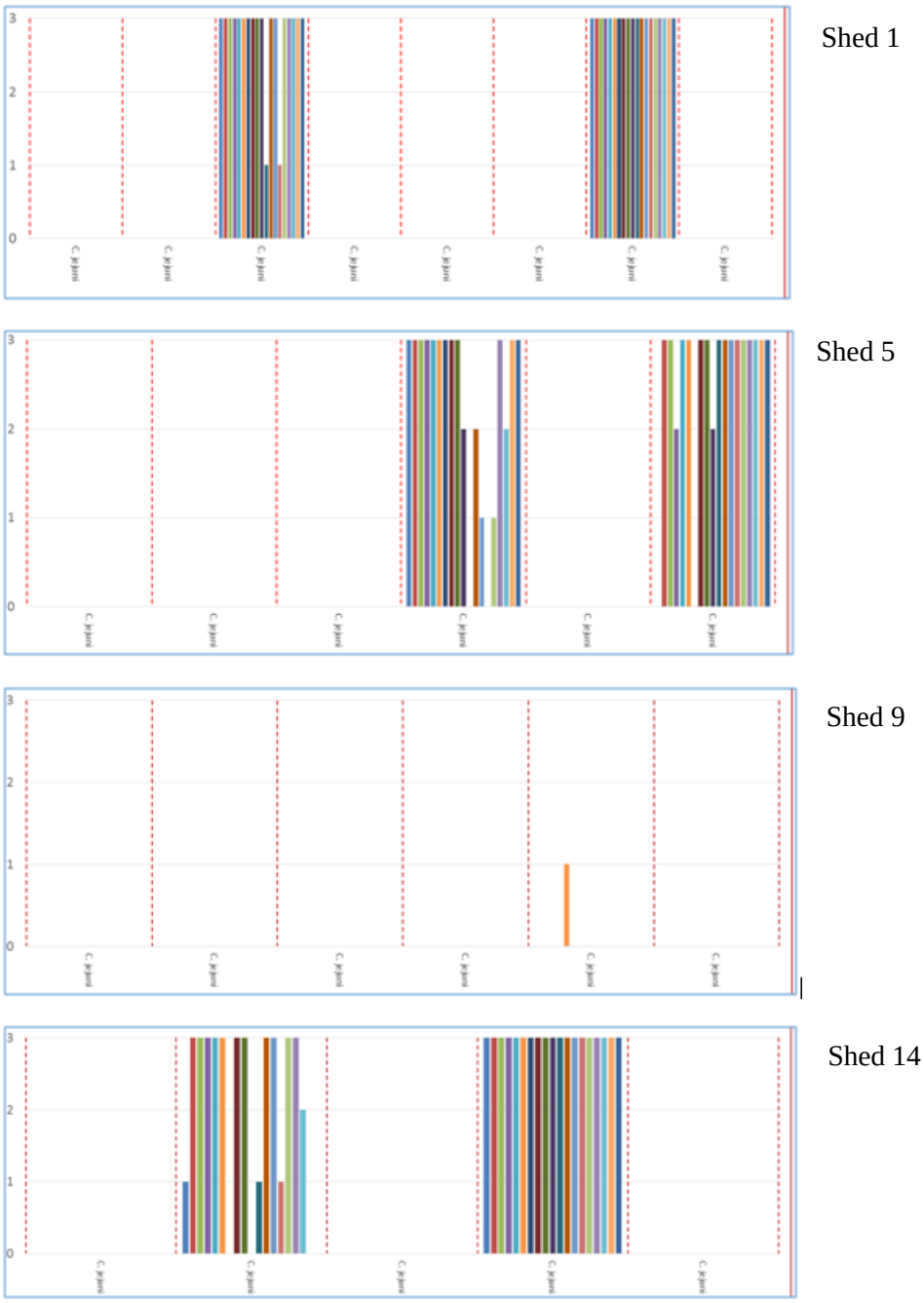


Figure 18 Activity of candidate phage panel (PH 1- 19) against selected isolates (all C. jejuni) from Farm SH, across sheds 1, 5, 9 and 14 (all isolates taken on the same day)

2.4.8 Farm RD against – 19 member panel

This farm is linked to company 1 and as in the previous instance multiple sheds were sampled on the same day. A total of five isolates were tested against the 19 member cocktail candidate panel. All isolates lysed, two phages PH 18 and 19, (Figure 19) which was also commonly lysed by other farm *Campylobacter* isolates as previously described.

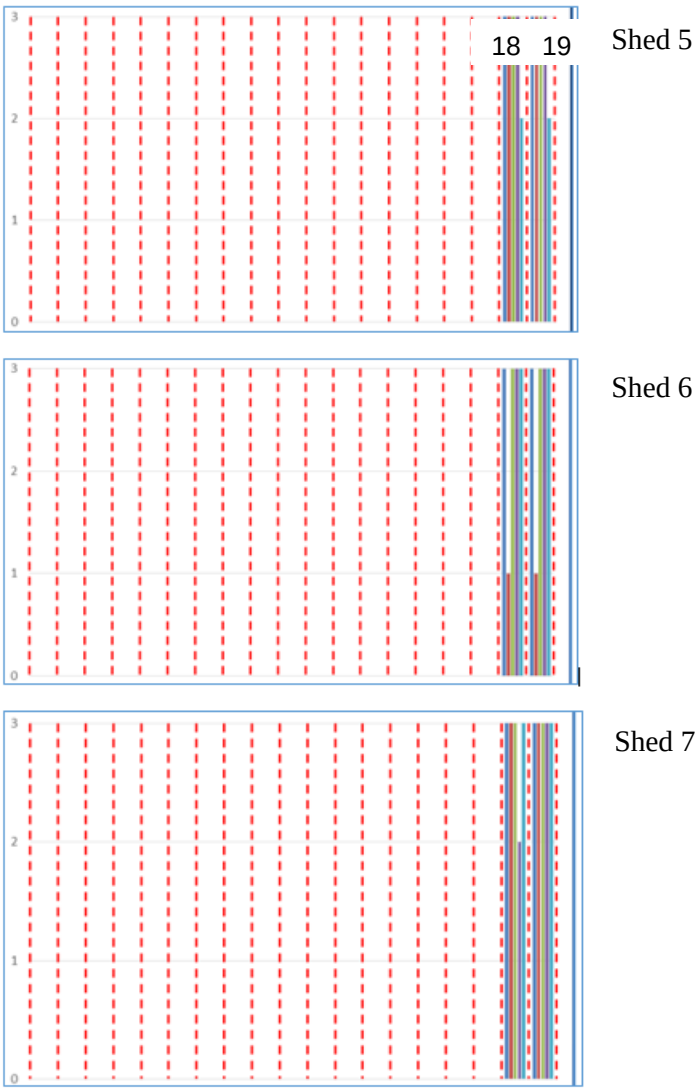


Figure 19 Activity of candidate phage panel (PH 1- 19) against selected isolates (all C. jejuni) from Farm RD, across sheds 5, 6 and 7 (all isolates taken on the same day)

2.4.9 Farm DK against – 19-member panel

Farm DK is a conventional re-use farm and belongs to company 1. The isolates were sourced on the same day across sheds 2, 3 and B on the same day. A total of 10 isolates per shed was sourced for carrying out lytic profiles. All isolates were *C. jejuni*. In this instance phages PH 18 and 19 were sensitive to the *Campylobacter* isolates across the three sheds.

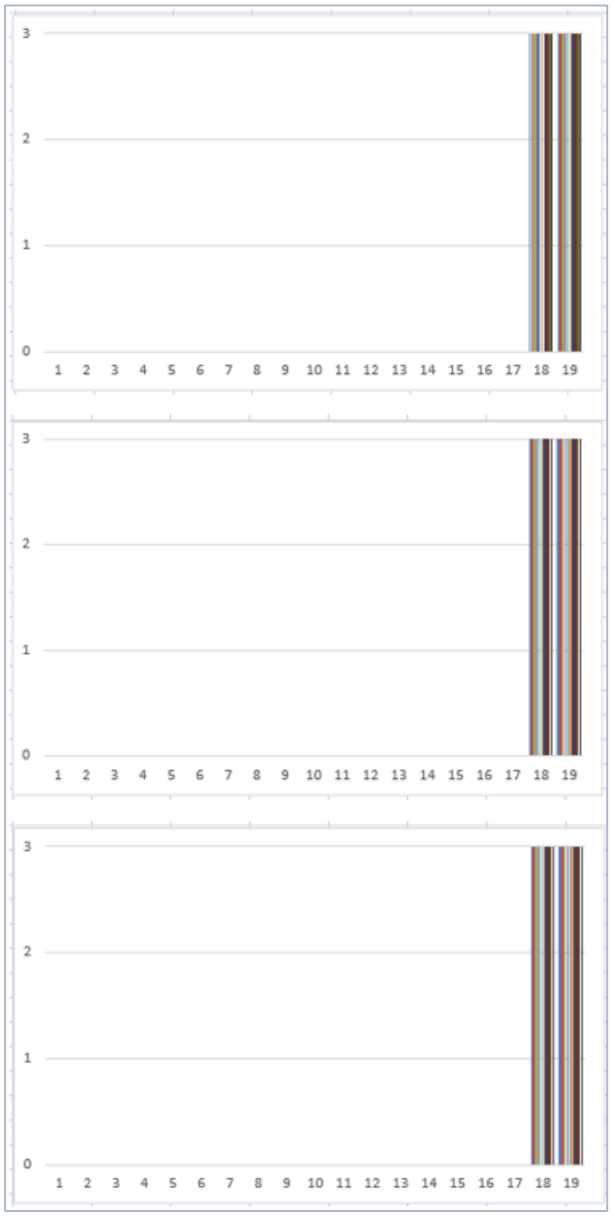


Figure 20 Activity of candidate phage panel (PH 1- 19) against selected isolates (all C. jejuni) from Farm DK, across sheds 2, 3 and B (all isolates taken on the same day)

2.4.10 Summary of farm screening data

This data was generated during the previous study to select candidates but the farm to farm details remained unanalysed. The analysis was undertaken during the current study to compare the activity of the 19-member (where data was available) (a) across farms (b) across years (c) across sheds on the same farm on the same day. Selected phage candidates such as PH 16, PH 17, PH 18 and PH 19 showed activity across most farms and both species. The pattern naturally varied on the same farm across sequential years due to different populations that appeared, whilst in general the sheds across a single farm at a particular time had a similar *Campylobacter* – cocktail candidate activity

2.5 Combined analysis – 19-member panel

Overall analysis of a group of 241 isolates against the cocktail candidates is presented in Figure 21, displaying good coverage across the candidate panel. More isolates were lysed by phages PH 18 and 19. This analysis is based on the screening done with the data generated during the Poultry CRC study.

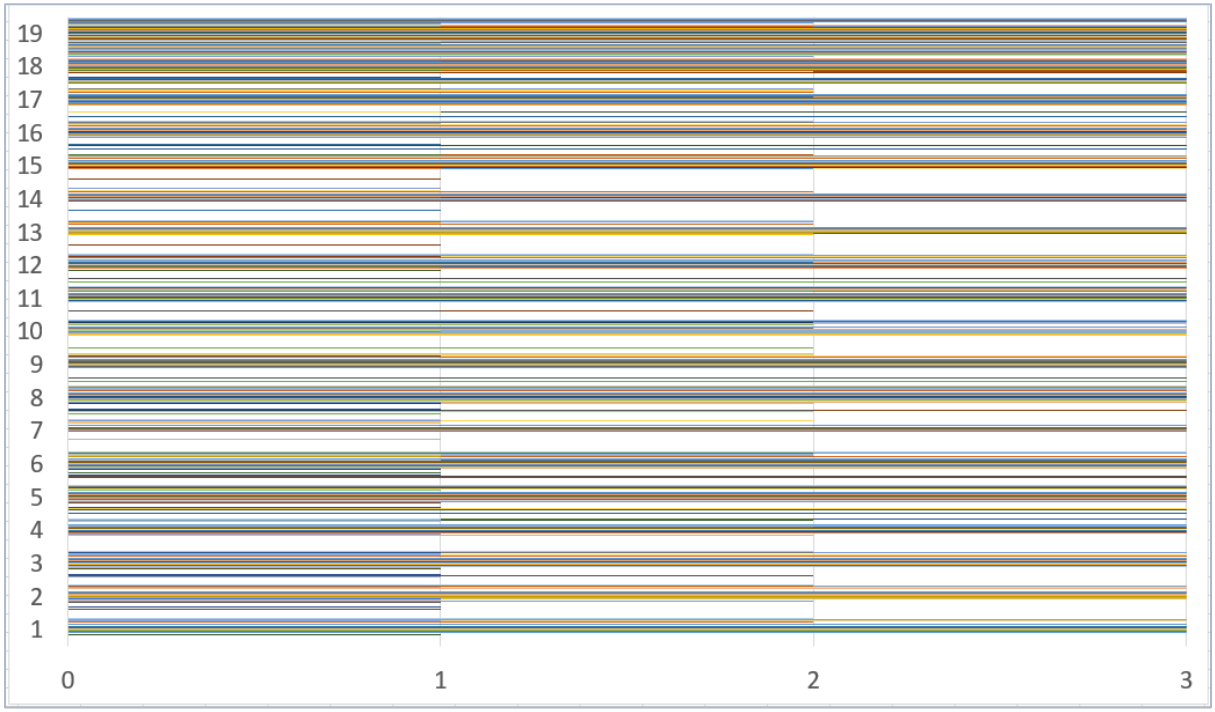


Figure 21 Combined analysis of 241 farm Campylobacter isolates against the 19 member phage cocktail candidate panel representing scores 0 - 3 based on their lytic profiles

2.6 Statistical analysis of candidate performance – 19-member panel

Lytic profiles using a panel of 19 phage cocktail candidates was carried across a random selection of *Campylobacter* (241) isolates sourced from 2012 – 2016 from 11 Queensland farms. The outcomes were statistically analysed and involved using 23 shed/year combinations which commonly had *C. jejuni* or *C. coli* on a single farm. Lytic profiles were carried as in Carrillo et al. (2005) following the scoring (i.e. 0 – 3 with 3 representing clear lysis and 0 no lysis). Data that represented trial farms (CRC) R (prior to the trial) and D (during the trial) were included.

For the initial screening of activity scores across farms, generalised linear mixed models (GLMM) were used with restricted maximum likelihood (REML) in (GenStat 2016). The fixed effects were species, year and phage, along with their interactions. The random effects were the farms, years, cultures within farm/year, and the position of the phages on each culture. These effects were restricted to not permit negative estimated variance components for comparing the test and control chickens.

From an overall perspective representative phage activity of phage cocktail candidates was observed across both *C. jejuni* and *C. coli* 241 farm isolates analysed, Figure 22.

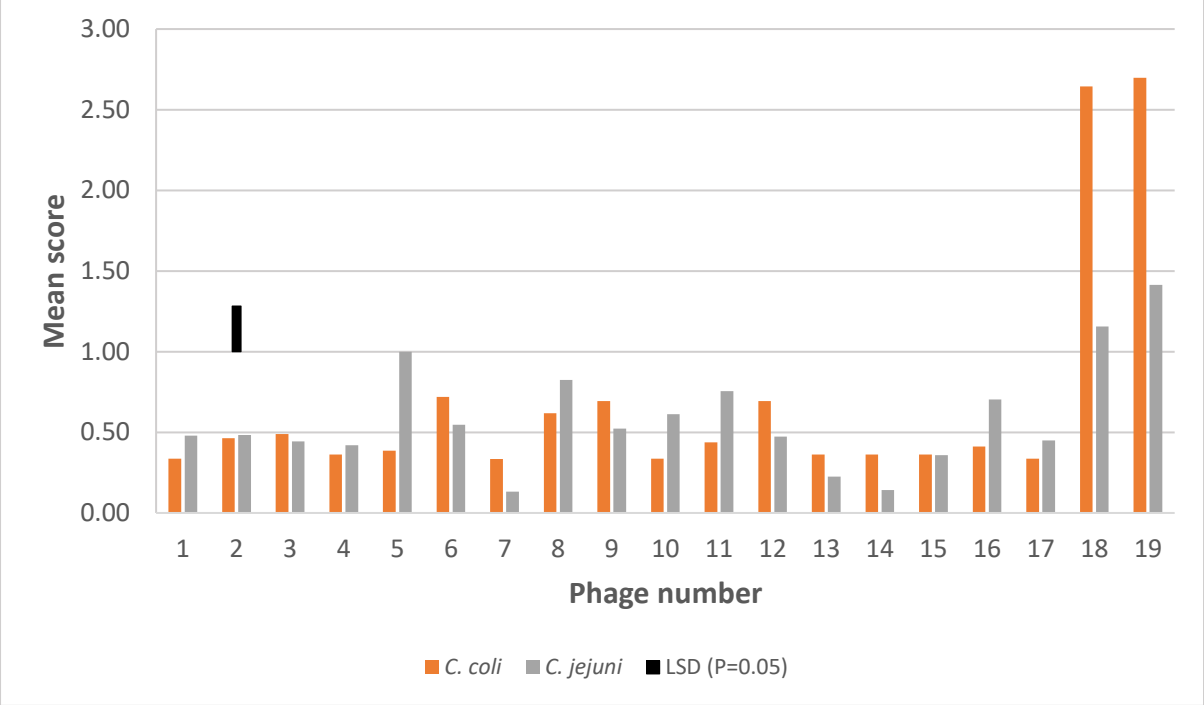


Figure 22 Analysis of the lytic scores (0 -3) of a group of C. jejuni and C. coli isolates (241) for their activity against the 19 member phage cocktail panel.

2.7 Expanded set of *Campylobacter* isolates to assess 23-member panel phage cocktail panel performance

Whilst the analysis just described in section 2 was presented via the detailed analysis of data generated by the Poultry CRC study, the current analysis was undertaken to both build upon those outcome/understandings and also include the recently added for cocktail candidates that completed the panel from 19 – 23 members.

A representative sub-set of *Campylobacter* isolates were created from our 2000 *Campylobacter* collection (2003 – 2016, RIRDC / CRC projects). The grouping followed four sequential (and logical) steps for selection which included year sourced, farm/location, origin (i.e. litter of caeca) and species. Thus, based on the former the overall group consisted of a total of 74 *Campylobacter* isolates.

Of these 47%, 12% and 39% were sourced from caeca, carcass rinses and litter respectively. The remaining 2% of isolates had no recorded source sample. In total, the source samples were taken from 11 different farms and included varying litter practices.

Among the total, 27% of the isolates were sourced from farms using the conventional practice (i.e. new litter utilised) and 54% with either partial reuse or full litter re-use. It is worth mentioning that the full litter re-use practice was adopted specifically for our RIRDC funded study (which compared three litter practices under commercial farming conditions).

Amongst the isolates (with a known species recorded), 29% are *C. coli* with the remaining 71% being identified at *C. jejuni*. This is comparable to the overall ratio for the species identity (of known isolates), which in the entire collection is 25:75 (*C. coli: C. jejuni)*.

From an overall perspective phages PH 4, 5, 11, 16, 17, 18 and 19 dominated compared to the rest of the panel members, Figure 23. Generally, over five farms showed sensitivity to each individual phage cocktail candidate.

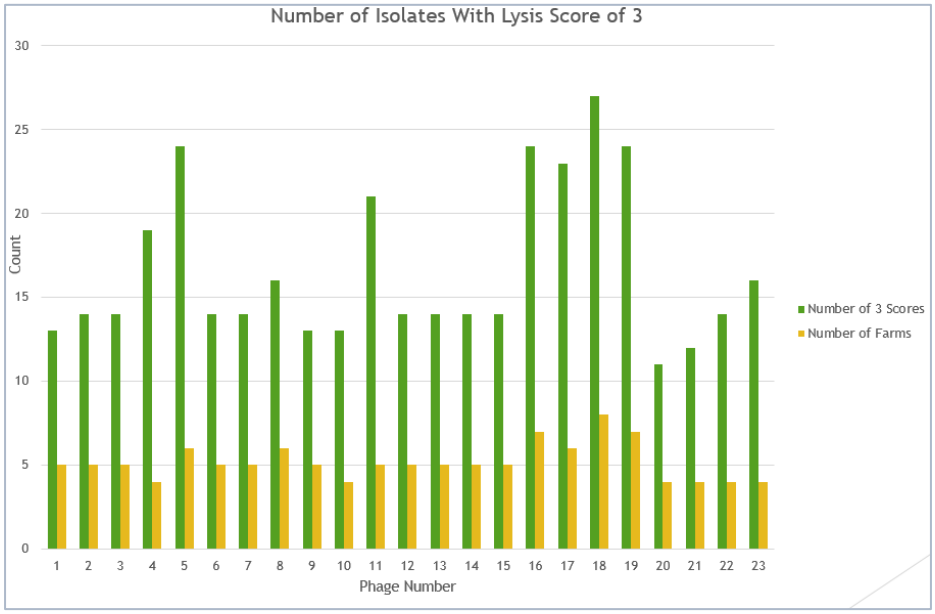


Figure 23 Number of isolates with a score of 3 against the panel of 23 members (and the number of farms that represent those isolates)

The total number of *Campylobacter* isolates lysed by each phage (PH 1 – 23) is also presented in Figure 24, showing an overall good representation of the 23-member phage cocktail candidate panel.

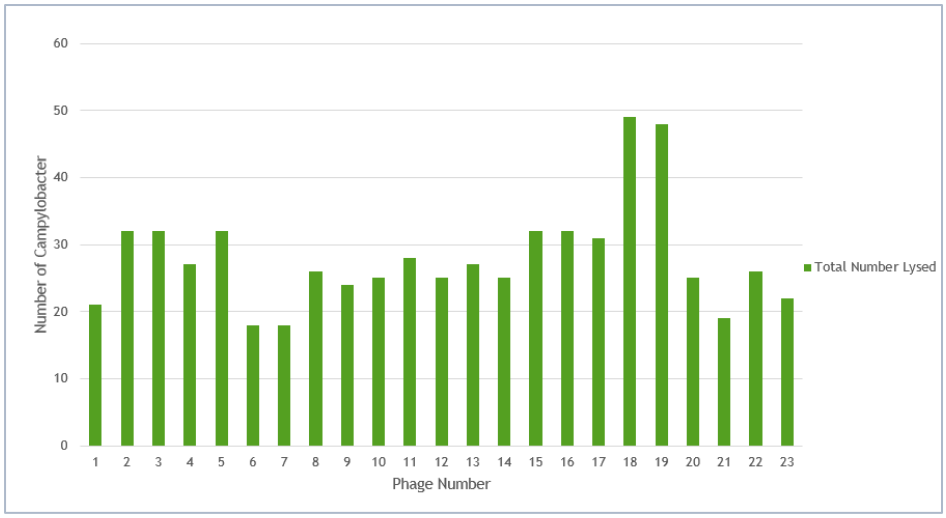


Figure 24 Number of Campylobacter isolates lysed (score 3) from the total logical selection of Campylobacter isolates (74 number)

2.8 *Campylobacter* log reduction

European studies indicate that on-farm interventions (such as phage therapy) can be very effective, with a 2-log reduction in faecal Campylobacter counts contributing to a 75% reduction in human infections. Similarly, a 1-log reduction in faecal count supported by a 1-log reduction in contamination of the exterior of chickens, during processing is predicted to result in a 90% reduction of human infections (Havelaar et al. 2007). Additionally, a 3-log reduction in *Campylobacter* numbers in the intestines of infected birds at slaughter, can contribute to a 90% reduction in public health risks (Crotta et al. 2017).

Thus, achieving a two-log reduction on-farm can contribute to a reduction in human illness. A two-log reduction was achieved on-farm during the CRC trial. The following section describes the work undertaken to assess in-vitro log reduction.

The aim to demonstrate *in-vitro* log reduction of *Campylobacter* following phage application was to validate the concept of using a phage cocktail (as a biocontrol agent) to reduce *Campylobacter* levels in the caeca of commercially farmed chickens. The achievement of log reductions of *Campylobacter* in the laboratory was an indication of that ability to be transferred on-farm and hence be able to progress to chicken trials, though this has already been demonstrated by the CRC farm trials.

2.8.1 Methodology for log reduction

An appropriate *Campylobacter* host and phage were used for the purpose and are listed as follows:

Host: *Campylobacter jejuni* PT14 Phage: PH 19

The basis for the selection of *Campylobacter jejuni* PT14 and Phage: PH 19 for log reduction studies is as follows

Campylobacter jejuni PT14 is a universal international host commonly used to isolate *Campylobacter* phages from poultry (Atterbury et al. 2003). This host was thus used to isolate all phages (750 numbers) in our collection. This was possibly due to the common receptor recognition between *C. jejuni* PT 14 (host) and the phages which were isolated (including the cocktail candidates). Based on this common link, (i.e. between our cocktail phages and PT14), *C. jejuni* PT 14 was used as host to assess *in-vitro* log reduction.

The phage selected was PH 19 and was a member of our 19 panel phage cocktail candidates. PH 19 was also one of the candidates of a "two-phage cocktail" used during farm trial 2 (CRC – Proof of concept study). Whilst a combination of four other phage cocktail candidates successfully contributed to a 2-log reduction in the caeca of chicken during Farm trial 1 (of the CRC study). Whereas PH 19 had the potential to lyse *Campylobacter* prior to the trial at day 40 (a requirement to address the proof of concept), log reduction attributed to the combined cocktail (i.e. PH 19 and PH 18) did not occur, during farm trial 2 as a reduction in *Campylobacter* levels were also observed in the control birds. As a result, there were no statistically significant differences between the test and control birds. This was due to the incursion of a native – competing phage that was present in both the test and control birds at the time. Thus, this was not potentially a reflection of phages PH 18 and 19. Thus, PH 19 was chosen for the present *in-vitro* study to be able to better understand phage – bacteria relationships (a) as it potential further use in cocktails and (b) try better understanding the activity of this phage *in-vitro*.

An overnight culture of *C. jejuni* PT14 (in logarithmic phase) was standardised to around log 6.00 cfu/ml and set up ready for incubation (at 42^{o}C for 24 hours) with shaking. To this phage PH 19 (a standardised concentration of around log 3.0 pfu/ml) was added. Phage and *Campylobacter* levels were assessed every 2h for 24h. Figure 25, presents the growth curve.

Campylobacter: *Campylobacter* (test and control) was introduced at log 6.4 cfu/ml (at time 0). These levels increased to log 8.0 cfu/ml, following which a drop in the phage infected *Campylobacter* host occurred at 8h (to log 5.9 cfu/ml, almost two logs) and difference to controls is even greater (3.3 logs).

2.8.2 Results of log reduction studies

The control *Campylobacter* continued to increase to log 10.0 cfu/ml. The infected *Campylobacter* host continued to gradually increase (to 20h). The levels of both control and infected *Campylobacter* reached log 10 cfu/ml almost 12h later at 25h.

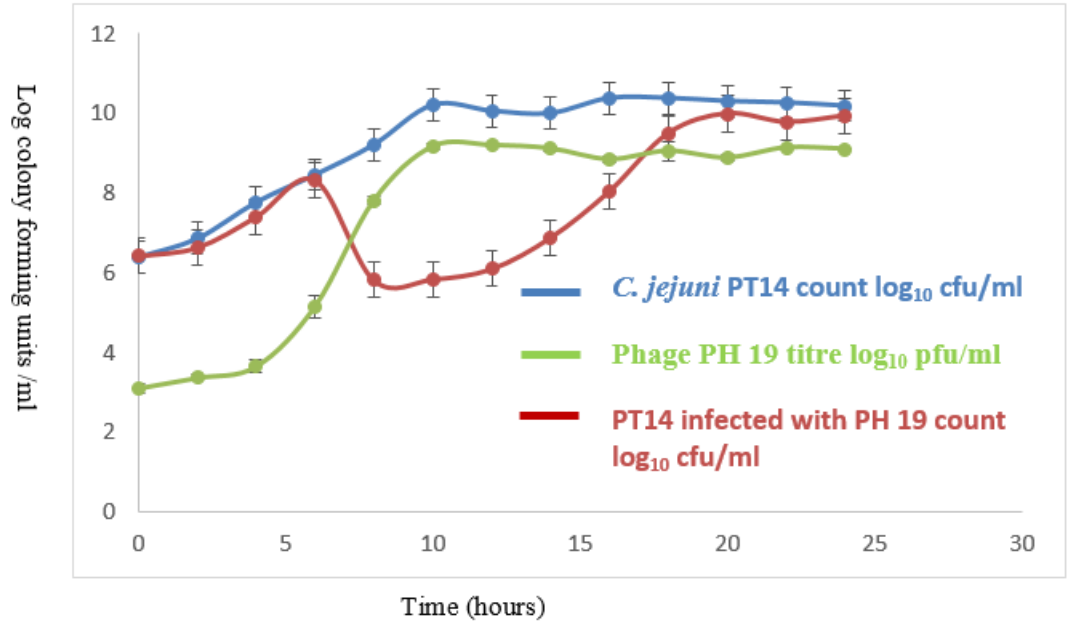


Figure 25 Growth studies demonstrating log reduction using C. jejuni PT14 and phage PH 19

In conclusion, this study has demonstrated *in-vitro* 2 log reduction in *Campylobacter* levels within 5h of infection with phage.

2.8.3 Outcome of the above trial and its relevance to *in-vivo* bird trials

PH 19 has demonstrated its potential to reduce *Campylobacter* levels *in-vitro* and is thus worthy as a phage cocktail candidate. However, when used as a cocktail candidate (along with a partner phage) and in the presence of native phages in the chickens, no statistically significant differences between the test and the control were observed during the farm trial. There may have been some cross-interference under the circumstances that prevailed at the time. The fact that there was cross interference using this phage and its partner cocktail candidate (and native phages) needs to be further understood.

2.9 Phage resistance – in vitro studies

The "phage-*Campylobacter* dynamics" in the chicken caeca is an on-going natural phenomena that supports both the survival of the phage and the bacteria. The genetic diversity in *Campylobacter* in chickens is naturally caused by the presence of phages in the gut. This is an on-going process, irrespective of whether options for bio-control are adopted. *Campylobacter* temporarily develops resistance in the presence of the phage, but reverts to a sensitive form in the absence of the phage. The sensitive form is an active coloniser of the chicken gut, thus the trend for *Campylobacter* to revert to a form that allows it to successfully "exploit" this "niche" which is favourable for its on-going survival.

Published studies (Loc Carrillo et al. 2005, Scott et al. 2007, Hammerl et al. 2014 and Fischer et al. 2013) have demonstrated the proportion of resistant campylobacters in the chicken caeca to be small and the rapid reversal of those resistant forms to sensitivity (in the absence of the phage). This is simply due to the fitness cost associated with maintaining resistance traits (i.e. the loss of flagella) required to continuously colonise the chicken gut.

This aspect is addressed by Loc Carrillo et al. (2005). The study shows that "campylobacters resistant to phage infection were recovered from phage-treated chickens at a frequency of <4%. These resistant types were compromised in their ability to colonize experimental chickens and rapidly reverted to a phage-sensitive phenotype, *in vivo*. The selection of appropriate phage and their dose optimization are key elements for the success of phage therapy to reduce campylobacters in broiler chickens". *C. jejuni* populations that survive phage predation in broiler chicken display genomic re-arrangements resulting in resistance to phages as well as inefficient colonisation of the broiler chicken intestine (Scott et al. 2007). When these strains were reintroduced into chickens in the absence of bacteriophage further genomic rearrangements at the same locations resulted in, reversion to bacteriophage sensitivity and colonisation proficiency (Scott et al. 2007). The resistance phonotype is of temporary nature with a high potential to revert to a sensitive phenotype. Thus, genomic instability of *C. jejuni* in the avian gut has been adopted as a mechanism to temporarily survive phage predation and subsequent competition for resources in order to survive local environmental pressures.

Based on this evidence, we predict that if any *Campylobacter* survive phage bio-control treatments via resistance they will readily revert to sensitivity, and therefore there will not be any net increase in phage resistance in the *Campylobacter* population on farm. Nevertheless, this prediction needs to be validated. These in-vitro studies are a step in that direction. However, the following needs to be noted in relation to in-vitro studies.

During active therapy the phage will be required to replicate in the host bacteria which can select phage resistant escape mutants. These mutants can rapidly overtake a laboratory culture under ideal host growth conditions, but phage-sensitive cells are out-competed far less frequently in chickens. This is because many of the useful phage have requirement for a functional flagella apparatus. In culture, losing motility has little or no penalty and *in-vitro,* the outcome is quite different to that what occurs in the chicken gut. Non-motile campylobacters (in the chicken gut) do not colonise chickens, do not efficiently adhere or invade human cells and cannot compete with motile campylobacters that remain phage sensitive. Thus, the outcome of in-vitro studies may not reflect as to what may occur in the chicken. Nevertheless, this was explored in the current section.

The poultry CRC farm trials have demonstrated a log-reduction (and an absence of resistance post phage treatment in isolates sourced from the chicken gut). Thus, there can be differences in in-vivo and in-vitro testing of phage resistance.

In summary, the concerns of phage resistance on-farm can be addressed by the following practices

- The use of cocktails and not single phages to treat the birds

- The introduction of phage to chickens around 24h prior removal for slaughter (to prevent the development of resistance).

These measures were adopted during the CRC trial which yielded no resistance and a demonstrated a 2-log reduction in the caeca of the commercially farmed bird (on-farm).

In-vitro resistance studies were addressed using two basic approaches,

- Using *Campylobacter* – phage growth experiments in liquid media – University of Nottingham method
- Using a stipulated MOI (multiplicity of infection) – ESR method

2.9.1 Methodology adopted to evaluate in-vitro resistance – University of Nottingham methodology

Basis: The levels of both phage and bacteria were assessed over time (i.e. via a "growth experiment") using liquid media. The time series nature of the study enables the assessment of frequency at which resistant mutants may arise, following a crash in *Campylobacter* population (as a consequence of phage infiltration).

Approach: Growth experiments were carried out using a chosen farm hosts and phages. *Campylobacter* and phage levels were assessed at time chosen time intervals (from 0 – 24h). Colonies were picked from the enumeration plates of a growth experiment when the *Campylobacter* populations started to increase post phage induced crash.

2.9.2 Step 1 Comparison of growth media for isolating mutants

Both CCDA and Horse Blood Agar (HBA) were compared for their suitability for use as plating media for growth studies and both media were found suitable.

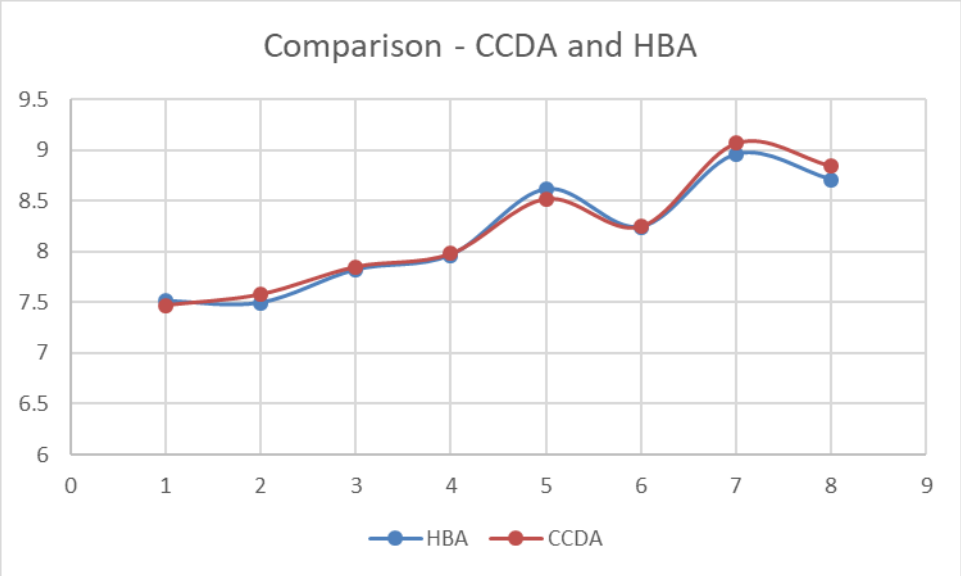


Figure 26 Comparison of using HBA and CCDA as potential media for growth studies

In summary, there was no difference in the recovery of *Campylobacter* (colonies) following growth experiments using either CCDA or HBA (Figure 25). HBA was used.

2.9.3 Step 2 Growth studies

Three trials were carried out with the following phage - *Campylobacter* combinations (i.e. NC 3351 – PH 21, NC 3330 – PH 20 and NC 3037 – PH 22). All three *Campylobacter* isolates were farm isolates and phages used were new cocktail candidates. We were only able to see a small drop (and thus try isolate resistant mutants) from a single combination which is described below.

Methodology:

- *Campylobacter* NC3037 – farm isolate
- Phage 22 – New cocktail candidate
- Two multiplicity of infections (i.e. *Campylobacter* – phage ratio) were used (Table 9)

Table 10 Multiplicity of infections used for growth study

Campylobacter NC 3330	Phage 726 (non-cocktail phage)
MOI 1	
10^5 CFU/ml	10^5 PFU/ml
MOI 0.1	
10^5 CFU/ml	10^4CFU/ml

Figure 4 presents the *Campylobacter* – phage growth curve when subjected to two MOI's i.e. 0.1 and 1.0.

More specifically,

- There was a drop in *Campylobacter* levels for both MOI 1 at 5h (log 0.2 when compared with the control) and occurred at 5h (Figure 3).
- This was followed a small rise (log 5.50 to log 5.60). We isolated colonies at this stage for MOI 1
- The drop in *Campylobacter* levels for MOI 0.1 was also 0.2 and occurred at 6h (Figure 3).
- Unfortunately we did not pursue the experiment beyond 6h to see any potential rise that may have occurred as with MOI 1. No colonies were sourced.
- Generating resistance *in-vitro* was challenging

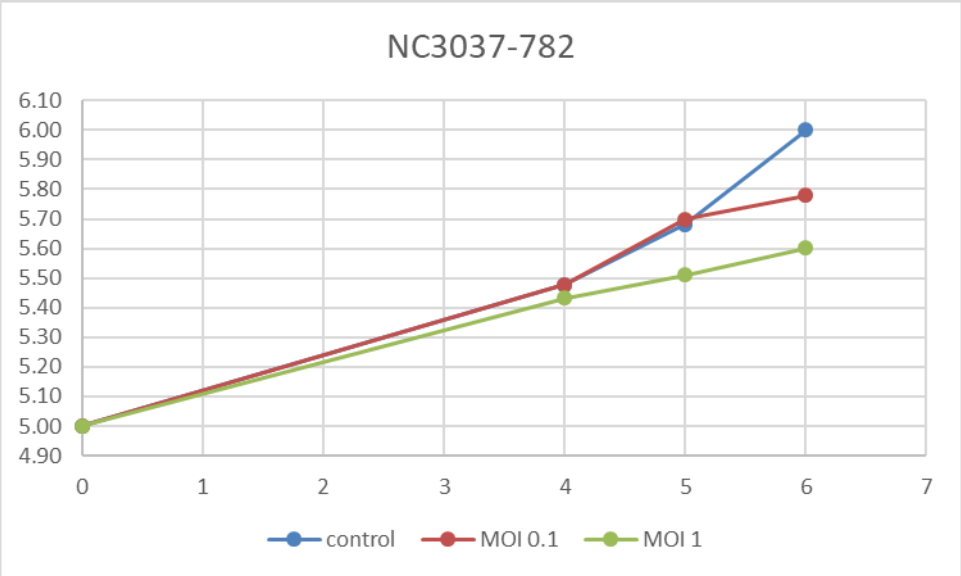


Figure 27 Growth curves generated for selecting and isolating phage resistant mutants

2.9.4 Resistance testing

The cultures were tested against phage stocks 10^3 to 10^6 pfu/ml which were used to do spot tests. Essentially both test cultures and the parental strain showed full lysis at the highest phage concentration of 10^6 pfu/ml, Table 11 and Figure 28. There was a lack of resistance.

There could be two reasons:

1. The drop obtained was not sufficient to be indicative of a "crash" but we tested nevertheless to try to understand.

2. As a result, the colonies isolated (post "crash") were not indicative of resistance and remained sensitive.

Table 11 Resistance testing via spot test MOI 0.1

Phage concentrations	10^6	10^5	10^4	10^3
culture				
1	FL	FL	FL	TNTC grainy
2	FL	FL	FL	41
3	FL	FL	~100	6
4	FL	FL	~65	7
5	FL	FL	FL	30
parental	FL	FL	FL	TNTC grainy

FL = fully lysed TNTC – too numerous to count

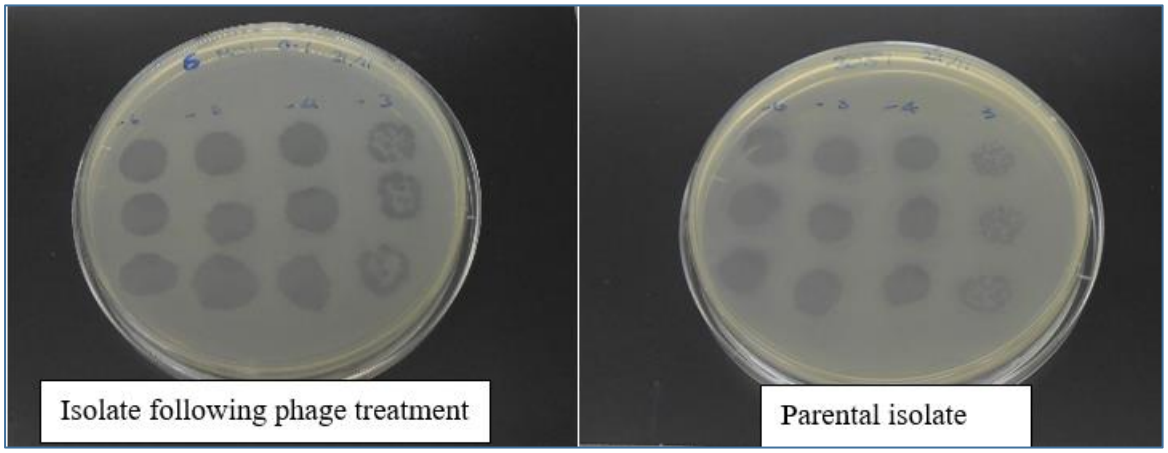


Figure 28 Illustration of a spotted isolate from MOI 0.1

2.9.5 Methodology adopted to evaluate in-vitro resistance – ESR methodology

Table 12 presents the description of the phage cocktail candidates used. The source of some of *Campylobacter* isolates chosen originated from our *Campylobacter* screening panel developed for the CRC study. The *Campylobacter* screening panel was created using a diversity of *Campylobacter* isolates sourced across farms and screening them against select groups of phages, and then grouped (based on the resultant lytic profiles). Finally, select representatives from each group formed the *Campylobacter* screening panel. The panel included campylobacters that had a good, medium and difficult lytic potential.

Table 12 Description of phage cocktail candidates used

Candidate used Farm RD, CRC – farm trial	Candidate used for DK, Farm, CRC – farm trial	New Candidates
PH 5	PH 18	PH 20
PH 8	PH 19	PH 21
PH 11		PH 22
PH 13		PH 23

The second set of *Campylobacter* isolates used originated from a CRC farm trial. These campylobacters were isolated from chicken caeca representative of birds that demonstrated a successful log reduction following treatment with a cocktail. These isolates remained sensitive to the phage used to treat the chickens. The caeca of chickens treated with the cocktail also demonstrated successful log reduction and were the source of the isolates. All details are presented in Table 13.

2.9.6 Outcome

The resultant infected plates were compared with the controls. Three general categories were apparent as listed below.

The lysis patterns were categorised as follows:

Category 1 – Clear plaques visible with bacterial growth inside the plaque (only 1 combination had this pattern) Figure 29. Bacterial growth emerged within a clear plaque, indicative of the emergence of a resistant population following lysis.

Category 2 - Isolated colonies in a partially lysed lawn (when compared with control). Intermittent and isolated single colonies were visible; but were not indicative of emerging against previous bacterial lysis (plaque) representative of a true mutant Figure 30.

Category 3 – Just grainy i.e. some area lysed some not (merged colony growth), no isolated colonies Figure 31.

Only Category 1 was typical of a resistant mutant. Some colonies were also picked from Category 2. No colonies were visible in the Category 3, which had grainy lawns with joined colonies.

The red arrows are indicative of the type of colonies picked to assess resistance testing,

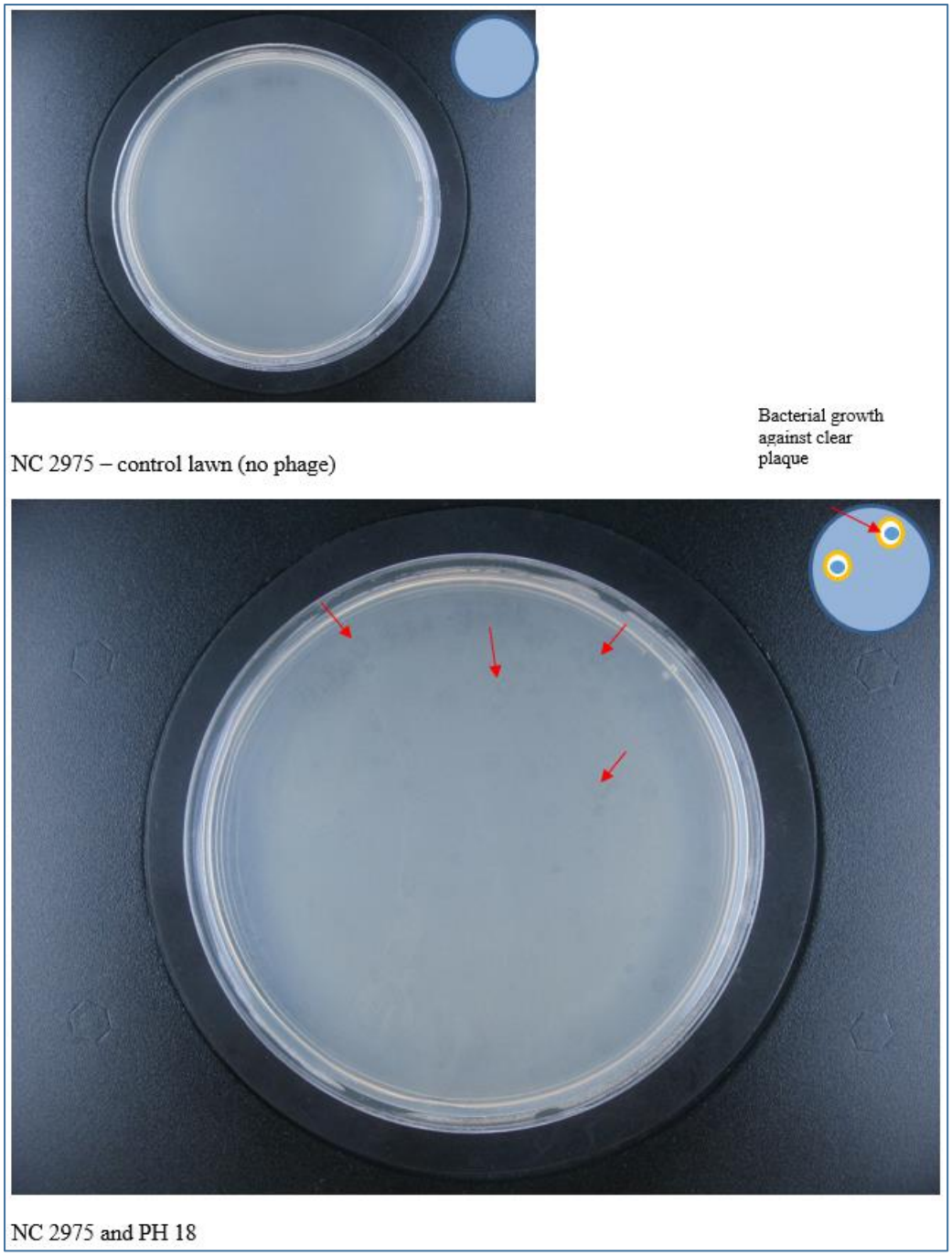


Figure 29 Category 1 - Bacterial growth inside lysed area (phage plaques) - indicative of resistant growth following lysis

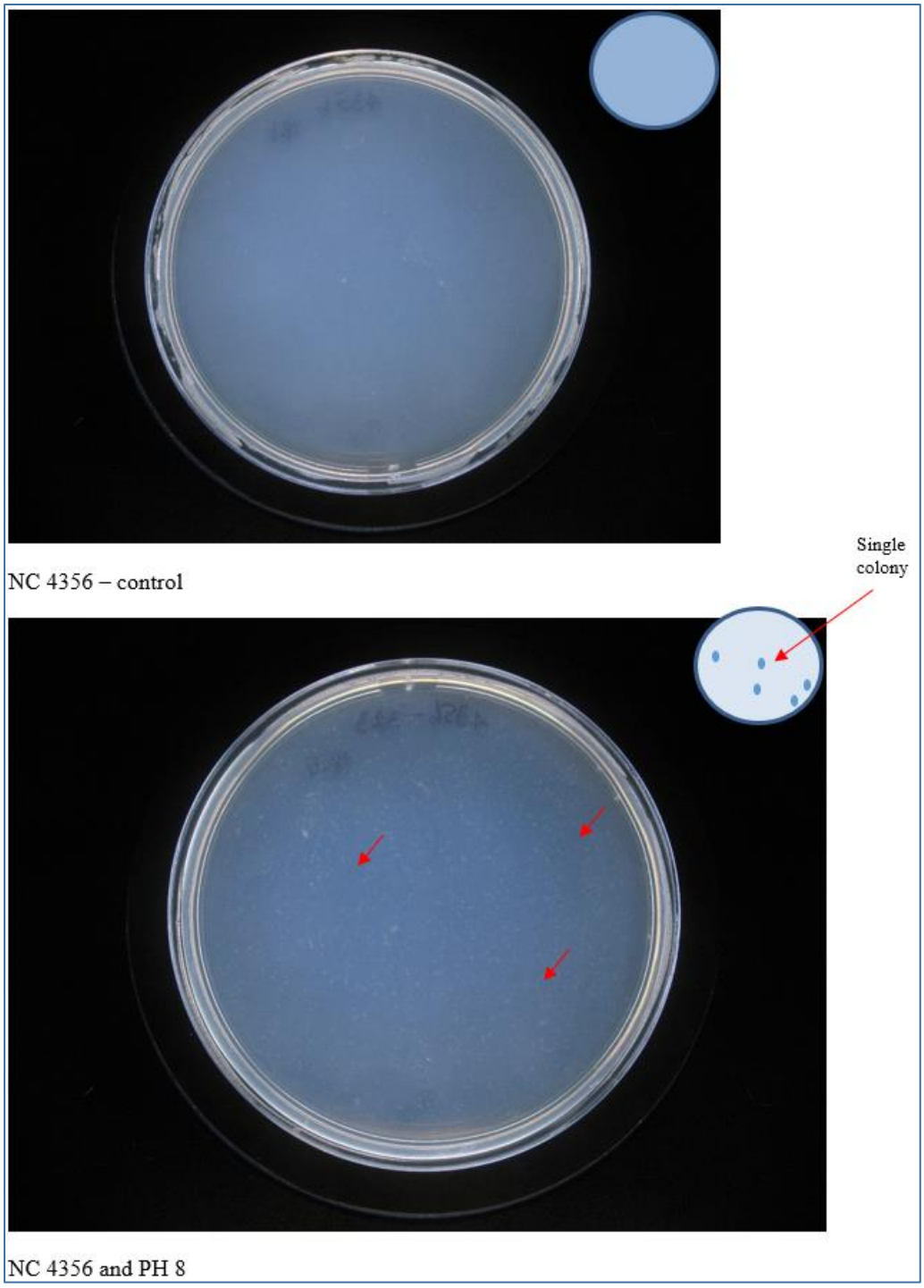


Figure 30 Category 2 – isolated bacterial colonies on a lysed lawn (compared to control)

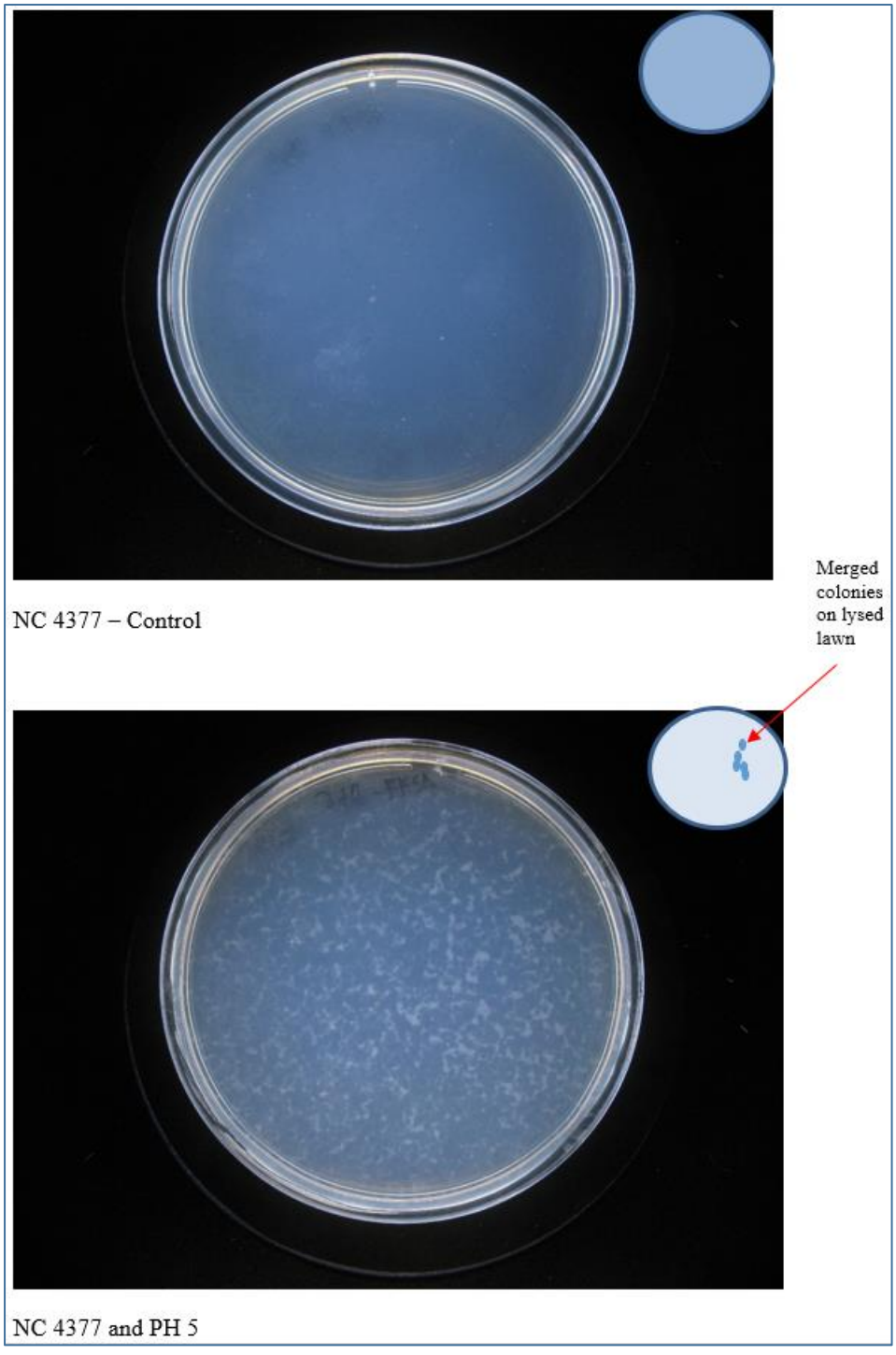


Figure 31 Category 3: Grainy areas (no colonies)

Table 13 Details of Campylobacter isolates and phages used and outcome following testing for resistance

NC number	Source	Details	Description on plate	Colony ID	Resistance
3330 – PH 20	Caeca Redland farm 2012	Campy panel	isolated colonies in a partially lysed lawn	17	Not typical
3351 - PH 21	Carcase Redland farm 2012	Campy panel	Looked like control nothing to see	No lysis?? Not used	Not typical
3037 - PH 22	Litter Redland farm 2011	Campy panel	isolated colonies in a partially lysed lawn	8, 9	Not typical
2482 - PH 2	Caeca Carbrook 2009	Campy panel	isolated colonies in a partially lysed lawn	15	Not typical
3333 - **PH 5**	Caeca Redland 2012	Campy panel	Did not pick control contamination	Not used	Not typical
3217 – **PH 11**	Caeca Redland 2012	Campy panel	isolated colonies in a partially lysed lawn	13	Not typical
2992 – **PH 13**	Caeca Redland 2011	Campy panel	isolated colonies in a partially lysed lawn	10,11	Not typical
2975 – PH 18	Caeca Redland 2011	Campy panel	Very good, typical outcome of resistance	1,2,3,18,19,16,24	5% plate Typical
4164 - PH 19	Caeca Redcliffe 2016	Redcliffe shed 7 before trial	Grainy nothing to pick	Not used	Not typical
4346 – **PH 8**	Caeca farm test Redcliffe 2016	Redcliffe Trial TEST	No indication	12	Not typical
4347 – PH 19	Caeca farm test Redcliffe 2016	Redcliffe Trial TEST	Some isolated colonies	14	Not typical
4349 - **PH 5**	Caeca farm test Redcliffe 2016	Redcliffe Trial TEST	Grainy nothing to pick (no resistance good result for cocktail??)	Not used	Not typical
4352 - **PH 5**	Caeca farm test Redcliffe 2016	Redcliffe Trial TEST	Is a Redcliffe combination, isolated colonies in partially lysed lawn (joint plaque, very faint)	6, 7,20	Not typical
4356 – **PH 8**	Caeca plant control Redcliffe 2016	Redcliffe Trial control	isolated colonies in a partially lysed lawn	4,5,21,22,23	Not typical
4377 – **PH 5**	Caeca plant test Redcliffe 2016	Redcliffe Trial TEST	Grainy nothing to pick (no resistance good result for cocktail??)	Not used	Not typical

In bold – Farm Redcliffe cocktail phage Highlighted – Farm DK cocktail phage The rest – New cocktail member

2.9.7 Evaluation of the outcomes of the screening:

A total of fifteen phage – *Campylobacter* combinations were screened (Table 13), the isolates selected in a manner to cover both *Campylobacter* panel and farm trial isolates. The *Campylobacter* isolates were paired with cocktail phages that were used to reduce *Campylobacter* on-farm (Redcliffe farm trial phages) and others were from the cocktail member panel.

Table 14 presents the detailed screening of the phage bacteria combinations that yielded colonies and Table 15 presents a summary of the different patterns. Only one combination was truly representative of demonstrating "typical resistance" NC 2975 (which was a normal farm isolate) and PH 18 which was used during Farm trial 2 (Farm DK), Table 14, Figure 32.

Thus, based on the total isolates tested only 7% resistance was observed during *in-vitro* testing. Among those which presented dispersed colonies across partially lysed lawns 42% of the combinations yielded resistant and 21% sensitive isolates. Among those that remained sensitive, were two isolates from the *Campylobacter* panel and one farm isolate that originated from the Redcliffe farm trial. The rest, (21%) simply had grainy lawns (i.e. joined bacterial colonies among areas of clearing with no visible colonies as described under Category 3).

Interestingly three of the Redcliffe farm *Campylobacter* isolates – post phage (which were tested with phages used in cocktail during both farm trials i.e. PH 5 at Redcliffe and PH 19 at Farm DK) did not yield any resistance colonies, only grainy lawns. PH 5 was among a combination that demonstrated successful *in-vivo* log reduction on-farm. Maybe this approach can be adopted to further narrow down and select suitable cocktail candidates.

2.9.8 Implications to future farm trials:

This has been discussed at the beginning on the differences between in-vitro and in-vivo resistance. Whilst among the carefully selected phage *Campylobacter* combinations only one combination presented a pattern of true resistance during in-vitro testing.

2.10 Overall summary – in-vitro log reductions and resistance studies

Studies towards the demonstration of *in-vitro* log reductions and evaluation of potential resistance to the candidate phage cocktail were completed. A two log-reduction was demonstrated *in-vitro* using the universal *Campylobacter* host, which was the source of all phage isolations, and a phage used in farm trials during the CRC proof of concept study. Resistance testing was carried out using two approaches (a) development of resistant mutant over time (growth curves in liquid media) and (b) plating *Campylobacter* – phage combinations via soft agar overlay. Using (a) we could not achieve a sufficient crash in host numbers with the *in-vitro* assay to assess the potential development of mutants. The second approach (b) however generated some resistant mutants. Among the 15 phage-host combinations logically selected at a MOI (multiplicity of infection) of 10, only one combination (7%) demonstrated the development of true resistant mutants' *in-vitro*. Of the remainder, 42% yielded resistant colonies sourced from partially lysed lawn (not a representation of true mutants, as the former). Among the other combinations 21% yielded sensitive isolates and rest (21%) had merged bacterial growth (colonies). To better address the outcomes of the *in-vitro* resistance encountered in the present study and its implication to chicken trials, a brief summary of literature addresses the implications of resistance to *Campylobacter* colonising the chicken gut. *In-vivo* resistance (in the chicken gut), unlike *in-vitro* is reversible, due to the fitness cost to the bird. Nevertheless both criteria addressed via the current milestone were also the focus of the CRC farm trials. During these trials we demonstrated a 2-log reduction in the caeca of treated birds and continued sensitivity to isolates tested post phage treatment. These outcomes highlight the challenges in comparing *in-vivo* and *in-vitro* resistance for *Campylobacter* (where the organism's main niche is the chicken gut).

Table 14 screening of isolates against phage concentrations 10^6 to 10^2

		Phage Concentration				
Source	**Colony ID**	**10^6**	**10^5**	**10^4**	**10^3**	**10^2**
2975-677	parental host	FL	FL	TNTC	17	2
	Test No: 1	-	-	-	-	-
	Test No:2	-	-	-	-	-
	Test No:3	-	-	-	-	-
	Test No:16	-	-	-	-	-
	Test No:18	-	-	-	-	-
	Test No:19	-	-	-	-	-
	Test No:24	-	-	-	-	-
4356-323	parental host	FL	FL	TNTC	6	1
	Test No:4	-	-	-	-	-
	Test No:5	-	-	-	-	-
	Test No:21	-	-	-	-	-
	Test No:22	-	-	-	-	-
	Test No:23	-	-	-	-	-
4352-265	parental host	FL	FL	TNTC	10	1
	Test No: 6	-	-	-	-	-
	Test No: 7	-	-	-	-	-
	Test No: 20	-	-	-	-	-
3037-782	parental host	FL	FL	TNTC	16	1
	Test No: 8	-	-	-	-	-
	Test No: 9	-	-	-	-	-
2992-431	parental host	FL	TNTC	20	2	0
	Test No: 10	-	-	-	-	-
	Test No: 11	-	-	-	-	-
4346-323	parental host	FL	FL	TNTC	12	1
	Test No: 12	-	-	-	-	-
3217-377	parental host	FL	FL	60	5	1
	Test No: 13	-	-	-	-	-
4347-722	parental host	TNTC	TNTC	60	5	0
	Test No: 14	FL	TNTC	30	1	0
2482-232	parental host	FL	FL	TNTC	12	0
	Test No: 15	32	3	0	0	0
3330-726	parental host	FL	FL	f	TNTC	12
	Test No: 17	FL	FL	TNTC	33	3

- No lysis FL fully lysed; TNTC too numerous to count

The highlighted is indicative of true resistant mutants

Table 15 Overall summary of the assessment of in-vitro resistance

Description of category	Percentage
Bacterial growth emergence within a cleared plaque area "typical resistant mutants"*	7
Resistant colonies (individual) from partially lysed bacterial lawn (compared to control)	42
Sensitive colonies (individual) from partially lysed bacterial lawn (compared to control)	21
No lysis (similar to control)	7
Grainy – joined bacterial colonies among areas of clearing	21

one combination was not tested due to contamination of the control

*The category highlighted in green was the only category typical of a resistant mutant, all seven isolates tested were resistant

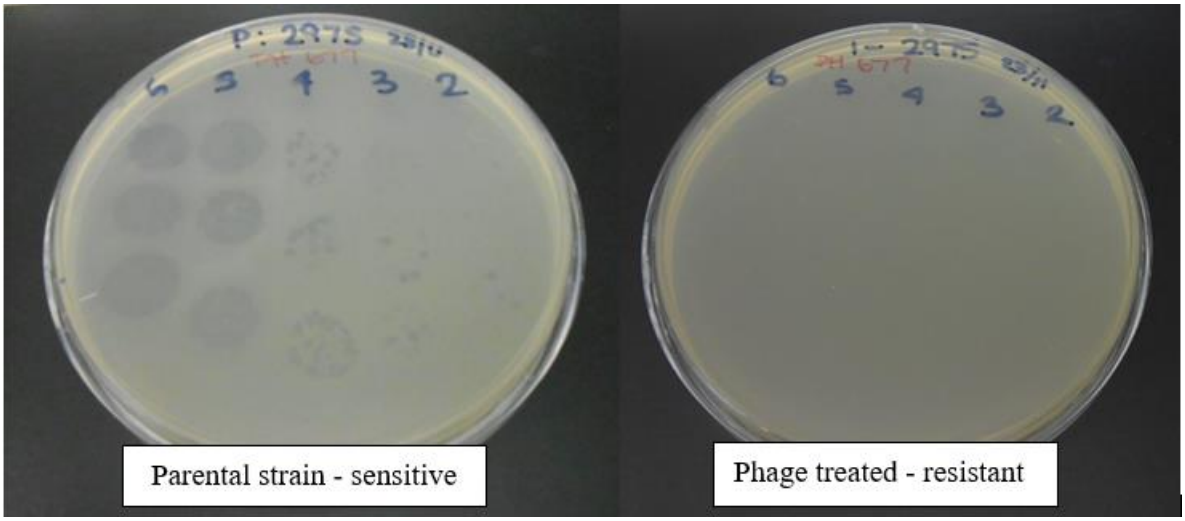


Figure 32 Screening for resistance combination NC2975 – PH18

2.11 Transmission Electron Microscopy (TEM) of phage images

Figures 33 and 34 present the TEM images of selected candidates. The phages have isometric heads (91-96 nm) and contractile tails (110-115 nm), which places them as members of the *Myoviridae* family and suitable for phage therapy applications. The phage dimensions are typical of group 3 phage that are now taxonomically classified as Ecampyvirinae Fletchervirus.

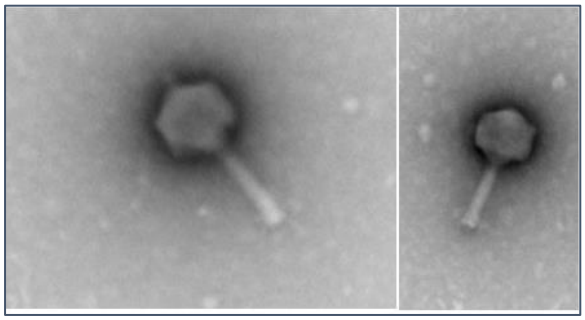


Figure 33 PH2 phage (head diameter 91 nm, tail 110 nm)

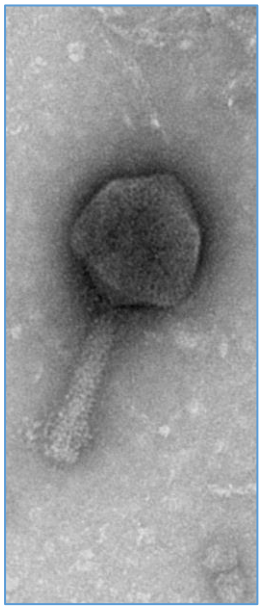


Figure 34 PH19 phage (head 95 nm diameter, tail 112 nm)

2.12 Phage genome sequences

The complete genome sequences of PH181 (non – cocktail candidate) and cocktail candidates. PH 1 and PH 2 were determined using the Illumina MiSeq platform, Appendix 2. The genome sequences confirm the phage are group 3 phage with genome sizes of 132-135 kb. There are no virulence or antibiotic resistance determinants discernible using the available search engines PathFinder and CARD. Appendix 3 presents the sequence annotation files (entire coding capacity) of all three phages.

BlastP searches of the putative phage tail fibre (gp047 homologue in NCTC12673 – Kropinski et al. 2011) protein encoding genes within the phage PH181, PH 1 and PH 2 genomes were undertaken to assess the binding mechanisms and compare these with the host range of these phage. Homologues in phages PH181 and PH 2 showed high sequence identity with GP047 (1364 amino acids), whereas a stop codon is present after the first 83 amino acids of phage PH 2 due to genetic mutation. The C-terminal regions of this homologue will be expressed from an internal start codon to create a protein missing the N-terminal 219 amino acids. PH 2 shows a broader host range than PH 1. Considering the finding from Javed et al. (2015) that the actual binding site of GP047 is located in the C-terminal quarter, this may suggest that binding of the shortened tail fibre is less hindered and is available to bind a greater variety of *Campylobacter* types.

These analyses are work in progress, which will require further work to complete due to time and funding limitations. The provisional work demonstrates how detailed analysis can provide a greater understanding of phage – *Campylobacter* binding (in addition to other factors assessed within the project) to enable intelligence-based refinement of the phage cocktails.

Chapter 3: Achieve a suitable log reduction of *Campylobacter* with the possible inclusion of either “active” or “passive” phage therapy strategy, which is assessed in-vitro (micro titre plates)

3.1 Background

The intestines of poultry become colonised by campylobacters often without noticeable effects on bird health but their presence represents a foodborne hazard to humans when transferred to poultry meat during processing. Control of *Campylobacter* is an obvious target for phage therapy because of the large proportion of poultry reared for meat harbours these organisms as a part of their intestinal microbiota with few practical alternatives for reduction (Connerton et al. 2011).

Two forms of phage therapy are recognised:

1. Active therapy, which requires ongoing replication of phage in order that the phage concentration reaches or is maintained at levels sufficient to control the bacteria;

2. Passive therapy, which requires the initial phage dose to inundate the bacteria present to affect a reduction bacterial numbers.

The two modes are not mutually exclusive, and can occur in the same treatment, for example where the initial phage dose is large enough to suppress the bacterial population and is maintained at that level by phage replication. To understand the basic kinetic properties of phage therapy one must appreciate that active therapy can occur only when the concentration of host bacteria exceeds that required to productively produce more phage progeny - known as the *proliferation* threshold, and passive therapy can occur only when the initial concentration of phage exceeds the host bacteria such that all are bound and killed – known as the *inundation* threshold.

Phages have been applied directly to foods and environmental surfaces in processing facilities to reduce the numbers of foodborne pathogens, a process that has been termed biosanitization. As atmospheric oxygen in these circumstances would normally prevent the growth of *Campylobacter* and replication of phages (since *Campylobacter* are microaerophilic), the numbers of campylobacters are probably reduced through “lysis from without” or by pre-adsorption of phages, which then resume their lytic lifecycle when conditions become conducive for *Campylobacter* growth (Atterbury et al. 2003). These are examples of passive phage therapy in the absence of replication and are the basis of industrial applications for biosanitization. We have examined the survival of *Campylobacter* treated with phage on an inert plastic surface or on chicken skin.

Active therapy requires phage proliferation that may occur in chickens when host bacterial concentrations frequently surpass the phage proliferation threshold (Carrillo et al. 2005). In the laboratory the action of phage may be modelled by examining their effect on growing cultures of host bacteria (Cairns et al. 2009).

3.2 Material and methods

The experimental details for active and passive therapy are presented in the following section

3.2.1 Passive therapy experiments

Campylobacter jejuni PT14 was cultured on horse blood agar plates (blood agar base No. 2 supplemented with 5% defibrinated horse blood), under a microaerobic atmosphere containing 5% O2, 5% H2, 10% CO2, 80% N2 at 42 ºC for 24 h. Phages PH13, PH19 and PH2 were propagated using the soft agar method and enumerated as previously described earlier. Campylobacters were applied to microtiter dishes at a range of concentrations and treated at 4 ºC with either mock or phage suspensions before the mixtures were recovered and diluted to determine the viable count at 42 ºC under microaerobic conditions.

Chicken portions were obtained from supermarkets and cut into 2 cm^2 sections and transferred to square Petri dishes divided into 25 sections at 4 ºC. For *Campylobacter* enumeration skin samples were aseptically transferred into individual stomacher bags 10 ml of MRD and stomached in a Seward Stomacher 80 Biomaster for 2 min. The suspensions were diluted 1:10 in MRD. Twenty 10 µl droplets of both the neat stomachate and the 1:10 dilution were dispensed onto the surface of plates of dried mCCDA (2% agar), incubated at 42 ºC under microaerobic conditions and the colonies counted after 24-72 h.

3.2.2 Active therapy experiments

One step growth curves for phage against *C. jejuni* PT14. Overnight cultures of *C. jejuni* PT14 were transferred into 100ml of MH broth with appropriate antibiotics to give a final concentration of approximately 7 $\log_{10}$ CFU /ml and incubated at 42°C under microaerobic conditions with 150 rpm shaking for 2 hours. The viable counts were measured after incubation as described earlier. Phage were diluted and added to bacterial suspension at the titre of 10^6 PFU/ml. The bacteria/ phage mix was further incubated at 42°C under microaerobic conditions with 150 rpm shaking for 3 hours and aliquoted samples were taken every 15 minutes. Aliquots were centrifuged at 13,000 x g for 5 minutes and the supernatant containing free phages were removed for titration. All measurements were made in triplicate and the mean ± standard deviation reported. The adsorption constant was calculated using the equation: k = -ln (Pt/P0)/Nt,

Pt = phage titer at time point t (PFU ml-1), P0 = initial phage titer (PFU ml-1), N = bacterial viable count (CFU ml-1) and t = time (min).

3.3 Results

3.3.1 Passive therapy

Campylobacters survive at 4 ºC in moist conditions such as those encountered in the processing environment and at retail. Similarly, *C. jejuni* PT14 survived in an aqueous film on plastic (microtiter plate) and on chicken skin as indicated by the minimal reductions in the viable count observed in the control samples over 24 hours compared to that at time zero, Table 16.

Figures 35, 36 and 37 present the survival of *C. jejuni* PT14 at 4 ºC in aqueous films in microtiter plates. The x-axis indicates the target bacterial count applied in $\log_{10}$ CFU. The controls (blue) were administered with SM buffer and the experimental $\log_{10}$ 8 PFU phage (as indicated) in SM buffer (red). The viable counts were determined immediately post mixing and 24 h later. Triplicate counts were performed and are recorded as the mean ± standard deviation.

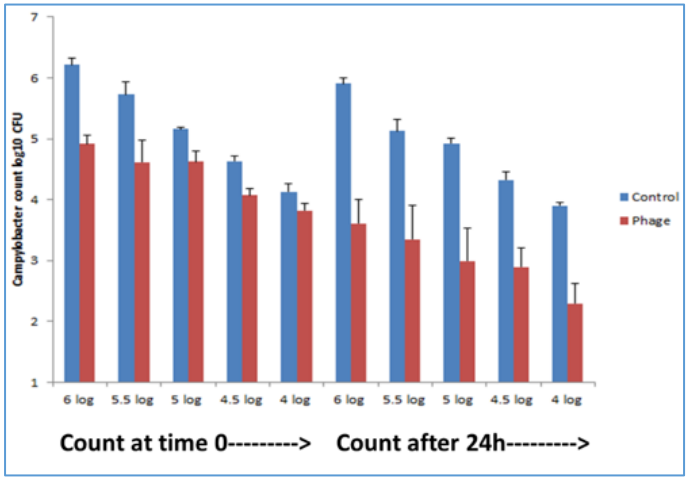


Figure 35 C. jejuni levels with $\log_{10}$ 8 PH 13 phage

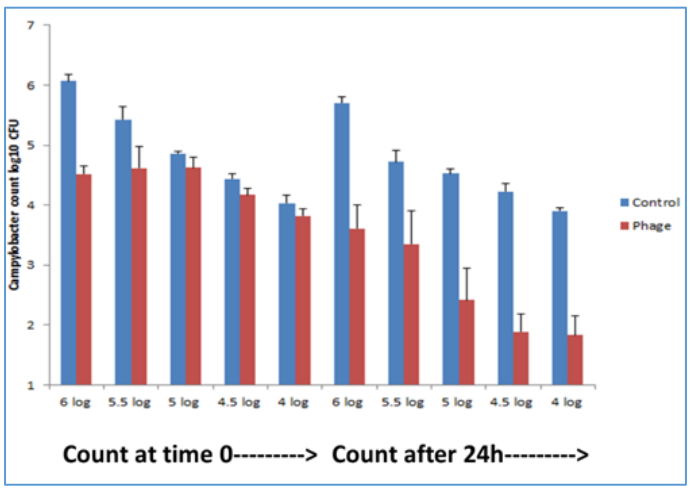
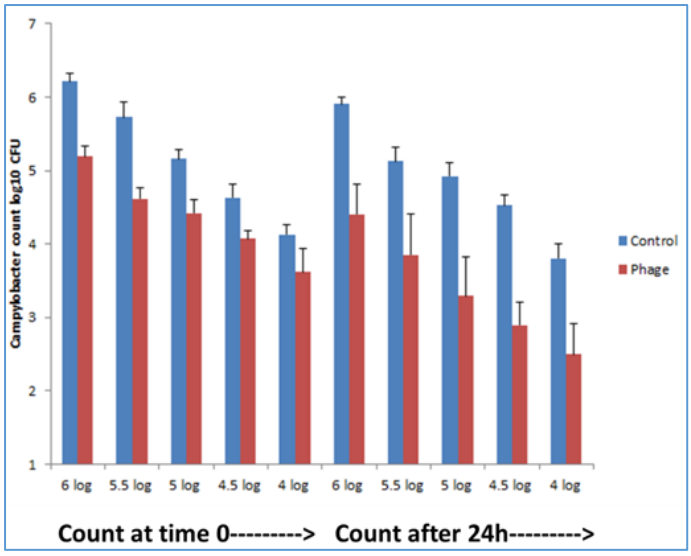


Figure 36 C. jejuni levels with $\log_{10}$ 8 PH 19 phage



The addition of phage reduced the viable count of the bacteria from time zero when mixed in the microtiter plates. The reductions were greater after 24 h with the phage achieving 1 to 2 $\log_{10}$ CFU reductions in the viable count. The most effective phage treatment under these circumstances was phage PH19 with 2 $\log_{10}$ CFU reductions observed at the highest multiplicities of infection (MOI s of 3,100 and 10,000).

The decline in *Campylobacter jejuni* counts after storage of chicken skin at 4 ^{o}C were examined. *C. jejuni* PT14 was applied to chicken skin at 5 $\log_{10}$ CFU/cm2 and treated with either 10^5 or 10^8 PFU/cm^2 phage. Table 16 shows significant reductions in the viable campylobacters recovered after stomaching contaminated chicken skins were recorded compared to controls without phage (MRD buffer alone). In this assay phage PH19 achieved the greatest reductions at applications of 10^5 or 10^8 PFU/cm^2. Phages PH13 and PH 2 could bring about reductions in the recoverable viable count with the greater phage applications.

Table 16 Mean decline in Campylobacter count (log10 CFU/cm2) on broiler chicken skin (n=10)

Days post PH13 treatment	10^5 PFU/cm^2	10^8 PFU/cm^2
1	0.8	1.7*
2	0.9	1.7*
3	0.9	1.7*
Days post PH19 treatment	10^5 PFU/cm^2	10^8 PFU/cm^2
1	1.2*	1.8*
2	1.4*	1.9*
3	1.4*	1.9*
Days post PH2 treatment	10^5 PFU/cm^2	10^8 PFU/cm^2
1	0.6	1.5*
2	0.7	1.6*
3	0.7	1.6*

* Significant differences at P= <0.05 by ANOVA

3.3.2 Active therapy

To compare and quantitate the log reductions observable with the phage isolates in actively growing cultures a series of growth curves were performed. From these the phage replication parameters were calculated, Table 17. Typical of *Campylobacter* phages the burst sizes are low at ~2 phage per cell due to the small size of the host bacterium (3-5 µm in length and 0.2-0.5 µm in width) compared to the assembled phage (190-210 nm in length with head diameters of 90-100 nm).

Table 17 Replication parameters for phage on C. jejuni PT14

Phage	Maximum host reduction (log_{10} CFU ml^{-1})_	Adsorption constant (k) $x10^{-10}$ (ml min^{-1})	Burst size (PFU $cell^{-1}$)	Latent period (min)
PH13	2.1	1.18±0.31	1.9±0.3	70
PH19	2.3	1.21±0.07	2.2±0.4	70
PH2	1.8	1.14±0.22	2.2±0.4	70

3.4 Conclusion

The application of phage isolated in this study can reduce the contamination of surface deposited campylobacters and on chicken carcass surfaces at refrigeration temperatures by 1-2 $\log_{10}$ CFU. However, to achieve these reductions requires high phage numbers and will require the propagation of high phage titres for commercial application (10^9 PFU per application).

Phage isolated in the course of this project are typical of group 2 and group 3 phage isolated from farm environments. Upon active replication when the host bacteria have reached the phage proliferation threshold of 7 $\log_{10}$ CFU /ml the phage achieve a reduction of 2 $\log_{10}$ CFU/ml. Of the phage investigated PH19 exhibits the greatest adsorption constant, indicating it binds to the host more efficiently, which likely contributes to the observation of the greatest *Campylobacter* host population crash. Active therapy requires a greater concentration of target bacteria but requires lower phage titres to achieve meaningful population reductions (10^7 PFU per application).

Chapter 4: Based on the knowledge of all of the above develop a cocktail of phages

4.0 Background

The progression to develop phage cocktails was undertaken in two stages, they included, undertaking the preliminary work and the validation of methodologies and the second stage included the assembling and analysing of selected phage cocktail activity against the host *Campylobacter*.

4.1 Preliminary work undertaken towards progressing cocktail formulation, Stage 1

This work was carried out at ESR in New Zealand by Dr Craig Billington and was done through two stages. During stage 1 the following was undertaken to initiate and progress the collaborative research. The work included and the detailed steps undertaken are listed as follows:

- Successfully reviving Queensland *Campylobacter* hosts and phages, Figure 38.
- Screening and analysis Queensland phages, Figure 39.
- Using above data picking the most promising phages for cocktail, Figure 40.
- Making some high titre stocks using the original phage stocks.
- Testing a 3-phage cocktail on 10 isolates for which the performance was good (100% coverage), Figure 41.
- Establishing high-throughput screening method for phage cocktails to commence screening, Figures 42 and 43.

All the above were successfully achieved to enable progression to the next stage.

On the initial arrival of Queensland *Campylobacter* isolates and phages work progressed to revive and validate stocks against data generated by the project in Queensland to enable progression of work.

		Phage (10ul spot)		
host	strain ID	PH5	PH16	PH19
Campylobacter	NC2480	0	0	0
C.coli	NC2905	0	3	0
C. jejuni	NC2981	3	3	3
C. jejuni	NC2992	3	3	3
C.jejuni (sam)	PT14	3	3	0
	pfu/ml	1.80E+05	5.00E+05	4.00E+04

DAF scoring system	
3	clear
2	many plaques / opaque
1	few plaques
0	no plaques

Figure 38 Initial testing of shipped frozen stocks

strain ID	Phages (spot test 10ul Sams stock)																		
	PH5	PH16	PH19	PH1	PH4	PH8	PH11	PH14	PH15	PH17	PH18	PH2	PH3	PH6	PH7	PH9	PH10	PH12	PH13
NC 2480	0	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	2
NC 2905	0	0	0	0	0	0	0	0	0	0	0	3	1	0	0	0	0	0	3
NC 2981	2	1	1	0	3	0	0	1	1	0	1	3	3	1	0	0	0	0	3
NC2992	3	1	1	0	3	1	0	0	0	0	1	1	1	0	0	0	0	0	3
PT 14	3	1	0	1	3	1	0	0	0	1	1	ND	ND	ND	ND	ND	ND	ND	ND
NC2487	0	1	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	3
NC2498	0	1	0	0	0	0	0	0	0	0	0	ND	ND	ND	ND	ND	ND	ND	ND
NC 3037	3	1	0	0	3	1	3	0	0	0	0	3	3	0	0	0	1	0	3
NC3548	1	3	0	1	1	0	0	0	0	0	0	3	3	0	0	0	0	0	3
NC3964	1	0	0	0	1	1	0	0	0	0	0	3	1	0	0	0	0	0	3
NC4076	3	1	1	0	3	1	1	0	0	0	0	1	1	0	0	0	0	0	3

Figure 39 Full screening of Queensland phages

The phages were narrowed down based on screening against QLD, "NC *Campylobacter* hosts"

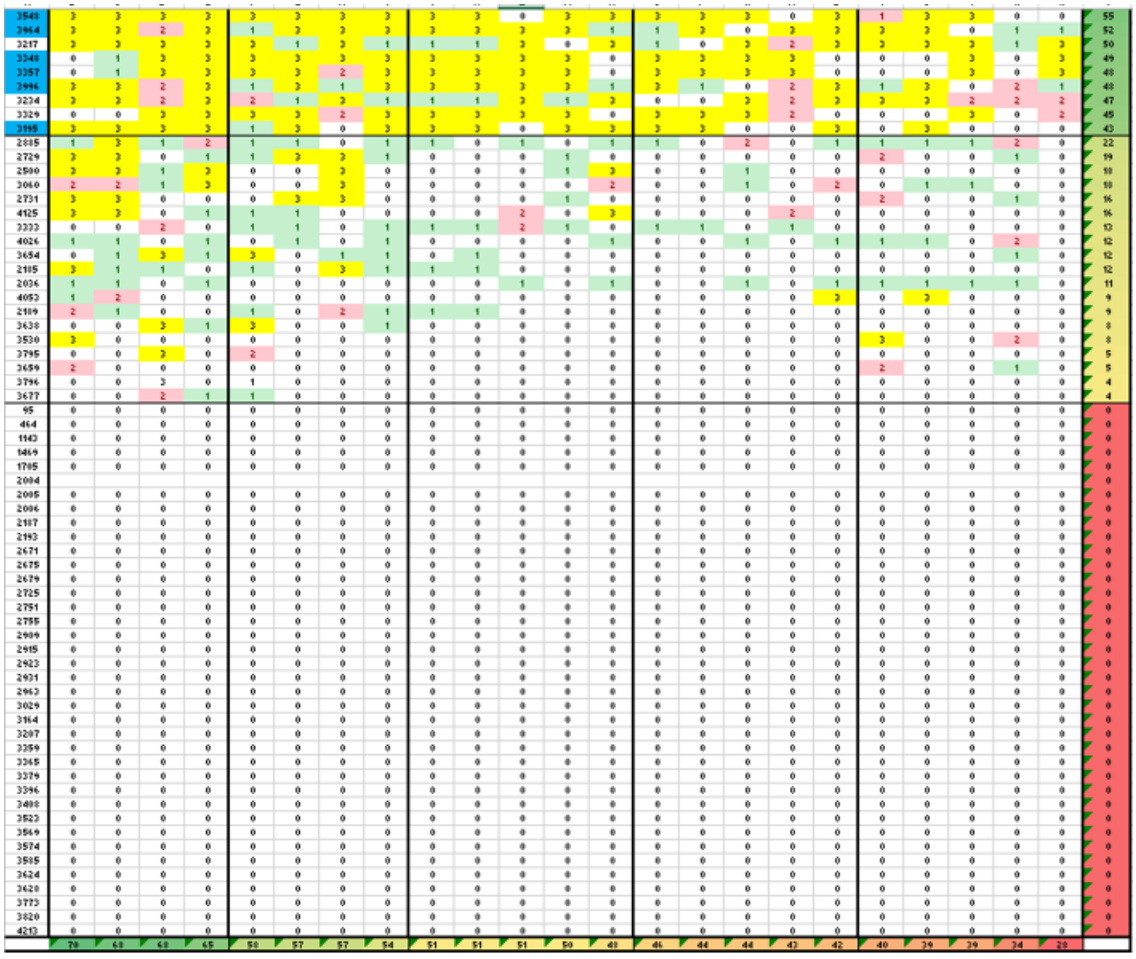


Figure 40 Narrowed down phages (with DAF, NC- hosts)

This work concluded to start with phage numbers PH5, PH2, PH13, PH8, PH16, PH19

Host	3E+5 pfu/spot	3E+3 pfu/spot	3E+1 pfu/spot
NC2981	3	3	2
NC2487	3	0	0
NC2480	3	2	0
NC2905	3	1	0
NC2498	3	0	0
NC3964	3	1	0
NC3548	3	3	0
NC 2992	3	3	0
NC 4076	3	3	2
NC 3037	3	repeat	repeat

3-phage cocktail* (3.1E+8 PFU/ml; NC2992)	
PH 5	propagated on NC2981
PH 2	propagated on NC3037
PH 13	propagated on NC2992

*original (old) stocks

Figure 41 Testing 10 hosts with a 3 phage cocktail

Growth of hosts in various liquid media (for high throughput screen)

Time (h)	NC2480	NC2981	NC2992	NC3307	PT14
0	0.063	0.037	0.009	0.096	0.017
4	0.076	0.059	0.018	0.081	0.013
23	0.075	0.055	0.068	0.052	0.054
100	0.090	0.144	0.095	0.100	0.039
116	0.159	0.142	0.112	0.173	0.076

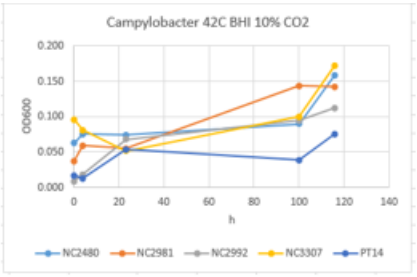


Figure 42 outcome when BHI, 42ºC, 10% CO2 – combination was used

Time (h)	NC2480	NC2981	NC 2992
0	0.119	0.0565	0.0625
2	0.1	0.0615	0.0635
4	0.1035	0.0815	0.0665
21	0.1155	0.124	0.143
26	0.106	0.1245	0.143
28	0.1075	0.1395	0.136

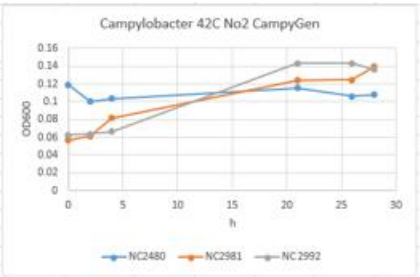


Figure 43 outcome when No2, 42ºC, CampyGen (MGS), 100 rpm was used

In conclusion: BHI+10% CO2 gives better media performance in liquid growth.

4.1.1. High throughput screen initial data

Some examples of 3-phage cocktail biocontrol on broth are presented in Figures 44 and 45.

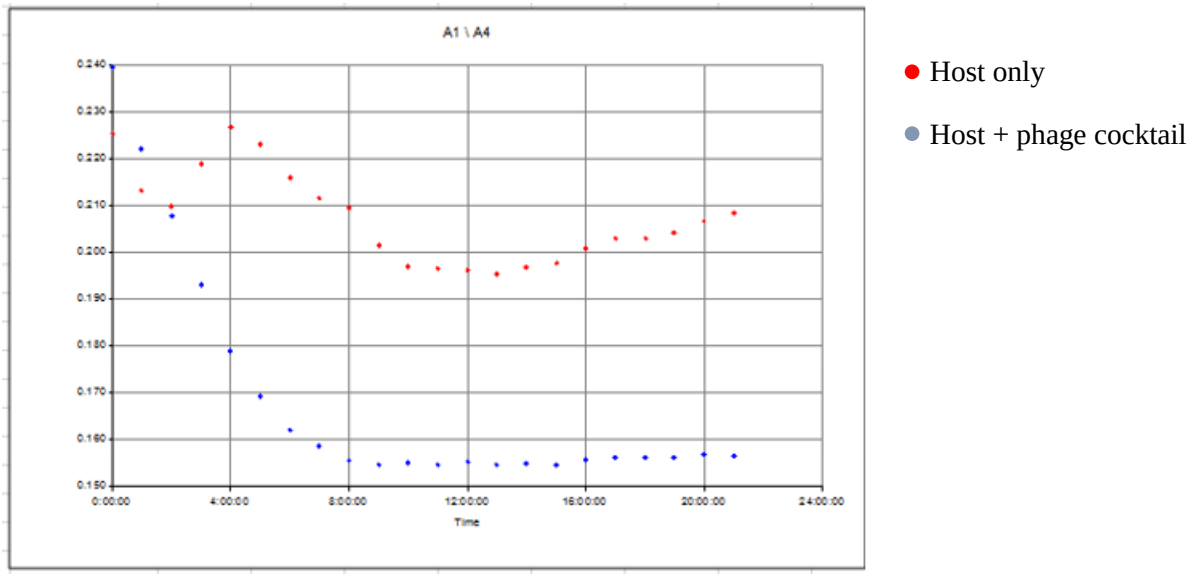


Figure 44 Lytic activity of cocktail on NC 2981 at 42°C in BHI

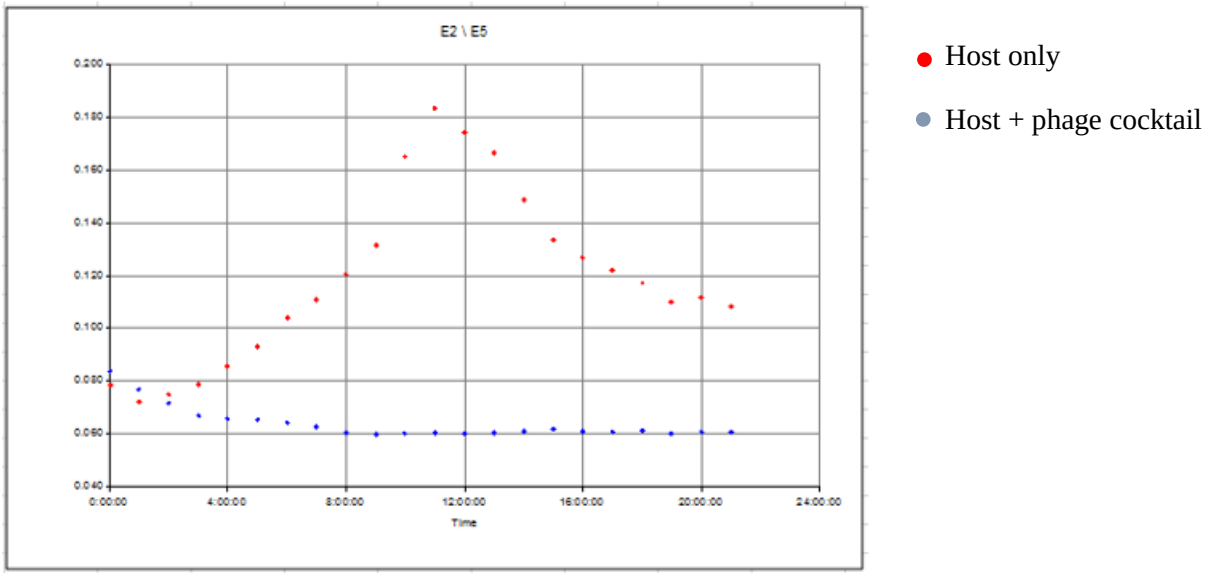


Figure 45 Lytic activity of 3 phage Campylobacter cocktail on NC 3037 at 42°C in BHI

4.1.2 Conclusion

In conclusion, these sequential outcomes demonstrated that a “3-phage cocktail” is exerting good performance in liquid media

This work concluded the validation work undertaken and enabled progression to the next stage i.e. carrying out the kinetic assay to screen the phages against different host panels.

4.2 ESR *Campylobacter* phage characterisation (stage 2 cocktail optimisation)

The aim of this work was to establish kinetic assay for screening different phage combinations against *Campylobacter* host panel.

4.2.1 Modify existing phage kinetic methods to work with *Campylobacter* (A)

The Billington lab at ESR is familiar with setting up high throughput screening of phages against host bacteria, but this is usually with aerobic bacteria so methods needed to be adapted for use with the microaerophilic *Campylobacter*. Variables tested included media, atmosphere, temperature, agitation, incubation and concentrations of phages and bacteria. Data from some of these optimization steps are presented below in Figures 46 and 47, where generally NZCYM media performed better than BHI media, with No 2. Broth media the poorest performer.

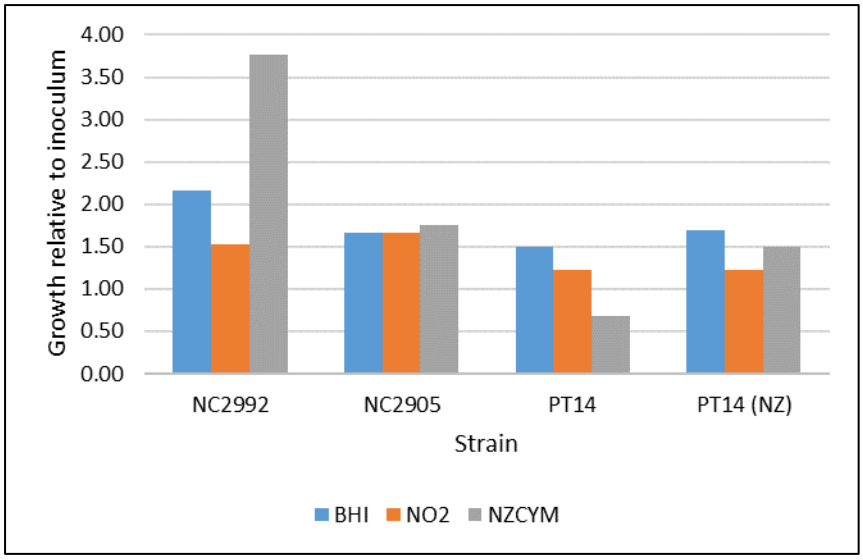


Figure 46 Comparison of growth of Campylobacter in different media - 10 ml tubes

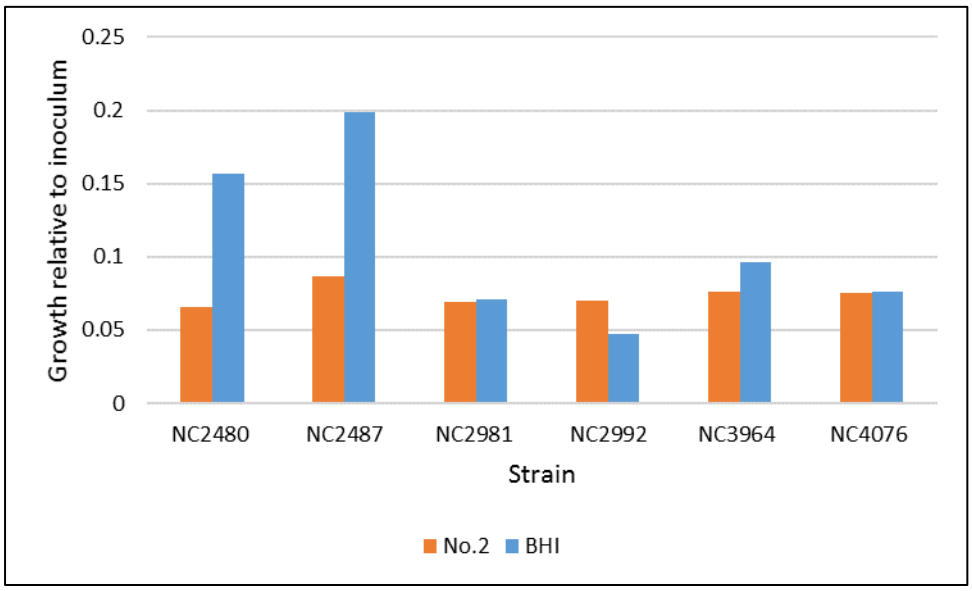


Figure 47 Comparison of growth of Campylobacter in different media – microtitre plate

4.2.2 Testing of *Campylobacter* phage cocktails – (B)

Host range and qualitative lysis (plaque morphology) data from the Chinivasagam lab were used alongside confirmatory data from our own work to establish the phage stocks to be included in the cocktails to be used for kinetic screening experiments. Five phages were chosen from Queensland stocks: PH13, PH8, PH5, PH2 and PH16 (Table 18). These five phages were made up into 10 cocktails (Table 19) for testing against 10 *Campylobacter* hosts (Table 20) selected to be broadly representative of Australian isolates from poultry farms. Later, a further phage (PH18) was added to make an 11th cocktail.

Table 18 Phage candidates

Strain	Isolated
PH13	Caeca
PH8	Caeca
PH5	Litter
PH2	Soil
PH16	Caeca
PH18	Pig effluent

Table 19 Phage cocktail composition

Cocktail	Phages		
A	PH13	PH5	PH2
B	PH13	PH8	PH16
C	PH13	PH8	PH2
D	PH13	PH8	PH5
E	PH13	PH2	PH16
F	PH8	PH5	PH2
G	PH5	PH2	PH16
H	PH8	PH2	PH16
I	PH13	PH5	PH16
J	PH8	PH5	PH16
K	PH13	PH2	PH18

Table 20 Campylobacter testing panel

Strain	Identification	Origin	Isolated
NC2480	*Campylobacter* spp.	Carbrook	Caeca
NC2487	*C. jejuni*	Carbrook	Caeca
NC2498	*C. jejuni*	Carbrook	Litter
NC2905	*C. coli*	Redland Bay	Litter
NC2981	*C. jejuni*	Redland Bay	Caeca
NC2992	*C. jejuni*	Redland Bay	Litter
NC3037	*C. jejuni*	Redland Bay	Litter
NC3964	*C. jejuni*	Carbrook	Caeca
NC4076	*C. jejuni*	Moreton Bay	No data
PT14 (NCTC 12662)	*C. jejuni*	United Kingdom	No data

Phage cocktails were tested by the standard method and relative effectiveness, as measured by decrease in optical density, was determined. Representative data from testing of the phage cocktails are illustrated in Figures 48, 49, and 50.

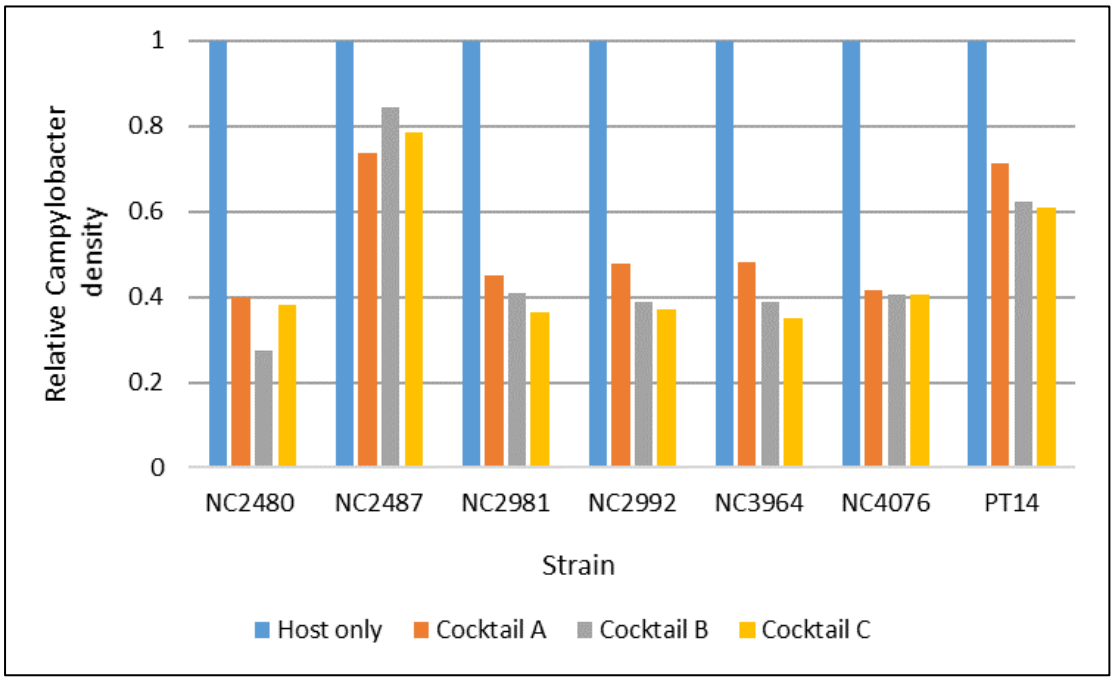


Figure 48 Comparison of phage cocktails A-C

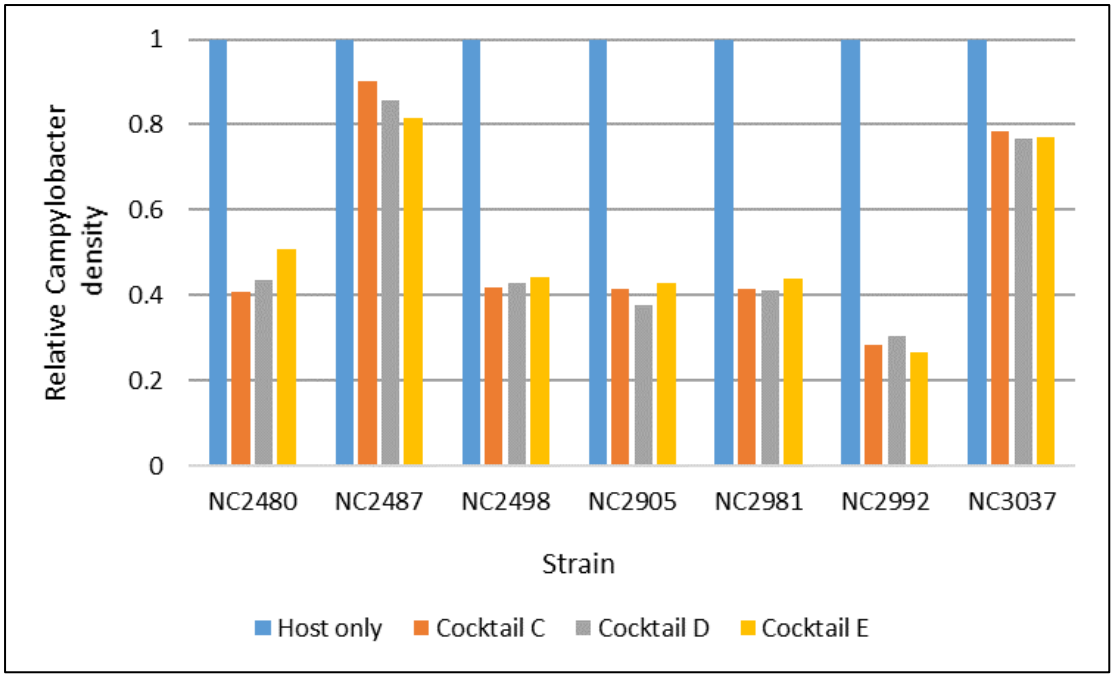


Figure 49 Comparison of phage cocktails C-E

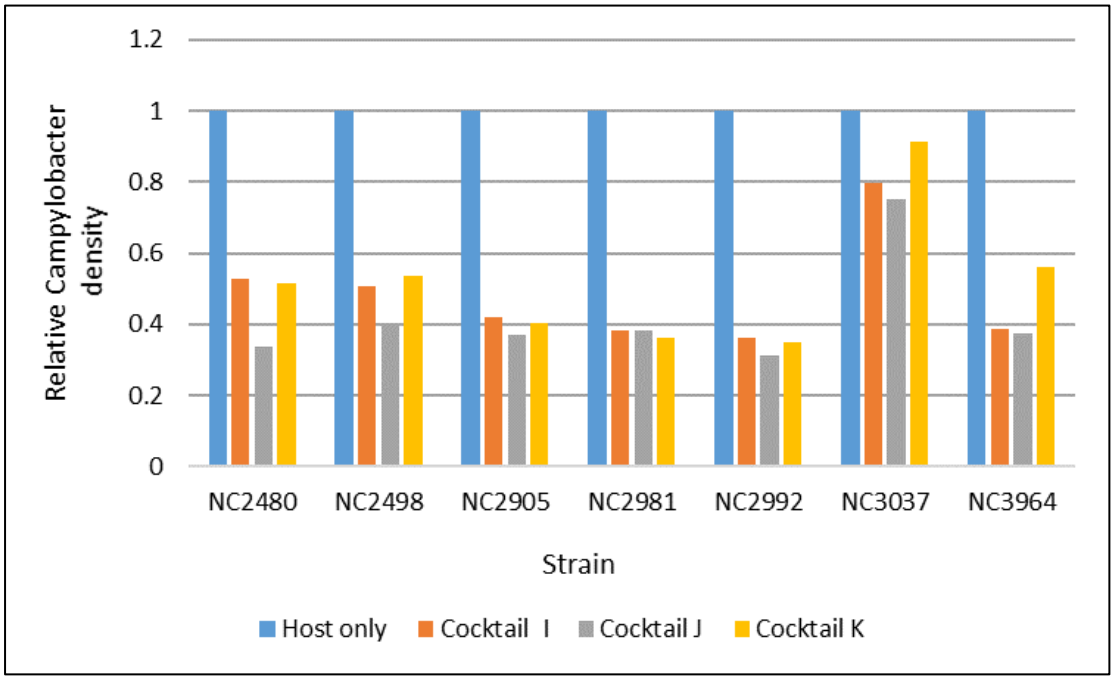


Figure 50 Comparison of phage cocktails I-K

4.2.3 Testing of *Campylobacter* phage cocktails – combination of Australian and New Zealand isolated phages (C)

Some of the Australian phage cocktails were further tested by addition of New Zealand isolated phages to determine if there is any added benefit. The cocktails tested are listed in Table 21, where New Zealand *Campylobacter* phage Cj6 was originally isolated from chicken faeces and phage C62.1 from chicken feathers.

Table 21 AU-NZ phage cocktail composition

Cocktail	Phages			
L	PH13	PH8	PH2	CJ6
M	PH13	PH8	PH5	CJ6
N	PH8	PH2	PH16	CJ6
O	PH13	PH8	PH5	C62.1
P	PH13	PH5	PH16	CJ6
R	PH8	PH5	PH16	CJ6
S	PH13	PH2	PH18	CJ6

The performance of these cocktails (Figures. 51 & 52), which contained four phages rather than three, was similar to that observed for Australian only phage cocktails. Note that the total phage titre was equivalent in all treatments to eliminate this as a factor.

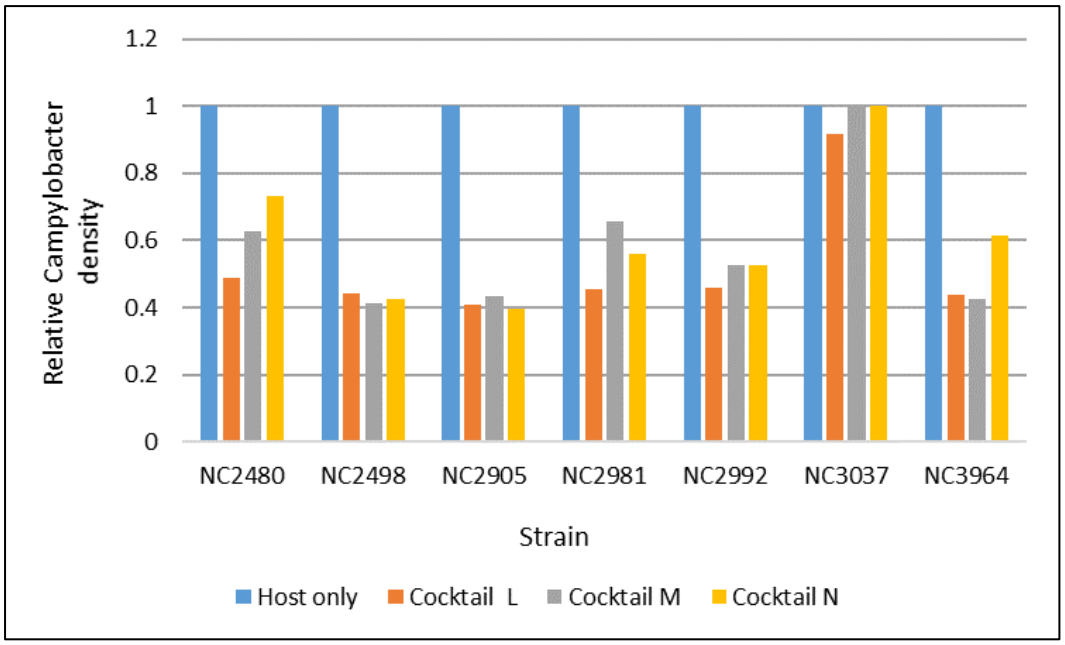


Figure 51 Combined AU-NZ phage cocktails L-N

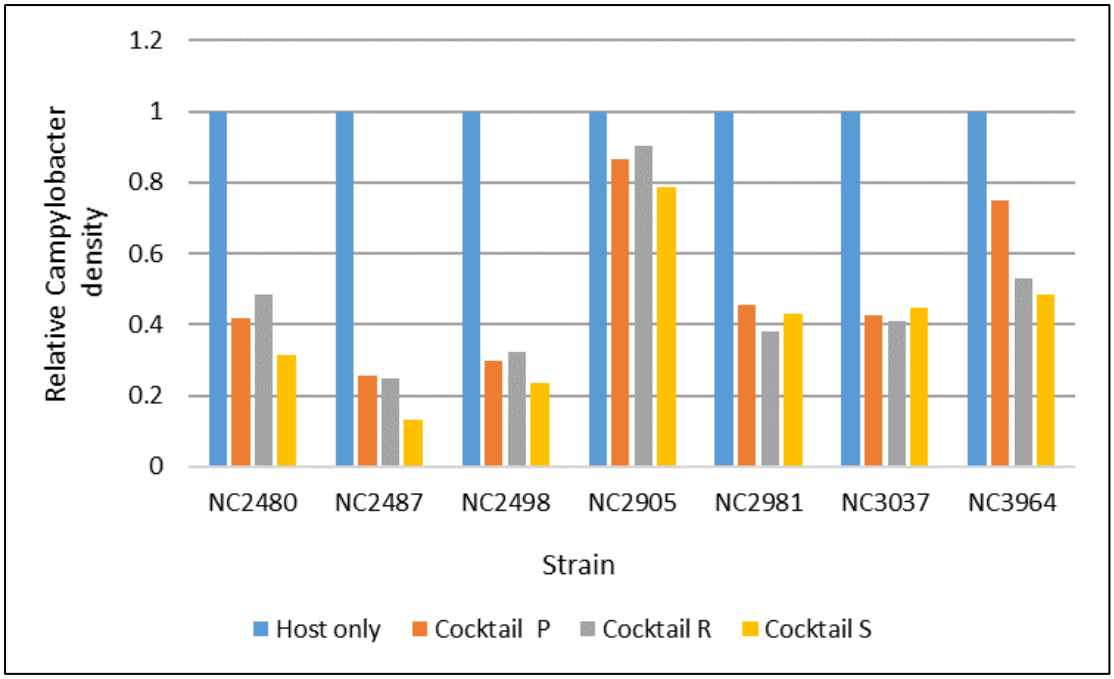


Figure 52 Combined AU-NZ phage cocktails P-S

An experiment was also performed where the Australian phage cocktail "D" was compared to the same cocktail with the addition of either phage Cj6 "M" or phage C62.1 "O" (Figure. 53). For 4/7 isolates "M" performed better than "D", and for 5/7 isolates "O" performed better than "D". This indicates there may be value in addition of New Zealand phages to cocktails of Australian phages to control Australian *Campylobacter*.

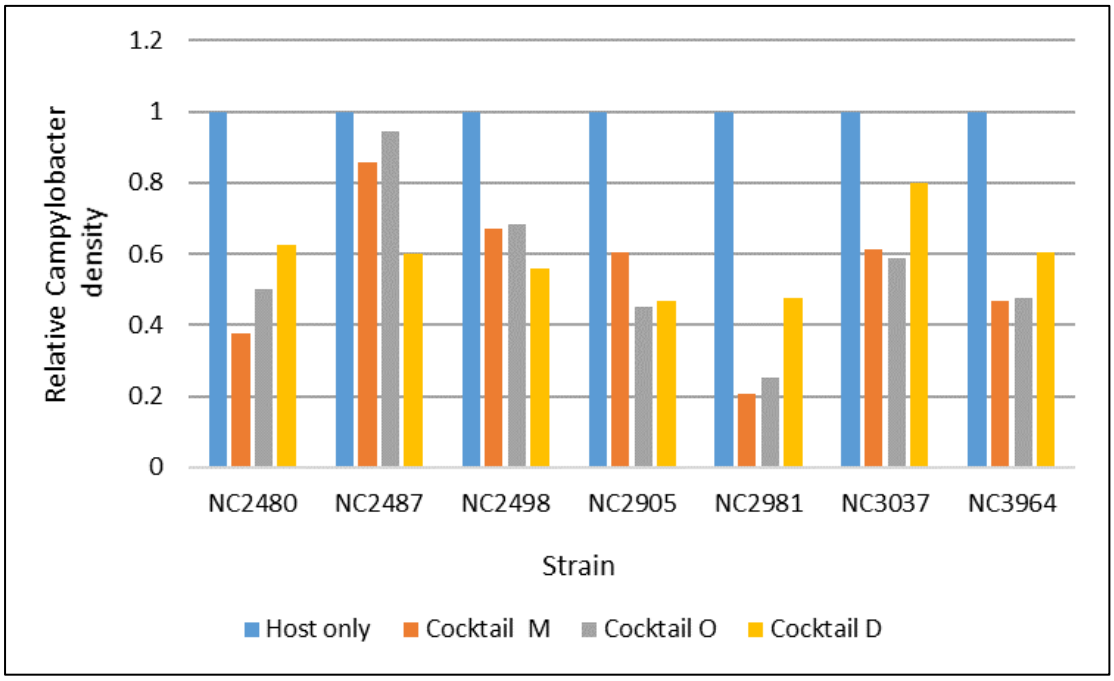


Figure 53 Combined AU-NZ phage cocktails M and O compared to AU cocktail D

4.2.4 Overall trend analysis of phage cocktail performance (D)

The relative efficacy of each cocktail was calculated to determine if there were any trends in performance of the different phage cocktails (Figure 54). Cocktail "S" was the best performer, having the greatest ability to decrease the concentration of *Campylobacter* in culture, whereas cocktails "H", "F": and "G" were the least effective. It is notable that combined Australia-New Zealand isolated phage cocktails were amongst the best performing.

When examining the data on the susceptibility of the *Campylobacter* isolates tested (Figure. 55), it does appear that some strains are more susceptible to the phage cocktails than others. It will be interesting to see if there are any genetic determinants which could be linked to these observations – this work will be performed later in the project.

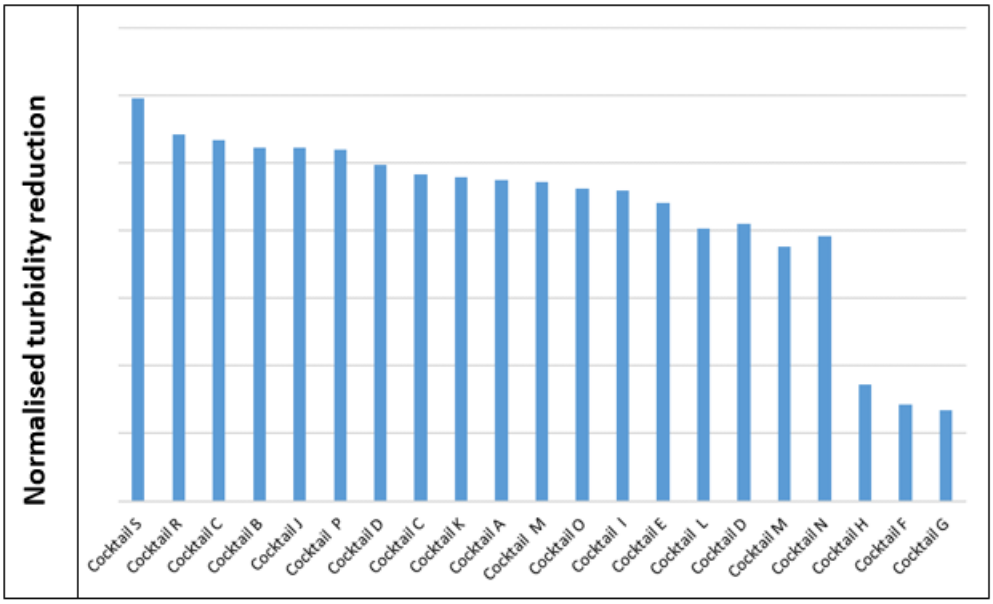


Figure 54 Overall relative effectiveness of phage cocktails against Campylobacter strains

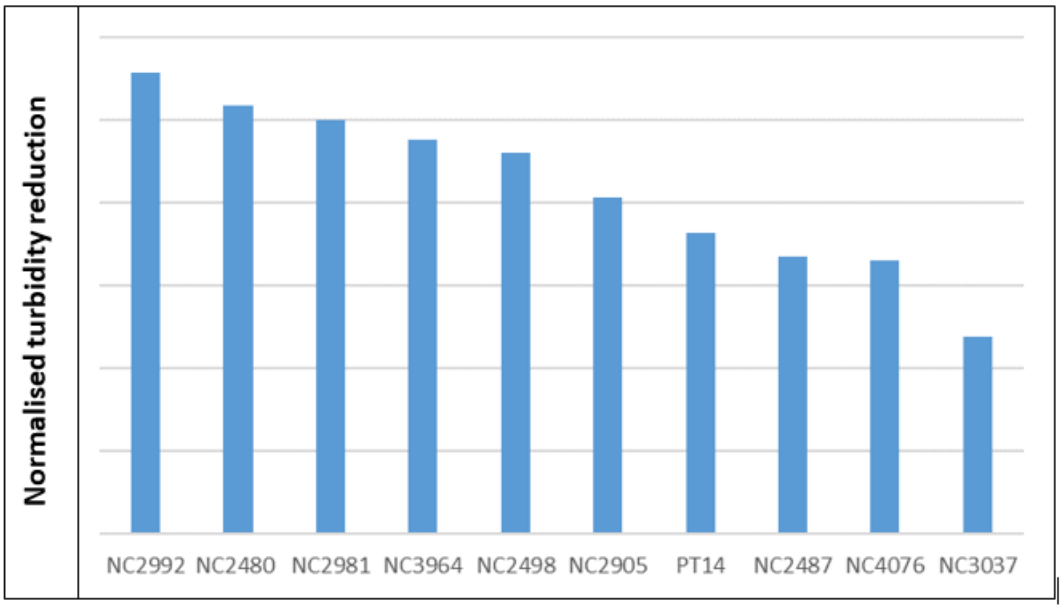


Figure 55 Overall relative susceptibility of Campylobacter strains to phage cocktails

4.2.5 Conclusions

Combinations of three and four phages were tested in 18 different formulations (cocktails) for efficacy against a panel of *Campylobacter* hosts. The cocktails all resulted in reductions in *Campylobacter* concentrations in broth. Addition of New Zealand isolated phages to Australian phage cocktails may give an added performance benefit. Overall, most phage cocktails were similar in their ability to kill *Campylobacter*. Some strains of *Campylobacter* had lower reductions in numbers than others. Further work to optimise phage cocktail formulations will be guided by this data.

Chapter 5: Generate data to support necessary Australian regulatory framework for the use of phages as bio-control agents by the Australian Poultry Industry

Provide the Australian Poultry Industry an efficacious environmentally friendly option to control *Campylobacter* that will benefit the poultry industry and the consumer.

5.0 Background

This section draws outcomes across two previous studies Chinivasagam et al. (2015) and Chinivasagam (2017) along with the current study to provide a comprehensive summary in pursuing this environmentally friendly option. The initial study (RIRDC funded) provided the basis for the isolation of *Campylobacter* phages and creating a large phage collection which led to the subsequent Poultry CRC study to address phage bio-control. The proof of concept (Poultry CRC funded) provided previously unavailable outcomes and is only one of the two studies relating to on-farm phage bio-control (only one published study exists to date, Kittler et al. 2013, the CRC study is accepted for publication). The CRC study provided an understanding of the natural incursion of intrinsic phage that co-contributed to *Campylobacter* reduction along with the cocktail candidate to facilitate *Campylobacter* reduction. This is the first time the need to understand this approach has been identified. The current study has thus focused on generating a detailed understanding of phage activity both at a laboratory and farm level. Host – phage relationships were furthered by *in-vitro* cocktail development and assessment and detailed molecular understanding of the candidate phages to help assess performance. All these outcomes have contributed to

- Generating data to support necessary Australian regulatory framework for the use of phages as bio-control agents by the Australian Poultry Industry
- Providing the Australian Poultry Industry an efficacious environmentally friendly option to control *Campylobacter* that will benefit the poultry industry and the consumer

These aspects are discussed in this Chapter.

5.1 Conclusions from the "proof of concept trial" with consequences to application in Australia

5.1.1 *Campylobacter* reduction in treated birds

Managing *Campylobacter* numbers in the chicken gut, on-farm, is a promising strategy to reduce disease burden attributed to human illness from poultry meat consumption. Whilst other options are available, one of the reasons that phage therapy has proved successful over treatments such as antibiotic therapies is that utilizing a biological agent requires care in selection of the appropriate agent and in application. However, the subtlety of being able to target pathogenic species within a complex microbiota within the chicken gut with no dysbiosis represents a major advantage. Campylobacters are not overt pathogens of chickens thus the ability to target the zoonotic component of the microbiota of the chicken is a key advantage to bird welfare, the integrity of the treatment and the quality of the product (Richards et al. 2019).

Two farms, Farm A and B were selected for these trials based on the absence of phage in the caeca of the bird one week before application, having a high *Campylobacter* count in the caeca the campylobacters relevant to the cycle being tested being sensitive to two or more members of the 19 – phage cocktail panel. Selection of the optimum phages, which are active against the dominant *Campylobacter* in the relevant flock is key to a successful intervention. This occurred in Farm A where phage treatment brought about a significant decline of a 2-log reduction in the *Campylobacter* count within the ceca that represents the major reservoir of intestinal contamination, when compared to control birds. A strong negative correlation was also observed between the *Campylobacter* count and the phage titre where a high *Campylobacter* counts in the treated birds represented birds where the phages have not attained a great enough titre in the caeca to shift the population.

As all birds were treated in the similar manner, the failure is likely due to low host concentrations encountered in the amplification phase, for example in the intestinal tract prior to reaching the caeca. Thus, one of the outcomes of the trial on Farm A was to increase the treatment beyond 24h (as adopted in the trial) to allow the phage titre to achieve titre and /or allow time for the required dispersion within the intestine. Whilst a statistically significant reduction was achieved on Farm A (at the farm), the reductions were not statistically significant following transport. The longer treatment period would allow the build-up of sufficient phage numbers to ensure host reduction in the caeca. However, in the majority of the phage treated birds on Farm A, the phage did replicate and were effective at reducing *Campylobacter* numbers in the caeca.

During the current study, a two log-reduction was demonstrated *in-vitro* using the universal *Campylobacter* host *C. jejuni* PT 14, which was the source of all phage isolations, and a phage used in farm trials during the CRC proof of concept study.

5.1.2 Co-contribution of inherent phages to log reduction

Indigenous phage can alter Phage – *Campylobacter* dynamics and outcomes as phage are already present in the chicken gut and have been isolated across poultry environments, (as described in Chapter 1. During the previously carried out farm trials, Farm B, tested negative a week prior phage treatment and the *Campylobacter* of the relevant cycle was sensitive to two candidates. Following phage treatment, the flock was phage positive either as a consequence of the on-going phage *Campylobacter* interactions or the shed environment. These phages most likely reduced the numbers of *Campylobacter* in caecal contents of both control and test birds, either before or concurrently, with the phage intervention. Following treatment and subsequent sampling, the average *Campylobacter* number in the caeca was 5.6 $\log_{10}$ CFU/g in contrast to 7.8 $\log_{10}$ CFU/g, when pre-screened, a week

earlier, in the absence of phage. This aspect sheds light on the process of co-contribution phages that are already a part of the natural *Campylobacter* – phage interactions occurring in the intestinal tracts of farm chickens. This further confirms earlier reports that the presence of phage in broiler flocks can reduce caecal *Campylobacter* population levels (Atterbury et al. 2005). Thus, in addition to the contribution to the reduction afforded by the cocktail candidates there is also need to take into account the action of concurrent phage infections, which may make phage intervention more effective, if optimized correctly. The outcomes from the study Farm B, highlights the need to understand system specific phage–host interactions that are likely critical for successful treatment outcomes.

5.1.3 Phage resistance

Phage resistance is often cited as a barrier to phage treatment. But resistance to the selected phage cocktails was not detected on either farm. This was possibly between the time difference between phage application and slaughter which was 24 hours. Irrespective of this, one of the key criteria for addressing resistance is the use of a cocktail of phages which target different receptors in the host bacteria. The short exposure of the birds to the phage cocktail treatment may have contributed to low phage titres observed and the strong correlation with the *Campylobacter* counts observed on Farm A in the absence of emerging phage resistant populations.

In-vitro testing of resistance undertaken by the current study also demonstrated low resistance (7%) as demonstrated by the development of true resistant mutants' *in-vitro*. Interestingly three of the *Campylobacter* isolates (from farm trial) following phage treatment did not yield any resistance colonies, only grainy lawns, during in-vitro testing.

5.1.4 Absence of phage in processed carcass – prior chlorination

This is a key criterion for consumer acceptance of phage bio-control, i.e. the absence of phage in the processed carcass. This was demonstrated from carcasses that originated for both farms.

5.2 *Campylobacter* phages occur in litter only in the presence in the bird

This was observed during the study that assessed *Campylobacter* dynamics across four litter practices (they were the conventional practice of full-clean-out, conventional litter re-use, free-range – with full clean-out and free-range with re-use). This involved the sampling of the birds (caeca) litter, soil and carcasses across 17 farms (24 farm samplings) over a two-year period (2012 – 2013). Phages were only isolated in conjunction with the host *Campylobacter* as illustrated in Figure 56.

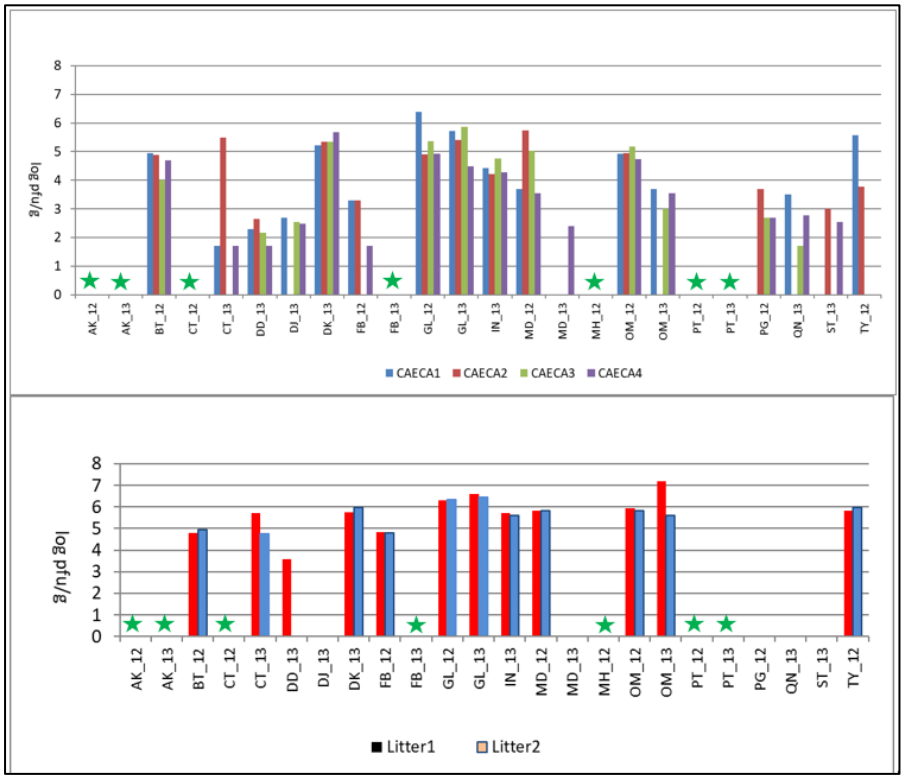


Figure 56 Levels of Campylobacter (CFU/g) and phages (PFU/g) in caeca of chickens from four 24 farms

This work is currently being prepared for a peer review publication

5.3 Survival in water

The delivery of phages does not require complicated options. They can be delivered via drinking water (tap water) as was done with both farm trials. High titre stocks were prepared and assessed over time. Figures 57 and 58 illustrate the phage levels in water compared to the common storage media SM buffer over time. Thus, high titre stocks can be calibrated to be delivered via the in-shed water delivery system.

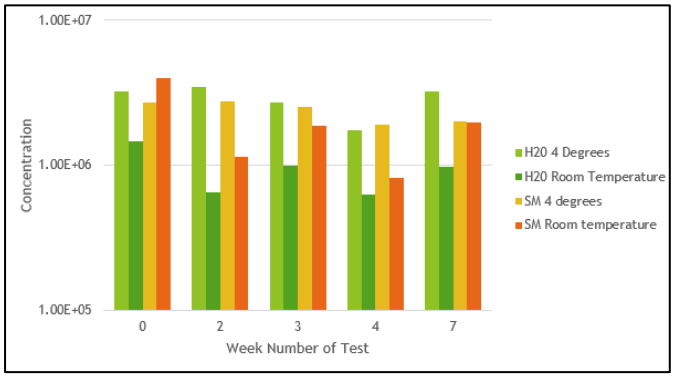


Figure 57 Storage studies PH18 in tap water and SM buffer at room temperature and 4ºC

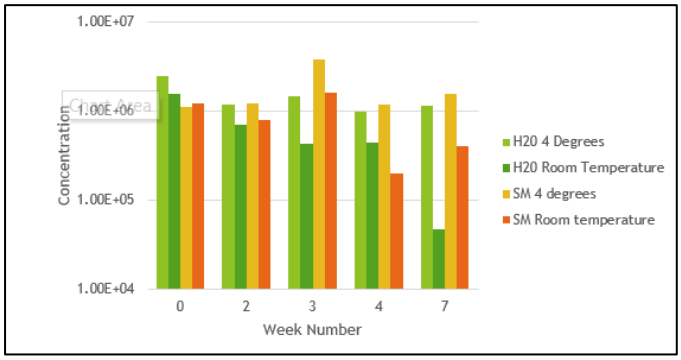


Figure 58 Storage studies PH19 in tap water and SM buffer at room temperature and 4ºC

5.4 Additional outcomes from current study

The current study has provided the Australian Poultry Industry an efficacious environmentally friendly option to control *Campylobacter* that will benefit the poultry industry and the consumer and the outcomes are summarised as follows:

- Provided an expanded set of phage cocktail candidates
- Evaluated the activity of these candidates on farm basis using previously generated data from the Poultry CRC study
- Expanded the set of *Campylobacter* isolates by creating a group based on chronological isolation, litter practice, source and species to further validate screening undertaken during the previous study
- Evaluated the activity of these candidates against various farm *Campylobacter* isolates to assess activity of candidates
- Demonstrated the use of select cocktails using both New Zealand and Australian phages
- Demonstrated the use of select cocktails using both New Zealand and Australian *Campylobacter* isolates
- Demonstrated the overall relative susceptibility of *Campylobacter* strains to phage cocktails to aid selection and combination of cocktail
- Demonstrated *in-vitro* log reduction (also supported by farm trial outcomes)
- Demonstrated minimum resistance via *in-vitro* resistance trials (also supported by farm trial outcomes)
- Provided PFGE details to have a detailed understanding of the cocktail candidates
- Provided detailed genomic data to support suitability for inclusion in cocktails and address Australian regulatory framework for the use of phages as bio-control agents by the Australian Poultry
- Demonstrated how detailed genomic analysis can provide a greater understanding of phage – *Campylobacter* binding (in addition to other factors assessed within the project) to enable intelligence-based refinement of the phage cocktails, which address both safety and efficiency.

5.5 Future needs to address commercialisation

Extensive studies have progressed the outcomes to use *Campylobacter* phage bio-control to date. The studies carried out across three countries has paved the way for successful data sharing, collaborative outcomes and previously unavailable data on *Campylobacter* phage bio-control. This has been achieved by both farm and detailed laboratory studies.

One of the key outcomes that needs to be furthered is the co-contribution of the natural phage – *Campylobacter* interaction which can be harnessed to enhance cocktail contribution. This requires a deeper understanding of *Campylobacter* – phage interactions.

There is a need to formulate and address selection of cocktails from a scale up perspective to ensure a viable commercialisation pathway to market.

There is a need to seek potential commercial entities to understand the way forward in providing a Australian regulatory frame work for the use of phages as bio-control agents by the Australian Poultry Industry.

There is a need to continue sequence annotation for the rest of the cocktail candidates as demonstrated in this section.

Implications

Poultry are a major source of *Campylobacter*, although a zoonotic pathogen the organism has minimal impact on birds. Campylobacteriosis is the most common form bacterial foodborne disease worldwide, and the single most important source of *Campylobacter* is broiler meat (European Food Safety Authority 2016). European studies indicate that on-farm interventions can exert effective control, with a 2.0 log reduction in faecal *Campylobacter* counts predicted to reduce human infections by 75% or a 1.0 log reduction in faecal count supported by a 1.0 log reduction in contamination of the exterior of processed chicken meat a 90% reduction of human infection (Havelaar et al. 2007). Hence, the development of an on-farm intervention to control *Campylobacter* levels by 1.0 to 2.0 logs is of significance to industry and policymakers to bring about reductions in human infections from 50,000 to 5,000 case per year.

This study represents progress towards delivering a sustainable and low environmental impact option, which is likely to gain consumer acceptance for the control of one of the key foodborne pathogens responsible for human illness.

In Summary:

Implications for relevant stakeholders

- Poultry are a major source of *Campylobacter*, with the most important single source of campylobacteriosis considered to be broiler meat.
- Modelling indicates that on-farm poultry interventions can be very effective in reducing human infections.
- Development and validation of on-farm control options for reducing *Campylobacter* levels by 1.0 to 2.0 logs can realistically result in a 90% reduction of human infections.
- This study is progressing towards delivering an environmentally compatible option for the industry to achieve these reductions in *Campylobacter* on-farm.

Recommendations

Work to develop a *Campylobacter* bio-control solution for the poultry industry has been significantly advanced in this work. This work now needs to be capitalised upon to bring this closer to a commercial reality.

Appendix 1 Variation to project

Research in Progress Report No. 2	- Agree work plan and finalise resourcing with international collaborators - Data analysis for interim phage resistance experiments - Re-evaluation of original Campylobacter screening panels to optimise Campylobacter genome sequencing work - NZ collaborator visit DAF to discuss collaborative work	Summary Report on Research in Progress submitted in Clarity, providing an update on the following: - Contracts finalised, materials and data in place to progress work - Data on phage resistance is expanded - A grouped set of Campylobacter isolates selected to progress collaborator work - Collaborator visit complete, work plans in place	31/5/2018
Annual Progress Report No. 3	- Undertake kinetic studies to inform phage cocktail formulation - Bioinformatics analyses of phage sequences to reveal host receptors and determine biosafety - Evaluate the potential for overseas phages to improve phage cocktail	Annual progress report submitted in Clarity, reporting on: - Formulation of the phage cocktail is advanced - Initial biosafety analysis complete	30/11/2018
Research in Progress Report No. 3	200-word summary report, providing update on project. - Cross-reference Campylobacter genome sequence data with phage susceptibility data to improve cocktail performance - Use in vitro evolution to improve cocktail performance - Investigate nature of phage escape mutants - Determine commercial potential for cocktail to perform in other markets	Summary report on Research in progress to date, submitted in Clarity, reporting on - In vitro performance of phage cocktail is optimized	30/5/2019

	Please contact AgriFutures Australia's Chicken Meat Extension Officer to develop the project's reporting outputs.		

Appendix 2 Phage genome sequences

PH 181

CDS_POSITION BLAST_HIT EVALUE PRO_SEQ

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region 1

complement(4..609) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00001; phage(gi100059) 1.17e-132
MYSKFLNESSENLWVFAKNDIKLRKLILPVIQDNIEYVMFLNDRSIEEGKLKDICLDIEIFGVFEHYNIGNYKKIEPSIVVNVTDLKKDALKSIEDKLKNCKSKDEPVL
SLKLDMITEYNVARLLEKEYYINNFTDIIQNELKSKQFKIVEGNIGESVVELFNDYGESMIFTLKNNKVIKVNGQVGTKYNYLYSSLVIQKI

complement(626..1582) PHAGE_Campyl_PC14_NC_031909: dihydrofolate reductase; PP_00002; phage(gi100060) 0.0
LKSINEKEYVWAEKYRPSKIDDMILPDKLYAKIKEWINSGEIPNLGFFSNTPGTGKTSLNKAICNELGATHLFINSSKESGVDLARNKITSFASSVSIDGSLKIISLSECD
GMTNELQRSIRDILDEYTQNCRFILTANYTDRLIEPILTRVTCIDFDKEFNDNKTELGVKILDRLEFILQNEKVEYDKKDLQKLIQCFYPCIREMLIVMQHNTIDNKLVI
DEKVFETINNYSNLIEALKKKNFTEARKIIAQTVSYSGFYQYLFKNIDNIFELESIPQAVMLIEHYSDHDRTSRDRELCLSALVAALIKYDIKYKNS

complement(1640..2197) PHAGE_Campyl_CP81_NC_042112: ssDNA binding protein; PP_00003; phage(gi100044) 4.12e-123
MKLHYYDIYNISNGVFLTFQKNLKEKLLCVSHSKDIMDKKIGFYPLNFSDRGDFILLCVYIMFKHSPSSIYGLCEYLRNYNKTEYEKFKNTIKFYKNMIKKDIALLEE
KYKKPMFKEVMREYSIKQISFVTVYWYLMLYDIKDFNGINNTIICESILNVFKFLKFTDESKDYIKDVFKQIEGEVL

complement(2210..2470) PHAGE_Campyl_PC14_NC_031909: ribonucleotide reductase A subunit; PP_00004; phage(gi100062) 1.45e-48
VESKTELFNKLFEFRKQKDMMDDCILDVIIEFGNHINMDPELIASELSDYAIFRDIVEKDLKKFKFTKYDPNQSDIDISDIDILWE

complement(2460..2906) PHAGE_Campyl_PC14_NC_031909: aerobic ribonucleotide reductase B subunit; PP_00005; phage(gi100063) 2.09e-103
MCVLKTWLEDSNAKLPEISVMGSACYDIFSIEDKTIQPGGFEYVENGVRLIIPDGYYIRFNTRSSLGFIKDLFVYPGILDASWSGNLKVKVYNFGKEPYTIKKGDKYC
QFELLKCNESKIENISKDDFDNITKKLIRGNNGGWGSSGK

complement(2894..3286) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00006; phage(gi100123) 3.60e-83
MKNIEILNMVEELVKLNPILLISENFSHTYELLKENVRESKSIENKKIKLNCISVKLDDDTKLPCYGTVLSVLMKDNLENIINKNPQSLLEISFKISINVLLDLIDNFVEIY
DFNNESLLLINRIKICVY

complement(3298..4566) PHAGE_Campyl_PC14_NC_031909: endonuclease II; PP_00007; phage(gi100065) 0.0
MKYVFIGGGVANIYTICYGIMNNIINMKHDEVIVIEKGKHINDRIPTIDIVNGLLGGGAFSDNKNVFSLHDDQPIFEYINKQQVLEYYDFFKNKLFKMFLPENASIHIT
QPVETGSKFVSGYGDIALKQSECYHVGSTLGLEMCKNMIKWLEDKGVTIYCNSTYIPSKLDKCIIVRDTNGIESYITYDKLFIGLGRSGMKDIKETFELNNIKSVADQI

HIGFRFECEYNNTIQELANNIQYDFKFSKNINKNHLKELRTFCVNHGTAEVVTEKVKGYSIPIREQANGHAYGLHVKNKWTGKSNWAILGSFKNVNVEDYLSQIETI
TNGKIYELNQKSSLEFLNCFDNLGDSLSEFVKELCDILDIKEWKGYFPEIKIIGPRVSYNDNFTVQGFSKNIFFVGDSAITRGIIPAAVTGIHALLN

complement(4619..5023) PHAGE_Campyl_CP81_NC_042112: RegA; PP_00008; phage(gi100039) 2.63e-90
MSYSFEQYCNSNNFNEFQRYLITQLGYINNKNVVAIQDSEYIDVFKAIKQEYYKASSCKHSDKEEVIPEHYTKLAIEPIDFIYKNNLNFCEGNIIKYVSRLGSKDDNKS
ELKKIFFYFDYLLHGNYDLTKRTFS

complement(5027..5203) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00009; phage(gi100126) 1.22e-29
MTIKNKINDINEILQSYVGELVLSDIDTQKIVENLTELETIIKDAISKQLNNSKLILG

complement(5259..5825) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00010; phage(gi100037) 4.14e-127
MEKLIYIVIFLCIVFTTTSQSVIFHAKYNFEDIIQERLSYLKQNMINHISKYNNKNATEITNYIFEASLKYNINPVFIMSLIQSESYFKHKVKHKYNNVKGISGINYKMW
KIVLAKHNIKHINSLKNQIEATAIIINYIKQKYKTNDDLEILHYYKGRGYDKYLNKSGLDLAQYSYSMYIKNIKIIYN

complement(5844..6479) PHAGE_Campyl_CP81_NC_042112: DNA polymerase; PP_00011; phage(gi100036) 1.02e-146
MKFNCKNFAKALFYSKDINYLIKLFKYAKQEDKKQAMQILLWARDVNGGNIKNSILLLKYIAEKTNNINDMFLASVVKYGCFKDLNEMYKVASDSNKRKILSFYS
NELKLKNQLAAKWAPRKGPLFYALANSLCLKIGDFRRYITSLYISVEAKMCDNMWDSISLDEIPERAIKKYKKVLEKRLKITIYCRSPKQRRLKFKGCEKLLKQY

complement(6694..8010) PHAGE_Campyl_PC14_NC_031909: 3'phosphatase, 5'polynucleotide kinase; PP_00012; phage(gi100070) 0.0
MNINTLFNDNLCQYASYDNIRSIASLIDGFKNSGRKIVYFSKDLANYKKVSTLKSEIASKSQYLHNEDILPDIITNFARDFDCGPVTLPLFKPLSAIGCRTSPTSAQPRY
SSIKKSDYYDLLFNKDDEEILDHQYFEGQKIEPRFLLPTLPLILLINNNGMGVGFAQNIMQRSAEDVKQAIKDILDNKQPKPLVPYFKGYKGTVELLNTEHGKKQWK
FKGVYEKIDTYNLKITETTPYATNESMLIHFNSLKEKKIIKDYKDYSLGDNFEYVINVSGDFWNNQNIHKLLGIETTDTENFTCADRNNFIKTYKDEIEILKEYIDVKL
EYIQKRKQYKLSKYSDQIELISNKIKFIQAVLDKKVIFERKKKEDIIKQINNIGIVHNIDTLINMPLYSLSEESINNLNEQLSGLQQSFNELSQKHVKNIWLDDINKLFER
L

complement(8045..9670) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00013; phage(gi100071) 0.0
MTNQEKIEYLNTLGFQVISENLTTNLIVKCSKEHVFKREFYDFQKGYTACPTCEIEQKITFLNSLGFEPISENLGKKLEVKCQKGHIFKRTFGSFKNGILSCPECEKKEK
HNFLKELGFEIVSNNLGTNLEVKCDEGHIFKRPYKSFKNGHISCPICETNNKHSFINNLGFEILSNNITNDLEIKCRKGHIFKRTFNSFKNGQQFCPICEAENKNTYLNS
LGFTIISDNLADNLEVKCQQGHVFKRTFGNFSKGHHLCPFCYPNSSTFEQEVRELTGGTNNWEILNGKELDIYLPEYNLAIECNGDFWHSESMNKDKRYHLTKTEK
CAEKNIQLIHIFESSWNKKKDIWISIINNKLGKSERIFARKCVLREVPKIEEKEFLENNHLQGFTGSSVCYGLYFNNELVCLISFGKPRFTDKYDWELIRLCTKMGVNV
VGGASRLLKHFHKHNKGSLISYSDRLYSDGSIYLKLGFTFSHYSKPGYFYFKNNTRYSRQQFMKHLLKDKLEIFDSNKTEYENMVENGYHRVWDCGQGVWVKEIL
S

complement(9680..11530) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00014; phage(gi100131) 0.0
MIENKIVHAENEVEYYLNLPHLITGALTSFNNTVKVLENNKIINKEIVYNQTLTKQIDEAIQNSIDEFTRTGGKYANKISLKIDKDSGIITISDNGRGLPIDTYVMATTK
FRTSSNYTFLEKEKKDRITIGAHGIGSKLIPLFSSEYQLTTITLEGDRGIVKCLNNMSTIEHKEDKAPASSTHGVTIKFKPDFERLELKEINDNLINHIHALLINIAYSNPG
IEFTFQGKLIKVKEFKEFIKYYSDNFSILQSDENLELAIFPTDEYKFVHIVNSLDLNKGGVALDYISNNIVNAFGNRLRKGYSKITNTAVKSRIGVILILKNKKNLRFGG
GQTKEEIKNTITELGIPTLKYIDFAELLFKNTHIKDPIIELYKVQQELENRKQNTFERKEAKERFNPKFTKHTKDPKFMYIAEGDSALSSLIQAVGRDCSSFLPLTGKLQ
NALKCSTAQLLKNQRVMDIVEAMGLGLPETKYENMVIATDADLDGNHIACLITALVYKLQPNLLTEGRVYRLKTPIISVLQNDKLIKWYYTLGEYQKDQDNLPKN
AEVIYMKGLGSWSAANYRIVFAKDGIDNCLEKIEWKDNDEKVLEQWMSDNGIDFRKQILSTKSFNIENL

complement(11630..12832) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00015; phage(gi100132) 0.0
MSIKHVISDSSFGIPKPGFALKNKFICDNYNEQLEDIKIPIDKLDELLDEIKTVLKTSYYEWNGIEGDKSVFIFRLSNIYIEITYKIGKYVKLDMYSNSINFLKGVYNNIL
KKYITGTDELLIKIKSFYEEKGELVYVDSSKTKDNYKNIDYDYYPFLDLNEMFIQFLFANSNILILYGQPGTGKTKLAECYLNFLLNLDYKKYKHLELEEKVFDKSD

DDGNCINVAVVKNESLLAGDAFWNELLSNRYNLVLFDDLDYLLPRSDIQNGIDAQRNQFMSHFLSFTEGINNDITCKTKFIITTNRNINEIDPALLRAGRTFDILNLRT
LTKKEALKIWENNGLPKKSFNKLVNDNILQCNLSNIIEGEKYNIACKNNFKNYLKENDISHMKNINNKKIGLI

complement(12993..13442) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00016; phage(gi100133) 2.81e-94
MNIYAKYLNEFTKSSIKLNEADIDFDDFISEVKEIAGTSGDKLHNPRTSPVFRNYMYSLYINDDGISAEKAWRMFEELNIMDSRKIIQYIEEDDDWYVNRLKDEYNIS
LDDFKQMDEYDQIRTFCEIHNCQYIEGTDNKMYVMLPKYYV

complement(13495..13755) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00017; phage(gi100134) 5.80e-54
MDKQLIKDITINGLSQFAKGHEIEAITETLQIVQEYNIEHHSHNFEFDVEPITSLEDFIKEINILITYEDLNLFHEVLVESLKYYK

13810..14211 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00018; phage(gi100076) 2.46e-86
MTFVEKNMVKELKKTISSKKPLVLCFMSKLLQKEIQKLLKGNKLITIIKIILYAFDKTPVEVKRGVLGYVENEKNIPFQYKYDNTTKTLTFSLDKKSYNFNLCTANEY
IKVLANETNWMILKKNLNNALKNIK

complement(14229..14747) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00019; phage(gi100077) 2.15e-119
MAITNYTEFEKLCPKNGEIADQDVLGKPSLQLKRELDTVMSQVNSIIGITDPSNWDTGTTYTQNQIVKYNNYIYVSLSDGNRGNQPDTSPSKWKKISGGSISSSVNIIV
SSSDYNTPVTEVSDNSLSLKPSKVYVVNGNLIPTTNYTHDGTLTKITFINGMSVYKNDVVTVEY

complement(14780..15421) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00020; phage(gi100078) 2.53e-156
MGILNTAVGAISDFFGGNKTQSAITELAQKIQKAYSTNFDLESLYSIDTFALKNEVPGAGRINILDLPNMDILIQRVSIDPISFAEINEWIGSSWVYTQGRHELQQLTITF
RDSDGGFLYSAFKKLAGHLKDQYPDDQMWIIKIRKRTLRESRNYINQSVQNNEFKNGGHVIIDTQCAMIRSHGGLSLDQNSNGLATFDVTFLFDPFPPQISY

15467..16120 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00021; phage(gi100027) 1.41e-152
MELEIWKGKHSILLNKLYNDNNYIYDSDIIDVLVYKCLNQPKYITNDEARFLFFKKYFAEVCSKIDSSFKCPYCNEMNDIKFTNDDISITEYSLKPIEINVDNVIVTMY
FKKELSQDDSLSLITETKNMIDHEKRLLELYYMIDYISINGEELRGNHIIFEKYINELPLSCFNKIFDYFINSIPKHSIIKNCSCKNCNSEINVELKELPESVRRNLF

16117..16779 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00022; phage(gi100026) 2.40e-156
LTKDIIINNRHYCLNVWKIKDEIGILHQFIDWIELPLEDQVNKIADILIPQTKDLDYISRLYIMIILSSYANGDYSDILLTCPHCGNPIDTRINIRENLEFIPPKTVEVEINNK
KYTISKQNIELCNELPLKDYNSILNQLNDDGDLKLCAKVKCIMCNNDVLAIRELKDLFENYVIMLDLEWYYSTLKYFISQLGFSKTDFDNLYPFEIELLTNENKDE

16772..19570 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00023; phage(gi100081) 0.0
MSDIIKIDGQMVSLDVDSLKDASIETIIKILSYTEDTFKPLLDYMSNNGIPYYMILYGRFNNESLYKQMGINILKTLGAVAMLFPPVRLIGSGSRVITVVPKLVFSKGGL
VNVTLISAGAALKTEENNELYTLETMLKNAIVFIFEDIMVSTFKMAKDGIIKLSLGIAEKIKKDGSVLVNGLPIYLYTDLDNMDPTLLSKNSETYDKLRPDLLIIFEYIT
TQAKTNKFVDNYYFESLSLMKEKDPKLYSMVKNSIFGKQHVRQGFIRLVHNAMYYFSNSYEVTYDDFNDNIDDVLPSNILNDFKKMILDNSLEPLKDKKGKQKTS
LFGDKLYKVVYDKSASQSYNIGDVQDLNRLTKAQFFNVNKKLQNQTVLSQFDIEPQKTEKNTANVSTPSTIVGRVNSVLQKHVGRAKLTSEGVAHVKKYGITTTK
SSLTLEGFDPSKYYFSYSGTEPFNTGIGKLDSNLLYNLNLMAYDYFNIYKKQFIVTSGYRSMESQQKLYNNFINGKGSPANRPGYSLHEYGMAVDINSADAIKLDSS
GMLSKYDFWRPIPNKEPWHVQPKNITDKNGDGMLEADIVETKKKQANTLQKTKPINTTSINTNVKKQLFTNTVVSTSGKYYSIDIGKSVYVSNIKQEKPIKANTRD
VKPTTNKAITDTKTIEPTANKEVITDINTKTINHSNISRKYAPEDTIEINKEVKRLGDEFAPKNNKGASIPGDIRYKDTGNGVSIPGDIGYKDTGNGVSIPGDIGYKDTG
NGVSIPGDIRYKDTGNGVSIPGDIGYKDTGNGVSIPGDIGYKDTGNGVSIPGDIGYEEKKIATSYDVKTQKAKNITYKKGKDDNTYYTSDGNFITKKTRIYDDGTKE
DYYLTNTGLELTENMLQNDTDEQFTEMSGLSKDQFQKGINLINNKQSSTNGDGDKPSVDAVKSVEITKKLGL

19572..20528 PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00024; phage(gi100141) 0.0
MAEVINIPGLDNEKYLVKITAYDIDNLGIGKEVMDSWDDLIKKVDESGSTDINSEGEYSSIDQLSETSSNILKRTVELMIDRDSAIISTDAAGTFYFPLPNSLSDQYVQS

YEVQSMNLLGSAISKASSYAGQTSIKNISEQALKRSGIQLDPNILSIYRSSNPRNIDMSWNIIPKSRKQYDAYVAQISKLKNWTKAKRNPITLGSVGNIIPMNFLIMKYI
FCIEIISLQNDKTPLVSNLLSASRDVTEGFFISLINTNIGSRQLMLRHDGNPTEFSLSIQFIERKPLWRDDWEKKINSLYNDQGKSETSLKEDDIYKE

20544..20897 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00025; phage(gi100083) 5.63e-80
MNDTQTIQIFDLIGDSQARDYIAIKAYKIGSDVSGIKDSINDILDDDPSKAFDNLLNMAENNISNIINPSNWEAGPRLKPGVPCKYIWILPIPSSLAEAFSHEFNQDEIDPI
GDMIG

20905..21666 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00026; phage(gi100084) 0.0
MASIRSFANFFKKGPKKVHNTEVPPHTIKPNKPKPNKMSTVKGKIKKGGAIVGMATGAALPFGYNLLKRNNIRTDPHIINTYNGTPNRVFNFETILLPNNAKHAEDI
VKALLQLKSIMTGTQLGTDKTGLLISQDYVFTIEFGSKDPAKGEQLKKVLNELLQLNHEENGETELNLRMCNINYMGQASALYGNGLPRDLSIALQFEEKRPLRMT
SDIVETTDTSNPNGNEKISEPNIGLTEEELNYKYSQDENS

21688..22149 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00027; phage(gi100085) 8.83e-107
MKNSVLNNKIMVDFNGFSLSPTYSVNIPKLREFMKNNLSMFYVKEMNDNVRFEVLALREYNDSSLWDILMILNFGENGILNFAKGDTWVSDNAENQYKEQQEYFS
PNFKPEDLYNQILSKIQKKNESRRKVIFIKRQFIPQFKESIKDMLNVF

22139..23275 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00028; phage(gi100019) 0.0
MFSDFKIMPEAYYAILLYSNNKKSELPLDPANISDFTIIWDYNDLCVEGYVIFNDTQKITELLPPHNGICFKVSLKDHFNIKFERVFKVTKIDRDFEGQSVATIKFELVD
EYYNMFANTFISKGYNNVKSTDVIKDIFNTKSDLISTPLNVIIKDTPKNTYENYVIQGNKNLLYLLNNMQKFDDLLIINTRKGIVVIPTDNIGKLSPDLSKVVKFSPTQT
QEYSPYSVKDFTLIQGDMLTQNAILPPSITYQVDSKKITKEEHNTKISHSKSGLKTSLTINDKDGIQGIKIFPYLHNIVDSIYNTEILESSAININVAGMFNHNLMCKVSF
DANSSIETLKSKMPYVTGEYFITKIVDHISSGNVFTQTITLGRIGSV

23272..24054 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00029; phage(gi100087) 0.0
MRVNEKNFKILTQTLPFYKGVIEDDKDPLESQRYRVRIIGIDDETIPTETLPWATSLDFSLFSGMGFTSFIKKGAYVLVHLFQNDRNQPIIIGVLKGVNNQNEELQSFK
DPTGQYPLNDYKNQPDTNNKSKGEKYLKNQVFETESGHYMEFDDSNGDERIHIFHRTGTEILVDKEGTVTINVVKDRNLNVKENQTSVIDKNDTTHIKENKNLTVD
KDNTTNIKGNNTINIDKDCNITIKGECNITVTGNANIKASNINLN

complement(24041..24382) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00030; phage(gi100147) 1.37e-68
MFLEDNNKQLSKVLNDNIVIKEDEKNIYIKFKKNIIIESDNNVIFLAKDYIVNSAKEIHLNPDVKISVDDNVDDIIKKIDDKKNEINISVEKLTHNHKHCKIKCFFKKLF
NLN

complement(24366..24653) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00031; phage(gi100089) 7.88e-64
MPPVTRLGDIALGHSCYPPSPTIEASSNVFANSIAVHRLGDKIQSHACPDTPPHGRNSSSGSTSVFTNSKATCGIGDAVNCGGIIAQGSNNVFRG

complement(24641..26260) PHAGE_Campyl_PC14_NC_031909: DNA ligase; PP_00032; phage(gi100090) 0.0
MDKIKFLNNLGYKVVSEDLVRNLYVKCKNNHIFKREFGDFKKGYIKCSKCEEEQKLEFIKGLGYEVVTMDKKGKLLLKCKSNHIIEKSFGNLKKGSILCSECIKEEK
IKFIKSCGYEPASENLAHDLFIKCKNGHIFKREYNDLKKGYVNCPKCNEEDKIKLITSFGYTIINQYDSEELELMCKNGHISKRIFNNFKKFPLCSECVEDKRTSFIKEL
GYKVVGKNLFECKNGHTFSREVKSFRKGCVYCPICSPSISSFEKEMSELLGNYISNDYSVLGDKELDFYVPNHKLAIECNGDYWHSEQMGKDKNYHLDKTNKCLE
KGIQLLHIFEHSWYSKKNIWTSIINNKLGKSKKIMARKCTLKEVTKTEEKEFLDTNHLQGFTGSTVCYGLYYQDKLVCLMSFGKSRFTGRYDWELIRLCTKKNINVI

GGASKLLKHFEKENEGSLISYSDRLYSDGSIYKQLGFEFSHFSKPGYFYYKNGTKYSRQQFMKHKLKDKLEKFDPNLTESENMVENGYHKVWDCGQGVWIKNRK
GILCHQ

complement(26272..26718) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00033; phage(gi100014) 3.42e-97
MEKNYNTFLRKKSVTIKLNDDLKDKLKDTIENINDYDIIKIKLGRTFFNQKRYYKIYARKKFGFYKTLLSENDDSYFFMENTSKIIRRVFNEYDVNCYNLYPNKKYR
YGLSIFILICCSIILIALSLGVGALSYIFKGYFLAFGFSLF

complement(26778..27350) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00034; phage(gi100092) 3.19e-138
MGLESGELRNEAQGGYNPPFELSIYKHQVKFTPPNNFESYIKWELLGDIPLHLTINEQTGLITGNIELLSKQPSAKNAIYEYQLMKIDGSNWRHLGILKNGQTFTFNFQ
VKLTYTVQANSGGSRLSNTVTEVSDVTITILQDNDIISTLFCKNYIDEAKFPLKIGDKVYTDAVEFMKNHPNKNNFKINLV

complement(27367..27894) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00035; phage(gi100012) 1.65e-129
MPLYTVDKLANALKGGAKSDKYFIEIGTPLGAPEVAFTEEDIILCKTASFPERTLGEVEAFVQGRKLKLPGDSTFDAAWSPVFYQTPDHNIRAKFLTWIDKIDVYKN
NYHTCDPYSLMVTAKVHQVNCNGEPVATYEFFNVWPSKVGEIEVAADKTNSIQEFTVDFTYSHWEKIA

complement(27923..28501) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00036; phage(gi100094) 1.96e-139
MSLYNIDRLRSSLKQGGAINSKYKIDIKIPTLLRSLPFFKTVNISGEYLSIMANRTSIPGKSMSTVKVYHRGQPFVIRGAAQFNNTHKITFYNTPDMDIHQLFSDWIYRI
DSFDSTITQSIFLGNYVGFNSVGAGYMSDIIVSQLSSDGRTETEFKLCYTFPIDIAEVELSASGKEISSTEVTFAYTYWERI

complement(28503..29063) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00037; phage(gi100010) 6.08e-137
MVESINPPKGYFKIELLDKDRNVIDTFEKHNLVVNGSRPVLASHMAGRSTTPVNKLVLGTRGHIGNNLMMPKTANEGFTAARTQLFAEEEGEFCYHVNFTPPQSDG
QAVVTEDDVGAGSTVEVTNSNNTITYRIELSTTAGNGTLGAVGYTEAGLYAGNDLFCMRTFAVRSKDVSSILRITWTLIF

complement(29047..30603) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00038; phage(gi100155) 0.0
MIDRVDLPNIYNENKLHKDSVEALYEVLDELNPYSLDIYNIFKRPNDSITENIVKIYAESLYYGMQKALTNPVVIQRMKEKIGTTDNYQPFDIKEFYKKLLKDYFVNF
TSFKEKKGLDVAIEYAYNIIFTSGLQPGLDVNGSSGFNLKWGTEDNPNEPFFIRIEGLLDPILYEGSVKSIAHPVGFGYNYVISLVLEFIEYIDDLINFNVKTLEIVSTNY
RKEFDKDKVEDIYTSKNIQNQERIVITFNDGKQLIKDFNGSITYNEKDGSVIENWNNTYILKLDYDISLKFRLKDEFDNSENNLIVYDCVWNRLNSFDTPIIGEAIVNK
FRVADKYYSSLVIGKIDDNTIYTLPDDPIKYTPDKMPLFLTNAINRGLFEHIHDDIDLYSTNNFTDNVINEKGISNTVGNKIIVGSFKVGSQSENPEGGVILDDSFSIERE
MIPTEYSETVTKNLKTNFYTTILDNFDEKVVNDDIKITVGSFKVGNINIGAEYIDNGVILDDAFDINILKIRKNNGRIN

complement(30600..32693) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00039; phage(gi100097) 0.0
MADNILIPYNYDDIKDEVIKLLKNKGYNADVKSSNANLLADILSYLAYSINVNTSFQAGEMLLSTAQYRKNILMGARQLGYEASRKVSYVYSLEIKPLKDDTKDDD
NEDKRIYSIPKYTMFNSGSNTYYYMGSDIEVELSNKDITTGKASTIKIDVKEGILHKWDKNKDTQVFTIKAIEQNRSIKSSNKISLYQDNIEENGLEVFVTYIDIETGDS
KVDEYWEKSDQFMIDADSDTNKKYFVLNNIDYSGVDIYFSISGIGTNLLPGSTVKVTYLESKGSSGKCGDNFAFSQNTYPFNLMEIDKFETKIVGTDEETNSSIKENA
PIFHNSANRAVTVRDYIAICNRYTNIYQTQVWGGDEEQVVQLGHIWFSFIPEYRNQDFSLDETTQTYSLVNKNDSYYLKQSELRSNTLDKNGYLVNKGIFDELDSY
KIMTMELHNRYPIYMDFDYEIRIIKQNIVVSKNETQDKLFNILKDYFKSDIESFESSYFHSSVIKRLGTELYDLSGIQVDVSMNIPLYLRNKEPNKDILYIYLAIPFEQIIT
KTQDDQNELHVNLLPQISSDDFGGKLEVDFKNPIKGFTVIGSSNAIIGTFDVGNGQSAVFNGKNVVTSDGLIIKNTNISFNIFANGTIIGTYKIIYDNRRRFIVIEITDSIV
LSSLDNITPKYIRVKYSDDNLSFYKNTIARLSSVKFVSESDVI

complement(32693..33040) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00040; phage(gi100007) 2.88e-75
VIQYKDINPKNIEKDIINVDTFYVSLKNIVSTTIGDIAGFPEFSNNAQLLFDQYSSVALDAYKTSLKTSIQKFDYRIIVDNINISKGDADNSVYIEIKYRVRDTTISDTASI
KVG

complement(33072..33782) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00041; phage(gi100158) 2.86e-165
MLLNSKTIALVNSLQLINESIIFSSKLTGIKDSAGSIIAFIDLEKLENKPFPKDFGILKIKEFMDLLKIIGEDANITMDDKNIIHISKDGMSCKYLTTNVEALSNACGVKPTI

LENVNNAELVSSFELDMTVSDKIKKAATLLGFDDMVLNIDDIITVSTSEQGINGNEFSLNVTPNVINSKANIFISIKNLKRIPTTDYIVSVHKHSSRQDTYLLKLIPKNN
DALIILIPSKVVK

complement(33831..34814) PHAGE_Campyl_CP81_NC_042112: DNA topoisomerase II large subunit; PP_00042; phage(gi100005) 0.0
MLQNFVGNSSIPSVLMAAPYGIIDSTPNNKWMEDLKKDGKFTPNIQKIEKQFFELQKTISSVASIYTIPAEKGLQDLAYVANLGMIFPHLNPNEDRRVLVSNFKSEPR
KGETKVGYEYFKKLGFDPIIMPDVNEKGEPMYFEGEADLKWLYGNVYVGADGNRTNGAALDWIAKTFNCEIIKFPSIDEYLYHLDCNVFPLGPDTEACLVNTYNL
DKDIIKELEKHVEVIPLGVDSHDDPDQYDFALAGTTNSVLLPGGIVITPSDISELNKKSDKDLYEMEKDKIEFMDEICSELGLQLVVQNISGYYVSGASLSCNVMHLN
QRSYLN

complement(34894..36135) PHAGE_Campyl_CP81_NC_042112: DNA topoisomerase medium subunit; PP_00043; phage(gi100004) 0.0
MISGLILKNLINDEIYFDKVYSILKPEHFIGVDSDIYKTIQKLVKEYNKKPTPKEVALKLKDNFKDEQQENCINRFKEIMLDKQNVSPEFLNNETAEFIKQAEMRSCIIQ
GAKLIQEKKDIGKIYERLGQAISFTMDTDIGMKDIDAQERDILRRETKIGISTGVEILDEVLAGGYMPSTLNFICSVTHGGKSMFLSHFCANAMLKGYNCLYITLEMP
SIKIWDRIESNIFNIDISELRNYNVSEGYEKLPNLGRCVVKEYGAGSFDVLQLKSLVQKVESSLEINLNCIIIDYLALMASYALQPSVGLYSYYKKIAEELHAYAKESK
KCVLSAAQLNRNAYNNSNADTSTIAESLGIAQTADTIAMLHRSPELDELGQAIISFTKNRNSGNLSQKYIGINFKQSRFFDIDQPD

complement(36135..36821) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00044; phage(gi100003) 1.44e-155
MIVCNYNVVPVIISLYRNDFNMQEVKICGYNQLNEYIKDDSNKFEIIGFNTDSINLPKNIVNLEINFENIPKYLQNPLKSYYEWDKNNQRDFLFGYYLDLYFKKNKLP
ALVDLLKNNTEENNIYNIVKNNFISLEYSLQQNIIKEKIINDTYIMKGNYNSFVYKMVKSQCKTYILDDDLGKLTIFSDDLKIIYDRISHLKIDIIKTENCIILNDIDNKQ
QIVKLMLGL

complement(36994..41088) PHAGE_Campyl_PC14_NC_031909: base plate hub; PP_00045; phage(gi100103) 0.0
MIEPKREPTQDFFVCLLKEPRWISTDDLYPILLIPGVNYPAEIAMMHPDFFGGDDIVFKPEPPIDPDGPDLSNYYTKPETNSLLDKKADKVHTHVVADITDLNLNKFA
TKEETYTKQEVDNKIDEIVPPEIDLTDYAKKDTANIFTKANTFTEAPSVEVDATLDNHVIRKKQFDNSIKEVKDLLSNVFSYKGSKPTYTEIEAIVDKKIGDVWYAED
TGYMYIWNGKTWYDLGKSFDASKFVDITSDQVAINGIKKFTGKLKALTPVDSDDVAILSWTTKQINDKVKSVIGDLNSLNNEVSKDNLVNAINSVDDKFKTTAKT
NKSNTFTGDQTYVDHILLESVPSERNHAVNLGYILDNPGGIKLPDHTALTQNSVTEITFGYANPVVYSAQQLKNVFLKDIVGNEYKAIMADKTSFTENPSKEMVILS
RTDYTKNTDVKFDITKTVDELKQYELKEGEVRVILSYDTISVYSSGYGYGAMFARNANKKDGDLIYDYYTGSQNDITNNRKISIKIDKLGINIPDIVSISMTTNGSEK
LTVKTDTLDPVENTYESADMTYIHTPVSKIAGDVLYSNISQAIKSIHVLENNICSLKPANMELQLVRLKEFKQTINNILQSMFDESPVALKNGDYINVSFSGSASYGTG
YCGYVNIKDTIRNITYKAYKVSLNAFDTTSGTKVIAVLTSDNSKTNVTYSDSVSTLESYEVAENEILLEISFSTAKQYSAKYGYGAMLEYWGSVSDLCYDYYMGSN
LDMDCPFKITLLKIGSSVKADTIQIGAPTFAGSLVMHLRKNINDVINFLVSTGVNVTGRDGAESGSVYNLVEKSLKPLKVLTSEAHQSINGITTFNNKVYMNIDNEKI
TDSKQLIHKEYLDKNIADNVAYNISNTPLVPYNDVSSLNTKNIGVRISATTDSSNYSSGDTVVVSNFKIKLKGDNEYLKPYGVEVIDRENNKIGLNLIGDDTVYNDN
DALLSTRPSDFNSSSVDLSSGSNALATVKTNGAYDYSGVYDIPNPFREYNKKYSLFLSNDGLKNPYYQVDISSSKQVDNISFQLFGTSATNPFLYSKDCKIELFIENTI
VKTFNIKGSSGNNSPVNINIDYKDGMFLVSVLDSINYINNRINKNAELLTGSGKPNFSLNPNKIGSLYSDTTNKAVYMCIDNTSGANKWVNIVTGDEIKPNLRKIEITC
NVRLRSGQYGGCMSGVKIGFDNGYASTKQIVKGLNSGQILLSLDGLGNLSGYSEVSSLTPSGQDIKVDVDTTGIYNDPSYHCVTNIFKEYLGNADQCSLWSDASVK
QLKITLLSENIPTKILYVGNGYYGQTSVSDVKAVWYYVNDSGDKIEGSIDNDLEISNNDSETNDSSYIYAFNIN

complement(41139..42164) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00046; phage(gi100164) 0.0
MVLIDFMHLAFKSLYVAVGKDMYSKQKLSFEKYHGMFVHLIFNYLKLIQTEYARDYGNEIILALEGSNSWRKSYYPEYKTNRKLSDVFDWENEVFPAVNEIIDVIK
KSLPYKVLRVKGAEGDDIIAVLANHTAKPVLVVSEDKDFMQLLINKHITLFKPIKKEFFRNIEESEITKTLTMHILLGDKADNIPSIMEGTTFTPDFIKFLETNGIFETDV

NNFNKLEISKTLYDLYSKQSEKSPFKPAYFGEVGAKKFLENLNENLEKNKLVYDNFIRNKTLIDFREIPDNIKESIIEQYNLEKPTIDLNNLLKFFLKYNCKKHSDSIAS
FNSNMGTSLFDDWM

complement(42151..42285) PHAGE_Campyl_PC14_NC_031909: baseplate hub assembly protein; PP_00047; phage(gi100106) 2.63e-21
MKRDGSIIKSFKREINLQTRFIKNKTKYTRKEKHKKGAIINGFN

complement(42282..42668) PHAGE_Campyl_PC14_NC_031909: baseplate hub subunit; PP_00048; phage(gi100107) 1.17e-91
MDITHSQYEVMVSAYKKDFIPNKNEMNLLNSFMLCRWMSNDIHSVEFANFINNHTDIPINVQYWFARSIMNKVTYMGRPPKEDKLNEYEEAVSKYYNVSFDVAK
QYCSILPKEKQEEVLNMFKGGRIK

complement(42720..43637) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00049; phage(gi100167) 0.0
MNEFDILTGFSGADLMQKMPQNVGQKSYIDNRFWKLSKNKEGSGAAVIRLVTDKHKTPFVHIYHYNSKKNVGGKDRWLIANSPSTIGLPCPIQEEYFEVLNSGDEK
LARSLYGRKVKYYTNILVVKDPANPENEGKVFLFEFGSKLKEKFLAWMNPDETQRSLGHTEKELYNPINGYNIELTIKKDPQSGFFNYDNTSLAPSPSKLGGLEKNE
DIIDIILNKTYDLSEFTKPEYFPSYEELKEKLERFKNPFGTKTSSVPSVVGKTNDNPPFETQESKPQSQQQVVQQQKPKQENSQDDDWLNNL

complement(43749..45983) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00050; phage(gi100168) 0.0
MTVNNKIEFLNNLGYETISDSLGHDLEVQCKNGHIFKRSFSRFKSGSTACPECERQENIKYLNKLGYEVISENLSNDLTVKCKNGHAFKRTLNNFKKGQLTCNECER
QRKLLFINSLGYKVVSKELNNDLTVECQNGHIFKRPYKAFKSGITICTICEKQEKLEYLNNLGYEVISDNLGNDLEVRCKSGHVFKRAFGDFKKGYTNCPGCIISEKT
KFLEDLGYKITSYTLGDNLEVECKNGHVFKRTYGNFKKGMTDCPKCTKEHKIKFITNLEYEIVSDNLGHDLEVKCKNGHIFKRPFGNFKMGNIDCPECIIHTKIKFLN
NLGYEVVSENLADYLEVKCSKGHIFKRTFRTFEKGTTDCPVCMEHEKTEVLNNLGYKTISHSNVQCKNGHVFKRSFSLFKQGVITCSECTKEYKTKFLSSLEYKIISE
NLADNLEVQCKNGHVFKRSFDNFKRGVTLCPICYPSTSSFEKEISKLLDNHVSNDYSILGDKELDFYLPDHNLAIECNGDYWHSESNGKDKNYHLDKTERCKEKGI
NLIHIFESSWIEKKDIWTSIINNKLGKSDKIMARKCVIKEVSKLEEKGFLDKNHLQGFTGSSVCYGLYFNNELVCLMSFGKPRFTGKYDWELIRLCAKMNTNIVGGA
SKLLSYFHKNNSGSLISYSDRLYSDGSIYKQLGFSFSHFSKPGYFYFKNGIKYSRQQFMKHMLKDKLEEFYPDLTESENMRLNGYHKVWDCGQGVWVKLS

complement(46019..46756) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00051; phage(gi100110) 2.32e-176
MPNYFSSSKPGSNQSNIVDSTKPGFVSSYQKKTKETQSISEEAKNINTGKKLIKDTVDDALKEKTTKEQEKAALNIVKQLMKKGTRNFKAEDFRFSNMIFMQYDAK
FKDEVYDKTPLILVLSTSRSYVLGLNLHWTPVPLRIALIKVLFKMNKAAIQKNKQLKITYKMVKPLLSALHLGPVIRLYIKKRISRRGIIIPQDLWLVAARLRAESFSG
GYSADKLYAKAIQNYKKSKSKNIRKNRKMF

complement(46765..47112) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00052; phage(gi100180) 1.11e-79
MNTVYSKYLCESSHYDQYKETRDIETANVEMKNMDRDLEFLKYRIEQKLEKANIEITEPYIEGECIKFALKNYNNEDNKKVKDILYDMRDISWGPISGDYSDMSQG
YEVSLDLED

complement(47163..47879) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: protector from prophage-induced early lysis; PP_00053; phage(gi100001) 7.34e-174
MVKDIQQLKDDKINYLNKLLPQDENGYFLDISNQKVSYGNNPQLSYINTKLPLKEEHIIEIQKCSTDIIYFVESYVKIRSLDEGLVYPDLRDYQKELIQQYYENRFNVV
LAGRQSGKSVTTLLYILWKLCFCPDTIVGICANKFTMAAENLQRLMDMYADLPIWLKPSVKVYNKESFVNEIGCKAYISATTPDAFRGLSINLIFIDECVAGDTKITV
RNKKTGVIEDITMEELYNRIG

complement(47899..48285) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00054; phage(gi100112) 2.17e-85
MNLISIDYEDKFYRKLLEDELTNFKSYPFKISEDVYWDFRNYGANSIDKPEKEIKLNLSKRKVRFIINRLEYYNENGYWNNVSLIQKHYQEERKLEKLAETHAKTFM
SAVWLCIPIFALLALLKYIFE

complement(48366..49031) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00055; phage(gi100113) 6.89e-156
MKNIEVKLLHHTPLEITIDAIRTCWNSGCKKDSVYENGRFVLGNQDKALLDRIVNHHKHLSTIEHVYYNFFIKGISRACLQELARHRHASLSVESTRYTLKKHLKNE

EGFKYEQDFDRASKYVVLTEDLESNLQILSNLDNLLRLVKQNKSNDVVKYALPEAFRTNLYWTINARSLRNFLELRSSNHALHEIRILANKVYESLPELHKQTLFKN
IIKEYNE

49271..50722 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00056; phage(gi100115) 0.0
MNVTEKLKFLNDLGYEVVSYDLSKNLIVRCKSGHEFKRRFYDFQRGTIICIQCDHNSKLSYLNSLGYSVKSKLINNDLEVICKNGHSFKRAWSEFKNGNIRCAMCYE
QHKIDFLNKLGYTILDINKIKVKCKHGHVFDRVWSHFNSGVVECKQCKNNIKIEYMKLAELEPISENIADSLELKCKNGHVFKRTFSNLKKCNVCPICYSNISSFEKEI
KEILPKCIENDYSILGDKELDFYLPGHNLAIECNGDYWHSEQMGKDKSYHLNKTEKCKEKGIQLLQIFESSWIEKKDIWKSIINNKLGKSKKIMARKCILKEVPKTEE
KEFLDENHLQGFTGSIVCYGLYFNDELVCLMSFGKPRFTDKYDWELIRLCTKKNTNIIGGASKLLSYFHKNNKGSIISYSDRLYSDGSIYKQLGFEFSHYSAPGYFYC
KNKIKYPRQQFMKHKLKDKLEKFDLNLTEYKNMLLNGYNRVWDCGQGVWVK

50738..52561 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00057; phage(gi100116) 0.0
MTLDEKIEFIKSVGFDIIAHKSNSITLQCNYGHVFNKKVSNIIPNTNIICDKCVVMSKEKTLRELGFTPLLINGDKCTVKCDKCNHIFNRTWYAFNTRKNTKCPECVEA
ERWNNINSHLNNMKVSYISDIQGNYTLQCKNGHIFKQSIAEIIKEVGCYQCEVEYRKEYIRNLNFTIIEYNSKIFNVKCNKCNHIFTRDWNGFYNRKHTICSNCIEIGK
KNLAKKHGFTLTDTKFGNDIREFICNKCNTTFKRGWSNFTSRGNKECYNCKQLSRINLAKSYGLDIINKNITSKYTFKCNKGHVFERPFTVVENKNQTKCPICYPRTS
NFEIEVKNLLTELCIKYIQNDRNILDGLELDFYLPDYNLAIECNGDYWHSDSVISDKKYHLNKTLKCNSQGIQLLHIFESNWIKNRNIWESIIKNKLGLSFKIYARKCEI
KEVNKIEEKEFLNKNHLQGFTGSAVCYGLYYQNELVELMSFGRSRFNKNISWELIRLCTKINVNVIGGASRLLKIFENNYPNQTLLSYSNNLYSNGKIYNTLGFEFSH
TSSPGYFYYKNGMTYDRQQFMKHKLKDKLEKFNPNLTEAENMSINGYNRVWDCGQGVWVKGSI

complement(52576..54486) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00058; phage(gi100117) 0.0
MALLSPGVEVKEIDLSLTVSSASSSFGAFCGIFPKGPCDGAVFINDIPTLESVFGKPTNSNYNDFFQAYCFLRRAGSLYVVRAIDKLGKSTRKDSGLTINAVLSEKATE
ITLADTTGLYVGQQIMFGEKTDANVYTIASIQANTKITFTPEIQTGDGTGNSSKIYICYPSMNATGEVLKTGSSNTITDAKLKETLKIIPNNDVYETLEPSIKFSDTETKL
KFIAKSAGFWGNNIKVAVATKADFGANKNIIKGIPLDDNFEYVPDTDQVAVIILENNEIKETYMVSIKEGAKDYNNKSNYIEDVINRKSSYVYCKNNTTITDLPKSAL
DSEAITLKFGEDGAPTKADIISGYTDNFSSKEEIDIDIVIANEMANKECADFCVTRGDVIGYGGVPFGEVVGLKAEDCVKNLLEYRSTGEMNIDNKYFSFIGNYGYIY
DKYNDKYRWINLAGATAGLRAYTNQARQPWFAAAGLNQGQYLDIIKLAFNPNNGQRDLLYKSAINPVVSFPSLGICLWGQKTCTQKPSAFDRVNVRMLFNYLER
NIANSARYVVFEQNDTHTQNMFVSMCTPLLTQVQAGRGIDAFKIVCDDSNNTPLVKSNNQFVASFLIKPTYAIEFITLNFVAVGATISFEEAIGSI

complement(54648..54995) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00059; phage(gi100007) 7.37e-74
METKLLNILLNIGEKYGIYFKQNPIEDEYNVEILLWTKESPESWDKIIKDIKTELLVNFTRNIKISSWGKNSVNIKMKLDRLYQVNILYNLEEPKLNITISYPKIINESAY
DNFL

complement(54985..55938) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00060; phage(gi100119) 0.0
MNTSTLYNDKGKVVLQWVKNVPKSIPSEEVIESIKLASKKFKKYPFKNVSKLKSLNTNSLTLYNISDMHFGMLALKEETNDSDWNLDIALKTLDQLSTELINGADK
TEECIICNLGDLIDINDFTHKTPRSGNVLDVDKKFPQILSVAYNSIINMIYKALGKHKYVYYYINIPGNHDILPSMAVQYIIKEHFAGNKRVICDESLMNIKYHSFGNVL
MAFTHGDNIKMKDVGQIIAFDNKENFVHSKHVYAYFGHYHVDKVIDTPLCRCESFRNLAPLNKWASNSGFRRGIGTISSITIHKSYGEISRRTYNMDMVNGN

complement(55960..57282) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00061; phage(gi100171) 0.0
MLVNIINNLKNENTDAGKIAIIKNNKDNQNFIKLLDIVYNPKTRLGITDFELPSETGNDILDNIISSLDYLQNGIYRGNDAETFIIKLAKQLDYENQLLLQKVIRKNLQA
DLGIKTINSAIPNFVKKPPYMRCALLNEKTSSKIKYPAYIQEKLDGQFCNVIVTKNSIQFVSRAGTEYKFKRDFSKLQQLIYYTLGECVIMGELLCTENGNILPREIGN
GIINKSSETNQTITEEESNKVILKAWDCIPYSDYLERKCNIPYETRFNNIRKITETPNGFIYPVVYNIVNNMEEIMEHYKNLVSQDQEGVIVKNRFATWGDKTSNDQLK

LKIKFQVDLRIKGYQCGKSGTSFEDTLGALICESDEGSLEVCVGTGFKESDRDFFWNNNMIGKIVTVEAHRAMEKNGKYSLILPVFIELRQDKDEADGIEKILEQEKS
AKYK

complement(57328..57456) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00062; phage(gi100010) 9.38e-21
MTTSGDIATTPSRLTLKRGKIKPKVIKYKQTKTLTLKKLSKN

complement(57453..57752) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00063; phage(gi100122) 8.28e-63
MYTKYLYESSLDLQFEVTDQDFDESFLNFNKELPVSLSETLKLKYNIKLSLKFQSKYDDIGILVKLNDNGKYVVYSNSIENIDKFIIFVDTLNQNKGNL

complement(57742..58242) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00064; phage(gi100012) 3.95e-117
MANKSKSKGNTFERTVAKMLSDNYADVFNVAQSFQRNISSGSMFGGSNSYRGMNVLDEHTFYAGDIICPSEFKYTVECKHYATAPSFNSLIIQECAQWDKWILQV
EADCEISNKLPMLVVKYDNIKPFVFIKHNFEGFIFKYRDYYAYNFEMFIKEYKKELINNVY

complement(58259..58636) PHAGE_Campyl_PC14_NC_031909: cytosine-specific methyltransferase; PP_00065; phage(gi100124) 1.45e-84
MKVQFINSKELSANVVSTKNLHKLNRKILVPGVVDISGTIYLASPSKELPTIRVEMDAVFKCGECSSFKIKHYVVNKKVYGSNSEIYDGISKFLRKYAKLILVSKDEI
MFFNYTYTGFAKYFKNK

complement(58753..59532) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00066; phage(gi100125) 2.16e-175
MKKSTTLNEAIKRKAKNMNKGKSITLNEAAKKGYFKYIKRKISINESEINGLKDALENMEEFSDENIMGSVVGKDYVISIFEKVCIILVNGTTPFLIEREDITEDEQTLI
DDIFETLNLELDDDLDNVDDNQGDDGLDDLDDDLEDDDLDDNSMNESRKIDKKIGLYFYNSKPIKDGNTVVSVDDKGNTEVKLHGNLIAVKNKNGDEKYSLAGY
NSQTTRARLNGLGFNVVQRKGKLFVDNNEINADDWYDIFGNKVSW

complement(59543..60124) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00067; phage(gi100126) 2.28e-137
MVTYEEIQQLIRNCLDVGIKAPASAYSKLLRHGYCVMYGGDAKFNKLEELEDNFDVKQFDRDTWVIKEYKKELTPEEWKDVNSQALYNGGTPDQIAKDIEDGEK
NPILENAFNKLDEAKLKQISKDDLKNIWNENDLETKREKTLKLISELKYKSPSLEKIIDIIKTTKDKNKIDQIITNIMFVGTGDKVIKI

60220..61302 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00068; phage(gi100164) 0.0
MDKIEYLKSLGYNLLSVEGSYVKVECKNKHVFRRAFASFKIRNTPCPECEIENRKQFLDSINYSLISVKGRKVEVKCKTCNTIFSKEYCNFKQGKITCNYCETNNKIE
YIQSLGYNIVDFESRGYVKIQCKYNHIFSRAYNSLKNGFISCPYCEHEQRETFFKFINLELITFDKGKITAKCKKNHIFNRTYGSFKRGSILCPICYPKSSSFEKEVKNILP
RNVIINDRTVLDGKELDFYLPEYNLAIECNGDYWHSEQMGKDKNYHLGKSLKCINKGIYLIHIFESKWRSNKQFYINLIKNHINGTIKRYPNKVISDISCENQLIFPKL
GYKLVDNVEPNFEIFQNTLKVYNCGYNIWLK

complement(61323..62705) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00069; phage(gi100128) 0.0
MNEINVVKTYTNGEIALCNLASINLHEYDQLSDTEKYNLVYDIINTMDNTIDLAYYMVKDAQTANKKYRYLGIGVSNLAVLLAKHKIIIDSQESLEFQAKLFDELLY
NCVKASMQLAIEKGRAEGFSETKWAKGLYPYLIGNEKAKKLIQFKPDENKWNKLMEDVKKYGMRNCALTAIAPTACVTKETKIKTENGIKSYKDIMKEQGINFNE
IENYGIPSWIDFKVPFKVQTRHGLKEVNRIWFNGKQPTKTITFEDNTILTLTYNHKLLVKLDSGIEEWIEARDLKKGMEIVSITNNIKIKSISNNTDVLFNTWDIEVPDV
HEYLLENGCISHNTSGRSINASESIEPIQKLLYKEDGNINVKTLAPMFKEYNKYYKLAQECDPMMLIKAAAVRQLFLDQSQSVNMYSYTFNGELNYIQKSSHKLSLL
HMYAHQLGLKTLYYFKSEKDNGVEHECESCS

complement(62743..64629) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00070; phage(gi100129) 0.0
MDKIKYLKSLGYTPVSSNLTNNLEVLCHKCNNTFKRSFYTFKNGSVDCPNCQNIERLNYLKSIGFEAVDLYNVKCLKGHIFKRRFSEFKNGATACPICIDNEKQEFIK
GLGYVIKDIKGDNFTVECQKGHIFNRVYSSFRSKNITFCPECKNNEKTLFLNSVGLKQIKSDGDKMTLQCSKGHTFVRRYCDIKRGSINCPECIIHMKEEYLKSIGFTL
IKTNVVKCSKGHIFNRSYSDFVNGSIACPTCQKENILNFIESNGLQLVSLGKSIKLKCQSDHIFTRAFNTLKVNTTCPICDKEKRKLFIESFGIKLLKDGNRLQLQCSKG
HVFEREYCNFKKCTLCPVCNPSTSSFEKEISELLTNYNKNDRNILDGKELDFYLPEYNLAIECNGDYWHSESNGKDKNYHLNKTNKCLERGIQLLHIFESSWIEKKDI

WKSIINNKLGKSNKIMARKCVLREVPKTEEKEFLDTNHLQGFTGSTVCYGLYCRDELVCLMSFGKPRFTDKYDWELIRLCTKMDHNIIGGASKLLKHFHKNHPGSLISYSDRLYSDGSIYLRLGFTFSHYSKPGYYYFKNGTKYSRQQFMKHKLKDKLEKFDPNLTELENMSINGYHKIWDCGQGVWVKGNLS

complement(64678..65985) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00071; phage(gi100130) 0.0
MDKIEYLKSLGYIPVSSNLAGNLEVQCKNGHKFKRSLGNFQRGTIHCPECEKQEKISFLNSLGYTPISSNLGNNLEVMCKNGHIFKRRYEHFKNGISTCIMCDEQNKSNYLDDIGFSIISDNTADDLEVICKNGHIIKRSYHNFKKGAKICPVCSPSTSSFEKEVSKLLDNYIENDYSVLGDKELDFYIPNYKLAIECNGVYWHSDKFKDKNYHLNKTEKCKEKDIQLLHIFEHSWAEKKDIWKSIINNKLGKSEKIMARKCVIKEVPKIEEKEFLDTNHLQGFTGSSICYGLYYQDKLVCLMSFGKPRFTNKYDWELIRLCTKMGLNVIGGASKLLSYFHKHNKGSLISYSDRLYSDGEIYKQLGFEFSHYSEPGYFYFKNNQVYSRQQFMKHKLKDKLEKFDPNLTESENMNINGYSRIWDCGQGVWVKLSIP

complement(66080..67477) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00072; phage(gi100131) 0.0
MADKYLLDESTKEKFITSNLYPNLNESEKNIMRTVLENQGKEVKMLMESTVTGDIAQFTPILVPVIRRALPTLIGTEIAGVQALKTPTAYLYAMVPHYVGDGNNSVSPTKNAIVLKLKTESANKDDFNYTGTPIEVSFKTATTVKGKIVYSEKQAGTDNIVNVLLRLESNSTGSVTIGDEVDKAATFATKKATIEAVYTNEALWLKVLKNYTGPYATATGEKLGKDMKEMGISVQRVLAEAKTRKVKGTYTIEMLQDLKAQHGINAEKELADILSAEVALEIDRTIIEKANEVATVCTDFDVNSADGRWFIEKARGLSMRISNEAREIGRQTRKGGGNKLIVSPKVATILDEIGSFVLSPAGSKINAIDSGIKPNVGKFDNRYDVIVDNFAEFDYCTVAYKGASNFDAGIFFAPYNITLQQNLTDPVSGQPAMILNNRYDVVGAPLHPEAFIRTFVVNLNNYIIS

complement(67509..68255) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: DNA helicase; PP_00073; phage(gi100021) 5.68e-156
MEELLSKLDKNIFTPEVVDEIKGLFEAAVDNKVEAALKIADIHAIEVDKHYEKQVKMLKESAEMYKQQVNKNNQKVIHNAITKIKKDYNKLVEGIIKGKVDEFVKKGSMNLEMLVESSNKKVVDACIKTADKIHGPVNALKRINESVKKEKNVKKLEEKNKKLQMKLEEAQKNNIYNNIRNTVSIGNRDMFDTLAESVAYTGDISYESNLKSIANKIALKSKTISRKSTGRKQQLSESQNNTTYGNFL

complement(68266..68895) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00074; phage(gi100159) 9.26e-153
MKLIIEEPVKIKGSVELNESKGEKNYYIQGIFATINQQNINGRVYPRPIWESAVNSYQHHITTPTTSSLMEYQHPNRQYVDPLEAVAKIVDLRIEGDYVMGKAKLLDNPKANQLKNLIDEGISIGVSSRGCGELMNGTVTEYELITFDIVPNPSDRNAHTKGLNESFDNGILKDKNYIKDKNGILVEADESNINNKSITSQFVDLFSQL

complement(68892..69059) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00075; phage(gi100158) 1.84e-30
MYNYIKYAERKDMNGLSNVIQKKLQQEYNNHPKVVNHIETIKKNEALIKVLKEYK

complement(69060..70766) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00076; phage(gi100136) 0.0
MANMFNGLVESVKKTFLKIENQEGSIKSDDPHKEANLTRDDIVLGYFDEGNYRYNNFETDTINDVSKQASLIKEYRRIAAYPEVADAIDEITNEMSFVPNNIDCCYLGFKDNILSDNLKEAFQSLFDMSCEILQLNENIDVLCRRFYIDGQLVIGLSYDDNNSILDAVIMNPSGLYFNKSTNKWQYFNNSNNYGVADDTSEVYDPEEIIRIDSGLYSDNLILSHLHSVIKIVNQLQTLEDLMIPLRYSRSVSRRVFNIDVGNLGYEKAIAAVEDIKNKFKYKKYYNTETGSISNGASIQSMVEDYYFPNRGGTKGTQVDVLDETGNLGETGDLDYFKNKLYNALKVPTSRLMGDNKTVFDFSSTSIESTEIKFFAFVNRLRQRFNVLLIEIMKRYAITNNILTEDEFDNYSKYIFIGWEKESNFLERQNLDILKQRLDLYTEFKEYEGDIFSRSYLLKNVLKMTDEEIDQMREEILQEGSQTTPGEDEFGNEITDDEDITDDEDNFNNDIEDESEDNSLDNIENKDLKIKDDISNNKRNIVKKATKLGIPKNIIKRKISKATKLIKGE

70811..71512 PHAGE_Campyl_vB_CjeM_Los1_NC_041896: DNA primase subunit; PP_00077; phage(gi100025) 1.41e-165
MTNIPKQNKFAYTEDKPKYIDINGTTNYILPGFEYPSDVAVKFPQFFGGKDNVFYPDLQVTLTPDSLTFENSKKSQAITYTATDGSSITSAVVTIEPSDLATWNEGDKTFTGNEEGSGKAIFELTDDKGRTAIKELPLTVTKAAVVTTLTLSPDNLTFANASAAMQEVTVTTNASDFMLEFNNQNIQAVKSGNKIQVTPKTGKTGSFTITVKAQASGGNQVSKTLNITVNAGG

71515..72246 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00078; phage(gi100155) 1.72e-177
MATRQSLKDYIFGMLGSPVITVELTDFQIDENINFTIQKFSEFAMYGKLKGTLLIDLPKGVRKIKLDSRISEVITLRIYPSGGGFLGLSIPGGLVITPTEMQAMLFGGTV

QGNFSMQNVYSVLANMSILDTYFTIIPNYAFNPFTNMLEFFEDITSEKVLLEVRYKYIPEEEDGIYEQPWVKEYALNLCKRTWGSNIGKYDAPLIGGIKANYERIIQE
ANTELERLETVLLENYCEPLPLLRG

72276..73604 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00079; phage(gi100139) 0.0
MYEVLTPNGFSSFDDISREKKDVYKVITEDDFIKVTKGHKFETPNGFKQLKYLKINDLIKYKNKFSKIVSIDYIGVEYVYDLINVHKNNEYYTNNFVSHNCAFIDKWS
EFSNSVIPTISASKKSQIIAASTPVGLNHWYKMWSDAVEGKSSYKPFKVEWWKVPGRDENYKELMIKTLEGGIRTWNQEYACEFIGSSDTLVDMTVLSNIKFGNTL
REPNFGETIRVYEAPQENHKYMVLADAAKGAIDGFVFHVIDVTNIPFKQVASGKIPESYLMAPPIFYNILRTYNEAMFVCENNEGAGTSVVDLLFQMYEYENIYQEP
DKKWLGVRTTKSNRSKNLSNMKLFIENNKLILQDEPTVKELLTFCNVNGKYQAQNSKAHDDYVMALSLLFVPLLDLNNIVDYDVFLNKINSDSETTDGDVKYLQ
MGFFDDGTSSFYGIFDD

73633..73854 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00080; phage(gi100153) 8.05e-44
MPPIKHMSVADRIAQKRYRKQPKVKRKLKIRAKKNAKAPSENMSWSSKKRGYVRKDPKLRRTMKLVAKLRRKS

73857..74588 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00081; phage(gi100152) 2.67e-173
MGLNKFDSVDYILSSGQRPFRYKVSLILPTKIAKISGALYDNAVNILCKGATLPAPSILTTPIGLDGRNINIPTLMKLDNTTNMTFFIDEKSSVRRILEYWHFCIDSGITA
NEETPSVPGAGVANIVGSVANIGAGFISDITSDIPIIGNAVNSFLGINKGVSGNTDINMTGELKLTLLNYSGNAVGSYTYKNIFPIDVTGSDMQDDQTETINEFSVTFGY
THYVYKKETESIIDAVTGLVGL

complement(74583..76028) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00082; phage(gi100151) 0.0
MNLLELNQNKINMLKEWGFTPISSNLNYGLEVKCDKCGSNIKRSWNQMLKYNKCLSCDDNKLLLELNNLGYTVTDIRLSKLEIQCRNNHIFNRNKADFKRGVISCP
ECDELEKLEFIKSCGFTKIDVNHMRCNKCNNIVKKSYPTLKSGITFCKFCDENNKKSLLDNINLEMVDKNIFKCNKGHTFYRTYDNLIKSNNLCPECYPNNTMFEKE
LKEILPKCIENDYSVLGDKELDFYLPGYNLAIECNGVYWHSDKFKDKNYHLNKTEKCNGKGIQLLQIFESSWIEKKDIWKSIINNKLGKSEKIMARKCIIKQVPKTEE
KEFLENNHLQGFAGSSICYGLYFNDGLVCLMSFGKPRFTDKCNWELIRLCTKMGLNVVGGASKLLSYFHKNHPGSLISYSDRLYSDGSIYKQLGFKFSHFSKPGYM
YTKNGRTLNRQQFMKHKLKDKLEKFDPNLTESENMSINGYYKIWDCGQGVWVKL

complement(76000..76767) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00083; phage(gi100143) 0.0
MAKSLREWYRTHVKSMADNFEDFEIFRTQFYRNPHRAIVKNSSAFKSPADGVIINQTQVNDIDDEVLKIKGKKYTLRNALGNNEEMLDLIKERGGALVIDVFMTYY
DVHYNRIPTDGFLTYEKLLPTESYNNESMLAVEEGLFANNFKKAVTELGYMFCNERLLNIIYSPVLQEKYAVVQIADEQINCIQTAWVPARGEPNTHLYQQGDIFGN
IRKGSQCTIVIPFSKKWNYIPILEPSFHVEAGIDELVRVEPK

complement(76778..77074) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00084; phage(gi100144) 8.84e-65
MDNFDVNSFKIVHPHDVLLEVAYPSEIKSESGIIVTVHPSLIDDRQTQGKVLQIGSEVKDIEIGDTVVFGKQHGIDLHKNDKVKYMLIRDESLMGILR

complement(77130..77639) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00085; phage(gi100145) 1.27e-115
MAKLILQRNKEYKDIKWQNSDKIEDSTIGELSLLDDNDNVIFKCASCENIGPSTDESGTDKRIVAREYKLKWCNSSKNGLLSKKYPEWKADNGSNIAIWVVSDEVE
GFNNRLIRIHTGNAPQHTEGCILPGSDLNNGTVGSSVDITHKLFTKIKELGIENIVFEIKEID

complement(77642..78139) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00086; phage(gi100146) 5.63e-113
MYYSNVVFPLNEVIPGFTYNVKKSKSNIYIRFVAYGYSVDDLEIVYNNSIITISTIKDYHEVKTDPKFSNNFPQQDKFYIQFWCPKISGINAEYSGNFIKLNCSLGDTSV
NLGVVPIKFINEDNDIDILENTSDDTMNIIQLNGFMDKLEDTKDDFDSEITNNKD

complement(78174..78317) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00087; phage(gi100146) 5.64e-25
MVEIIASFFVGGLIGFIAGYFVYHNNKKKASEIGDKIESVKDEIIKK

complement(78349..80712) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00088; phage(gi100145) 0.0
MKYIFTVIDNTSKTKVLKTDIDNKVNFRNVICPSINSFAQLIESNFILSRPIHSNGLFERKRENMDYLHDCGYIILDLDKVTKGNFQKIIDYFKNTKWECLICNSRSYNF
VDNFNLKVICKIDYKSTDENIRNTLLFFKEQLKGLCSIDESATRHSSYQAPSLKISVFYKNENNIGIPFSILPKSQSKTTLINCSNKQVEWCLNYVKTKLKGNIKEYVG

YYSINLPSEKKSKYSYCLYETNPFVIFHPNPSKNINILQEYLKTKDGKAFLQEKQSKIILSSLKYTPDIHINQKFLKNVDIPDTRVVCIKSPMGSGKSNIINQYIKDKSKIL
FISVRQTLAKDISLKYGCKYYLEDKKILYGENYVCQINSLHKINLDYFDYVVLDEFETLLMYIVTSIEDSPYALNILRKFYNILNSKYLLILDAFLSDHSDILSDVCRIK
NHYKDQTNVSLYTKKNTFFSVLEYVCKNKNKNEVVTMSFSTLSEFKTVESLLIKSNLKVISINSNTNRFIRDNIFTEYFKKKYVNYDCILFSPSITVGVSIMNNISHHF
HFDNSASIDAITSIQMVKRSRLASNIHIFVEGSTNMITPLEVEKNIIDSFEIDDLEYLSEFYNKLCYYYETIELNHKMSFCLLLQDQFNNINTVDSIVNYNIVQADIPKEIE
LNEFENSKIKDELIYAIKKDKNYLNYIRNFKFYTLNKNKNEFLENYLLNNPSNLLELSYRAKFLKYCVTYPDIRLKDIFTYNDIQNIKYTTDYFSFSNFLKELGYKKM
NGNYYLPLQYIKHLSKI

complement(80769..82289) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00089; phage(gi100149) 0.0
LIKIEKINESAYKIVSETQLYLDEIKQLCSAKIPNAQFLPAVRMGYSDGVKYFYKDCGDYLIVPKGFIKGIIKRLNEKYKLELSFDDEIEKITEEEFNKFVKSLKLPFEPY
DFQLKAAFDSINTGNNICVMATGSGKSLTIYILCRWFIEKYKNTDDKILIIVPSVVLLNQMYSDFKEYGFTDIDKYVDRLGGDFKVVSFVKKLNISTWQSLYRNVSLF
KDITVIIEDECHTAASDVHESIIFPSATNAKYRFGFTGTLPQNYCDKLSLMAVLGTAKTYVTPRELIDMGLATEMEIKPIILKYNDATSSIVRTVKNYQQEVSFFLGIPE
RDNIIAKLICKVSQKGNSIVLFTRVSNGENLARKVCKLKHGVDVEISELRKLNKYNIFFVSGETKASDREAIRQIMESCDDAIIFGTTSIMSTGVNIRKLKNLVSTMPG
KSYIKINQSIGRMLRKHETKNNIVYLYDIVDDARGRYAKKNYMFKHYEERLKYYNENQYVIDEVVVNI

complement(82330..82749) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00090; phage(gi100038) 4.38e-96
MTIDDLKSFHKKIIEEYDMDSNWNPSTIKHHLTTLSGTIAKYLNYWSRLKHIIIQIDEEYNEKYMILYSHYRENSNINYTVTEIKDLISKDNELCNIRVKKSTAILIMEYI
EKCVDNLNKTRYDLSNYIEIEKFLNGKG

complement(82751..83479) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00091; phage(gi100151) 2.73e-170
MLKKLCFIVTLASSLFAYNYIDSTVIEDKGNNIVIELSFCTKDLDSEKEYIIDHFNNQIDGLEQQQVKSEVYQYRGKQYVFNKGKNVKYNKPIITFVPTSTNGCYIATA
LYKIKHDDIKTSVNNKYESYFNGFITKNTSTKNEVENEIRQNLENEIKENIIIKPEQIKNSHETFVEVPKYLYAQTKENYYINIICEVTNSDNEFIYNFEIKDYKRPLIVK
GKIWGDLTPYFNTNCKVELVGK

complement(83652..85034) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00092; phage(gi100141) 0.0
MKFVNSLSNLSYTENGALTLSSSLNVALDLFFIIGTTNENNIDNVFEKVKESFNIDKELTSRILLWTRDAREGAGRREIFKRFLDFIAENNKEIYKRIIRKVPELGRFDD
LITYKQLDLVGNELIKILDFNNQLCAKWMPREKSSKSKLAKKLMKLLKLNAKDYRKLLSSNTCVVENKMCSKEWNLIEYEKIPSKAMTKYNDAFERNDKERFGN
YQESLIKGESKVNTSAIYPYEIIKLMFKNDILANEMWKNQKDWMEDSKKTLFPIIDVSGSMYTAVQGSTTALNIAISLGMYLSERNDKDFKDYFITFSANPEMVKIEG
NDLKEKYHSIKISNWGMNTNLAKTFDLILNRAKADNLSQEDLPDALVVLSDMEFDEAQQGKTNFEYIRDSFKNSGYKMPELIFWNIYGRSGNIPVRKDENGTCLIS
GFSPSIVKGLLTNDLNPEKIMFETINKERYDF

complement(85798..86442) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00093; phage(gi100134) 2.20e-149
MILTFDPYYDIKESNEFIKNLKENKINFNTYILSKSPYYWFYEVADKYKPVFLKFNEANSTDLRFMLPKLKELTPSDENYLRRIPKTPSDFERYVSPNIFKKAKYAEYF
CVFRYKNISEINKITETLGIKIYILPKKVKEWNIAFTFNKMIRNFVFGHYILLEKTKKTQFNKVGEIELYLNNKVFVTDKMKFKTRELPFSEDGTYYPLKFQIKQ

complement(86426..87604) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00094; phage(gi100154) 0.0
MNINKNYLIKGDNLEVMNSILPFYKGKVKLIYIDPPYNTGNKNFQYNDNFESIDLIIKYFNVDEEEAKKIRSQDKFIGSKVWLKFMKERLEVAREFLRDDGVIFVQCD
DNEQAYLKVLMDEIFGRENFVNCIVVKMNESKGLKNANCHKKLPKNKEYILLYKKQDNKSILKQIRLKKTQNELSSYIKYYNKYITNIENDYKEWEIKYFDPKLNK
QDYLKNLIYLVKPDNNININMEEGTFEKIINSKGKTNYYYMNNGVIMKVLFLHENLDYSLGDLWTNISTIGICKEGLKTTFKNGQKPEYLLKIILDLSTNENDLVMDF
FAGSGTTLAVAHKMKRKWIGIEQMDYIETITKERLKKVIEGEQGGISKEVQWQGGGDFEYLNKEHDDTNI

complement(87610..88341) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00095; phage(gi100155) 1.11e-177
VKYRYSYSRLECFRQCKLKFKYSYIDKISVPKDQTALIKGSYIHWLIEQSFKEEPIEVSKSYHNPLINADQYKEYNEIFEKFKETEKYKNIKDLPALGNEVNWALDSK

LNPTNYYGNDYVIRGTIDYIAIKNRCAIIIDWKTGKTKDKKYIPDANQLALYAIWAEKVLNVDKIICQFVYVETNDFHTYTYTSDDLVPLKKQFAQDIMSIENEKAFI
ANPSILCNWCEFKSMCDSFKNSSYNRE

complement(88351..88695) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00096; phage(gi100130) 2.13e-71
MENIDEFIELKSQKLNVTDFIEKNSINEDELVKNAIKQIFDLEKQKREIDVEIRDIKTKLSKDGINITEFNRVLSTLKNELKMSIDSLSANISMYNSIVSDKELLQNLKDQ
IND

complement(88752..89366) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00097; phage(gi100157) 5.27e-142
MKLFEKLEEWLKERHLDKKEYDHLTLLGYLHEEIDEGIKKRDSEHESIDWRCDCIVFLINSLYQDGYNPKICMDECLKEIEERTGEYSESERKFKKHMGAYTYKEA
LDEIIKNYNCRKEDITLHGDHREFWYFLVNGKQIKVKKWYKADYSKSIRDDISNERYITKAYKLGKKIMFRQLNTKNRWKLLRDENLNFKEFDYKVVD

complement(89741..92404) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: rnaseH; PP_00098; phage(gi100048) 0.0
MFKYEYVFEHNFKLYARLYDEVTKNSIIKEYKSTEYVPELFIRTNEKTEYKDFYTHGYLKKKTFKATYEIYQYLKNVSPSTPLYGNINRPQKYIRENFKDIDCNHEFR
TQYLDIETRAINGYAKPSNPTEEISLIQVYDNYLNKFIIFGAKDLNISLESDIGEVIYKKCDNEIQMLKKYLTFVVKTNPTIIAGFNSNLFDIPYIVNRMIHLGIDDYIELS
PIKAITHKKMKTNDDIEYDGVKIEGIIQLDLRDLYIKYTTQKPSRFSLDEISKLELGDTKVNYDGSIEDLYKDFNKFVSYGLKDVELLIKLERKLKLLKVCQLVAYKC
GVNADEVSGTLMQWASLMYNYALSKNVILPLRQLKIINYDPPYPGGWVRVIEGLHKNVCSYDFTSLYPNIIIEFKIGLDNYIPVSNIPYEKAKILEENRARFINEEPNE
VISTSLPEDLKDMLNKYFYFYSETYDKTNNDSMEEFYYFKNIIDNKDEIKQICKKYGVNVTPNGCLYFSNGTSLFAELIESFFKDRLNHKSFLKNDNLTASEIDYHDL
MQYMFKILMNSAYGSTSLAINPFSFGKKMSESITTTGRFLNMWVSYKVNKFCNETYNLNIDVNSRPLSIQCDTDSNYFEFKFLETPKDLQENAKFLKSYCETTISPVI
DDAISEAVTAINGLDKNSNLGMEQETICDRLISCARKRYVGRYFNKKKSDKGFKITGLPMIDKTTPKWTKLKLNECLDLILDSDLHGLRQFINNIKNEFKQQLLSDIC
MNKSVSSLSYIISNGKWVSSINGNPCPIQSRGSIHYNNLTNKYKLKKIMEGEKVYIVYLKTPNTITCDNVICIPDDEIVREIPSINEFVDYETMFEKYFIQKLDIMSKHIG
FDYKNIFANTLDEWL

complement(92544..92933) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00099; phage(gi100161) 5.90e-82
MKFIECIQILLENNSIGSLSLENDYIKIYKDNDKLKIVDSKDNNVLLSSEHINNENWELNNKLFELILGSMWINDSDIVTKVEDNSFYNNIQYTTFRNMLTNEISILESD
KYYTNYCKNKWFQPEPLKV

complement(92930..93370) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00100; phage(gi100162) 2.30e-102
MENISKDLITIYRYGNNFELYNDFYFIFDFDVTSKGFKLEKYLVGNNIIRIPKGFRTDFGSIPQLFQSIISPVGKPTKAYVLHDFLCGKSNKGDIPRALADELFLDAMKL
LGVNVVKRYVVWAWVRVYGIIYKPLAKFFKDIWNKL

complement(93372..93875) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: recombination endonuclease subunit; PP_00101; phage(gi100052) 2.97e-114
MIKLIIGPMRSGKSLELLREAEKLHFGRKKYILIRPEIDDREFISRSYKTLHNLNVIKTNNINTIVNEYDYILLDEFQFFDNSITNIIIDNISKNWILCGLNINYESKLFENII
NILPYADRICKLSSICEKCGSEYGNHNISNTGEICIGDDYTILCSTCKLQLKG

complement(93872..94081) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00102; phage(gi100121) 1.26e-33
MQIEDVVIDTFKSILILLISAIMLKVYVILFLIISLGVLYYDLTIGIPVTATLMFISIYLANKFEKFIS

complement(94060..95004) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00103; phage(gi100165) 0.0
MLNPINVKYWEIIHNKEDLGIKKSDDYNCKCDVCGDSKYKNKKRLHLYRKDSYTDDSIKCFNCGYTATMYSYIKTFHPMYLNNYLNEIGEKYIDDLNIQNITLTKK

EPQKPKEFFSLNLPKASEIKEAKEYILKRGGNPDDFYYCKESFVINDKTFKLPNFIIYLNTVNDNAFSFYSRSINDKIFYIFNSDDGFKVMNYFNIDPLKEVYVFEGLFD
MLCTPFKNKIAMLGATLPKGMKVIPYIIWCCDNDETGRKEMLKHTNNPNHKFVVWCDDEKFKKYKDINEIYQSGVNIENFIKEHTFDGLIAECKLRMW

complement(94988..95497) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00104; phage(gi100166) 4.77e-118
MKKVLCSAVMVAGLMFVGCSTTTPQQQFAKPMLEKYDDLPSWVKEYGDIDTAVGSAMYMGQNYIQQQTEAIAVAKMNLTQKLSSKVDSMIKQYYQNKGVVKT
NNSQVSVQVSSSLVKNVKVVDTYVADDGELFVKIEAYSTNLLETIKNDDSKSLFDELDRRVGNVKSN

complement(95584..95910) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00105; phage(gi100167) 1.23e-72
MYFSLKETLEFLSTNSKNGVWEYDDISEADTTVFCSYFSDNSDENDIYIILSNPTGKSDIDLQGNVTDTDSEDGIPDRFSTCIMKVNLAKLNISNFDELGNAIKKYRL

95996..96451 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00106; phage(gi100117) 2.54e-105
MNFRNIALNSNIVFRTLLFSDDTQYYCQKVKLPRISLEGQKVGHSTGTLTLGGEVAKFDSITLTLLVDENLEVWKNFVNLINKYNKISTNTGCGIEATSWLEIHDSKN
KYLFKVEFYKSKLDEVSELEYSTTDNNIITLDITLNFDYMKII

complement(96452..96733) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00107; phage(gi100058) 3.41e-60
MNYLLELSPIFIVGLICGLSNYLSDEEDTCAGKHIKCILKYIFNSAVLCTIIYCILTSLELPYLTKIGVAGAITYLGIDKAMSLIKEFIHLKK

complement(96919..97581) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00108; phage(gi100059) 1.12e-155
MIISKKTLADQGQLNKNVILWAIDIGSELALLNRPMTVRKNSENMMVEYVDDITPEEIEAGKQAIKEYCISNNIMDIYYNFLIATTQESNKLDILKEKKRYEIQSNRD
KALENGIVYNGHTFQTREKDKLNINGAVTNLMLDIQSGTNSVSEIIWIDINDEKVTFNPQEFLKFTSMVAYNTQEITFKANVLKAKIEAAKTIEELEKIQWDDSVKTT
QKKR

complement(97617..98321) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00109; phage(gi100171) 2.21e-153
MKTYGQTKFKDIIDNTPELAYNLEFTIGNGGNFTNILDALNHCKRYINYPYYTITLKLLNNLTIDYTINIANTDFRNLIFDGNGFTISKNCKSQYDTVFHSDMSIYPWI
KNLTVENTNNRSFGIAFTNYHGSIFASHANVENNLTIKNFWNGIRHACSYLFVPGLTLDNCEYGLYAFRKSDTCLDAFVNIKNCGTGIAVYHGSEVVAQGVTFAGN
TTDCNISYNTPTTNGTIWK

complement(98498..99106) PHAGE_Campyl_PC14_NC_031909: protector from prophage-induced early lysis; PP_00110; phage(gi100001) 2.05e-127
LQTAINEANKYINYSNKSITIKLISDLVINEYINIVNIHSPFLNIDFNDYSIILNNASYDIGFSMYNSILGHINKLKINCNNKSINTAILLQKNSFCCFYYMKGILNCLGNAF
ALSTNSEAFVSDSTCELSAGSSGYYSKGILSVGSRLLFHTCKFTQNSGTLSQSVETSGIIDNFYTTFSGSVTGKSQVVGTWTKNGYISA

complement(99091..99216) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: ribonucleotide reductase A subunit; PP_00111; phage(gi100062) 3.96e-14
MLEYGRSSIKDIIDNSAKLLTSNLEWTVGTGGASSKTCKLL

complement(99261..100058) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: aerobic ribonucleotide reductase B subunit; PP_00112; phage(gi100063) 0.0
LSDALAKALEYISVKNNCNINIILKSGYKLNEQIILRNALANHINILSEDDEVLLNNFDTQDYIFMFYGCKAPNIKIMINAVGTRARGWYFRESSVTMVPSTSNAYKY
GIKNCYKNAVLSLSSKILISKYSFINNGNNLDGTQEQSLLYCNDQGELTGFDLKLDNNGSENCNGWLYYCGYGSKMTLTNSSITNNKSAANILNNNNSYMNLQYPN
FTGSKAANLLLCYNGAHTNITGRNVTNCTWSKYEFPFATNTITANGIIHAP

complement(100043..100165) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: aerobic ribonucleotide reductase B subunit; PP_00113; phage(gi100063) 1.88e-13
MINYGNSNIKEIINGSVKILTESKTYTVGRGGGSPNCQML

complement(100183..101520) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00114; phage(gi100064) 0.0
MAYGIDNVWSFVNDSQTGIDKVPVNKIILLKSENKLYLKKQEGGLTATSTVNEAILNNSIVSLSSDGNLGAVDSSIKVINDPEFTTTDNISKGKKMFKIAIEPDTIIQVL
GLYIENAANSSIDAVPFDYIIKNNNVVIYTDNDTIPIKKIIYSKTKSSQLSLSSLPKLLTENLEWTVGANGTFSNLADALQEASKYISVTNYKITITMKSSYKLTESLHIN
NANLGHVVLTSEDDYVDFDGTMTPNPSFINQYATTPIAVSFTFGISPTISFKLRFSSIPTMFSMAFGFLQTNFKLNNSGVYNAKWGVGSVGCIGLVQNSTFENCTKSG

VVADNGSILNVLENNTFKTCSGNILWSADSSKIYAGSVTFDGTYNNVAANCGVSHIASELGFNIPIFKNISNSNSYALFASYGGKITCGSNIVVSGFNKTNITANVFSS
SGCIFLY

complement(101544..103190) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: endonuclease II; PP_00115; phage(gi100065) 0.0
LNNINFKSITLQNFMKYGNKKTKFEFTNGIHLVTGKNGAGKSSLFLALHYCLFGKTYNGKTIGSLVNNINKKGMYVEVEMNINGDEFTIKRGTNPSIFEIYKNNELIP
LLSTNSAYQEFLENNILKFTEQAFRNLIYLGGDLLSQSFVRLSKKEKEDVFAILSDTATFLELTEKIKLLKKEKTTVQTNTLFKINTLQDVISKAKIKYEYDLKAYNDY
IENKNNNINEIENKIKEESGKVEKLKELKTQYDSILTQDPSNKINDLLKIINEQKSALQLMEKYKMCKGCEKLKQIIPSNIDVSNHDDLLKQLEVLQNENEVYIKNKD
DIYTKMLELKPSIENKKIYEDLLEKSKIEHIEKPSNDDIISNEKELQEVSNEYNEINTYISNLNQLEILLNNNNLKGAFLNMHLPFINKTINKYINMFDEFNFTFLLDSNL
KETITKDNKPFEYKSMSNGEALRLTFSIMLAFLDICRNKFDVKCNLLILDEVLDSSLDSVGKNELLKILTKNTDLMSMYVISHNSEIKNQLDYFTSTVNIINDGKFSEIE
YK

complement(103232..103552) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: RNA ligase 1; PP_00116; phage(gi100066) 1.74e-64
MIINVDKNMFQERMQKQGLSYGASDVLFDYIEQLEDDIGEQIEFDPIAIMSDFSVAEGEDELKDQLETLGYFDMEGDDSDLDDAKQRAINDGVLVYEDDDYYVFKS

complement(103610..104605) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00117; phage(gi100007) 0.0
MGKLIALIGDLHFGCKNFDHDILEVQLNSLEKYRDILKEKNCSTIYQLGDMFDNRKLIDLKLLHTLSTRFRNIFEGFNFYTFAGNHDMYNRDNRDIVSSELFADLLGI
KYIKEPSYHIFGKYKIGISPWLCGDEELLKECDILLGHAELKGFKYNHTSIAEEGLNIDNSKYKKVYMGHYHFNQNNVYIGTPYQMTFNEINSVPGIILLNENLEEEFI
ENTWDRRYFTVTVLKDKIILQYKDEPELFTGNLPDFCKVGKIVLKEKNEKEDKILEYFGARARISRIFYKYEEEKLYESVNLNNSVAESLDFIKEYILKEHKHLESVL
NDVINN

complement(104593..105462) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00118; phage(gi100008) 0.0
MDYLKEEDLRDEIIKLQKVEKLKELLKIEDKTDDDIQQIEKLREEGISEHYKKTKFGEMCLLLIKRILTMPKFSGYTYKDDFYSNATEKLMLYVIPNFDANKVSKISK
EPVKAFAYCTQIIVNSILQVINERKAEQELLKNYYTDYTELELRLEQKEYTCCYKTDDENIEYDVEIYPIVVIDDKLYIVEDINKKVETDLNLDISKRYFIVNEDIIQSN
TLWDILKNIDNNKTVRMIYHHDYLLKTDEYNKITGKNFKTLDIMKFRNTYIPSFPKKEKKTVESELDIWEN

105555..106517 PHAGE_Campyl_CP81_NC_042112: baseplate subunit; PP_00119; phage(gi100104) 0.0
MSKVINESTTTVDIAGVELKLAKLIYRIYTESLLNRIGARINVAVPNGSIFAFKGKYLTDYTGTDKSSTPYATILPDFAGNRDNNQETDVKAEMNYKIVKRTINCQTK
KIRSKWSIEAITDLVALTGKTTVEDILEKELLTEIIQEIDFSALKMMTTKATKTQLTLKAPNDPLVGIELFNAAQKKILEMAASTKRAITMCITAPYETCAKLMSHPNF
KANEDFTNSYFMGSIGATEIYCDYYNSLNKEYMLISYKHRNKEVEIADGSTCFAFYSYNITKAFDATSGAESYFHFLRYDVVQHPLDNTNDGQSIFLHCIEIQ

106525..107172 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00120; phage(gi100010) 6.98e-158
MAWNLNNRQNEYQLFGTLSAEIIDMYGFQLTYIKTTRLGHDKVLDDIVNYGTEATYQIFALPENAEMFDERGDILNKFGIFTMDSMNLFVSANTMKRIFQDDSKIPS
AVGDLLLLPSGKYIEITSIEHQVPGANNQFTYSNSKNVYMLRCKSFNYNHDNIPTLEEVNNEEVNESLDEIFNLVGSAENSKDKIKEEQDKESPLVKGTDSVFGYLDS

complement(107157..108935) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00121; phage(gi100071) 0.0
MDNDNKIDYLNNLGYEVISKNLSVNLEVRCSKGHTFKRAFSVFEKGCTTCPKCKDEAKMQFLHSLGYKIISKDKSDYFEVECKHGHVFKRALSVFKKGTHSCPKCE
LESKINHLHNLGFKYKSDNLVECPSGHTFKRQFSKFTDGHIICPDCNKQNKLDFLRKCGYETVSDDLTYNLMVKCPKGHIFKRTYYTFEKGIVTCPECDKNKKEIYL
SNLGFTIQSESLGHSLEVKCPKGHIFQRSFSNFFGKNVTYCPKCKDDEKMLIINEIGYKITSENLAKYLTVECPEGHIFQRSFGHFKRGNILCPICNPSTSSFEKEVSNLL
DNYIENDYSVLGDKELDFYLPEHNLAIECNGDYWHSESNGKDKNYHLNKTEKCKEKGIQLLHIFESSWIEKKDIWKSIINNKLGKSERIFARKCVLREVPKIEEKEFL
ENNHLQGFTGSSVCYGLYFNNELVCLMSFGKPRFTDKYDWELIRLCTKKNTNVIGGASKLLKYFEKENEGSLISYSDRLYSDGSIYKQLGFIFSHYSEPGYFYIKGNN
KYSRQQFMKHKLKDKLEKFDPSLTEYENMFLNGYNRVWDCGQGVWVKDQLSK

109044..110075 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00122; phage(gi100012) 0.0
MEFFFFETTKKYCKGLLDIFNSIQVKKKIDEKTDKYVTVPISFGSKDAASVFNDTELDQLLSGNFNILPRMSLALMSMERDDQRATSRFQIPIKDIDGKNITFQHNCVP
YSFDFVLSIATRSLTDLTSILEQILPFFNPNINLRVRELEWLTEPTTIQVELISVDYELPDENDGADIRVCSANVTMRLHGNIYPPIKNGAVIQQVKLYLSPVVDFSEDSK

EIVHKFNVNENTHMMDIDSFVRIDYGEEWNKVKPVIDGVKGEVKNLPIQENIKYRILYTDDTDDNIKFIINVLEDNGVNPIISKQLNYFTVFAKNKGTLKLSIQAVNS
FDLQSNIYEMELEFQ

110072..110527 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00123; phage(gi100100) 1.55e-102
MKEKAEALGKKLDKINDIFNITEKTIVEVEKSDLVKSNPEENLKFTYLKEDFNLMRESLVNTIKRGQDILEVISNNILADPLSSNQAVMAYSTLVDTINNSTKLLTDIY
KNIVDIQIKIAPKEAEKGSGKQEIMTIAQITKMISKNQQSQN

complement(110524..111075) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00124; phage(gi100099) 4.96e-112
MADLKKIEELIALAYGYEYGISHIDESDIDVFIKGFDEKNAEQQLKKADIDLESLLSNNFDKNALIMINYKKYYPIKLYGFNNLIKEFPSLNNINFYGALSGASTIIIKD
DEIMCLVDPNDYEKFKESFDSMLIELMKFIANSNSAEKAMDYLVSNDVGVGSYYNENKELTQMIFNAIELNKA

complement(111068..111259) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00125; phage(gi100098) 7.00e-26
MFKKLLNWFMNNFCACILLLYLILLLVIIDGEISLSNVITVIVITGCYIVERIENTIKGNKNG

complement(111283..111582) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00126; phage(gi100097) 2.60e-62
MKSSNFKTCKINKKYHCINTKSALVQENYKMEKSKYSVVKEFINLNYNIPIEKIDKETELFFFSIKLLCDIIELCPKHKKEIEDKVGELCDFREYQLES

complement(111569..111736) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00127; phage(gi100016) 1.02e-29
MLEYFNCYTSKKELYNYEKLKQELNEHGLNIKDDENSIKEDIDENILKRKNNEIK

complement(111730..112152) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00128; phage(gi100017) 2.94e-79
MTNRCFIGILENNNNVKYSFCMYDGNIELAGRILLQNYNKLCELLNIGKDIRFLSNRIDLCNFFEYEYNYNHDVKMNLETFKNIVFDDHYCDIKYIYLFKDGKYYFA
DRNNYKNLLENALEDFICYSMNNEDNLIEEIKC

complement(112245..112682) PHAGE_Campyl_PC14_NC_031909: exonuclease A; PP_00129; phage(gi100018) 3.71e-86
MENYKSVYNDCLLLFLELQKSDDNKKLQIYDLMLKCIKLKLPEITTKENIKKVQEVLKNYKEIETLDKDKTYGTISWYYLLYYIGNVYNIGYKVVFYGTNGRYSYN
DDYFEDIINLYSTITFLKEKLQKGCPDNVSLAVFNKEGN

complement(112806..113399) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00130; phage(gi100019) 1.36e-72
MTEIQFNKIKERLTQWREERHLTYENQQAEFFGNVFEKVSEYFRAKDDLEKIDAICDIVIYFFNAFDFKYIAVSSNMYCYTFSDVVVYNIYSLFGARTDNLCVVENE
NDFINLEKNLNLTMFEIEQLYENLDFDFYKCMLEKIKEIESRTGYYDEKLKKFIKDTSDEAKAKWYKADYESCMFEGWEIISKLIKEFKK

complement(113380..113721) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00131; phage(gi100091) 1.47e-63
MVSTVFENDYVEVVTRKDAESIVENFIKTCDCDWNDDENCDKCASIDNLKFHLEANRDCNIFVRFKFNKDDKTNLRWSGNLCVNSISEYVENELENDIKVVKYNR
RLNDRNTI

complement(113765..113968) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00132; phage(gi100022) 1.67e-42
MNKIKQWTIELMCMFYPIKIKSTAKDNYYISYKFKFNKYYVFGDKGGALFAENYKDALRIVEWMDDN

complement(113971..114120) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00133; phage(gi100023) 4.33e-28
MKIEITRDISNVVKKSPEIILNDEFYKLYVKYIGPSEELLFYKNCNKGR

complement(114347..114823) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00134; phage(gi100084) 5.29e-110
MYSKFINEAVSDDMLKAINVANWKTGLDFRKDYEEIESHGKKALEILDKLAKGGYNSKQYYNIYSDLRDELWNIHDRLLSYKNKMPWFRDELQSPELKRYREIIK
DYIYEVNQAMKDLKSDYAVVSHISNRNLESIIKAIIDEYERLYEIVEKIALSQ

complement(114950..115081) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00135; phage(gi100085) 6.33e-18
VKLKSFNFRIYDENTTINLLVDHKYDLFETLCGEFEPDKCEYC

complement(115093..115374) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00136; phage(gi100080) 3.56e-57
MALYKFSVKLYDDKHENIQKFCLIDGKHWHLLKDFRNCLISPDNVYFYDEKDLISISDYEDALKVFKKPIHRRMFIEYGSSYQEPDDKFITEY

complement(115494..115946) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00137; phage(gi100091) 2.26e-98
MLLEVVFENFKFCRQDRVEINFDKLYSPDYFKKTFRKVKCKCNPLKSLFFVDCDLPKYILKAIKRDKSLCNEITKDYGVITLTYRQDDFLIDYILKITESEIIQTTDLVY
LDLYLKDENSDCAKTINENTKLKPSEKKALEKVKQFEKIQ

complement(116057..116371) PHAGE_Campyl_CP30A_NC_018861: hypothetical protein; PP_00138; phage(gi410493054) 1.39e-68
MRITFNFEKEYTSTPYARNAEHDKEKNGEDFEKNYLSKWIDEKQETLIKVDNLELPFSDSFVDASFCKLIRQNKKLFYKYIKIDDKTDDEKDLLNTIKEVLARK

complement(116527..116715) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00139; phage(gi100076) 4.00e-10
MDKKCRDSYGQIDYLDAYGNYVKTIFESNTERHRNYSGENIRRGNGTKRLEESIKKCKGAKM

complement(116721..117335) PHAGE_Campyl_CP81_NC_042112: co-chaperonin for GroEL; PP_00140; phage(gi100075) 6.32e-107
MIESKFIIKRKLNFKNMEFGYKLFDVSGYFEFVEKPIYPRILEEFKKLDPTMKNKTILNRLRYIDRVRYDLLYDFTFTLAYSKSKLDKTIKNGKDLCEYDLYDLKPDW
LLKMVSDIIDEKTLLKYLPDIFEYMDDIIKSINDNFDLSNNAIFKWFQNVRNYIKLLLDGKIDYKNYCINIDLVIKSNMENALLFEKEVIEELNRC

complement(117496..117882) PHAGE_Campyl_PC14_NC_031909: membrane-associated initiation of head vertex; PP_00141; phage(gi100034) 5.89e-75
MAMILSQEEIDALLECDSRPTNLGIRSIVDKKISELREEHSKLSIKMKAIQGLNLLAHTDDFTIKDYMSIINDLIDCLKYKISHCQSFRDNISNKEAEKEFLKELGSFKLT
LLDFELNMNTGEENGEI

complement(117961..118116) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00142; phage(gi100072) 2.42e-27
MRELRGIVFNFYKKYFCKCESCNFREFGKLFKNYFIYLNLFQLYKITDEGI

complement(118304..118705) PHAGE_Campyl_CP81_NC_042112: 3'phosphatase, 5'polynucleotide kinase; PP_00143; phage(gi100070) 9.18e-90
MNNATVISFKFETEQLAFLNNCICYYDDEFYNVKYMCNLSDDEFKRITNFISCMKNNIKYLEINDKNVDIETLINRLGTHIFRYAHTDTPKEHKDTEYMLLKDYLLL
HIKDYGDNELVKQILKKSEELNSKYL

complement(118756..119199) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00144; phage(gi100038) 2.47e-103
MPEFKQGFYKPINPEKYIDDVTNIIYRSSWEYKFMLWCDNNAGVLKWASESIVIPYEFLGKKHRYFPDFYIEVKDKDNNIKKYIIEIKPQKDAIFKKPKIITEKNKKRV
VEQALTVSKNQAKWEAAREFCRINNMEFMVLTENELFK

complement(119199..119582) PHAGE_Campyl_PC14_NC_031909: RegA; PP_00145; phage(gi100039) 2.74e-74
MNESLADYGLDVNGFYKHIDGKESIVETDDFKIKITYDSVNSEFDGDNEELLLKMHCNIELRYIAGIEDAMRVSDEINNKIVEIIEEDLKKYDDVSKYLILVDSGVFID
PDDPDYIQNAYIIIQPKY

complement(119579..119902) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00146; phage(gi100099) 5.69e-60
MNIYSIFLNEEVEPQKDLAKKSLDFLGEKLNATHSVSEKGNTLIATYKDKNGNKLCDVNITVNDNNIKVTKVTDNKGKPKQIDLVIHRINDIIGSRMMSYINKVKKQ

complement(120203..120478) PHAGE_Weisse_WCP30_NC_031101: DCTP pyrophosphatase; PP_00147; phage(gi100024) 4.39e-05
MNNKRKNNGTRRFTGYFDKNGNKIYKDDIIIFNDIVHDTNRIGVIIKRQHSGEFRLEFSKDDTLGLKILDESKLLVIGNINENAELLEAKE

complement(120638..120880) hypothetical; PP_00148 N/A
MKIGTDKNGKEIKIGDVLFCLELVATEVEDEGDEVEYEEFEHYIQVLEKDNEIIVCDLDSDEWWFLHQFSFADYKIVSDY

complement(120877..121344) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00149; phage(gi100087) 8.74e-13
MKLKDFDFRIWDDTNKGYIEEIEIHKFQNYPIEAGYTFMETDRIGEVEFIKNKNDLEIELFTGLYDKNGTKIYEGDIVCCSTSQGKTLFYFITTNKNINTFQIFVISDLEK
FKICNEIDINSLLYCDLSNLEDMKLNSEVIGNIHNREGISKELK

complement(121341..121547) hypothetical; PP_00150 N/A
MKEKVQNISIDVNVEELLEQVETEYLLHELSRRPLLYVDITSLIWDTLDEDELKILKKEVHQMIKEKQ

complement(121882..122052) PHAGE_Campyl_CP81_NC_042112: aerobic ribonucleotide reductase B subunit; PP_00151; phage(gi100063) 1.03e-30
MDIKKLKESLEGKDNGKYFCEIFNTNVDILVVDNGMKKSEAIIQVLEDVKELYKND

complement(122098..122379) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: baseplate subunit; PP_00152; phage(gi100104) 6.97e-53
MEKVIHKESGKEYSYFKPVLNKTTNEVMICYTDGVNFYVRTKNDFFDKFEILETPEKYDTIKYFHDLVNNKLWALKRQEELLDKVSKFDLSLI

complement(122386..122628) PHAGE_Campyl_PC14_NC_031909: ssDNA binding protein; PP_00153; phage(gi100044) 1.85e-46
MKLIISLLILASMAFSIEVCSFKEPLKRGFFSIDNSIVFLCIDKKLFVRNFPGETDYSYSVTQVFEEGMKPQACSCQAEE

complement(122625..122792) PHAGE_Campyl_PC14_NC_031909: loader of DNA helicase; PP_00154; phage(gi100045) 4.14e-21
MTPKKIQKIFEKVLKEKEKEYTDGRLEEIRKEREYVESIVNEGIQKANNMLKEFK

complement(123150..124190) PHAGE_Campyl_PC14_NC_031909: dsDNA binding protein; PP_00155; phage(gi100047) 0.0
MINKKALINHMYSEMLHKCLNGTETVDNPYHLEKTVLDHTIMVLNKVEDLFKNDKDYKVLMFGAALHDLGKIFTREVITKDNRTVKVRFINHENVGVYYACDVL
SKFDLSEEEIIKIIKIVAYHDIYKYNIDELKRKFTYDDLQLLYKFSICDLLGRITHTPKPTDIYKQIKSLEYYETKGIDSSKPTITMLIGVPGVGKSILCNQYENVVSRDDV
LMSYGKNKFNLETYSEIWSKLSQDDQKEIDNIFKFKLNRLLQQGKDIIIDKTNTSIKSRKSLLNSSSLIKSYNKVAIVVLCPYNTILERIEKRSLETGKEISKNIVDDFIKS
MRLPTLEEFDEISFKWSI

complement(124393..125766) PHAGE_Campyl_PC14_NC_031909: rnaseH; PP_00156; phage(gi100048) 0.0
MLPVKTLTELNDININVIKRNGTVEKYSPDKMYKFLLKVCDNKESYAINILSKSKIKLRDNIKIQDLYDEILSTTVNEISMLYPMYEKFAAKLYIIKYRKNIGDEISLSS
VLKLGLSSGVYSSDFVNSFSEDEIQELDRYIDNNRDYLFQNYKAISMFYTKYCLNRTKTIKLETPQITYMRVAMFICMNESNRVEKIKRIYDLISTHKFTYATPIMLNS
GINKGQLSSCVLAKMGDDSHSILATNDNLAIYSKNKGGTACDVSALRATGSIIDGVGVSSGPIPFIKLLDSTISAWNQGSTRKGSCCVYYPTWHMDVQNLIMLKDN
GGTESTRARNLQYAIKIDDVFVKRWYNNENYTLFDPKDTPKLLDTFGDDFEKYYLEYEQKSNIRKKSINARELFDEILKYRVETGNIYIFFIDNVNKQGMLNRIVTQS
NLCCEIVLPTSAPYKKDEKIVHYM

complement(125753..126889) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00157; phage(gi100055) 0.0
MLLSKKNLVTDKSKEKFFFGEYSGFQRYDWYSHNQLESLDRKQQAQLWFPEEISMIHEPKSFIELPEHNQKQIKANLTFQTLMDSGQNRGLDNILIPLVTSSGLEGC
LKTQAYFEYIHSRSYSHIIKSVFPNPTDVFDEYCEYPEIKTRINDEIDTYESLEGSLEENDENKLKILEACLRIQFLEGVKFYVSFLTTYMINKYSAGGNKIPNLTKIIKLI
NNDEDIHLIIFSFIIKTLRSEQHQGFSHLFDDSLSRKARKIAKKVYQDELEWAKYLLSMGPIPGLTIENIDGFLKFFVDDRLKKCGFQPIWNAQKTDLVKEFQEIKNISS
ENQMLQEVDSITYSKGVMKKDTKLEIYNGETLENELEKILNGEIGNVAS

127089..127226 hypothetical; PP_00158 N/A
MSISVYVSNNIVTYSFGFSKCTPTLSNTSKATGKLIKLMIIESTQ

complement(127254..127625) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00159; phage(gi100111) 6.26e-83
MKLLVAGSRDFNDYNLLKNKIFELNIQPSTIVCGMTRGADMLGYQYGIDNSLKIEKYKPNWNLYGKSAGPIRNKLMADSLNKETDMAIIFWDGISKGTKNMISILD
DKKINYKIIYYKEKENE

complement(127622..127828) PHAGE_Campyl_PC14_NC_031909: recombination endonuclease subunit; PP_00160; phage(gi100052) 4.52e-41
MFVKIKELICKFVNFKTLQKFITTDRQFIIEGQNGMKYSGDFFFVDEDGCICKISDGSYVGTMVKSSK

complement(127862..129337) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00161; phage(gi100053) 0.0
MTNHEKIIFLNNLGYKAISENLSKNLKVECKSGHVFGRMFDDFKRGSVNCPECDRLGKLNYLNNLGYKVASENLADSLHVECPKGHIFKRAFGDFKNGKINCPKC
NIQSKLDYLNSLGYEVISENLSKGLEVRCSNGHIFKRAFGKFKDGFTTCPKCKDTNKVNYINNLGYEIISNNLADELKVRCIQGHIFNRTYGNFKQGKIICPICNPSTSS
FEKEVSDLLDNYIENDYSILGDKELDFYLPEHNLAIECNGDYWHSESNGKDKNYHLDKTLKCESKGIHLLHVFEHSWYSKKNIWTSIINNKLGKSNKIMARKCVLR

EVPKTEEKEFLDENHLQGFTGSSICYGLYYQDKLVCLMSFGKPRFTGKYDWELIRLCTKMDHNIIGGASKLLKHFHKNHPGSLISYSDRLYSDGSIYLRLGFTFSHYS
KPGYYYFKNGTKYSRQQFMKHKLKDKLEKFDPNLTESENMVENGYHKVWDCGQGVWVKGNL

complement(129370..130416) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00162; phage(gi100114) 0.0
MSLIDKLLKSSTLGNRTSVLKESKYFGKDEFVETPIPMLNLALSGKLNGGLTSGLTVIAGPSKHFKSNYALVMMASYLKKYPDSVCIFYDSEFGITPDYMQNFGVDT
TRVIHTPVANVEELKFDIANQLENIGDNDKVIIVLDSLGNLASKAEIENAINEKSVVDMQRSKHIKSLFRIVTPYLSMKKIPMVVVNHTYDDIGSLWGGQVVSGGTG
VIYSADTIFVIGKAQEKDSKKNLQGWQFTINVEKSRFIKEKSKIPILVTFDNGINKWSGLADLGLELGFLQKQGDSHFNPFTEKKLYLKGAPQEQLDEFFSELLSNKD
FVDALEYKYSLLNITPNNNETTENNV

complement(130472..130765) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00163; phage(gi100116) 1.92e-53
MKRNILLLIFSSFLFIGCSTATKTVTITKKEYLKYPLDEKYIPHKLDVKIMKQKLNGKDYLLILPNDFITIYNQYKHLELNYNNLYDSVEKFNLQIK

complement(130734..131072) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00164; phage(gi100117) 1.44e-49
MFNIILSVIKSNIVYIIFGCLLVAITYRYISLEKSNAVLIENEKQLTQNLNESKKELEVLDKYNKITVEIFKEKETKYKEVLRNIKNIETKIKNLQPIGKDKNETQYIIIINF

PH 1

CDS_POSITION	BLAST_HIT	EVALUE	PRO_SEQ

region 1

complement(4..609) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00001; phage(gi100059) 1.17e-132
MYSKFLNESSENLWVFAKNDIKLRKLILPVIQDNIEYVMFLNDRSIEEGKLKDICLDIEIFGVFEHYNIGNYKKIEPSIVVNVTDLKKDALKSIEDKLKNCKSKDEPVL
SLKLDMITEYNVARLLEKEYYINNFTDIIQNELKSKQFKIVEGNIGESVVELFNDYGESMIFTLKNNKVIKVNGQVGTKYNYLYSSLVIQKI

complement(626..1582) PHAGE_Campyl_PC14_NC_031909: dihydrofolate reductase; PP_00002; phage(gi100060) 0.0
LKSINEKEYVWAEKYRPSKIDDMILPDKLYAKIKEWINSGEIPNLGFFSNTPGTGKTSLNKAICNELGATHLFINSSKESGVDLARNKITSFASSVSIDGSLKIISLSECD

GMTNELQRSIRDILDEYTQNCRFILTANYTDRLIEPILTRVTCIDFDKEFNDNKTELGVKILDRLEFILQNEKVEYDKKDLQKLIQCFYPCIREMLIVMQHNTIDNKLVI
DEKVFETINNYSNLIEALKKKNFTEARKIIAQTVSYSGFYQYLFKNIDNIFELESIPQAVMLIEHYSDHDRTSRDRELCLSALVAALIKYDIKYKNS

complement(1640..2197) PHAGE_Campyl_CP81_NC_042112: ssDNA binding protein; PP_00003; phage(gi100044) 4.12e-123
MKLHYYDIYNISNGVFLTFQKNLKEKLLCVSHSKDIMDKKIGFYPLNFSDRGDFILLCVYIMFKHSPSSIYGLCEYLRNYNKTEYEKFKNTIKFYKNMIKKDIALLEE
KYKKPMFKEVMREYSIKQISFVTVYWYLMLYDIKDFNGINNTIICESILNVFKFLKFTDESKDYIKDVFKQIEGEVL

complement(2210..2470) PHAGE_Campyl_PC14_NC_031909: ribonucleotide reductase A subunit; PP_00004; phage(gi100062) 1.45e-48
VESKTELFNKLFEFRKQKDMMDDCILDVIIEFGNHINMDPELIASELSDYAIFRDIVEKDLKKFKFTKYDPNQSDIDISDIDILWE

complement(2460..2906) PHAGE_Campyl_PC14_NC_031909: aerobic ribonucleotide reductase B subunit; PP_00005; phage(gi100063) 2.09e-103
MCVLKTWLEDSNAKLPEISVMGSACYDIFSIEDKTIQPGGFEYVENGVRLIIPDGYYIRFNTRSSLGFIKDLFVYPGILDASWSGNLKVKVYNFGKEPYTIKKGDKYC
QFELLKCNESKIENISKDDFDNITKKLIRGNNGGWGSSGK

complement(2894..3286) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00006; phage(gi100123) 3.60e-83
MKNIEILNMVEELVKLNPILLISENFSHTYELLKENVRESKSIENKKIKLNCISVKLDDDTKLPCYGTVLSVLMKDNLENIINKNPQSLLEISFKISINVLLDLIDNFVEIY
DFNNESLLLINRIKICVY

complement(3298..4566) PHAGE_Campyl_PC14_NC_031909: endonuclease II; PP_00007; phage(gi100065) 0.0
MKYVFIGGGVANIYTICYGIMNNIINMKHDEVIVIEKGKHINDRIPTIDIVNGLLGGGAFSDNKNVFSLHDDQPIFEYINKQQVLEYYDFFKNKLFKMFLPENASIHIT
QPVETGSKFVSGYGDIALKQSECYHVGSTLGLEMCKNMIKWLEDKGVTIYCNSTYIPSKLDKCIIVRDTNGIESYITYDKLFIGLGRSGMKDIKETFELNNIKSVADQI
HIGFRFECEYNNTIQELANNIQYDFKFSKNINKNHLKELRTFCVNHGTAEVVTEKVKGYSIPIREQANGHAYGLHVKNKWTGKSNWAILGSFKNVNVEDYLSQIETI
TNGKIYELNQKSSLEFLNCFDNLGDSLSEFVKELCDILDIKEWKGYFPEIKIIGPRVSYNDNFTVQGFSKNIFFVGDSAITRGIIPAAVTGIHALLN

complement(4619..5023) PHAGE_Campyl_CP81_NC_042112: RegA; PP_00008; phage(gi100039) 2.63e-90
MSYSFEQYCNSNNFNEFQRYLITQLGYINNKNVVAIQDSEYIDVFKAIKQEYYKASSCKHSDKEEVIPEHYTKLAIEPIDFIYKNNLNFCEGNIIKYVSRLGSKDDNKS
ELKKIFFYFDYLLHGNYDLTKRTFS

complement(5027..5203) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00009; phage(gi100126) 1.22e-29
MTIKNKINDINEILQSYVGELVLSDIDTQKIVENLTELETIIKDAISKQLNNSKLILG

complement(5259..5825) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00010; phage(gi100037) 4.14e-127
MEKLIYIVIFLCIVFTTTSQSVIFHAKYNFEDIIQERLSYLKQNMINHISKYNNKNATEITNYIFEASLKYNINPVFIMSLIQSESYFKHKVKHKYNNVKGISGINYKMW
KIVLAKHNIKHINSLKNQIEATAIIINYIKQKYKTNDDLEILHYYKGRGYDKYLNKSGLDLAQYSYSMYIKNIKIIYN

complement(5844..6479) PHAGE_Campyl_CP81_NC_042112: DNA polymerase; PP_00011; phage(gi100036) 1.02e-146
MKFNCKNFAKALFYSKDINYLIKLFKYAKQEDKKQAMQILLWARDVNGGNIKNSILLLKYIAEKTNNINDMFLASVVKYGCFKDLNEMYKVASDSNKRKILSFYS
NELKLKNQLAAKWAPRKGPLFYALANSLCLKIGDFRRYITSLYISVEAKMCDNMWDSISLDEIPERAIKKYKKVLEKRLKITIYCRSPKQRRLKFKGCEKLLKQY

complement(6694..8010) PHAGE_Campyl_PC14_NC_031909: 3'phosphatase, 5'polynucleotide kinase; PP_00012; phage(gi100070) 0.0
MNINTLFNDNLCQYASYDNIRSIASLIDGFKNSGRKIVYFSKDLANYKKVSTLKSEIASKSQYLHNEDILPDIITNFARDFDCGPVTLPLFKPLSAIGCRTSPTSAQPRY
SSIKKSDYYDLLFNKDDEEILDHQYFEGQKIEPRFLLPTLPLILLINNNGMGVGFAQNIMQRSAEDVKQAIKDILDNKQPKPLVPYFKGYKGTVELLNTEHGKKQWK
FKGVYEKIDTYNLKITETTPYATNESMLIHFNSLKEKKIIKDYKDYSLGDNFEYVINVSGDFWNNQNIHKLLGIETTDTENFTCADRNNFIKTYKDEIEILKEYIDVKL
EYIQKRKQYKLSKYSDQIELISNKIKFIQAVLDKKVIFERKKKEDIIKQINNIGIVHNIDTLINMPLYSLSEESINNLNEQLSGLQQSFNELSQKHVKNIWLDDINKLFER
L

complement(8045..9670) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00013; phage(gi100071) 0.0
MTNQEKIEYLNTLGFQVISENLTTNLIVKCSKEHVFKREFYDFQKGYTACPTCEIEQKITFLNSLGFEPISENLGKKLEVKCQKGHIFKRTFGSFKNGILSCPECEKKEK

HNFLKELGFEIVSNNLGTNLEVKCDEGHIFKRPYKSFKNGHISCPICETNNKHSFINNLGFEILSNNITNDLEIKCRKGHIFKRTFNSFKNGQQFCPICEAENKNTYLNS
LGFTIISDNLADNLEVKCQQGHVFKRTFGNFSKGHHLCPFCYPNSSTFEQEVRELTGGTNNWEILNGKELDIYLPEYNLAIECNGDFWHSESMNKDKRYHLTKTEK
CAEKNIQLIHIFESSWNKKKDIWISIINNKLGKSERIFARKCVLREVPKIEEKEFLENNHLQGFTGSSVCYGLYFNNELVCLISFGKPRFTDKYDWELIRLCTKMGVNV
VGGASRLLKHFHKHNKGSLISYSDRLYSDGSIYLKLGFTFSHYSKPGYFYFKNNTRYSRQQFMKHLLKDKLEIFDSNKTEYENMVENGYHRVWDCGQGVWVKEIL
S

complement(9680..11530) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00014; phage(gi100131) 0.0
MIENKIVHAENEVEYYLNLPHLITGALTSFNNTVKVLENNKIINKEIVYNQTLTKQIDEAIQNSIDEFTRTGGKYANKISLKIDKDSGIITISDNGRGLPIDTYVMATTK
FRTSSNYTFLEKEKKDRITIGAHGIGSKLIPLFSSEYQLTTITLEGDRGIVKCLNNMSTIEHKEDKAPASSTHGVTIKFKPDFERLELKEINDNLINHIHALLINIAYSNPG
IEFTFQGKLIKVKEFKEFIKYYSDNFSILQSDENLELAIFPTDEYKFVHIVNSLDLNKGGVALDYISNNIVNAFGNRLRKGYSKITNTAVKSRIGVILILKNKKNLRFGG
GQTKEEIKNTITELGIPTLKYIDFAELLFKNTHIKDPIIELYKVQQELENRKQNTFERKEAKERFNPKFTKHTKDPKFMYIAEGDSALSSLIQAVGRDCSSFLPLTGKLQ
NALKCSTAQLLKNQRVMDIVEAMGLGLPETKYENMVIATDADLDGNHIACLITALVYKLQPNLLTEGRVYRLKTPIISVLQNDKLIKWYYTLGEYQKDQDNLPKN
AEVIYMKGLGSWSAANYRIVFAKDGIDNCLEKIEWKDNDEKVLEQWMSDNGIDFRKQILSTKSFNIENL

complement(11630..12832) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00015; phage(gi100132) 0.0
MSIKHVISDSSFGIPKPGFALKNKFICDNYNEQLEDIKIPIDKLDELLDEIKTVLKTSYYEWNGIEGDKSVFIFRLSNIYIEITYKIGKYVKLDMYSNSINFLKGVYNNIL
KKYITGTDELLIKIKSFYEEKGELVYVDSSKTKDNYKNIDYDYYPFLDLNEMFIQFLFANSNILILYGQPGTGKTKLAECYLNFLLNLDYKKYKHLELEEKVFDKSD

DDGNCINVAVVKNESLLAGDAFWNELLSNRYNLVLFDDLDYLLPRSDIQNGIDAQRNQFMSHFLSFTEGINNDITCKTKFIITTNRNINEIDPALLRAGRTFDILNLRT
LTKKEALKIWENNGLPKKSFNKLVNDNILQCNLSNIIEGEKYNIACKNNFKNYLKENDISHMKNINNKKIGLI

complement(12993..13442) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00016; phage(gi100133) 2.81e-94
MNIYAKYLNEFTKSSIKLNEADIDFDDFISEVKEIAGTSGDKLHNPRTSPVFRNYMYSLYINDDGISAEKAWRMFEELNIMDSRKIIQYIEEDDDWYVNRLKDEYNIS
LDDFKQMDEYDQIRTFCEIHNCQYIEGTDNKMYVMLPKYYV

complement(13495..13755) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00017; phage(gi100134) 5.80e-54
MDKQLIKDITINGLSQFAKGHEIEAITETLQIVQEYNIEHHSHNFEFDVEPITSLEDFIKEINILITYEDLNLFHEVLVESLKYYK

13810..14211 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00018; phage(gi100076) 2.46e-86
MTFVEKNMVKELKKTISSKKPLVLCFMSKLLQKEIQKLLKGNKLITIIKIILYAFDKTPVEVKRGVLGYVENEKNIPFQYKYDNTTKTLTFSLDKKSYNFNLCTANEY
IKVLANETNWMILKKNLNNALKNIK

complement(14229..14747) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00019; phage(gi100077) 2.15e-119
MAITNYTEFEKLCPKNGEIADQDVLGKPSLQLKRELDTVMSQVNSIIGITDPSNWDTGTTYTQNQIVKYNNYIYVSLSDGNRGNQPDTSPSKWKKISGGSISSSVNIIV
SSSDYNTPVTEVSDNSLSLKPSKVYVNGNLIPTTNYTHDGTLTKITFINGMSVYKNDVVTVEY

complement(14780..15421) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00020; phage(gi100078) 2.53e-156
MGILNTAVGAISDFFGGNKTQSAITELAQKIQKAYSTNFDLESLYSIDTFALKNEVPGAGRINILDLPNMDILIQRVSIDPISFAEINEWIGSSWVYTQGRHELQQLTITF
RDSDGGFLYSAFKKLAGHLKDQYPDDQMWIIKIRKRTLRESRNYINQSVQNNEFKNGGHVIIDTQCAMIRSHGGLSLDQNSNGLATFDVTFLFDPFPPQISY

15467..16120 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00021; phage(gi100027) 1.41e-152
MELEIWKGKHSILLNKLYNDNNYIYDSDIIDVLVYKCLNQPKYITNDEARFLFFKKYFAEVCSKIDSSFKCPYCNEMNDIKFTNDDISITEYSLKPIEINVDNVIVTMY
FKKELSQDDSLSLITETKNMIDHEKRLLELYYMIDYISINGEELRGNHIIFEKYINELPLSCFNKIFDYFINSIPKHSIIKNCSCKNCNSEINVELKELPESVRRNLF

16117..16779 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00022; phage(gi100026) 2.40e-156
LTKDIIINNRHYCLNVWKIKDEIGILHQFIDWIELPLEDQVNKIADILIPQTKDLDYISRLYIMIILSSYANGDYSDILLTCPHCGNPIDTRINIRENLEFIPPKTVEVEINNK
KYTISKQNIELCNELPLKDYNSILNQLNDDGDLKLCAKVKCIMCNNDVLAIRELKDLFENYVIMLDLEWYYSTLKYFISQLGFSKTDFDNLYPFEIELLTNENKDE

16772..19345 PHAGE_Campyl_CP81_NC_042112: DCTP pyrophosphatase; PP_00023; phage(gi100024) 0.0
MSDIIKIDGQMVSLDVDSLKDASIETIIKILSYTEDTFKPLLDYMSNNGIPYYMILYGRFNNESLYKQMGINILKTLGAVAMLFPPVRLIGSGSRVITVVPKLVFSKGGL
VNVTLISAGAALKTEENNELYTLETMLKNAIVFIFEDIMVSTFKMAKDGIIKLSLGIAEKIKKDGSVLVNGLPIYLYTDLDNMDPTLLSKNSETYDKLRPDLLIIFEYIT
TQAKTNKFVDNYYFESLSLMKEKDPKLYSMVKNSIFGKQHVRQGFIRLVHNAMYYFSNSYEVTYDDFNDNIDDVLPSNILNDFKKMILDNSLEPLKDKKGKQKTS
LFGDKLYKVVYDKSASQSYNIGDVQDLNRLTKAQFFNVNKKLQNQTVLSQFDIEPQKTEKNTANVSTPSTIVGRVNSVLQKHVGRAKLTSEGVAHVKKYGITTTK
SSLTLEGFDPSKYYFSYSGTEPFNTGIGKLDSNLLYNLNLMAYDYFNIYKKQFIVTSGYRSMESQQKLYNNFINGKGSPANRPGYSLHEYGMAVDINSADAIKLDSS
GMLSKYDFWRPIPNKEPWHVQPKNITDKNGDGMLEADIVETKKKQANTLQKTKPINTTSINTNVKKQLFTNTVVSTSGKYYSIDIGKSVYVSNIKQEKPIKANTRD
VKPTTNKAITDTKTIEPTANKEVITDINTKTINHSNISRKYAPEDTIEINKEVKRLGDEFAPKNNKGASIPGDIGYKDTGNGVSIPGDIGYEEKKIATSYDVKTQKAKNI
TYKKGKDDNTYYTSDGNFITKKTRIYDDGTKEDYYLTNTGLELTENMLQNDTDEQFTEMSGLSKDQFQKGINLINNKQSSTNGDGDKPSVDAVKSVEITKKLGL

19347..20303 PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00024; phage(gi100141) 0.0
MAEVINIPGLDNEKYLVKITAYDIDNLGIGKEVMDSWDDLIKKVDESGSTDINSEGEYSSIDQLSETSSNILKRTVELMIDRDSAIISTDAAGTFYFPLPNSLSDQYVQS

YEVQSMNLLGSAISKASSYAGQTSIKNISEQALKRSGIQLDPNILSIYRSSNPRNIDMSWNIIPKSRKQYDAYVAQISKLKNWTKAKRNPITLGSVGNIIPMNFLIMKYI
FCIEIISLQNDKTPLVSNLLSASRDVTEGFFISLINTNIGSRQLMLRHDGNPTEFSLSIQFIERKPLWRDDWEKKINSLYNDQGKSETSLKEDDIYKE

20319..20672 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00025; phage(gi100083) 5.63e-80
MNDTQTIQIFDLIGDSQARDYIAIKAYKIGSDVSGIKDSINDILDDDPSKAFDNLLNMAENNISNIINPSNWEAGPRLKPGVPCKYIWILPIPSSLAEAFSHEFNQDEIDPI
GDMIG

20680..21441 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00026; phage(gi100084) 0.0
MASIRSFANFFKKGPKKVHNTEVPPHTIKPNKPKPNKMSTVKGKIKKGGAIVGMATGAALPFGYNLLKRNNIRTDPHIINTYNGTPNRVFNFETILLPNNAKHAEDI
VKALLQLKSIMTGTQLGTDKTGLLISQDYVFTIEFGSKDPAKGEQLKKVLNELLQLNHEENGETELNLRMCNINYMGQASALYGNGLPRDLSIALQFEEKRPLRMT
SDIVETTDTSNPNGNEKISEPNIGLTEEELNYKYSQDENS

21463..21924 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00027; phage(gi100085) 8.83e-107
MKNSVLNNKIMVDFNGFSLSPTYSVNIPKLREFMKNNLSMFYVKEMNDNVRFEVLALREYNDSSLWDILMILNFGENGILNFAKGDTWVSDNAENQYKEQQEYFS
PNFKPEDLYNQILSKIQKKNESRRKVIFIKRQFIPQFKESIKDMLNVF

21914..23050 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00028; phage(gi100019) 0.0
MFSDFKIMPEAYYAILLYSNNKKSELPLDPANISDFTIIWDYNDLCVEGYVIFNDTQKITELLPPHNGICFKVSLKDHFNIKFERVFKVTKIDRDFEGQSVATIKFELVD
EYYNMFANTFISKGYNNVKSTDVIKDIFNTKSDLISTPLNVIIKDTPKNTYENYVIQGNKNLLYLLNNMQKFDDLLIINTRKGIVVIPTDNIGKLSPDLSKVVKFSPTQT
QEYSPYSVKDFTLIQGDMLTQNAILPPSITYQVDSKKITKEEHNTKISHSKSGLKTSLTINDKDGIQGIKIFPYLHNIVDSIYNTEILESSAININVAGMFNHNLMCKVSF
DANSSIETLKSKMPYVTGEYFITKIVDHISSGNVFTQTITLGRIGSV

23047..23829 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00029; phage(gi100087) 0.0
MRVNEKNFKILTQTLPFYKGVIEDDKDPLESQRYRVRIIGIDDETIPTETLPWATSLDFSLFSGMGFTSFIKKGAYVLVHLFQNDRNQPIIIGVLKGVNNQNEELQSFK
DPTGQYPLNDYKNQPDTNNKSKGEKYLKNQVFETESGHYMEFDDSNGDERIHIFHRTGTEILVDKEGTVTINVVKDRNLNVKENQTSVIDKNDTTHIKENKNLTVD
KDNTTNIKGNNTINIDKDCNITIKGECNITVTGNANIKASNINLN

complement(23816..24157) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00030; phage(gi100147) 1.37e-68
MFLEDNNKQLSKVLNDNIVIKEDEKNIYIKFKKNIIIESDNNVIFLAKDYIVNSAKEIHLNPDVKISVDDNVDDIIKKIDDKKNEINISVEKLTHNHKHCKIKCFFKKLF
NLN

complement(24141..24428) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00031; phage(gi100089) 7.88e-64
MPPVTRLGDIALGHSCYPPSPTIEASSNVFANSIAVHRLGDKIQSHACPDTPPHGRNSSSGSTSVFTNSKATCGIGDAVNCGGIIAQGSNNVFRG

complement(24416..26035) PHAGE_Campyl_PC14_NC_031909: DNA ligase; PP_00032; phage(gi100090) 0.0
MDKIKFLNNLGYKVVSEDLVRNLYVKCKNNHIFKREFGDFKKGYIKCSKCEEEQKLEFIKGLGYEVVTMDKKGKLLLKCKSNHIIEKSFGNLKKGSILCSECIKEEK
IKFIKSCGYEPASENLAHDLFIKCKNGHIFKREYNDLKKGYVNCPKCNEEDKIKLITSFGYTIINQYDSEELELMCKNGHISKRIFNNFKKFPLCSECVEDKRTSFIKEL
GYKVVGKNLFECKNGHTFSREVKSFRKGCVYCPICSPSISSFEKEMSELLGNYISNDYSVLGDKELDFYVPNHKLAIECNGDYWHSEQMGKDKNYHLDKTNKCLE
KGIQLLHIFEHSWYSKKNIWTSIINNKLGKSKKIMARKCTLKEVTKTEEKEFLDTNHLQGFTGSTVCYGLYYQDKLVCLMSFGKSRFTGRYDWELIRLCTKKNINVI

GGASKLLKHFEKENEGSLISYSDRLYSDGSIYKQLGFEFSHFSKPGYFYYKNGTKYSRQQFMKHKLKDKLEKFDPNLTESENMVENGYHKVWDCGQGVWIKNRK
GILCHQ

complement(26047..26493) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00033; phage(gi100014) 3.42e-97
MEKNYNTFLRKKSVTIKLNDDLKDKLKDTIENINDYDIIKIKLGRTFFNQKRYYKIYARKKFGFYKTLLSENDDSYFFMENTSKIIRRVFNEYDVNCYNLYPNKKYR
YGLSIFILICCSIILIALSLGVGALSYIFKGYFLAFGFSLF

complement(26553..27125) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00034; phage(gi100092) 3.19e-138
MGLESGELRNEAQGGYNPPFELSIYKHQVKFTPPNNFESYIKWELLGDIPLHLTINEQTGLITGNIELLSKQPSAKNAIYEYQLMKIDGSNWRHLGILKNGQTFTFNFQ
VKLTYTVQANSGGSRLSNTVTEVSDVTITILQDNDIISTLFCKNYIDEAKFPLKIGDKVYTDAVEFMKNHPNKNNFKINLV

complement(27142..27669) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00035; phage(gi100012) 1.65e-129
MPLYTVDKLANALKGGAKSDKYFIEIGTPLGAPEVAFTEEDIILCKTASFPERTLGEVEAFVQGRKLKLPGDSTFDAAWSPVFYQTPDHNIRAKFLTWIDKIDVYKN
NYHTCDPYSLMVTAKVHQVNCNGEPVATYEFFNVWPSKVGEIEVAADKTNSIQEFTVDFTYSHWEKIA

complement(27698..28276) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00036; phage(gi100094) 1.96e-139
MSLYNIDRLRSSLKQGGAINSKYKIDIKIPTLLRSLPFFKTVNISGEYLSIMANRTSIPGKSMSTVKVYHRGQPFVIRGAAQFNNTHKITFYNTPDMDIHQLFSDWIYRI
DSFDSTITQSIFLGNYVGFNSVGAGYMSDIIVSQLSSDGRTETEFKLCYTFPIDIAEVELSASGKEISSTEVTFAYTYWERI

complement(28278..28838) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00037; phage(gi100010) 6.08e-137
MVESINPPKGYFKIELLDKDRNVIDTFEKHNLVVNGSRPVLASHMAGRSTTPVNKLVLGTRGHIGNNLMMPKTANEGFTAARTQLFAEEEGEFCYHVNFTPPQSDG
QAVVTEDDVGAGSTVEVTNSNNTITYRIELSTTAGNGTLGAVGYTEAGLYAGNDLFCMRTFAVRSKDVSSILRITWTLIF

complement(28822..30378) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00038; phage(gi100155) 0.0
MIDRVDLPNIYNENKLHKDSVEALYEVLDELNPYSLDIYNIFKRPNDSITENIVKIYAESLYYGMQKALTNPVVIQRMKEKIGTTDNYQPFDIKEFYKKLLKDYFVNF
TSFKEKKGLDVAIEYAYNIIFTSGLQPGLDVNGSSGFNLKWGTEDNPNEPFFIRIEGLLDPILYEGSVKSIAHPVGFGYNYVISLVLEFIEYIDDLINFNVKTLEIVSTNY
RKEFDKDKVEDIYTSKNIQNQERIVITFNDGKQLIKDFNGSITYNEKDGSVIENWNNTYILKLDYDISLKFRLKDEFDNSENNLIVYDCVWNRLNSFDTPIIGEAIVNK
FRVADKYYSSLVIGKIDDNTIYTLPDDPIKYTPDKMPLFLTNAINRGLFEHIHDDIDLYSTNNFTDNVINEKGISNTVGNKIIVGSFKVGSQSENPEGGVILDDSFSIERE
MIPTEYSETVTKNLKTNFYTTILDNFDEKVVNDDIKITVGSFKVGNINIGAEYIDNGVILDDAFDINILKIRKNNGRIN

complement(30375..32468) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00039; phage(gi100097) 0.0
MADNILIPYNYDDIKDEVIKLLKNKGYNADVKSSNANLLADILSYLAYSINVNTSFQAGEMLLSTAQYRKNILMGARQLGYEASRKVSYVYSLEIKPLKDDTKDDD
NEDKRIYSIPKYTMFNSGSNTYYYMGSDIEVELSNKDITTGKASTIKIDVKEGILHKWDKNKDTQVFTIKAIEQNRSIKSSNKISLYQDNIEENGLEVFVTYIDIETGDS
KVDEYWEKSDQFMIDADSDTNKKYFVLNNIDYSGVDIYFSISGIGTNLLPGSTVKVTYLESKGSSGKCGDNFAFSQNTYPFNLMEIDKFETKIVGTDEETNSSIKENA
PIFHNSANRAVTVRDYIAICNRYTNIYQTQVWGGDEEQVVQLGHIWFSFIPEYRNQDFSLDETTQTYSLVNKNDSYYLKQSELRSNTLDKNGYLVNKGIFDELDSY
KIMTMELHNRYPIYMDFDYEIRIIKQNIVVSKNETQDKLFNILKDYFKSDIESFESSYFHSSVIKRLGTELYDLSGIQVDVSMNIPLYLRNKEPNKDILYIYLAIPFEQIIT
KTQDDQNELHVNLLPQISSDDFGGKLEVDFKNPIKGFTVIGSSNAIIGTFDVGNGQSAVFNGKNVVTSDGLIIKNTNISFNIFANGTIIGTYKIIYDNRRRFIVIEITDSIV
LSSLDNITPKYIRVKYSDDNLSFYKNTIARLSSVKFVSESDVI

complement(32468..32815) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00040; phage(gi100007) 2.88e-75
VIQYKDINPKNIEKDIINVDTFYVSLKNIVSTTIGDIAGFPEFSNNAQLLFDQYSSVALDAYKTSLKTSIQKFDYRIIVDNINISKGDADNSVYIEIKYRVRDTTISDTASI
KVG

complement(32847..33557) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00041; phage(gi100158) 2.86e-165
MLLNSKTIALVNSLQLINESIIFSSKLTGIKDSAGSIIAFIDLEKLENKPFPKDFGILKIKEFMDLLKIIGEDANITMDDKNIIHISKDGMSCKYLTTNVEALSNACGVKPTI

LENVNNAELVSSFELDMTVSDKIKKAATLLGFDDMVLNIDDIITVSTSEQGINGNEFSLNVTPNVINSKANIFISIKNLKRIPTTDYIVSVHKHSSRQDTYLLKLIPKNN
DALIILIPSKVVK

complement(33606..34589) PHAGE_Campyl_CP81_NC_042112: DNA topoisomerase II large subunit; PP_00042; phage(gi100005) 0.0
MLQNFVGNSSIPSVLMAAPYGIIDSTPNNKWMEDLKKDGKFTPNIQKIEKQFFELQKTISSVASIYTIPAEKGLQDLAYVANLGMIFPHLNPNEDRRVLVSNFKSEPR
KGETKVGYEYFKKLGFDPIIMPDVNEKGEPMYFEGEADLKWLYGNVYVGADGNRTNGAALDWIAKTFNCEIIKFPSIDEYLYHLDCNVFPLGPDTEACLVNTYNL
DKDIIKELEKHVEVIPLGVDSHDDPDQYDFALAGTTNSVLLPGGIVITPSDISELNKKSDKDLYEMEKDKIEFMDEICSELGLQLVVQNISGYYVSGASLSCNVMHLN
QRSYLN

complement(34669..35910) PHAGE_Campyl_CP81_NC_042112: DNA topoisomerase medium subunit; PP_00043; phage(gi100004) 0.0
MISGLILKNLINDEIYFDKVYSILKPEHFIGVDSDIYKTIQKLVKEYNKKPTPKEVALKLKDNFKDEQQENCINRFKEIMLDKQNVSPEFLNNETAEFIKQAEMRSCIIQ
GAKLIQEKKDIGKIYERLGQAISFTMDTDIGMKDIDAQERDILRRETKIGISTGVEILDEVLAGGYMPSTLNFICSVTHGGKSMFLSHFCANAMLKGYNCLYITLEMP
SIKIWDRIESNIFNIDISELRNYNVSEGYEKLPNLGRCVVKEYGAGSFDVLQLKSLVQKVESSLEINLNCIIIDYLALMASYALQPSVGLYSYYKKIAEELHAYAKESK
KCVLSAAQLNRNAYNNSNADTSTIAESLGIAQTADTIAMLHRSPELDELGQAIISFTKNRNSGNLSQKYIGINFKQSRFFDIDQPD

complement(35910..36596) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00044; phage(gi100003) 1.44e-155
MIVCNYNVVPVIISLYRNDFNMQEVKICGYNQLNEYIKDDSNKFEIIGFNTDSINLPKNIVNLEINFENIPKYLQNPLKSYYEWDKNNQRDFLFGYYLDLYFKKNKLP
ALVDLLKNNTEENNIYNIVKNNFISLEYSLQQNIIKEKIINDTYIMKGNYNSFVYKMVKSQCKTYILDDDLGKLTIFSDDLKIIYDRISHLKIDIIKTENCIILNDIDNKQ
QIVKLMLGL

complement(36769..40866) PHAGE_Campyl_PC14_NC_031909: base plate hub; PP_00045; phage(gi100103) 0.0
MIEPKREPTQDFFVCLLKEPRWISTDDLYPILLIPGVNYPAEIAMMHPDFFGGDDIVFKPEPPIDPDGPDLSNYYTKPETNSLLDKKADKVHTHVVADITDLNLNKFA
TKEETYTKQEVDNKIDEIVPPEIDLTDYAKKDTANIFTKANTFTEAPSVEVDATLDNHVIRKKQFDNSIKEVKDLLSNVFSYKGSKPTYTEIEAIVDKKIGDVWYAED
TGYMYIWNGKTWYDLGKSFDASKFVDITSDQVAINGIKKFTGKLKALTPVDSDDVAILSWTTKQINDKVKSVIGDLNSLNNEVSKDNLVNAINSVDDKFKTTAKT
NKSNTFTGDQTYVDHILLESVPSERNHAVNLGYILDNPGGIKLPDHTALTQNSVTEITFGYANPVVYSAQQLKNVFLKDIVGNEYKAIMADKTSFTENPSKEMVVIL
SRTDYTKNTDVKFDITKTVDELKQYELKEGEVRVILSYDTISVYSSGYGYGAMFARNANKKDGDLIYDYYTGSQNDITNNRKISIKIDKLGINIPDIVSISMTTNGSEK
LTVKTDTLDPVENTYESADMTYIHTPVSKIAGDVLYSNISQAIKSIHVLENNICSLKPANMELQLVRLKEFKQTINNILQSMFDESPVALKNGDYINVSFSGSASYGTG
YCGYVNIKDTIRNITYKAYKVSLNAFDTTSGTKVIAVLTSDNSKTNVTYSDSVSTLESYEVAENEILLEISFSTAKQYSAKYGYGAMLEYWGSVSDLCYDYYMGSN
LDMDCPFKITLLKIGSSVKADTIQIGAPTFAGSLVMHLRKNINDVINFLVSTGVNVTGRDGAESGSVYNLVEKSLKPLKVLTSEAHQSINGITTFNNKVYMNIDNEKI
TDSKQLIHKEYLDKNIADNVAYNISNTPLVPYNDVSSLNTKNIGVRISATTDSSNYSSGDTVVVSNFKIKLKGDNEYLKPYGVEVIDRENNKIGLNLIGDDTVYNDN
DALLSTRPSDFNSSSVDLSSGSNALATVKTNGAYDYSGVYDIPNPFREYNKKYSLFLSNDGLKNPYYQVDISSSKQVDNISFQLFGTSATNPFLYSKDCKIELFIENTI
VKTFNIKGSSGNNSPVNINIDYKDGMFLVSVLDSINYINNRINKNAELLTGSGKPNFSLNPNKIGSLYSDTTNKAVYMCIDNTSGANKWVNIVTGDEIKPNLRKIEITC
NVRLRSGQYGGCMSGVKIGFDNGYASTKQIVKGLNSGQILLSLDGLGNLSGYSEVSSLTPSGQDIKVDVDTTGIYNDPSYHCVTNIFKEYLGNADQCSLWSDASVK
QLKITLLSENIPTKILYVGNGYYGQTSVSDVKAVWYYVNDSGDKIEGSIDNDLEISNNDSETNDSSYIYAFNIN

complement(40917..41942) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00046; phage(gi100164) 0.0
MVLIDFMHLAFKSLYVAVGKDMYSKQKLSFEKYHGMFVHLIFNYLKLIQTEYARDYGNEIILALEGSNSWRKSYYPEYKTNRKLSDVFDWENEVFPAVNEIIDVIK
KSLPYKVLRVKGAEGDDIIAVLANHTAKPVLVVSEDKDFMQLLINKHITLFKPIKKEFFRNIEESEITKTLTMHILLGDKADNIPSIMEGTTFTPDFIKFLETNGIFETDV

NNFNKLEISKTLYDLYSKQSEKSPFKPAYFGEVGAKKFLENLNENLEKNKLVYDNFIRNKTLIDFREIPDNIKESIIEQYNLEKPTIDLNNLLKFFLKYNCKKHSDSIAS
FNSNMGTSLFDDWM

complement(41929..42063) PHAGE_Campyl_PC14_NC_031909: baseplate hub assembly protein; PP_00047; phage(gi100106) 2.63e-21
MKRDGSIIKSFKREINLQTRFIKNKTKYTRKEKHKKGAIINGFN

complement(42060..42446) PHAGE_Campyl_PC14_NC_031909: baseplate hub subunit; PP_00048; phage(gi100107) 1.17e-91
MDITHSQYEVMVSAYKKDFIPNKNEMNLLNSFMLCRWMSNDIHSVEFANFINNHTDIPINVQYWFARSIMNKVTYMGRPPKEDKLNEYEEAVSKYYNVSFDVAK
QYCSILPKEKQEEVLNMFKGGRIK

complement(42498..43415) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00049; phage(gi100167) 0.0
MNEFDILTGFSGADLMQKMPQNVGQKSYIDNRFWKLSKNKEGSGAAVIRLVTDKHKTPFVHIYHYNSKKNVGGKDRWLIANSPSTIGLPCPIQEEYFEVLNSGDEK
LARSLYGRKVKYYTNILVVKDPANPENEGKVFLFEFGSKLKEKFLAWMNPDETQRSLGHTEKELYNPINGYNIELTIKKDPQSGFFNYDNTSLAPSPSKLGGLEKNE
DIIDIILNKTYDLSEFTKPEYFPSYEELKEKLERFKNPFGTKTSSVPSVVGKTNDNPPFETQESKPQSQQQVVQQQKPKQENSQDDDWLNNL

complement(43527..45761) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00050; phage(gi100168) 0.0
MTVNNKIEFLNNLGYETISDSLGHDLEVQCKNGHIFKRSFSRFKSGSTACPECERQENIKYLNKLGYEVISENLSNDLTVKCKNGHAFKRTLNNFKKGQLTCNECER
QRKLLFINSLGYKVVSKELNNDLTVECQNGHIFKRPYKAFKSGITICTICEKQEKLEYLNNLGYEVISDNLGNDLEVRCKSGHVFKRAFGDFKKGYTNCPGCIISEKT
KFLEDLGYKITSYTLGDNLEVECKNGHVFKRTYGNFKKGMTDCPKCTKEHKIKFITNLEYEIVSDNLGHDLEVKCKNGHIFKRPFGNFKMGNIDCPECIIHTKIKFLN
NLGYEVVSENLADYLEVKCSKGHIFKRTFRTFEKGTTDCPVCMEHEKTEVLNNLGYKTISHSNVQCKNGHVFKRSFSLFKQGVITCSECTKEYKTKFLSSLEYKIISE
NLADNLEVQCKNGHVFKRSFDNFKRGVTLCPICYPSTSSFEKEISKLLDNHVSNDYSILGDKELDFYLPDHNLAIECNGDYWHSESNGKDKNYHLDKTERCKEKGI
NLIHIFESSWIEKKDIWTSIINNKLGKSDKIMARKCVIKEVSKLEEKGFLDKNHLQGFTGSSVCYGLYFNNELVCLMSFGKPRFTGKYDWELIRLCAKMNTNIVGGA
SKLLSYFHKNNSGSLISYSDRLYSDGSIYKQLGFSFSHFSKPGYFYFKNGIKYSRQQFMKHMLKDKLEEFYPDLTESENMRLNGYHKVWDCGQGVWVKLS

complement(45797..46534) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00051; phage(gi100110) 2.32e-176
MPNYFSSSKPGSNQSNIVDSTKPGFVSSYQKKTKETQSISEEAKNINTGKKLIKDTVDDALKEKTTKEQEKAALNIVKQLMKKGTRNFKAEDFRFSNMIFMQYDAK
FKDEVYDKTPLILVLSTSRSYVLGLNLHWTPVPLRIALIKVLFKMNKAAIQKNKQLKITYKMVKPLLSALHLGPVIRLYIKKRISRRGIIIPQDLWLVAARLRAESFSG
GYSADKLYAKAIQNYKKSKSKNIRKNRKMF

complement(46543..46890) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00052; phage(gi100180) 1.11e-79
MNTVYSKYLCESSHYDQYKETRDIETANVEMKNMDRDLEFLKYRIEQKLEKANIEITEPYIEGECIKFALKNYNNEDNKKVKDILYDMRDISWGPISGDYSDMSQG
YEVSLDLED

complement(46941..47657) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: protector from prophage-induced early lysis; PP_00053; phage(gi100001) 7.34e-174
MVKDIQQLKDDKINYLNKLLPQDENGYFLDISNQKVSYGNNPQLSYINTKLPLKEEHIIEIQKCSTDIIYFVESYVKIRSLDEGLVYPDLRDYQKELIQQYYENRFNVV
LAGRQSGKSVTTLLYILWKLCFCPDTIVGICANKFTMAAENLQRLMDMYADLPIWLKPSVKVYNKESFVNEIGCKAYISATTPDAFRGLSINLIFIDECVAGDTKITV
RNKKTGVIEDITMEELYNRIG

complement(47677..48063) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00054; phage(gi100112) 2.17e-85
MNLISIDYEDKFYRKLLEDELTNFKSYPFKISEDVYWDFRNYGANSIDKPEKEIKLNLSKRKVRFIINRLEYYNENGYWNNVSLIQKHYQEERKLEKLAETHAKTFM
SAVWLCIPIFALLALLKYIFE

complement(48144..48809) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00055; phage(gi100113) 6.89e-156
MKNIEVKLLHHTPLEITIDAIRTCWNSGCKKDSVYENGRFVLGNQDKALLDRIVNHHKHLSTIEHVYYNFFIKGISRACLQELARHRHASLSVESTRYTLKKHLKNE

EGFKYEQDFDRASKYVVLTEDLESNLQILSNLDNLLRLVKQNKSNDVVKYALPEAFRTNLYWTINARSLRNFLELRSSNHALHEIRILANKVYESLPELHKQTLFKN
IIKEYNE

49049..50500 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00056; phage(gi100115) 0.0
MNVTEKLKFLNDLGYEVVSYDLSKNLIVRCKSGHEFKRRFYDFQRGTIICIQCDHNSKLSYLNSLGYSVKSKLINNDLEVICKNGHSFKRAWSEFKNGNIRCAMCYE
QHKIDFLNKLGYTILDINKIKVKCKHGHVFDRVWSHFNSGVVECKQCKNNIKIEYMKLAELEPISENIADSLELKCKNGHVFKRTFSNLKKCNVCPICYSNISSFEKEI
KEILPKCIENDYSILGDKELDFYLPGHNLAIECNGDYWHSEQMGKDKSYHLNKTEKCKEKGIQLLQIFESSWIEKKDIWKSIINNKLGKSKKIMARKCILKEVPKTEE
KEFLDENHLQGFTGSIVCYGLYFNDELVCLMSFGKPRFTDKYDWELIRLCTKKNTNIIGGASKLLSYFHKNNKGSIISYSDRLYSDGSIYKQLGFEFSHYSAPGYFYC
KNKIKYPRQQFMKHKLKDKLEKFDLNLTEYKNMLLNGYNRVWDCGQGVWVK

50516..52339 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00057; phage(gi100116) 0.0
MTLDEKIEFIKSVGFDIIAHKSNSITLQCNYGHVFNKKVSNIIPNTNIICDKCVVMSKEKTLRELGFTPLLINGDKCTVKCDKCNHIFNRTWYAFNTRKNTKCPECVEA
ERWNNINSHLNNMKVSYISDIQGNYTLQCKNGHIFKQSIAEIIKEVGCYQCEVEYRKEYIRNLNFTIIEYNSKIFNVKCNKCNHIFTRDWNGFYNRKHTICSNCIEIGK
KNLAKKHGFTLTDTKFGNDIREFICNKCNTTFKRGWSNFTSRGNKECYNCKQLSRINLAKSYGLDIINKNITSKYTFKCNKGHVFERPFTVVENKNQTKCPICYPRTS
NFEIEVKNLLTELCIKYIQNDRNILDGLELDFYLPDYNLAIECNGDYWHSDSVISDKKYHLNKTLKCNSQGIQLLHIFESNWIKNRNIWESIIKNKLGLSFKIYARKCEI
KEVNKIEEKEFLNKNHLQGFTGSAVCYGLYYQNELVELMSFGRSRFNKNISWELIRLCTKINVNVIGGASRLLKIFENNYPNQTLLSYSNNLYSNGKIYNTLGFEFSH
TSSPGYFYYKNGMTYDRQQFMKHKLKDKLEKFNPNLTEAENMSINGYNRVWDCGQGVWVKGSI

complement(52354..54264) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00058; phage(gi100117) 0.0
MALLSPGVEVKEIDLSLTVSSASSSFGAFCGIFPKGPCDGAVFINDIPTLESVFGKPTNSNYNDFFQAYCFLRRAGSLYVVRAIDKLGKSTRKDSGLTINAVLSEKATE
ITLADTTGLYVGQQIMFGEKTDANVYTIASIQANTKITFTPEIQTGDGTGNSSKIYICYPSMNATGEVLKTGSSNTITDAKLKETLKIIPNNDVYETLEPSIKFSDTETKL
KFIAKSAGFWGNNIKVAVATKADFGANKNIIKGIPLDDNFEYVPDTDQVAVIILENNEIKETYMVSIKEGAKDYNNKSNYIEDVINRKSSYVYCKNNTTITDLPKSAL
DSEAITLKFGEDGAPTKADIISGYTDNFSSKEEIDIDIVIANEMANKECADFCVTRGDVIGYGGVPFGEVVGLKAEDCVKNLLEYRSTGEMNIDNKYFSFIGNYGYIY
DKYNDKYRWINLAGATAGLRAYTNQARQPWFAAAGLNQGQYLDIIKLAFNPNNGQRDLLYKSAINPVVSFPSLGICLWGQKTCTQKPSAFDRVNVRMLFNYLER
NIANSARYVVFEQNDTHTQNMFVSMCTPLLTQVQAGRGIDAFKIVCDDSNNTPLVKSNNQFVASFLIKPTYAIEFITLNFVAVGATISFEEAIGSI

complement(54426..54773) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00059; phage(gi100007) 7.37e-74
METKLLNILLNIGEKYGIYFKQNPIEDEYNVEILLWTKESPESWDKIIKDIKTELLVNFTRNIKISSWGKNSVNIKMKLDRLYQVNILYNLEEPKLNITISYPKIINESAY
DNFL

complement(54763..55716) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00060; phage(gi100119) 0.0
MNTSTLYNDKGKVVLQWVKNVPKSIPSEEVIESIKLASKKFKKYPFKNVSKLKSLNTNSLTLYNISDMHFGMLALKEETNDSDWNLDIALKTLDQLSTELINGADK
TEECIICNLGDLIDINDFTHKTPRSGNVLDVDKKFPQILSVAYNSIINMIYKALGKHKYVYYYINIPGNHDILPSMAVQYIIKEHFAGNKRVICDESLMNIKYHSFGNVL
MAFTHGDNIKMKDVGQIIAFDNKENFVHSKHVYAYFGHYHVDKVIDTPLCRCESFRNLAPLNKWASNSGFRRGIGTISSITIHKSYGEISRRTYNMDMVNGN

complement(55738..57060) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00061; phage(gi100171) 0.0
MLVNIINNLKNENTDAGKIAIIKNNKDNQNFIKLLDIVYNPKTRLGITDFELPSETGNDILDNIISSLDYLQNGIYRGNDAETFIIKLAKQLDYENQLLLQKVIRKNLQA
DLGIKTINSAIPNFVKKPPYMRCALLNEKTSSKIKYPAYIQEKLDGQFCNVIVTKNSIQFVSRAGTEYKFKRDFSKLQQLIYYTLGECVIMGELLCTENGNILPREIGN
GIINKSSETNQTITEEESNKVILKAWDCIPYSDYLERKCNIPYETRFNNIRKITETPNGFIYPVVYNIVNNMEEIMEHYKNLVSQDQEGVIVKNRFATWGDKTSNDQLK

LKIKFQVDLRIKGYQCGKSGTSFEDTLGALICESDEGSLEVCVGTGFKESDRDFFWNNNMIGKIVTVEAHRAMEKNGKYSLILPVFIELRQDKDEADGIEKILEQEKS
AKYK

complement(57106..57234) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00062; phage(gi100010) 9.38e-21
MTTSGDIATTPSRLTLKRGKIKPKVIKYKQTKTLTLKKLSKN

complement(57231..57530) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00063; phage(gi100122) 8.28e-63
MYTKYLYESSLDLQFEVTDQDFDESFLNFNKELPVSLSETLKLKYNIKLSLKFQSKYDDIGILVKLNDNGKYVVYSNSIENIDKFIIFVDTLNQNKGNL

complement(57520..58020) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00064; phage(gi100012) 3.95e-117
MANKSKSKGNTFERTVAKMLSDNYADVFNVAQSFQRNISSGSMFGGSNSYRGMNVLDEHTFYAGDIICPSEFKYTVECKHYATAPSFNSLIIQECAQWDKWILQV
EADCEISNKLPMLVVKYDNIKPFVFIKHNFEGFIFKYRDYYAYNFEMFIKEYKKELINNVY

complement(58037..58414) PHAGE_Campyl_PC14_NC_031909: cytosine-specific methyltransferase; PP_00065; phage(gi100124) 1.45e-84
MKVQFINSKELSANVVSTKNLHKLNRKILVPGVVDISGTIYLASPSKELPTIRVEMDAVFKCGECSSFKIKHYVVNKKVYGSNSEIYDGISKFLRKYAKLILVSKDEI
MFFNYTYTGFAKYFKNK

complement(58531..59310) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00066; phage(gi100125) 2.16e-175
MKKSTTLNEAIKRKAKNMNKGKSITLNEAAKKGYFKYIKRKISINESEINGLKDALENMEEFSDENIMGSVVGKDYVISIFEKVCIILVNGTTPFLIEREDITEDEQTLI
DDIFETLNLELDDDLDNVDDNQGDDGLDDLDDDLEDDDLDDNSMNESRKIDKKIGLYFYNSKPIKDGNTVVSVDDKGNTEVKLHGNLIAVKNKNGDEKYSLAGY
NSQTTRARLNGLGFNVVQRKGKLFVDNNEINADDWYDIFGNKVSW

complement(59321..59902) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00067; phage(gi100126) 2.28e-137
MVTYEEIQQLIRNCLDVGIKAPASAYSKLLRHGYCVMYGGDAKFNKLEELEDNFDVKQFDRDTWVIKEYKKELTPEEWKDVNSQALYNGGTPDQIAKDIEDGEK
NPILENAFNKLDEAKLKQISKDDLKNIWNENDLETKREKTLKLISELKYKSPSLEKIIDIIKTTKDKNKIDQIITNIMFVGTGDKVIKI

59998..61080 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00068; phage(gi100164) 0.0
MDKIEYLKSLGYNLLSVEGSYVKVECKNKHVFRRAFASFKIRNTPCPECEIENRKQFLDSINYSLISVKGRKVEVKCKTCNTIFSKEYCNFKQGKITCNYCETNNKIE
YIQSLGYNIVDFESRGYVKIQCKYNHIFSRAYNSLKNGFISCPYCEHEQRETFFKFINLELITFDKGKITAKCKKNHIFNRTYGSFKRGSILCPICYPKSSSFEKEVKNILP
RNVIINDRTVLDGKELDFYLPEYNLAIECNGDYWHSEQMGKDKNYHLGKSLKCINKGIYLIHIFESKWRSNKQFYINLIKNHINGTIKRYPNKVISDISCENQLIFPKL
GYKLVDNVEPNFEIFQNTLKVYNCGYNIWLK

complement(61101..62483) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00069; phage(gi100128) 0.0
MNEINVVKTYTNGEIALCNLASINLHEYDQLSDTEKYNLVYDIINTMDNTIDLAYYMVKDAQTANKKYRYLGIGVSNLAVLLAKHKIIIDSQESLEFQAKLFDELLY
NCVKASMQLAIEKGRAEGFSETKWAKGLYPYLIGNEKAKKLIQFKPDENKWNKLMEDVKKYGMRNCALTAIAPTACVTKETKIKTENGIKSYKDIMKEQGINFNE
IENYGIPSWIDFKVPFKVQTRHGLKEVNRIWFNGKQPTKTITFEDNTILTLTYNHKLLVKLDSGIEEWIEARDLKKGMEIVSITNNIKIKSISNNTDVLFNTWDIEVPDV
HEYLLENGCISHNTSGRSINASESIEPIQKLLYKEDGNINVKTLAPMFKEYNKYYKLAQECDPMMLIKAAAVRQLFLDQSQSVNMYSYTFNGELNYIQKSSHKLSLL
HMYAHQLGLKTLYYFKSEKDNGVEHECESCS

complement(62521..64407) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00070; phage(gi100129) 0.0
MDKIKYLKSLGYTPVSSNLTNNLEVLCHKCNNTFKRSFYTFKNGSVDCPNCQNIERLNYLKSIGFEAVDLYNVKCLKGHIFKRRFSEFKNGATACPICIDNEKQEFIK
GLGYVIKDIKGDNFTVECQKGHIFNRVYSSFRSKNITFCPECKNNEKTLFLNSVGLKQIKSDGDKMTLQCSKGHTFVRRYCDIKRGSINCPECIIHMKEEYLKSIGFTL
IKTNVVKCSKGHIFNRSYSDFVNGSIACPTCQKENILNFIESNGLQLVSLGKSIKLKCQSDHIFTRAFNTLKVNTTCPICDKEKRKLFIESFGIKLLKDGNRLQLQCSKG
HVFEREYCNFKKCTLCPVCNPSTSSFEKEISELLTNYNKNDRNILDGKELDFYLPEYNLAIECNGDYWHSESNGKDKNYHLNKTNKCLERGIQLLHIFESSWIEKKDI

WKSIINNKLGKSNKIMARKCVLREVPKTEEKEFLDTNHLQGFTGSTVCYGLYCRDELVCLMSFGKPRFTDKYDWELIRLCTKMDHNIIGGASKLLKHFHKNHPGSLISYSDRLYSDGSIYLRLGFTFSHYSKPGYYYFKNGTKYSRQQFMKHKLKDKLEKFDPNLTELENMSINGYHKIWDCGQGVWVKGNLS

complement(64456..65763) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00071; phage(gi100130) 0.0
MDKIEYLKSLGYIPVSSNLAGNLEVQCKNGHKFKRSLGNFQRGTIHCPECEKQEKISFLNSLGYTPISSNLGNNLEVMCKNGHIFKRRYEHFKNGISTCIMCDEQNKSNYLDDIGFSIISDNTADDLEVICKNGHIIKRSYHNFKKGAKICPVCSPSTSSFEKEVSKLLDNYIENDYSVLGDKELDFYIPNYKLAIECNGVYWHSDKFKDKNYHLNKTEKCKEKDIQLLHIFEHSWAEKKDIWKSIINNKLGKSEKIMARKCVIKEVPKIEEKEFLDTNHLQGFTGSSICYGLYYQDKLVCLMSFGKPRFTNKYDWELIRLCTKMGLNVIGGASKLLSYFHKHNKGSLISYSDRLYSDGEIYKQLGFEFSHYSEPGYFYFKNNQVYSRQQFMKHKLKDKLEKFDPNLTESENMNINGYSRIWDCGQGVWVKLSIP

complement(65858..67255) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00072; phage(gi100131) 0.0
MADKYLLDESTKEKFITSNLYPNLNESEKNIMRTVLENQGKEVKMLMESTVTGDIAQFTPILVPVIRRALPTLIGTEIAGVQALKTPTAYLYAMVPHYVGDGNNSVSPTKNAIVLKLKTESANKDDFNYTGTPIEVSFKTATTVKGKIVYSEKQAGTDNIVNVLLRLESNSTGSVTIGDEVDKAATFATKKATIEAVYTNEALWLKVLKNYTGPYATATGEKLGKDMKEMGISVQRVLAEAKTRKVKGTYTIEMLQDLKAQHGINAEKELADILSAEVALEIDRTIIEKANEVATVCTDFDVNSADGRWFIEKARGLSMRISNEAREIGRQTRKGGGNKLIVSPKVATILDEIGSFVLSPAGSKINAIDSGIKPNVGKFDNRYDVIVDNFAEFDYCTVAYKGASNFDAGIFFAPYNITLQQNLTDPVSGQPAMILNNRYDVVGAPLHPEAFIRTFVVNLNNYIIS

complement(67287..68033) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: DNA helicase; PP_00073; phage(gi100021) 5.68e-156
MEELLSKLDKNIFTPEVVDEIKGLFEAAVDNKVEAALKIADIHAIEVDKHYEKQVKMLKESAEMYKQQVNKNNQKVIHNAITKIKKDYNKLVEGIIKGKVDEFVKKGSMNLEMLVESSNKKVVDACIKTADKIHGPVNALKRINESVKKEKNVKKLEEKNKKLQMKLEEAQKNNIYNNIRNTVSIGNRDMFDTLAESVAYTGDISYESNLKSIANKIALKSKTISRKSTGRKQQLSESQNNTTYGNFL

complement(68044..68673) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00074; phage(gi100159) 9.26e-153
MKLIIEEPVKIKGSVELNESKGEKNYYIQGIFATINQQNINGRVYPRPIWESAVNSYQHHITTPTTSSLMEYQHPNRQYVDPLEAVAKIVDLRIEGDYVMGKAKLLDNPKANQLKNLIDEGISIGVSSRGCGELMNGTVTEYELITFDIVPNPSDRNAHTKGLNESFDNGILKDKNYIKDKNGILVEADESNINNKSITSQFVDLFSQL

complement(68670..68837) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00075; phage(gi100158) 1.84e-30
MYNYIKYAERKDMNGLSNVIQKKLQQEYNNHPKVVNHIETIKKNEALIKVLKEYK

complement(68838..70544) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00076; phage(gi100136) 0.0
MANMFNGLVESVKKTFLKIENQEGSIKSDDPHKEANLTRDDIVLGYFDEGNYRYNNFETDTINDVSKQASLIKEYRRIAAYPEVADAIDEITNEMSFVPNNIDCCYLGFKDNILSDNLKEAFQSLFDMSCEILQLNENIDVLCRRFYIDGQLVIGLSYDDNNSILDAVIMNPSGLYFNKSTNKWQYFNNSNNYGVADDTSEVYDPEEIIRIDSGLYSDNLILSHLHSVIKIVNQLQTLEDLMIPLRYSRSVSRRVFNIDVGNLGYEKAIAAVEDIKNKFKYKKYYNTETGSISNGASIQSMVEDYYFPNRGGTKGTQVDVLDETGNLGETGDLDYFKNKLYNALKVPTSRLMGDNKTVFDFSSTSIESTEIKFFAFVNRLRQRFNVLLIEIMKRYAITNNILTEDEFDNYSKYIFIGWEKESNFLERQNLDILKQRLDLYTEFKEYEGDIFSRSYLLKNVLKMTDEEIDQMREEILQEGSQTTPGEDEFGNEITDDEDITDDEDNFNNDIEDESEDNSLDNIENKDLKIKDDISNNKRNIVKKATKLGIPKNIIKRKISKATKLIKGE

70589..71290 PHAGE_Campyl_vB_CjeM_Los1_NC_041896: DNA primase subunit; PP_00077; phage(gi100025) 1.41e-165
MTNIPKQNKFAYTEDKPKYIDINGTTNYILPGFEYPSDVAVKFPQFFGGKDNVFYPDLQVTLTPDSLTFENSKKSQAITYTATDGSSITSAVVTIEPSDLATWNEGDKTFTGNEEGSGKAIFELTDDKGRTAIKELPLTVTKAAVVTTLTLSPDNLTFANASAAMQEVTVTTNASDFMLEFNNQNIQAVKSGNKIQVTPKTGKTGSFTITVKAQASGGNQVSKTLNITVNAGG

71293..72024 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00078; phage(gi100155) 1.72e-177
MATRQSLKDYIFGMLGSPVITVELTDFQIDENINFTIQKFSEFAMYGKLKGTLLIDLPKGVRKIKLDSRISEVITLRIYPSGGGFLGLSIPGGLVITPTEMQAMLFGGTV

QGNFSMQNVYSVLANMSILDTYFTIIPNYAFNPFTNMLEFFEDITSEKVLLEVRYKYIPEEEDGIYEQPWVKEYALNLCKRTWGSNIGKYDAPLIGGIKANYERIIQE
ANTELERLETVLLENYCEPLPLLRG

72054..73382 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00079; phage(gi100139) 0.0
MYEVLTPNGFSSFDDISREKKDVYKVITEDDFIKVTKGHKFETPNGFKQLKYLKINDLIKYKNKFSKIVSIDYIGVEYVYDLINVHKNNEYYTNNFVSHNCAFIDKWS
EFSNSVIPTISASKKSQIIAASTPVGLNHWYKMWSDAVEGKSSYKPFKVEWWKVPGRDENYKELMIKTLEGGIRTWNQEYACEFIGSSDTLVDMTVLSNIKFGNTL
REPNFGETIRVYEAPQENHKYMVLADAAKGAIDGFVFHVIDVTNIPFKQVASGKIPESYLMAPPIFYNILRTYNEAMFVCENNEGAGTSVVDLLFQMYEYENIYQEP
DKKWLGVRTTKSNRSKNLSNMKLFIENNKLILQDEPTVKELLTFCNVNGKYQAQNSKAHDDYVMALSLLFVPLLDLNNIVDYDVFLNKINSDSETTDGDVKYLQ
MGFFDDGTSSFYGIFDD

73411..73632 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00080; phage(gi100153) 8.05e-44
MPPIKHMSVADRIAQKRYRKQPKVKRKLKIRAKKNAKAPSENMSWSSKKRGYVRKDPKLRRTMKLVAKLRRKS

73635..74366 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00081; phage(gi100152) 2.67e-173
MGLNKFDSVDYILSSGQRPFRYKVSLILPTKIAKISGALYDNAVNILCKGATLPAPSILTTPIGLDGRNINIPTLMKLDNTTNMTFFIDEKSSVRRILEYWHFCIDSGITA
NEETPSVPGAGVANIVGSVANIGAGFISDITSDIPIIGNAVNSFLGINKGVSGNTDINMTGELKLTLLNYSGNAVGSYTYKNIFPIDVTGSDMQDDQTETINEFSVTFGY
THYVYKKETESIIDAVTGLVGL

complement(74361..75806) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00082; phage(gi100151) 0.0
MNLLELNQNKINMLKEWGFTPISSNLNYGLEVKCDKCGSNIKRSWNQMLKYNKCLSCDDNKLLLELNNLGYTVTDIRLSKLEIQCRNNHIFNRNKADFKRGVISCP
ECDELEKLEFIKSCGFTKIDVNHMRCNKCNNIVKKSYPTLKSGITFCKFCDENNKKSLLDNINLEMVDKNIFKCNKGHTFYRTYDNLIKSNNLCPECYPNNTMFEKE
LKEILPKCIENDYSVLGDKELDFYLPGYNLAIECNGVYWHSDKFKDKNYHLNKTEKCNGKGIQLLQIFESSWIEKKDIWKSIINNKLGKSEKIMARKCIIKQVPKTEE
KEFLENNHLQGFAGSSICYGLYFNDGLVCLMSFGKPRFTDKCNWELIRLCTKMGLNVVGGASKLLSYFHKNHPGSLISYSDRLYSDGSIYKQLGFKFSHFSKPGYM
YTKNGRTLNRQQFMKHKLKDKLEKFDPNLTESENMSINGYYKIWDCGQGVWVKL

complement(75778..76545) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00083; phage(gi100143) 0.0
MAKSLREWYRTHVKSMADNFEDFEIFRTQFYRNPHRAIVKNSSAFKSPADGVIINQTQVNDIDDEVLKIKGKKYTLRNALGNNEEMLDLIKERGGALVIDVFMTYY
DVHYNRIPTDGFLTYEKLLPTESYNNESMLAVEEGLFANNFKKAVTELGYMFCNERLLNIIYSPVLQEKYAVVQIADEQINCIQTAWVPARGEPNTHLYQQGDIFGN
IRKGSQCTIVIPFSKKWNYIPILEPSFHVEAGIDELVRVEPK

complement(76556..76852) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00084; phage(gi100144) 8.84e-65
MDNFDVNSFKIVHPHDVLLEVAYPSEIKSESGIIVTVHPSLIDDRQTQGKVLQIGSEVKDIEIGDTVVFGKQHGIDLHKNDKVKYMLIRDESLMGILR

complement(76908..77417) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00085; phage(gi100145) 1.27e-115
MAKLILQRNKEYKDIKWQNSDKIEDSTIGELSLLDDNDNVIFKCASCENIGPSTDESGTDKRIVAREYKLKWCNSSKNGLLSKKYPEWKADNGSNIAIWVVSDEVE
GFNNRLIRIHTGNAPQHTEGCILPGSDLNNGTVGSSVDITHKLFTKIKELGIENIVFEIKEID

complement(77420..77917) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00086; phage(gi100146) 5.63e-113
MYYSNVVFPLNEVIPGFTYNVKKSKSNIYIRFVAYGYSVDDLEIVYNNSIITISTIKDYHEVKTDPKFSNNFPQQDKFYIQFWCPKISGINAEYSGNFIKLNCSLGDTSV
NLGVVPIKFINEDNDIDILENTSDDTMNIIQLNGFMDKLEDTKDDFDSEITNNKD

complement(77952..78095) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00087; phage(gi100146) 5.64e-25
MVEIIASFFVGGLIGFIAGYFVYHNNKKKASEIGDKIESVKDEIIKK

complement(78127..80490) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00088; phage(gi100145) 0.0
MKYIFTVIDNTSKTKVLKTDIDNKVNFRNVICPSINSFAQLIESNFILSRPIHSNGLFERKRENMDYLHDCGYIILDLDKVTKGNFQKIIDYFKNTKWECLICNSRSYNF
VDNFNLKVICKIDYKSTDENIRNTLLFFKEQLKGLCSIDESATRHSSYQAPSLKISVFYKNENNIGIPFSILPKSQSKTTLINCSNKQVEWCLNYVKTKLKGNIKEYVG

YYSINLPSEKKSKYSYCLYETNPFVIFHPNPSKNINILQEYLKTKDGKAFLQEKQSKIILSSLKYTPDIHINQKFLKNVDIPDTRVVCIKSPMGSGKSNIINQYIKDKSKIL
FISVRQTLAKDISLKYGCKYYLEDKKILYGENYVCQINSLHKINLDYFDYVVLDEFETLLMYIVTSIEDSPYALNILRKFYNILNSKYLLILDAFLSDHSDILSDVCRIK
NHYKDQTNVSLYTKKNTFFSVLEYVCKNKNKNEVVTMSFSTLSEFKTVESLLIKSNLKVISINSNTNRFIRDNIFTEYFKKKYVNYDCILFSPSITVGVSIMNNISHHF
HFDNSASIDAITSIQMVKRSRLASNIHIFVEGSTNMITPLEVEKNIIDSFEIDDLEYLSEFYNKLCYYYETIELNHKMSFCLLLQDQFNNINTVDSIVNYNIVQADIPKEIE
LNEFENSKIKDELIYAIKKDKNYLNYIRNFKFYTLNKNKNEFLENYLLNNPSNLLELSYRAKFLKYCVTYPDIRLKDIFTYNDIQNIKYTTDYFSFSNFLKELGYKKM
NGNYYLPLQYIKHLSKI

complement(80547..82067) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00089; phage(gi100149) 0.0
LIKIEKINESAYKIVSETQLYLDEIKQLCSAKIPNAQFLPAVRMGYSDGVKYFYKDCGDYLIVPKGFIKGIIKRLNEKYKLELSFDDEIEKITEEEFNKFVKSLKLPFEPY
DFQLKAAFDSINTGNNICVMATGSGKSLTIYILCRWFIEKYKNTDDKILIIVPSVVLLNQMYSDFKEYGFTDIDKYVDRLGGDFKVVSFVKKLNISTWQSLYRNVSLF
KDITVIIEDECHTAASDVHESIIFPSATNAKYRFGFTGTLPQNYCDKLSLMAVLGTAKTYVTPRELIDMGLATEMEIKPIILKYNDATSSIVRTVKNYQQEVSFFLGIPE
RDNIIAKLICKVSQKGNSIVLFTRVSNGENLARKVCKLKHGVDVEISELRKLNKYNIFFVSGETKASDREAIRQIMESCDDAIIFGTTSIMSTGVNIRKLKNLVSTMPG
KSYIKINQSIGRMLRKHETKNNIVYLYDIVDDARGRYAKKNYMFKHYEERLKYYNENQYVIDEVVVNI

complement(82108..82527) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00090; phage(gi100038) 4.38e-96
MTIDDLKSFHKKIIEEYDMDSNWNPSTIKHHLTTLSGTIAKYLNYWSRLKHIIIQIDEEYNEKYMILYSHYRENSNINYTVTEIKDLISKDNELCNIRVKKSTAILIMEYI
EKCVDNLNKTRYDLSNYIEIEKFLNGKG

complement(82529..83257) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00091; phage(gi100151) 2.73e-170
MLKKLCFIVTLASSLFAYNYIDSTVIEDKGNNIVIELSFCTKDLDSEKEYIIDHFNNQIDGLEQQQVKSEVYQYRGKQYVFNKGKNVKYNKPIITFVPTSTNGCYIATA
LYKIKHDDIKTSVNNKYESYFNGFITKNTSTKNEVENEIRQNLENEIKENIIIKPEQIKNSHETFVEVPKYLYAQTKENYYINIICEVTNSDNEFIYNFEIKDYKRPLIVK
GKIWGDLTPYFNTNCKVELVGK

complement(83430..84812) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00092; phage(gi100141) 0.0
MKFVNSLSNLSYTENGALTLSSSLNVALDLFFIIGTTNENNIDNVFEKVKESFNIDKELTSRILLWTRDAREGAGRREIFKRFLDFIAENNKEIYKRIIRKVPELGRFDD
LITYKQLDLVGNELIKILDFNNQLCAKWMPREKSSKSKLAKKLMKLLKLNAKDYRKLLSSNTCVVENKMCSKEWNLIEYEKIPSKAMTKYNDAFERNDKERFGN
YQESLIKGESKVNTSAIYPYEIIKLMFKNDILANEMWKNQKDWMEDSKKTLFPIIDVSGSMYTAVQGSTTALNIAISLGMYLSERNDKDFKDYFITFSANPEMVKIEG
NDLKEKYHSIKISNWGMNTNLAKTFDLILNRAKADNLSQEDLPDALVVLSDMEFDEAQQGKTNFEYIRDSFKNSGYKMPELIFWNIYGRSGNIPVRKDENGTCLIS
GFSPSIVKGLLTNDLNPEKIMFETINKERYDF

complement(85576..86220) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00093; phage(gi100134) 2.20e-149
MILTFDPYYDIKESNEFIKNLKENKINFNTYILSKSPYYWFYEVADKYKPVFLKFNEANSTDLRFMLPKLKELTPSDENYLRRIPKTPSDFERYVSPNIFKKAKYAEYF
CVFRYKNISEINKITETLGIKIYILPKKVKEWNIAFTFNKMIRNFVFGHYILLEKTKKTQFNKVGEIELYLNNKVFVTDKMKFKTRELPFSEDGTYYPLKFQIKQ

complement(86204..87382) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00094; phage(gi100154) 0.0
MNINKNYLIKGDNLEVMNSILPFYKGKVKLIYIDPPYNTGNKNFQYNDNFESIDLIIKYFNVDEEEAKKIRSQDKFIGSKVWLKFMKERLEVAREFLRDDGVIFVQCD
DNEQAYLKVLMDEIFGRENFVNCIVVKMNESKGLKNANCHKKLPKNKEYILLYKKQDNKSILKQIRLKKTQNELSSYIKYYNKYITNIENDYKEWEIKYFDPKLNK
QDYLKNLIYLVKPDNNININMEEGTFEKIINSKGKTNYYYMNNGVIMKVLFLHENLDYSLGDLWTNISTIGICKEGLKTTFKNGQKPEYLLKIILDLSTNENDLVMDF
FAGSGTTLAVAHKMKRKWIGIEQMDYIETITKERLKKVIEGEQGGISKEVQWQGGGDFEYLNKEHDDTNI

complement(87388..88119) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00095; phage(gi100155) 1.11e-177
VKYRYSYSRLECFRQCKLKFKYSYIDKISVPKDQTALIKGSYIHWLIEQSFKEEPIEVSKSYHNPLINADQYKEYNEIFEKFKETEKYKNIKDLPALGNEVNWALDSK

LNPTNYYGNDYVIRGTIDYIAIKNRCAIIIDWKTGKTKDKKYIPDANQLALYAIWAEKVLNVDKIICQFVYVETNDFHTYTYTSDDLVPLKKQFAQDIMSIENEKAFI
ANPSILCNWCEFKSMCDSFKNSSYNRE

complement(88129..88473) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00096; phage(gi100130) 2.13e-71
MENIDEFIELKSQKLNVTDFIEKNSINEDELVKNAIKQIFDLEKQKREIDVEIRDIKTKLSKDGINITEFNRVLSTLKNELKMSIDSLSANISMYNSIVSDKELLQNLKDQ
IND

complement(88530..89144) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00097; phage(gi100157) 5.27e-142
MKLFEKLEEWLKERHLDKKEYDHLTLLGYLHEEIDEGIKKRDSEHESIDWRCDCIVFLINSLYQDGYNPKICMDECLKEIEERTGEYSESERKFKKHMGAYTYKEA
LDEIIKNYNCRKEDITLHGDHREFWYFLVNGKQIKVKKWYKADYSKSIRDDISNERYITKAYKLGKKIMFRQLNTKNRWKLLRDENLNFKEFDYKVVD

complement(89519..92182) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: rnaseH; PP_00098; phage(gi100048) 0.0
MFKYEYVFEHNFKLYARLYDEVTKNSIIKEYKSTEYVPELFIRTNEKTEYKDFYTHGYLKKKTFKATYEIYQYLKNVSPSTPLYGNINRPQKYIRENFKDIDCNHEFR
TQYLDIETRAINGYAKPSNPTEEISLIQVYDNYLNKFIIFGAKDLNISLESDIGEVIYKKCDNEIQMLKKYLTFVVKTNPTIIAGFNSNLFDIPYIVNRMIHLGIDDYIELS
PIKAITHKKMKTNDDIEYDGVKIEGIIQLDLRDLYIKYTTQKPSRFSLDEISKLELGDTKVNYDGSIEDLYKDFNKFVSYGLKDVELLIKLERKLKLLKVCQLVAYKC
GVNADEVSGTLMQWASLMYNYALSKNVILPLRQLKIINYDPPYPGGWVRVIEGLHKNVCSYDFTSLYPNIIIEFKIGLDNYIPVSNIPYEKAKILEENRARFINEEPNE
VISTSLPEDLKDMLNKYFYFYSETYDKTNNDSMEEFYYFKNIIDNKDEIKQICKKYGVNVTPNGCLYFSNGTSLFAELIESFFKDRLNHKSFLKNDNLTASEIDYHDL
MQYMFKILMNSAYGSTSLAINPFSFGKKMSESITTTGRFLNMWVSYKVNKFCNETYNLNIDVNSRPLSIQCDTDSNYFEFKFLETPKDLQENAKFLKSYCETTISPVI
DDAISEAVTAINGLDKNSNLGMEQETICDRLISCARKRYVGRYFNKKKSDKGFKITGLPMIDKTTPKWTKLKLNECLDLILDSDLHGLRQFINNIKNEFKQQLLSDIC
MNKSVSSLSYIISNGKWVSSINGNPCPIQSRGSIHYNNLTNKYKLKKIMEGEKVYIVYLKTPNTITCDNVICIPDDEIVREIPSINEFVDYETMFEKYFIQKLDIMSKHIG
FDYKNIFANTLDEWL

complement(92322..92711) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00099; phage(gi100161) 5.90e-82
MKFIECIQILLENNSIGSLSLENDYIKIYKDNDKLKIVDSKDNNVLLSSEHINNENWELNNKLFELILGSMWINDSDIVTKVEDNSFYNNIQYTTFRNMLTNEISILESD
KYYTNYCKNKWFQPEPLKV

complement(92708..93148) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00100; phage(gi100162) 2.30e-102
MENISKDLITIYRYGNNFELYNDFYFIFDFDVTSKGFKLEKYLVGNNIIRIPKGFRTDFGSIPQLFQSIISPVGKPTKAYVLHDFLCGKSNKGDIPRALADELFLDAMKL
LGVNVVKRYVVWAWVRVYGIIYKPLAKFFKDIWNKL

complement(93150..93653) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: recombination endonuclease subunit; PP_00101; phage(gi100052) 2.97e-114
MIKLIIGPMRSGKSLELLREAEKLHFGRKKYILIRPEIDDREFISRSYKTLHNLNVIKTNNINTIVNEYDYILLDEFQFFDNSITNIIIDNISKNWILCGLNINYESKLFENII
NILPYADRICKLSSICEKCGSEYGNHNISNTGEICIGDDYTILCSTCKLQLKG

complement(93650..93859) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00102; phage(gi100121) 1.26e-33
MQIEDVVIDTFKSILILLISAIMLKVYVILFLIISLGVLYYDLTIGIPVTATLMFISIYLANKFEKFIS

complement(93838..94782) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00103; phage(gi100165) 0.0
MLNPINVKYWEIIHNKEDLGIKKSDDYNCKCDVCGDSKYKNKKRLHLYRKDSYTDDSIKCFNCGYTATMYSYIKTFHPMYLNNYLNEIGEKYIDDLNIQNITLTKK

EPQKPKEFFSLNLPKASEIKEAKEYILKRGGNPDDFYYCKESFVINDKTFKLPNFIIYLNTVNDNAFSFYSRSINDKIFYIFNSDDGFKVMNYFNIDPLKEVYVFEGLFD
MLCTPFKNKIAMLGATLPKGMKVIPYIIWCCDNDETGRKEMLKHTNNPNHKFVVWCDDEKFKKYKDINEIYQSGVNIENFIKEHTFDGLIAECKLRMW

complement(94766..95275) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00104; phage(gi100166) 4.77e-118
MKKVLCSAVMVAGLMFVGCSTTTPQQQFAKPMLEKYDDLPSWVKEYGDIDTAVGSAMYMGQNYIQQQTEAIAVAKMNLTQKLSSKVDSMIKQYYQNKGVVKT
NNSQVSVQVSSSLVKNVKVVDTYVADDGELFVKIEAYSTNLLETIKNDDSKSLFDELDRRVGNVKSN

complement(95362..95688) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00105; phage(gi100167) 1.23e-72
MYFSLKETLEFLSTNSKNGVWEYDDISEADTTVFCSYFSDNSDENDIYIILSNPTGKSDIDLQGNVTDTDSEDGIPDRFSTCIMKVNLAKLNISNFDELGNAIKKYRL

95774..96229 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00106; phage(gi100117) 2.54e-105
MNFRNIALNSNIVFRTLLFSDDTQYYCQKVKLPRISLEGQKVGHSTGTLTLGGEVAKFDSITLTLLVDENLEVWKNFVNLINKYNKISTNTGCGIEATSWLEIHDSKN
KYLFKVEFYKSKLDEVSELEYSTTDNNIITLDITLNFDYMKII

complement(96230..96511) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00107; phage(gi100058) 3.41e-60
MNYLLELSPIFIVGLICGLSNYLSDEEDTCAGKHIKCILKYIFNSAVLCTIIYCILTSLELPYLTKIGVAGAITYLGIDKAMSLIKEFIHLKK

complement(96697..97359) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00108; phage(gi100059) 1.12e-155
MIISKKTLADQGQLNKNVILWAIDIGSELALLNRPMTVRKNSENMMVEYVDDITPEEIEAGKQAIKEYCISNNIMDIYYNFLIATTQESNKLDILKEKKRYEIQSNRD
KALENGIVYNGHTFQTREKDKLNINGAVTNLMLDIQSGTNSVSEIIWIDINDEKVTFNPQEFLKFTSMVAYNTQEITFKANVLKAKIEAAKTIEELEKIQWDDSVKTT
QKKR

complement(97395..98099) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00109; phage(gi100171) 2.21e-153
MKTYGQTKFKDIIDNTPELAYNLEFTIGNGGNFTNILDALNHCKRYINYPYYTITLKLLNNLTIDYTINIANTDFRNLIFDGNGFTISKNCKSQYDTVFHSDMSIYPWI
KNLTVENTNNRSFGIAFTNYHGSIFASHANVENNLTIKNFWNGIRHACSYLFVPGLTLDNCEYGLYAFRKSDTCLDAFVNIKNCGTGIAVYHGSEVVAQGVTFAGN
TTDCNISYNTPTTNGTIWK

complement(98276..98884) PHAGE_Campyl_PC14_NC_031909: protector from prophage-induced early lysis; PP_00110; phage(gi100001) 2.05e-127
LQTAINEANKYINYSNKSITIKLISDLVINEYINIVNIHSPFLNIDFNDYSIILNNASYDIGFSMYNSILGHINKLKINCNNKSINTAILLQKNSFCCFYYMKGILNCLGNAF
ALSTNSEAFVSDSTCELSAGSSGYYSKGILSVGSRLLFHTCKFTQNSGTLSQSVETSGIIDNFYTTFSGSVTGKSQVVGTWTKNGYISA

complement(98869..98994) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: ribonucleotide reductase A subunit; PP_00111; phage(gi100062) 3.96e-14
MLEYGRSSIKDIIDNSAKLLTSNLEWTVGTGGASSKTCKLL

complement(99039..99836) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: aerobic ribonucleotide reductase B subunit; PP_00112; phage(gi100063) 0.0
LSDALAKALEYISVKNNCNINIILKSGYKLNEQIILRNALANHINILSEDDEVLLNNFDTQDYIFMFYGCKAPNIKIMINAVGTRARGWYFRESSVTMVPSTSNAYKY
GIKNCYKNAVLSLSSKILISKYSFINNGNNLDGTQEQSLLYCNDQGELTGFDLKLDNNGSENCNGWLYYCGYGSKMTLTNSSITNNKSAANILNNNNSYMNLQYPN
FTGSKAANLLLCYNGAHTNITGRNVTNCTWSKYEFPFATNTITANGIIHAP

complement(99821..99943) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: aerobic ribonucleotide reductase B subunit; PP_00113; phage(gi100063) 1.88e-13
MINYGNSNIKEIINGSVKILTESKTYTVGRGGGSPNCQML

complement(99961..101298) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00114; phage(gi100064) 0.0
MAYGIDNVWSFVNDSQTGIDKVPVNKIILLKSENKLYLKKQEGGLTATSTVNEAILNNSIVSLSSDGNLGAVDSSIKVINDPEFTTTDNISKGKKMFKIAIEPDTIIQVL
GLYIENAANSSIDAVPFDYIIKNNNVVIYTDNDTIPIKKIIYSKTKSSQLSLSSLPKLLTENLEWTVGANGTFSNLADALQEASKYISVTNYKITITMKSSYKLTESLHIN
NANLGHVVLTSEDDYVDFDGTMTPNPSFINQYATTPIAVSFTFGISPTISFKLRFSSIPTMFSMAFGFLQTNFKLNNSGVYNAKWGVGSVGCIGLVQNSTFENCTKSG

VVADNGSILNVLENNTFKTCSGNILWSADSSKIYAGSVTFDGTYNNVAANCGVSHIASELGFNIPIFKNISNSNSYALFASYGGKITCGSNIVVSGFNKTNITANVFSS
SGCIFLY

complement(101322..102968) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: endonuclease II; PP_00115; phage(gi100065) 0.0
LNNINFKSITLQNFMKYGNKKTKFEFTNGIHLVTGKNGAGKSSLFLALHYCLFGKTYNGKTIGSLVNNINKKGMYVEVEMNINGDEFTIKRGTNPSIFEIYKNNELIP
LLSTNSAYQEFLENNILKFTEQAFRNLIYLGGDLLSQSFVRLSKKEKEDVFAILSDTATFLELTEKIKLLKKEKTTVQTNTLFKINTLQDVISKAKIKYEYDLKAYNDY
IENKNNNINEIENKIKEESGKVEKLKELKTQYDSILTQDPSNKINDLLKIINEQKSALQLMEKYKMCKGCEKLKQIIPSNIDVSNHDDLLKQLEVLQNENEVYIKNKD
DIYTKMLELKPSIENKKIYEDLLEKSKIEHIEKPSNDDIISNEKELQEVSNEYNEINTYISNLNQLEILLNNNNLKGAFLNMHLPFINKTINKYINMFDEFNFTFLLDSNL
KETITKDNKPFEYKSMSNGEALRLTFSIMLAFLDICRNKFDVKCNLLILDEVLDSSLDSVGKNELLKILTKNTDLMSMYVISHNSEIKNQLDYFTSTVNIINDGKFSEIE
YK

complement(103010..103330) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: RNA ligase 1; PP_00116; phage(gi100066) 1.74e-64
MIINVDKNMFQERMQKQGLSYGASDVLFDYIEQLEDDIGEQIEFDPIAIMSDFSVAEGEDELKDQLETLGYFDMEGDDSDLDDAKQRAINDGVLVYEDDDYYVFKS

complement(103388..104383) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00117; phage(gi100007) 0.0
MGKLIALIGDLHFGCKNFDHDILEVQLNSLEKYRDILKEKNCSTIYQLGDMFDNRKLIDLKLLHTLSTRFRNIFEGFNFYTFAGNHDMYNRDNRDIVSSELFADLLGI
KYIKEPSYHIFGKYKIGISPWLCGDEELLKECDILLGHAELKGFKYNHTSIAEEGLNIDNSKYKKVYMGHYHFNQNNVYIGTPYQMTFNEINSVPGIILLNENLEEEFI
ENTWDRRYFTVTVLKDKIILQYKDEPELFTGNLPDFCKVGKIVLKEKNEKEDKILEYFGARARISRIFYKYEEEKLYESVNLNNSVAESLDFIKEYILKEHKHLESVL
NDVINN

complement(104371..105240) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00118; phage(gi100008) 0.0
MDYLKEEDLRDEIIKLQKVEKLKELLKIEDKTDDDIQQIEKLREEGISEHYKKTKFGEMCLLLIKRILTMPKFSGYTYKDDFYSNATEKLMLYVIPNFDANKVSKISK
EPVKAFAYCTQIIVNSILQVINERKAEQELLKNYYTDYTELELRLEQKEYTCCYKTDDENIEYDVEIYPIVVIDDKLYIVEDINKKVETDLNLDISKRYFIVNEDIIQSN
TLWDILKNIDNNKTVRMIYHHDYLLKTDEYNKITGKNFKTLDIMKFRNTYIPSFPKKEKKTVESELDIWEN

105333..106295 PHAGE_Campyl_CP81_NC_042112: baseplate subunit; PP_00119; phage(gi100104) 0.0
MSKVINESTTTVDIAGVELKLAKLIYRIYTESLLNRIGARINVAVPNGSIFAFKGKYLTDYTGTDKSSTPYATILPDFAGNRDNNQETDVKAEMNYKIVKRTINCQTK
KIRSKWSIEAITDLVALTGKTTVEDILEKELLTEIIQEIDFSALKMMTTKATKTQLTLKAPNDPLVGIELFNAAQKKILEMAASTKRAITMCITAPYETCAKLMSHPNF
KANEDFTNSYFMGSIGATEIYCDYYNSLNKEYMLISYKHRNKEVEIADGSTCFAFYSYNITKAFDATSGAESYFHFLRYDVVQHPLDNTNDGQSIFLHCIEIQ

106303..106950 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00120; phage(gi100010) 6.98e-158
MAWNLNNRQNEYQLFGTLSAEIIDMYGFQLTYIKTTRLGHDKVLDDIVNYGTEATYQIFALPENAEMFDERGDILNKFGIFTMDSMNLFVSANTMKRIFQDDSKIPS
AVGDLLLLPSGKYIEITSIEHQVPGANNQFTYSNSKNVYMLRCKSFNYNHDNIPTLEEVNNEEVNESLDEIFNLVGSAENSKDKIKEEQDKESPLVKGTDSVFGYLDS

complement(106935..108713) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00121; phage(gi100071) 0.0
MDNDNKIDYLNNLGYEVISKNLSVNLEVRCSKGHTFKRAFSVFEKGCTTCPKCKDEAKMQFLHSLGYKIISKDKSDYFEVECKHGHVFKRALSVFKKGTHSCPKCE
LESKINHLHNLGFKYKSDNLVECPSGHTFKRQFSKFTDGHIICPDCNKQNKLDFLRKCGYETVSDDLTYNLMVKCPKGHIFKRTYYTFEKGIVTCPECDKNKKEIYL
SNLGFTIQSESLGHSLEVKCPKGHIFQRSFSNFFGKNVTYCPKCKDDEKMLIINEIGYKITSENLAKYLTVECPEGHIFQRSFGHFKRGNILCPICNPSTSSFEKEVSNLL
DNYIENDYSVLGDKELDFYLPEHNLAIECNGDYWHSESNGKDKNYHLNKTEKCKEKGIQLLHIFESSWIEKKDIWKSIINNKLGKSERIFARKCVLREVPKIEEKEFL
ENNHLQGFTGSSVCYGLYFNNELVCLMSFGKPRFTDKYDWELIRLCTKKNTNVIGGASKLLKYFEKENEGSLISYSDRLYSDGSIYKQLGFIFSHYSEPGYFYIKGNN
KYSRQQFMKHKLKDKLEKFDPSLTEYENMFLNGYNRVWDCGQGVWVKDQLSK

108822..109853 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00122; phage(gi100012) 0.0
MEFFFFETTKKYCKGLLDIFNSIQVKKKIDEKTDKYVTVPISFGSKDAASVFNDTELDQLLSGNFNILPRMSLALMSMERDDQRATSRFQIPIKDIDGKNITFQHNCVP
YSFDFVLSIATRSLTDLTSILEQILPFFNPNINLRVRELEWLTEPTTIQVELISVDYELPDENDGADIRVCSANVTMRLHGNIYPPIKNGAVIQQVKLYLSPVVDFSEDSK

EIVHKFNVNENTHMMDIDSFVRIDYGEEWNKVKPVIDGVKGEVKNLPIQENIKYRILYTDDTDDNIKFIINVLEDNGVNPIISKQLNYFTVFAKNKGTLKLSIQAVNS
FDLQSNIYEMELEFQ

109850..110305 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00123; phage(gi100100) 1.55e-102
MKEKAEALGKKLDKINDIFNITEKTIVEVEKSDLVKSNPEENLKFTYLKEDFNLMRESLVNTIKRGQDILEVISNNILADPLSSNQAVMAYSTLVDTINNSTKLLTDIY
KNIVDIQIKIAPKEAEKGSGKQEIMTIAQITKMISKNQQSQN

complement(110302..110853) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00124; phage(gi100099) 4.96e-112
MADLKKIEELIALAYGYEYGISHIDESDIDVFIKGFDEKNAEQQLKKADIDLESLLSNNFDKNALIMINYKKYYPIKLYGFNNLIKEFPSLNNINFYGALSGASTIIIKD
DEIMCLVDPNDYEKFKESFDSMLIELMKFIANSNSAEKAMDYLVSNDVGVGSYYNENKELTQMIFNAIELNKA

complement(110846..111037) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00125; phage(gi100098) 7.00e-26
MFKKLLNWFMNNFCACILLLYLILLLVIIDGEISLSNVITVIVITGCYIVERIENTIKGNKNG

complement(111061..111360) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00126; phage(gi100097) 2.60e-62
MKSSNFKTCKINKKYHCINTKSALVQENYKMEKSKYSVVKEFINLNYNIPIEKIDKETELFFFSIKLLCDIIELCPKHKKEIEDKVGELCDFREYQLES

complement(111347..111514) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00127; phage(gi100016) 1.02e-29
MLEYFNCYTSKKELYNYEKLKQELNEHGLNIKDDENSIKEDIDENILKRKNNEIK

complement(111508..111930) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00128; phage(gi100017) 2.94e-79
MTNRCFIGILENNNNVKYSFCMYDGNIELAGRILLQNYNKLCELLNIGKDIRFLSNRIDLCNFFEYEYNYNHDVKMNLETFKNIVFDDHYCDIKYIYLFKDGKYYFA
DRNNYKNLLENALEDFICYSMNNEDNLIEEIKC

complement(112023..112460) PHAGE_Campyl_PC14_NC_031909: exonuclease A; PP_00129; phage(gi100018) 3.71e-86
MENYKSVYNDCLLLFLELQKSDDNKKLQIYDLMLKCIKLKLPEITTKENIKKVQEVLKNYKEIETLDKDKTYGTISWYYLLYYIGNVYNIGYKVVFYGTNGRYSYN
DDYFEDIINLYSTITFLKEKLQKGCPDNVSLAVFNKEGN

complement(112584..113177) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00130; phage(gi100019) 1.36e-72
MTEIQFNKIKERLTQWREERHLTYENQQAEFFGNVFEKVSEYFRAKDDLEKIDAICDIVIYFFNAFDFKYIAVSSNMYCYTFSDVVVYNIYSLFGARTDNLCVVENE
NDFINLEKNLNLTMFEIEQLYENLDFDFYKCMLEKIKEIESRTGYYDEKLKKFIKDTSDEAKAKWYKADYESCMFEGWEIISKLIKEFKK

complement(113158..113499) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00131; phage(gi100091) 1.47e-63
MVSTVFENDYVEVVTRKDAESIVENFIKTCDCDWNDDENCDKCASIDNLKFHLEANRDCNIFVRFKFNKDDKTNLRWSGNLCVNSISEYVENELENDIKVVKYNR
RLNDRNTI

complement(113543..113746) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00132; phage(gi100022) 1.67e-42
MNKIKQWTIELMCMFYPIKIKSTAKDNYYISYKFKFNKYYVFGDKGGALFAENYKDALRIVEWMDDN

complement(113749..113898) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00133; phage(gi100023) 4.33e-28
MKIEITRDISNVVKKSPEIILNDEFYKLYVKYIGPSEELLFYKNCNKGR

complement(114125..114601) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00134; phage(gi100084) 5.29e-110
MYSKFINEAVSDDMLKAINVANWKTGLDFRKDYEEIESHGKKALEILDKLAKGGYNSKQYYNIYSDLRDELWNIHDRLLSYKNKMPWFRDELQSPELKRYREIIK
DYIYEVNQAMKDLKSDYAVVSHISNRNLESIIKAIIDEYERLYEIVEKIALSQ

complement(114728..114859) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00135; phage(gi100085) 6.33e-18
VKLKSFNFRIYDENTTINLLVDHKYDLFETLCGEFEPDKCEYC

complement(114871..115152) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00136; phage(gi100080) 3.56e-57
MALYKFSVKLYDDKHENIQKFCLIDGKHWHLLKDFRNCLISPDNVYFYDEKDLISISDYEDALKVFKKPIHRRMFIEYGSSYQEPDDKFITEY

complement(115272..115724) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00137; phage(gi100091) 2.26e-98
MLLEVVFENFKFCRQDRVEINFDKLYSPDYFKKTFRKVKCKCNPLKSLFFVDCDLPKYILKAIKRDKSLCNEITKDYGVITLTYRQDDFLIDYILKITESEIIQTTDLVY
LDLYLKDENSDCAKTINENTKLKPSEKKALEKVKQFEKIQ

complement(115835..116149) PHAGE_Campyl_CP30A_NC_018861: hypothetical protein; PP_00138; phage(gi410493054) 1.39e-68
MRITFNFEKEYTSTPYARNAEHDKEKNGEDFEKNYLSKWIDEKQETLIKVDNLELPFSDSFVDASFCKLIRQNKKLFYKYIKIDDKTDDEKDLLNTIKEVLARK

complement(116305..116493) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00139; phage(gi100076) 4.00e-10
MDKKCRDSYGQIDYLDAYGNYVKTIFESNTERHRNYSGENIRRGNGTKRLEESIKKCKGAKM

complement(116499..117113) PHAGE_Campyl_CP81_NC_042112: co-chaperonin for GroEL; PP_00140; phage(gi100075) 6.32e-107
MIESKFIIKRKLNFKNMEFGYKLFDVSGYFEFVEKPIYPRILEEFKKLDPTMKNKTILNRLRYIDRVRYDLLYDFTFTLAYSKSKLDKTIKNGKDLCEYDLYDLKPDW
LLKMVSDIIDEKTLLKYLPDIFEYMDDIIKSINDNFDLSNNAIFKWFQNVRNYIKLLLDGKIDYKNYCINIDLVIKSNMENALLFEKEVIEELNRC

complement(117274..117660) PHAGE_Campyl_PC14_NC_031909: membrane-associated initiation of head vertex; PP_00141; phage(gi100034) 5.89e-75
MAMILSQEEIDALLECDSRPTNLGIRSIVDKKISELREEHSKLSIKMKAIQGLNLLAHTDDFTIKDYMSIINDLIDCLKYKISHCQSFRDNISNKEAEKEFLKELGSFKLT
LLDFELNMNTGEENGEI

complement(117739..117894) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00142; phage(gi100072) 2.42e-27
MRELRGIVFNFYKKYFCKCESCNFREFGKLFKNYFIYLNLFQLYKITDEGI

complement(118082..118483) PHAGE_Campyl_CP81_NC_042112: 3'phosphatase, 5'polynucleotide kinase; PP_00143; phage(gi100070) 9.18e-90
MNNATVISFKFETEQLAFLNNCICYYDDEFYNVKYMCNLSDDEFKRITNFISCMKNNIKYLEINDKNVDIETLINRLGTHIFRYAHTDTPKEHKDTEYMLLKDYLLL
HIKDYGDNELVKQILKKSEELNSKYL

complement(118534..118977) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00144; phage(gi100038) 2.47e-103
MPEFKQGFYKPINPEKYIDDVTNIIYRSSWEYKFMLWCDNNAGVLKWASESIVIPYEFLGKKHRYFPDFYIEVKDKDNNIKKYIIEIKPQKDAIFKKPKIITEKNKKRV
VEQALTVSKNQAKWEAAREFCRINNMEFMVLTENELFK

complement(118977..119360) PHAGE_Campyl_PC14_NC_031909: RegA; PP_00145; phage(gi100039) 2.74e-74
MNESLADYGLDVNGFYKHIDGKESIVETDDFKIKITYDSVNSEFDGDNEELLLKMHCNIELRYIAGIEDAMRVSDEINNKIVEIIEEDLKKYDDVSKYLILVDSGVFID
PDDPDYIQNAYIIIQPKY

complement(119357..119680) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00146; phage(gi100099) 5.69e-60
MNIYSIFLNEEVEPQKDLAKKSLDFLGEKLNATHSVSEKGNTLIATYKDKNGNKLCDVNITVNDNNIKVTKVTDNKGKPKQIDLVIHRINDIIGSRMMSYINKVKKQ

complement(119981..120256) PHAGE_Weisse_WCP30_NC_031101: DCTP pyrophosphatase; PP_00147; phage(gi100024) 4.39e-05
MNNKRKNNGTRRFTGYFDKNGNKIYKDDIIIFNDIVHDTNRIGVIIKRQHSGEFRLEFSKDDTLGLKILDESKLLVIGNINENAELLEAKE

complement(120416..120658) hypothetical; PP_00148 N/A
MKIGTDKNGKEIKIGDVLFCLELVATEVEDEGDEVEYEEFEHYIQVLEKDNEIIVCDLDSDEWWFLHQFSFADYKIVSDY

complement(120655..121122) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00149; phage(gi100087) 8.74e-13
MKLKDFDFRIWDDTNKGYIEEIEIHKFQNYPIEAGYTFMETDRIGEVEFIKNKNDLEIELFTGLYDKNGTKIYEGDIVCCSTSQGKTLFYFITTNKNINTFQIFVISDLEK
FKICNEIDINSLLYCDLSNLEDMKLNSEVIGNIHNREGISKELK

complement(121119..121325) hypothetical; PP_00150 N/A
MKEKVQNISIDVNVEELLEQVETEYLLHELSRRPLLYVDITSLIWDTLDEDELKILKKEVHQMIKEKQ

complement(121660..121830) PHAGE_Campyl_CP81_NC_042112: aerobic ribonucleotide reductase B subunit; PP_00151; phage(gi100063) 1.03e-30
MDIKKLKESLEGKDNGKYFCEIFNTNVDILVVDNGMKKSEAIIQVLEDVKELYKND

complement(121876..122157) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: baseplate subunit; PP_00152; phage(gi100104) 6.97e-53
MEKVIHKESGKEYSYFKPVLNKTTNEVMICYTDGVNFYVRTKNDFFDKFEILETPEKYDTIKYFHDLVNNKLWALKRQEELLDKVSKFDLSLI

complement(122164..122406) PHAGE_Campyl_PC14_NC_031909: ssDNA binding protein; PP_00153; phage(gi100044) 1.85e-46
MKLIISLLILASMAFSIEVCSFKEPLKRGFFSIDNSIVFLCIDKKLFVRNFPGETDYSYSVTQVFEEGMKPQACSCQAEE

complement(122403..122570) PHAGE_Campyl_PC14_NC_031909: loader of DNA helicase; PP_00154; phage(gi100045) 4.14e-21
MTPKKIQKIFEKVLKEKEKEYTDGRLEEIRKEREYVESIVNEGIQKANNMLKEFK

complement(122928..123968) PHAGE_Campyl_PC14_NC_031909: dsDNA binding protein; PP_00155; phage(gi100047) 0.0
MINKKALINHMYSEMLHKCLNGTETVDNPYHLEKTVLDHTIMVLNKVEDLFKNDKDYKVLMFGAALHDLGKIFTREVITKDNRTVKVRFINHENVGVYYACDVL
SKFDLSEEEIIKIIKIVAYHDIYKYNIDELKRKFTYDDLQLLYKFSICDLLGRITHTPKPTDIYKQIKSLEYYETKGIDSSKPTITMLIGVPGVGKSILCNQYENVVSRDDV
LMSYGKNKFNLETYSEIWSKLSQDDQKEIDNIFKFKLNRLLQQGKDIIIDKTNTSIKSRKSLLNSSSLIKSYNKVAIVVLCPYNTILERIEKRSLETGKEISKNIVDDFIKS
MRLPTLEEFDEISFKWSI

complement(124171..125544) PHAGE_Campyl_PC14_NC_031909: rnaseH; PP_00156; phage(gi100048) 0.0
MLPVKTLTELNDININVIKRNGTVEKYSPDKMYKFLLKVCDNKESYAINILSKSKIKLRDNIKIQDLYDEILSTTVNEISMLYPMYEKFAAKLYIIKYRKNIGDEISLSS
VLKLGLSSGVYSSDFVNSFSEDEIQELDRYIDNNRDYLFQNYKAISMFYTKYCLNRTKTIKLETPQITYMRVAMFICMNESNRVEKIKRIYDLISTHKFTYATPIMLNS
GINKGQLSSCVLAKMGDDSHSILATNDNLAIYSKNKGGTACDVSALRATGSIIDGVGVSSGPIPFIKLLDSTISAWNQGSTRKGSCCVYYPTWHMDVQNLIMLKDN
GGTESTRARNLQYAIKIDDVFVKRWYNNENYTLFDPKDTPKLLDTFGDDFEKYYLEYEQKSNIRKKSINARELFDEILKYRVETGNIYIFFIDNVNKQGMLNRIVTQS
NLCCEIVLPTSAPYKKDEKIVHYM

complement(125531..126667) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00157; phage(gi100055) 0.0
MLLSKKNLVTDKSKEKFFFGEYSGFQRYDWYSHNQLESLDRKQQAQLWFPEEISMIHEPKSFIELPEHNQKQIKANLTFQTLMDSGQNRGLDNILIPLVTSSGLEGC
LKTQAYFEYIHSRSYSHIIKSVFPNPTDVFDEYCEYPEIKTRINDEIDTYESLEGSLEENDENKLKILEACLRIQFLEGVKFYVSFLTTYMINKYSAGGNKIPNLTKIIKLI
NNDEDIHLIIFSFIIKTLRSEQHQGFSHLFDDSLSRKARKIAKKVYQDELEWAKYLLSMGPIPGLTIENIDGFLKFFVDDRLKKCGFQPIWNAQKTDLVKEFQEIKNISS
ENQMLQEVDSITYSKGVMKKDTKLEIYNGETLENELEKILNGEIGNVAS

126867..127004 hypothetical; PP_00158 N/A
MSISVYVSNNIVTYSFGFSKCTPTLSNTSKATGKLIKLMIIESTQ

complement(127032..127403) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00159; phage(gi100111) 6.26e-83
MKLLVAGSRDFNDYNLLKNKIFELNIQPSTIVCGMTRGADMLGYQYGIDNSLKIEKYKPNWNLYGKSAGPIRNKLMADSLNKETDMAIIFWDGISKGTKNMISILD
DKKINYKIIYYKEKENE

complement(127400..127606) PHAGE_Campyl_PC14_NC_031909: recombination endonuclease subunit; PP_00160; phage(gi100052) 4.52e-41
MFVKIKELICKFVNFKTLQKFITTDRQFIIEGQNGMKYSGDFFFVDEDGCICKISDGSYVGTMVKSSK

complement(127640..129115) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00161; phage(gi100053) 0.0
MTNHEKIIFLNNLGYKAISENLSKNLKVECKSGHVFGRMFDDFKRGSVNCPECDRLGKLNYLNNLGYKVASENLADSLHVECPKGHIFKRAFGDFKNGKINCPKC
NIQSKLDYLNSLGYEVISENLSKGLEVRCSNGHIFKRAFGKFKDGFTTCPKCKDTNKVNYINNLGYEIISNNLADELKVRCIQGHIFNRTYGNFKQGKIICPICNPSTSS
FEKEVSDLLDNYIENDYSILGDKELDFYLPEHNLAIECNGDYWHSESNGKDKNYHLDKTLKCESKGIHLLHVFEHSWYSKKNIWTSIINNKLGKSNKIMARKCVLR

EVPKTEEKEFLDENHLQGFTGSSICYGLYYQDKLVCLMSFGKPRFTGKYDWELIRLCTKMDHNIIGGASKLLKHFHKNHPGSLISYSDRLYSDGSIYLRLGFTFSHYS
KPGYYYFKNGTKYSRQQFMKHKLKDKLEKFDPNLTESENMVENGYHKVWDCGQGVWVKGNL

complement(129148..130194) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00162; phage(gi100114) 0.0
MSLIDKLLKSSTLGNRTSVLKESKYFGKDEFVETPIPMLNLALSGKLNGGLTSGLTVIAGPSKHFKSNYALVMMASYLKKYPDSVCIFYDSEFGITPDYMQNFGVDT
TRVIHTPVANVEELKFDIANQLENIGDNDKVIIVLDSLGNLASKAEIENAINEKSVVDMQRSKHIKSLFRIVTPYLSMKKIPMVVVNHTYDDIGSLWGGQVVSGGTG
VIYSADTIFVIGKAQEKDSKKNLQGWQFTINVEKSRFIKEKSKIPILVTFDNGINKWSGLADLGLELGFLQKQGDSHFNPFTEKKLYLKGAPQEQLDEFFSELLSNKD
FVDALEYKYSLLNITPNNNETTENNV

complement(130250..130543) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00163; phage(gi100116) 1.92e-53
MKRNILLLIFSSFLFIGCSTATKTVTITKKEYLKYPLDEKYIPHKLDVKIMKQKLNGKDYLLILPNDFITIYNQYKHLELNYNNLYDSVEKFNLQIK

complement(130512..130850) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00164; phage(gi100117) 1.44e-49
MFNIILSVIKSNIVYIIFGCLLVAITYRYISLEKSNAVLIENEKQLTQNLNESKKELEVLDKYNKITVEIFKEKETKYKEVLRNIKNIETKIKNLQPIGKDKNETQYIIIINF

PH 2

CDS_POSITION BLAST_HIT EVALUE PRO_SEQ

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region 1

complement(4..609) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00001; phage(gi100059) 1.17e-132
MYSKFLNESSENLWVFAKNDIKLRKLILPVIQDNIEYVMFLNDRSIEEGKLKDICLDIEIFGVFEHYNIGNYKKIEPSIVVNVTDLKKDALKSIEDKLKNCKSKDEPVL
SLKLDMITEYNVARLLEKEYYINNFTDIIQNELKSKQFKIVEGNIGESVVELFNDYGESMIFTLKNNKVIKVNGQVGTKYNYLYSSLVIQKI

complement(626..1582) PHAGE_Campyl_PC14_NC_031909: dihydrofolate reductase; PP_00002; phage(gi100060) 0.0
LKSINEKEYVWAEKYRPSKIDDMILPDKLYAKIKEWINSGEIPNLGFFSNTPGTGKTSLNKAICNELGATHLFINSSKESGVDLARNKITSFASSVSIDGSLKIISLSECD

GMTNELQRSIRDILDEYTQNCRFILTANYTDRLIEPILTRVTCIDFDKEFNDNKTELGVKILDRLEFILQNEKVEYDKKDLQKLIQCFYPCIREMLIVMQHNTIDNKLVI
DEKVFETINNYSNLIEALKKKNFTEARKIIAQTVSYSGFYQYLFKNIDNIFELESIPQAVMLIEHYSDHDRTSRDRELCLSALVAALIKYDIKYKNS

complement(1640..2197) PHAGE_Campyl_CP81_NC_042112: ssDNA binding protein; PP_00003; phage(gi100044) 4.12e-123
MKLHYYDIYNISNGVFLTFQKNLKEKLLCVSHSKDIMDKKIGFYPLNFSDRGDFILLCVYIMFKHSPSSIYGLCEYLRNYNKTEYEKFKNTIKFYKNMIKKDIALLEE
KYKKPMFKEVMREYSIKQISFVTVYWYLMLYDIKDFNGINNTIICESILNVFKFLKFTDESKDYIKDVFKQIEGEVL

complement(2210..2470) PHAGE_Campyl_PC14_NC_031909: ribonucleotide reductase A subunit; PP_00004; phage(gi100062) 1.45e-48
VESKTELFNKLFEFRKQKDMMDDCILDVIIEFGNHINMDPELIASELSDYAIFRDIVEKDLKKFKFTKYDPNQSDIDISDIDILWE

complement(2460..2906) PHAGE_Campyl_PC14_NC_031909: aerobic ribonucleotide reductase B subunit; PP_00005; phage(gi100063) 2.09e-103
MCVLKTWLEDSNAKLPEISVMGSACYDIFSIEDKTIQPGGFEYVENGVRLIIPDGYYIRFNTRSSLGFIKDLFVYPGILDASWSGNLKVKVYNFGKEPYTIKKGDKYC
QFELLKCNESKIENISKDDFDNITKKLIRGNNGGWGSSGK

complement(2894..3286) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00006; phage(gi100123) 3.60e-83
MKNIEILNMVEELVKLNPILLISENFSHTYELLKENVRESKSIENKKIKLNCISVKLDDDTKLPCYGTVLSVLMKDNLENIINKNPQSLLEISFKISINVLLDLIDNFVEIY
DFNNESLLLINRIKICVY

complement(3298..4566) PHAGE_Campyl_PC14_NC_031909: endonuclease II; PP_00007; phage(gi100065) 0.0
MKYVFIGGGVANIYTICYGIMNNIINMKHDEVIVIEKGKHINDRIPTIDIVNGLLGGGAFSDNKNVFSLHDDQPIFEYINKQQVLEYYDFFKNKLFKMFLPENASIHIT
QPVETGSKFVSGYGDIALKQSECYHVGSTLGLEMCKNMIKWLEDKGVTIYCNSTYIPSKLDKCIIVRDTNGIESYITYDKLFIGLGRSGMKDIKETFELNNIKSVADQI
HIGFRFECEYNNTIQELANNIQYDFKFSKNINKNHLKELRTFCVNHGTAEVVTEKVKGYSIPIREQANGHAYGLHVKNKWTGKSNWAILGSFKNVNVEDYLSQIETI
TNGKIYELNQKSSLEFLNCFDNLGDSLSEFVKELCDILDIKEWKGYFPEIKIIGPRVSYNDNFTVQGFSKNIFFVGDSAITRGIIPAAVTGIHALLN

complement(4619..5023) PHAGE_Campyl_CP81_NC_042112: RegA; PP_00008; phage(gi100039) 2.63e-90
MSYSFEQYCNSNNFNEFQRYLITQLGYINNKNVVAIQDSEYIDVFKAIKQEYYKASSCKHSDKEEVIPEHYTKLAIEPIDFIYKNNLNFCEGNIIKYVSRLGSKDDNKS
ELKKIFFYFDYLLHGNYDLTKRTFS

complement(5027..5203) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00009; phage(gi100126) 1.22e-29
MTIKNKINDINEILQSYVGELVLSDIDTQKIVENLTELETIIKDAISKQLNNSKLILG

complement(5259..5825) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00010; phage(gi100037) 4.14e-127
MEKLIYIVIFLCIVFTTTSQSVIFHAKYNFEDIIQERLSYLKQNMINHISKYNNKNATEITNYIFEASLKYNINPVFIMSLIQSESYFKHKVKHKYNNVKGISGINYKMW
KIVLAKHNIKHINSLKNQIEATAIIINYIKQKYKTNDDLEILHYYKGRGYDKYLNKSGLDLAQYSYSMYIKNIKIIYN

complement(5844..6479) PHAGE_Campyl_CP81_NC_042112: DNA polymerase; PP_00011; phage(gi100036) 1.02e-146
MKFNCKNFAKALFYSKDINYLIKLFKYAKQEDKKQAMQILLWARDVNGGNIKNSILLLKYIAEKTNNINDMFLASVVKYGCFKDLNEMYKVASDSNKRKILSFYS
NELKLKNQLAAKWAPRKGPLFYALANSLCLKIGDFRRYITSLYISVEAKMCDNMWDSISLDEIPERAIKKYKKVLEKRLKITIYCRSPKQRRLKFKGCEKLLKQY

complement(6694..8010) PHAGE_Campyl_PC14_NC_031909: 3'phosphatase, 5'polynucleotide kinase; PP_00012; phage(gi100070) 0.0
MNINTLFNDNLCQYASYDNIRSIASLIDGFKNSGRKIVYFSKDLANYKKVSTLKSEIASKSQYLHNEDILPDIITNFARDFDCGPVTLPLFKPLSAIGCRTSPTSAQPRY
SSIKKSDYYDLLFNKDDEEILDHQYFEGQKIEPRFLLPTLPLILLINNNGMGVGFAQNIMQRSAEDVKQAIKDILDNKQPKPLVPYFKGYKGTVELLNTEHGKKQWK
FKGVYEKIDTYNLKITETTPYATNESMLIHFNSLKEKKIIKDYKDYSLGDNFEYVINVSGDFWNNQNIHKLLGIETTDTENFTCADRNNFIKTYKDEIEILKEYIDVKL
EYIQKRKQYKLSKYSDQIELISNKIKFIQAVLDKKVIFERKKKEDIIKQINNIGIVHNIDTLINMPLYSLSEESINNLNEQLSGLQQSFNELSQKHVKNIWLDDINKLFER
L

complement(8045..9670) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00013; phage(gi100071) 0.0
MTNQEKIEYLNTLGFQVISENLTTNLIVKCSKEHVFKREFYDFQKGYTACPTCEIEQKITFLNSLGFEPISENLGKKLEVKCQKGHIFKRTFGSFKNGILSCPECEKKEK

HNFLKELGFEIVSNNLGTNLEVKCDEGHIFKRPYKSFKNGHISCPICETNNKHSFINNLGFEILSNNITNDLEIKCRKGHIFKRTFNSFKNGQQFCPICEAENKNTYLNS
LGFTIISDNLADNLEVKCQQGHVFKRTFGNFSKGHHLCPFCYPNSSTFEQEVRELTGGTNNWEILNGKELDIYLPEYNLAIECNGDFWHSESMNKDKRYHLTKTEK
CAEKNIQLIHIFESSWNKKKDIWISIINNKLGKSERIFARKCVLREVPKIEEKEFLENNHLQGFTGSSVCYGLYFNNELVCLISFGKPRFTDKYDWELIRLCTKMGVNV
VGGASRLLKHFHKHNKGSLISYSDRLYSDGSIYLKLGFTFSHYSKPGYFYFKNNTRYSRQQFMKHLLKDKLEIFDSNKTEYENMVENGYHRVWDCGQGVWVKEIL
S

complement(9680..11530) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00014; phage(gi100131) 0.0
MIENKIVHAENEVEYYLNLPHLITGALTSFNNTVKVLENNKIINKEIVYNQTLTKQIDEAIQNSIDEFTRTGGKYANKISLKIDKDSGIITISDNGRGLPIDTYVMATTK
FRTSSNYTFLEKEKKDRITIGAHGIGSKLIPLFSSEYQLTTITLEGDRGIVKCLNNMSTIEHKEDKAPASSTHGVTIKFKPDFERLELKEINDNLINHIHALLINIAYSNPG
IEFTFQGKLIKVKEFKEFIKYYSDNFSILQSDENLELAIFPTDEYKFVHIVNSLDLNKGGVALDYISNNIVNAFGNRLRKGYSKITNTAVKSRIGVILILKNKKNLRFGG
GQTKEEIKNTITELGIPTLKYIDFAELLFKNTHIKDPIIELYKVQQELENRKQNTFERKEAKERFNPKFTKHTKDPKFMYIAEGDSALSSLIQAVGRDCSSFLPLTGKLQ
NALKCSTAQLLKNQRVMDIVEAMGLGLPETKYENMVIATDADLDGNHIACLITALVYKLQPNLLTEGRVYRLKTPIISVLQNDKLIKWYYTLGEYQKDQDNLPKN
AEVIYMKGLGSWSAANYRIVFAKDGIDNCLEKIEWKDNDEKVLEQWMSDNGIDFRKQILSTKSFNIENL

complement(11630..12832) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00015; phage(gi100132) 0.0
MSIKHVISDSSFGIPKPGFALKNKFICDNYNEQLEDIKIPIDKLDELLDEIKTVLKTSYYEWNGIEGDKSVFIFRLSNIYIEITYKIGKYVKLDMYSNSINFLKGVYNNIL
KKYITGTDELLIKIKSFYEEKGELVYVDSSKTKDNYKNIDYDYYPFLDLNEMFIQFLFANSNILILYGQPGTGKTKLAECYLNFLLNLDYKKYKHLELEEKVFDKSD

DDGNCINVAVVKNESLLAGDAFWNELLSNRYNLVLFDDLDYLLPRSDIQNGIDAQRNQFMSHFLSFTEGINNDITCKTKFIITTNRNINEIDPALLRAGRTFDILNLRT
LTKKEALKIWENNGLPKKSFNKLVNDNILQCNLSNIIEGEKYNIACKNNFKNYLKENDISHMKNINNKKIGLI

complement(12993..13442) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00016; phage(gi100133) 2.81e-94
MNIYAKYLNEFTKSSIKLNEADIDFDDFISEVKEIAGTSGDKLHNPRTSPVFRNYMYSLYINDDGISAEKAWRMFEELNIMDSRKIIQYIEEDDDWYVNRLKDEYNIS
LDDFKQMDEYDQIRTFCEIHNCQYIEGTDNKMYVMLPKYYV

complement(13495..13755) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00017; phage(gi100134) 5.80e-54
MDKQLIKDITINGLSQFAKGHEIEAITETLQIVQEYNIEHHSHNFEFDVEPITSLEDFIKEINILITYEDLNLFHEVLVESLKYYK

13810..14211 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00018; phage(gi100076) 2.46e-86
MTFVEKNMVKELKKTISSKKPLVLCFMSKLLQKEIQKLLKGNKLITIIKIILYAFDKTPVEVKRGVLGYVENEKNIPFQYKYDNTTKTLTFSLDKKSYNFNLCTANEY
IKVLANETNWMILKKNLNNALKNIK

complement(14229..14747) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00019; phage(gi100077) 2.15e-119
MAITNYTEFEKLCPKNGEIADQDVLGKPSLQLKRELDTVMSQVNSIIGITDPSNWDTGTTYTQNQIVKYNNYIYVSLSDGNRGNQPDTSPSKWKKISGGSISSSVNIIV
SSSDYNTPVTEVSDNSLSLKPSKVYVVNGNLIPTTNYTHDGTLTKITFINGMSVYKNDVVTVEY

complement(14780..15421) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00020; phage(gi100078) 2.53e-156
MGILNTAVGAISDFFGGNKTQSAITELAQKIQKAYSTNFDLESLYSIDTFALKNEVPGAGRINILDLPNMDILIQRVSIDPISFAEINEWIGSSWVYTQGRHELQQLTITF
RDSDGGFLYSAFKKLAGHLKDQYPDDQMWIIKIRKRTLRESRNYINQSVQNNEFKNGGHVIIDTQCAMIRSHGGLSLDQNSNGLATFDVTFLFDPFPPQISY

15467..16120 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00021; phage(gi100027) 1.41e-152
MELEIWKGKHSILLNKLYNDNNYIYDSDIIDVLVYKCLNQPKYITNDEARFLFFKKYFAEVCSKIDSSFKCPYCNEMNDIKFTNDDISITEYSLKPIEINVDNVIVTMY
FKKELSQDDSLSLITETKNMIDHEKRLLELYYMIDYISINGEELRGNHIIFEKYINELPLSCFNKIFDYFINSIPKHSIIKNCSCKNCNSEINVELKELPESVRRNLF

16117..16779 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00022; phage(gi100026) 2.40e-156
LTKDIIINNRHYCLNVWKIKDEIGILHQFIDWIELPLEDQVNKIADILIPQTKDLDYISRLYIMIILSSYANGDYSDILLTCPHCGNPIDTRINIRENLEFIPPKTVEVEINNK
KYTISKQNIELCNELPLKDYNSILNQLNDDGDLKLCAKVKCIMCNNDVLAIRELKDLFENYVIMLDLEWYYSTLKYFISQLGFSKTDFDNLYPFEIELLTNENKDE

16772..19525 PHAGE_Campyl_CP81_NC_042112: DCTP pyrophosphatase; PP_00023; phage(gi100024) 0.0
MSDIIKIDGQMVSLDVDSLKDASIETIIKILSYTEDTFKPLLDYMSNNGIPYYMILYGRFNNESLYKQMGINILKTLGAVAMLFPPVRLIGSGSRVITVVPKLVFSKGGL
VNVTLISAGAALKTEENNELYTLETMLKNAIVFIFEDIMVSTFKMAKDGIIKLSLGIAEKIKKDGSVLVNGLPIYLYTDLDNMDPTLLSKNSETYDKLRPDLLIIFEYIT
TQAKTNKFVDNYYFESLSLMKEKDPKLYSMVKNSIFGKQHVRQGFIRLVHNAMYYFSNSYEVTYDDFNDNIDDVLPSNILNDFKKMILDNSLEPLKDKKGKQKTS
LFGDKLYKVVYDKSASQSYNIGDVQDLNRLTKAQFFNVNKKLQNQTVLSQFDIEPQKTEKNTANVSTPSTIVGRVNSVLQKHVGRAKLTSEGVAHVKKYGITTTK
SSLTLEGFDPSKYYFSYSGTEPFNTGIGKLDSNLLYNLNLMAYDYFNIYKKQFIVTSGYRSMESQQKLYNNFINGKGSPANRPGYSLHEYGMAVDINSADAIKLDSS
GMLSKYDFWRPIPNKEPWHVQPKNITDKNGDGMLEADIVETKKKQANTLQKTKPINTTSINTNVKKQLFTNTVVSTSGKYYSIDIGKSVYVSNIKQEKPIKANTRD
VKPTTNKAITDTKTIEPTANKEVITDINTKTINHSNISRKYAPEDTIEINKEVKRLGDEFAPKNNKGASIPGDIGYKDTGNGVSIPGDIGYKDTGNGVSIPGDIRYKDTG
NGVSIPGDIGYKDTGNGVSIPGDIGYKDTGNGVSIPGDIGYEEKKIATSYDVKTQKAKNITYKKGKDDNTYYTSDGNFITKKTRIYDDGTKEDYYLTNTGLELTENM
LQNDTDEQFTEMSGLSKDQFQKGINLINNKQSSTNGDGDKPSVDAVKSVEITKKLGL

19527..20483 PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00024; phage(gi100141) 0.0
MAEVINIPGLDNEKYLVKITAYDIDNLGIGKEVMDSWDDLIKKVDESGSTDINSEGEYSSIDQLSETSSNILKRTVELMIDRDSAIISTDAAGTFYFPLPNSLSDQYVQS

YEVQSMNLLGSAISKASSYAGQTSIKNISEQALKRSGIQLDPNILSIYRSSNPRNIDMSWNIIPKSRKQYDAYVAQISKLKNWTKAKRNPITLGSVGNIIPMNFLIMKYI
FCIEIISLQNDKTPLVSNLLSASRDVTEGFFISLINTNIGSRQLMLRHDGNPTEFSLSIQFIERKPLWRDDWEKKINSLYNDQGKSETSLKEDDIYKE

20499..20852 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00025; phage(gi100083) 5.63e-80
MNDTQTIQIFDLIGDSQARDYIAIKAYKIGSDVSGIKDSINDILDDDPSKAFDNLLNMAENNISNIINPSNWEAGPRLKPGVPCKYIWILPIPSSLAEAFSHEFNQDEIDPI
GDMIG

20860..21621 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00026; phage(gi100084) 0.0
MASIRSFANFFKKGPKKVHNTEVPPHTIKPNKPKPNKMSTVKGKIKKGGAIVGMATGAALPFGYNLLKRNNIRTDPHIINTYNGTPNRVFNFETILLPNNAKHAEDI
VKALLQLKSIMTGTQLGTDKTGLLISQDYVFTIEFGSKDPAKGEQLKKVLNELLQLNHEENGETELNLRMCNINYMGQASALYGNGLPRDLSIALQFEEKRPLRMT
SDIVETTDTSNPNGNEKISEPNIGLTEEELNYKYSQDENS

21643..22104 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00027; phage(gi100085) 8.83e-107
MKNSVLNNKIMVDFNGFSLSPTYSVNIPKLREFMKNNLSMFYVKEMNDNVRFEVLALREYNDSSLWDILMILNFGENGILNFAKGDTWVSDNAENQYKEQQEYFS
PNFKPEDLYNQILSKIQKKNESRRKVIFIKRQFIPQFKESIKDMLNVF

22094..23230 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00028; phage(gi100019) 0.0
MFSDFKIMPEAYYAILLYSNNKKSELPLDPANISDFTIIWDYNDLCVEGYVIFNDTQKITELLPPHNGICFKVSLKDHFNIKFERVFKVTKIDRDFEGQSVATIKFELVD
EYYNMFANTFISKGYNNVKSTDVIKDIFNTKSDLISTPLNVIIKDTPKNTYENYVIQGNKNLLYLLNNMQKFDDLLIINTRKGIVVIPTDNIGKLSPDLSKVVKFSPTQT
QEYSPYSVKDFTLIQGDMLTQNAILPPSITYQVDSKKITKEEHNTKISHSKSGLKTSLTINDKDGIQGIKIFPYLHNIVDSIYNTEILESSAININVAGMFNHNLMCKVSF
DANSSIETLKSKMPYVTGEYFITKIVDHISSGNVFTQTITLGRIGSV

23227..24009 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00029; phage(gi100087) 0.0
MRVNEKNFKILTQTLPFYKGVIEDDKDPLESQRYRVRIIGIDDETIPTETLPWATSLDFSLFSGMGFTSFIKKGAYVLVHLFQNDRNQPIIIGVLKGVNNQNEELQSFK
DPTGQYPLNDYKNQPDTNNKSKGEKYLKNQVFETESGHYMEFDDSNGDERIHIFHRTGTEILVDKEGTVTINVVKDRNLNVKENQTSVIDKNDTTHIKENKNLTVD
KDNTTNIKGNNTINIDKDCNITIKGECNITVTGNANIKASNINLN

complement(23996..24337) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00030; phage(gi100147) 1.37e-68
MFLEDNNKQLSKVLNDNIVIKEDEKNIYIKFKKNIIIESDNNVIFLAKDYIVNSAKEIHLNPDVKISVDDNVDDIIKKIDDKKNEINISVEKLTHNHKHCKIKCFFKKLF
NLN

complement(24321..24608) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00031; phage(gi100089) 7.88e-64
MPPVTRLGDIALGHSCYPPSPTIEASSNVFANSIAVHRLGDKIQSHACPDTPPHGRNSSSGSTSVFTNSKATCGIGDAVNCGGIIAQGSNNVFRG

complement(24596..26215) PHAGE_Campyl_PC14_NC_031909: DNA ligase; PP_00032; phage(gi100090) 0.0
MDKIKFLNNLGYKVVSEDLVRNLYVKCKNNHIFKREFGDFKKGYIKCSKCEEEQKLEFIKGLGYEVVTMDKKGKLLLKCKSNHIIEKSFGNLKKGSILCSECIKEEK
IKFIKSCGYEPASENLAHDLFIKCKNGHIFKREYNDLKKGYVNCPKCNEEDKIKLITSFGYTIINQYDSEELELMCKNGHISKRIFNNFKKFPLCSECVEDKRTSFIKEL
GYKVVGKNLFECKNGHTFSREVKSFRKGCVYCPICSPSISSFEKEMSELLGNYISNDYSVLGDKELDFYVPNHKLAIECNGDYWHSEQMGKDKNYHLDKTNKCLE
KGIQLLHIFEHSWYSKKNIWTSIINNKLGKSKKIMARKCTLKEVTKTEEKEFLDTNHLQGFTGSTVCYGLYYQDKLVCLMSFGKSRFTGRYDWELIRLCTKKNINVI

GGASKLLKHFEKENEGSLISYSDRLYSDGSIYKQLGFEFSHFSKPGYFYYKNGTKYSRQQFMKHKLKDKLEKFDPNLTESENMVENGYHKVWDCGQGVWIKNRK
GILCHQ

complement(26227..26673) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00033; phage(gi100014) 3.42e-97
MEKNYNTFLRKKSVTIKLNDDLKDKLKDTIENINDYDIIKIKLGRTFFNQKRYYKIYARKKFGFYKTLLSENDDSYFFMENTSKIIRRVFNEYDVNCYNLYPNKKYR
YGLSIFILICCSIILIALSLGVGALSYIFKGYFLAFGFSLF

complement(26733..27305) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00034; phage(gi100092) 3.19e-138
MGLESGELRNEAQGGYNPPFELSIYKHQVKFTPPNNFESYIKWELLGDIPLHLTINEQTGLITGNIELLSKQPSAKNAIYEYQLMKIDGSNWRHLGILKNGQTFTFNFQ
VKLTYTVQANSGGSRLSNTVTEVSDVTITILQDNDIISTLFCKNYIDEAKFPLKIGDKVYTDAVEFMKNHPNKNNFKINLV

complement(27322..27849) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00035; phage(gi100012) 1.65e-129
MPLYTVDKLANALKGGAKSDKYFIEIGTPLGAPEVAFTEEDIILCKTASFPERTLGEVEAFVQGRKLKLPGDSTFDAAWSPVFYQTPDHNIRAKFLTWIDKIDVYKN
NYHTCDPYSLMVTAKVHQVNCNGEPVATYEFFNVWPSKVGEIEVAADKTNSIQEFTVDFTYSHWEKIA

complement(27878..28456) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00036; phage(gi100094) 1.96e-139
MSLYNIDRLRSSLKQGGAINSKYKIDIKIPTLLRSLPFFKTVNISGEYLSIMANRTSIPGKSMSTVKVYHRGQPFVIRGAAQFNNTHKITFYNTPDMDIHQLFSDWIYRI
DSFDSTITQSIFLGNYVGFNSVGAGYMSDIIVSQLSSDGRTETEFKLCYTFPIDIAEVELSASGKEISSTEVTFAYTYWERI

complement(28458..29018) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00037; phage(gi100010) 6.08e-137
MVESINPPKGYFKIELLDKDRNVIDTFEKHNLVVNGSRPVLASHMAGRSTTPVNKLVLGTRGHIGNNLMMPKTANEGFTAARTQLFAEEEGEFCYHVNFTPPQSDG
QAVVTEDDVGAGSTVEVTNSNNTITYRIELSTTAGNGTLGAVGYTEAGLYAGNDLFCMRTFAVRSKDVSSILRITWTLIF

complement(29002..30558) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00038; phage(gi100155) 0.0
MIDRVDLPNIYNENKLHKDSVEALYEVLDELNPYSLDIYNIFKRPNDSITENIVKIYAESLYYGMQKALTNPVVIQRMKEKIGTTDNYQPFDIKEFYKKLLKDYFVNF
TSFKEKKGLDVAIEYAYNIIFTSGLQPGLDVNGSSGFNLKWGTEDNPNEPFFIRIEGLLDPILYEGSVKSIAHPVGFGYNYVISLVLEFIEYIDDLINFNVKTLEIVSTNY
RKEFDKDKVEDIYTSKNIQNQERIVITFNDGKQLIKDFNGSITYNEKDGSVIENWNNTYILKLDYDISLKFRLKDEFDNSENNLIVYDCVWNRLNSFDTPIIGEAIVNK
FRVADKYYSSLVIGKIDDNTIYTLPDDPIKYTPDKMPLFLTNAINRGLFEHIHDDIDLYSTNNFTDNVINEKGISNTVGNKIIVGSFKVGSQSENPEGGVILDDSFSIERE
MIPTEYSETVTKNLKTNFYTTILDNFDEKVVNDDIKITVGSFKVGNINIGAEYIDNGVILDDAFDINILKIRKNNGRIN

complement(30555..32648) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00039; phage(gi100097) 0.0
MADNILIPYNYDDIKDEVIKLLKNKGYNADVKSSNANLLADILSYLAYSINVNTSFQAGEMLLSTAQYRKNILMGARQLGYEASRKVSYVYSLEIKPLKDDTKDDD
NEDKRIYSIPKYTMFNSGSNTYYYMGSDIEVELSNKDITTGKASTIKIDVKEGILHKWDKNKDTQVFTIKAIEQNRSIKSSNKISLYQDNIEENGLEVFVTYIDIETGDS
KVDEYWEKSDQFMIDADSDTNKKYFVLNNIDYSGVDIYFSISGIGTNLLPGSTVKVTYLESKGSSGKCGDNFAFSQNTYPFNLMEIDKFETKIVGTDEETNSSIKENA
PIFHNSANRAVTVRDYIAICNRYTNIYQTQVWGGDEEQVVQLGHIWFSFIPEYRNQDFSLDETTQTYSLVNKNDSYYLKQSELRSNTLDKNGYLVNKGIFDELDSY
KIMTMELHNRYPIYMDFDYEIRIIKQNIVVSKNETQDKLFNILKDYFKSDIESFESSYFHSSVIKRLGTELYDLSGIQVDVSMNIPLYLRNKEPNKDILYIYLAIPFEQIIT
KTQDDQNELHVNLLPQISSDDFGGKLEVDFKNPIKGFTVIGSSNAIIGTFDVGNGQSAVFNGKNVVTSDGLIIKNTNISFNIFANGTIIGTYKIIYDNRRRFIVIEITDSIV
LSSLDNITPKYIRVKYSDDNLSFYKNTIARLSSVKFVSESDVI

complement(32648..32995) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00040; phage(gi100007) 2.88e-75
VIQYKDINPKNIEKDIINVDTFYVSLKNIVSTTIGDIAGFPEFSNNAQLLFDQYSSVALDAYKTSLKTSIQKFDYRIIVDNINISKGDADNSVYIEIKYRVRDTTISDTASI
KVG

complement(33027..33737) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00041; phage(gi100158) 2.86e-165
MLLNSKTIALVNSLQLINESIIFSSKLTGIKDSAGSIIAFIDLEKLENKPFPKDFGILKIKEFMDLLKIIGEDANITMDDKNIIHISKDGMSCKYLTTNVEALSNACGVKPTI

LENVNNAELVSSFELDMTVSDKIKKAATLLGFDDMVLNIDDIITVSTSEQGINGNEFSLNVTPNVINSKANIFISIKNLKRIPTTDYIVSVHKHSSRQDTYLLKLIPKNN
DALIILIPSKVVK

complement(33786..34769) PHAGE_Campyl_CP81_NC_042112: DNA topoisomerase II large subunit; PP_00042; phage(gi100005) 0.0
MLQNFVGNSSIPSVLMAAPYGIIDSTPNNKWMEDLKKDGKFTPNIQKIEKQFFELQKTISSVASIYTIPAEKGLQDLAYVANLGMIFPHLNPNEDRRVLVSNFKSEPR
KGETKVGYEYFKKLGFDPIIMPDVNEKGEPMYFEGEADLKWLYGNVYVGADGNRTNGAALDWIAKTFNCEIIKFPSIDEYLYHLDCNVFPLGPDTEACLVNTYNL
DKDIIKELEKHVEVIPLGVDSHDDPDQYDFALAGTTNSVLLPGGIVITPSDISELNKKSDKDLYEMEKDKIEFMDEICSELGLQLVVQNISGYYVSGASLSCNVMHLN
QRSYLN

complement(34849..36090) PHAGE_Campyl_CP81_NC_042112: DNA topoisomerase medium subunit; PP_00043; phage(gi100004) 0.0
MISGLILKNLINDEIYFDKVYSILKPEHFIGVDSDIYKTIQKLVKEYNKKPTPKEVALKLKDNFKDEQQENCINRFKEIMLDKQNVSPEFLNNETAEFIKQAEMRSCIIQ
GAKLIQEKKDIGKIYERLGQAISFTMDTDIGMKDIDAQERDILRRETKIGISTGVEILDEVLAGGYMPSTLNFICSVTHGGKSMFLSHFCANAMLKGYNCLYITLEMP
SIKIWDRIESNIFNIDISELRNYNVSEGYEKLPNLGRCVVKEYGAGSFDVLQLKSLVQKVESSLEINLNCIIIDYLALMASYALQPSVGLYSYYKKIAEELHAYAKESK
KCVLSAAQLNRNAYNNSNADTSTIAESLGIAQTADTIAMLHRSPELDELGQAIISFTKNRNSGNLSQKYIGINFKQSRFFDIDQPD

complement(36090..36776) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00044; phage(gi100003) 1.44e-155
MIVCNYNVVPVIISLYRNDFNMQEVKICGYNQLNEYIKDDSNKFEIIGFNTDSINLPKNIVNLEINFENIPKYLQNPLKSYYEWDKNNQRDFLFGYYLDLYFKKNKLP
ALVDLLKNNTEENNIYNIVKNNFISLEYSLQQNIIKEKIINDTYIMKGNYNSFVYKMVKSQCKTYILDDDLGKLTIFSDDLKIIYDRISHLKIDIIKTENCIILNDIDNKQ
QIVKLMLGL

complement(36949..40743) PHAGE_Campyl_PC14_NC_031909: base plate hub; PP_00045; phage(gi100103) 0.0
LNLNKFATKEETYTKQEVDNKIDEIVPPEIDLTDYAKKDTANIFTKANTFTEAPSVEVDATLDNHVIRKKQFDNSIKEVKDLLSNVFSYKGSKPTYTEIEAIVDKKIG
DVWYAEDTGYMYIWNGKTWYDLGKSFDASKFVDITSDQVAINGIKKFTGKLKALTPVDSDDVAILSWTTKQINDKVKSVIGDLNSLNNEVSKDNLVNAINSVDD
KFKTTAKTNKSNTFTGDQTYVDHILLESVPSERNHAVNLGYILDNPGGIKLPDHTALTQNSVTEITFGYANPVVYSAQQLKNVFLKDIVGNEYKAIMADKTSFTENP
SKEMVVILSRTDYTKNTDVKFDITKTVDELKQYELKEGEVRVILSYDTISVYSSGYGYGAMFARNANKKDGDLIYDYYTGSQNDITNNRKISIKIDKLGINIPDIVSIS
MTTNGSEKLTVKTDTLDPVENTYESADMTYIHTPVSKIAGDVLYSNISQAIKSIHVLENNICSLKPANMELQLVRLKEFKQTINNILQSMFDESPVALKNGDYINVSF
SGSASYGTGYCGYVNIKDTIRNITYKAYKVSLNAFDTTSGTKVIAVLTSDNSKTNVTYSDSVSTLESYEVAENEILLEISFSTAKQYSAKYGYGAMLEYWGSVSDLC
YDYYMGSNLDMDCPFKITLLKIGSSVKADTIQIGAPTFAGSLVMHLRKNINDVINFLVSTGVNVTGRDGAESGSVYNLVEKSLKPLKVLTSEAHQSINGITTFNNKV
YMNIDNEKITDSKQLIHKEYLDKNIADNVAYNISNTPLVPYNDVSSLNTKNIGVRISATTDSSNYSSGDTVVVSNFKIKLKGDNEYLKPYGVEVIDRENNKIGLNLIG
DDTVYNDNDALLSTRPSDFNSSSVDLSSGSNALATVKTNGAYDYSGVYDIPNPFREYNKKYSLFLSNDGLKNPYYQVDISSSKQVDNISFQLFGTSATNPFLYSKDC
KIELFIENTIVKTFNIKGSSGNNSPVNINIDYKDGMFLVSVLDSINYINNRINKNAELLTGSGKPNFSLNPNKIGSLYSDTTNKAVYMCIDNTSGANKWVNIVTGDEIK
PNLRKIEITCNVRLRSGQYGGCMSGVKIGFDNGYASTKQIVKGLNSGQILLSLDGLGNLSGYSEVSSLTPSGQDIKVDVDTTGIYNDPSYHCVTNIFKEYLGNADQCS
LWSDASVKQLKITLLSENIPTKILYVGNGYYGQTSVSDVKAVWYYVNDSGDKIEGSIDNDLEISNNDSETNDSSYIYAFNIN

complement(41096..42121) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00046; phage(gi100164) 0.0
MVLIDFMHLAFKSLYVAVGKDMYSKQKLSFEKYHGMFVHLIFNYLKLIQTEYARDYGNEIILALEGSNSWRKSYYPEYKTNRKLSDVFDWENEVFPAVNEIIDVIK
KSLPYKVLRVKGAEGDDIIAVLANHTAKPVLVVSEDKDFMQLLINKHITLFKPIKKEFFRNIEESEITKTLTMHILLGDKADNIPSIMEGTTFTPDFIKFLETNGIFETDV

NNFNKLEISKTLYDLYSKQSEKSPFKPAYFGEVGAKKFLENLNENLEKNKLVYDNFIRNKTLIDFREIPDNIKESIIEQYNLEKPTIDLNNLLKFFLKYNCKKHSDSIAS
FNSNMGTSLFDDWM

complement(42108..42242) PHAGE_Campyl_PC14_NC_031909: baseplate hub assembly protein; PP_00047; phage(gi100106) 2.63e-21
MKRDGSIIKSFKREINLQTRFIKNKTKYTRKEKHKKGAIINGFN

complement(42239..42625) PHAGE_Campyl_PC14_NC_031909: baseplate hub subunit; PP_00048; phage(gi100107) 1.17e-91
MDITHSQYEVMVSAYKKDFIPNKNEMNLLNSFMLCRWMSNDIHSVEFANFINNHTDIPINVQYWFARSIMNKVTYMGRPPKEDKLNEYEEAVSKYYNVSFDVAK
QYCSILPKEKQEEVLNMFKGGRIK

complement(42677..43594) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00049; phage(gi100167) 0.0
MNEFDILTGFSGADLMQKMPQNVGQKSYIDNRFWKLSKNKEGSGAAVIRLVTDKHKTPFVHIYHYNSKKNVGGKDRWLIANSPSTIGLPCPIQEEYFEVLNSGDEK
LARSLYGRKVKYYTNILVVKDPANPENEGKVFLFEFGSKLKEKFLAWMNPDETQRSLGHTEKELYNPINGYNIELTIKKDPQSGFFNYDNTSLAPSPSKLGGLEKNE
DIIDIILNKTYDLSEFTKPEYFPSYEELKEKLERFKNPFGTKTSSVPSVVGKTNDNPPFETQESKPQSQQQVVQQQKPKQENSQDDDWLNNL

complement(43706..45940) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00050; phage(gi100168) 0.0
MTVNNKIEFLNNLGYETISDSLGHDLEVQCKNGHIFKRSFSRFKSGSTACPECERQENIKYLNKLGYEVISENLSNDLTVKCKNGHAFKRTLNNFKKGQLTCNECER
QRKLLFINSLGYKVVSKELNNDLTVECQNGHIFKRPYKAFKSGITICTICEKQEKLEYLNNLGYEVISDNLGNDLEVRCKSGHVFKRAFGDFKKGYTNCPGCIISEKT
KFLEDLGYKITSYTLGDNLEVECKNGHVFKRTYGNFKKGMTDCPKCTKEHKIKFITNLEYEIVSDNLGHDLEVKCKNGHIFKRPFGNFKMGNIDCPECIIHTKIKFLN
NLGYEVVSENLADYLEVKCSKGHIFKRTFRTFEKGTTDCPVCMEHEKTEVLNNLGYKTISHSNVQCKNGHVFKRSFSLFKQGVITCSECTKEYKTKFLSSLEYKIISE
NLADNLEVQCKNGHVFKRSFDNFKRGVTLCPICYPSTSSFEKEISKLLDNHVSNDYSILGDKELDFYLPDHNLAIECNGDYWHSESNGKDKNYHLDKTERCKEKGI
NLIHIFESSWIEKKDIWTSIINNKLGKSDKIMARKCVIKEVSKLEEKGFLDKNHLQGFTGSSVCYGLYFNNELVCLMSFGKPRFTGKYDWELIRLCAKMNTNIVGGA
SKLLSYFHKNNSGSLISYSDRLYSDGSIYKQLGFSFSHFSKPGYFYFKNGIKYSRQQFMKHMLKDKLEEFYPDLTESENMRLNGYHKVWDCGQGVWVKLS

complement(45976..46713) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00051; phage(gi100110) 2.32e-176
MPNYFSSSKPGSNQSNIVDSTKPGFVSSYQKKTKETQSISEEAKNINTGKKLIKDTVDDALKEKTTKEQEKAALNIVKQLMKKGTRNFKAEDFRFSNMIFMQYDAK
FKDEVYDKTPLILVLSTSRSYVLGLNLHWTPVPLRIALIKVLFKMNKAAIQKNKQLKITYKMVKPLLSALHLGPVIRLYIKKRISRRGIIIPQDLWLVAARLRAESFSG
GYSADKLYAKAIQNYKKSKSKNIRKNRKMF

complement(46722..47069) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00052; phage(gi100180) 1.11e-79
MNTVYSKYLCESSHYDQYKETRDIETANVEMKNMDRDLEFLKYRIEQKLEKANIEITEPYIEGECIKFALKNYNNEDNKKVKDILYDMRDISWGPISGDYSDMSQG
YEVSLDLED

complement(47120..47836) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: protector from prophage-induced early lysis; PP_00053; phage(gi100001) 7.34e-174
MVKDIQQLKDDKINYLNKLLPQDENGYFLDISNQKVSYGNNPQLSYINTKLPLKEEHIIEIQKCSTDIIYFVESYVKIRSLDEGLVYPDLRDYQKELIQQYYENRFNVV
LAGRQSGKSVTTLLYILWKLCFCPDTIVGICANKFTMAAENLQRLMDMYADLPIWLKPSVKVYNKESFVNEIGCKAYISATTPDAFRGLSINLIFIDECVAGDTKITV
RNKKTGVIEDITMEELYNRIG

complement(47856..48242) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00054; phage(gi100112) 2.17e-85
MNLISIDYEDKFYRKLLEDELTNFKSYPFKISEDVYWDFRNYGANSIDKPEKEIKLNLSKRKVRFIINRLEYYNENGYWNNVSLIQKHYQEERKLEKLAETHAKTFM
SAVWLCIPIFALLALLKYIFE

complement(48323..48988) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00055; phage(gi100113) 6.89e-156
MKNIEVKLLHHTPLEITIDAIRTCWNSGCKKDSVYENGRFVLGNQDKALLDRIVNHHKHLSTIEHVYYNFFIKGISRACLQELARHRHASLSVESTRYTLKKHLKNE

EGFKYEQDFDRASKYVVLTEDLESNLQILSNLDNLLRLVKQNKSNDVVKYALPEAFRTNLYWTINARSLRNFLELRSSNHALHEIRILANKVYESLPELHKQTLFKN
IIKEYNE

49228..50679 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00056; phage(gi100115) 0.0
MNVTEKLKFLNDLGYEVVSYDLSKNLIVRCKSGHEFKRRFYDFQRGTIICIQCDHNSKLSYLNSLGYSVKSKLINNDLEVICKNGHSFKRAWSEFKNGNIRCAMCYE
QHKIDFLNKLGYTILDINKIKVKCKHGHVFDRVWSHFNSGVVECKQCKNNIKIEYMKLAELEPISENIADSLELKCKNGHVFKRTFSNLKKCNVCPICYSNISSFEKEI
KEILPKCIENDYSILGDKELDFYLPGHNLAIECNGDYWHSEQMGKDKSYHLNKTEKCKEKGIQLLQIFESSWIEKKDIWKSIINNKLGKSKKIMARKCILKEVPKTEE
KEFLDENHLQGFTGSIVCYGLYFNDELVCLMSFGKPRFTDKYDWELIRLCTKKNTNIIGGASKLLSYFHKNNKGSIISYSDRLYSDGSIYKQLGFEFSHYSAPGYFYC
KNKIKYPRQQFMKHKLKDKLEKFDLNLTEYKNMLLNGYNRVWDCGQGVWVK

50695..52518 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00057; phage(gi100116) 0.0
MTLDEKIEFIKSVGFDIIAHKSNSITLQCNYGHVFNKKVSNIIPNTNIICDKCVVMSKEKTLRELGFTPLLINGDKCTVKCDKCNHIFNRTWYAFNTRKNTKCPECVEA
ERWNNINSHLNNMKVSYISDIQGNYTLQCKNGHIFKQSIAEIIKEVGCYQCEVEYRKEYIRNLNFTIIEYNSKIFNVKCNKCNHIFTRDWNGFYNRKHTICSNCIEIGK
KNLAKKHGFTLTDTKFGNDIREFICNKCNTTFKRGWSNFTSRGNKECYNCKQLSRINLAKSYGLDIINKNITSKYTFKCNKGHVFERPFTVVENKNQTKCPICYPRTS
NFEIEVKNLLTELCIKYIQNDRNILDGLELDFYLPDYNLAIECNGDYWHSDSVISDKKYHLNKTLKCNSQGIQLLHIFESNWIKNRNIWESIIKNKLGLSFKIYARKCEI
KEVNKIEEKEFLNKNHLQGFTGSAVCYGLYYQNELVELMSFGRSRFNKNISWELIRLCTKINVNVIGGASRLLKIFENNYPNQTLLSYSNNLYSNGKIYNTLGFEFSH
TSSPGYFYYKNGMTYDRQQFMKHKLKDKLEKFNPNLTEAENMSINGYNRVWDCGQGVWVKGSI

complement(52533..54443) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00058; phage(gi100117) 0.0
MALLSPGVEVKEIDLSLTVSSASSSFGAFCGIFPKGPCDGAVFINDIPTLESVFGKPTNSNYNDFFQAYCFLRRAGSLYVVRAIDKLGKSTRKDSGLTINAVLSEKATE
ITLADTTGLYVGQQIMFGEKTDANVYTIASIQANTKITFTPEIQTGDGTGNSSKIYICYPSMNATGEVLKTGSSNTITDAKLKETLKIIPNNDVYETLEPSIKFSDTETKL
KFIAKSAGFWGNNIKVAVATKADFGANKNIIKGIPLDDNFEYVPDTDQVAVIILENNEIKETYMVSIKEGAKDYNNKSNYIEDVINRKSSYVYCKNNTTITDLPKSAL
DSEAITLKFGEDGAPTKADIISGYTDNFSSKEEIDIDIVIANEMANKECADFCVTRGDVIGYGGVPFGEVVGLKAEDCVKNLLEYRSTGEMNIDNKYFSFIGNYGYIY
DKYNDKYRWINLAGATAGLRAYTNQARQPWFAAAGLNQGQYLDIIKLAFNPNNGQRDLLYKSAINPVVSFPSLGICLWGQKTCTQKPSAFDRVNVRMLFNYLER
NIANSARYVVFEQNDTHTQNMFVSMCTPLLTQVQAGRGIDAFKIVCDDSNNTPLVKSNNQFVASFLIKPTYAIEFITLNFVAVGATISFEEAIGSI

complement(54605..54952) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00059; phage(gi100007) 7.37e-74
METKLLNILLNIGEKYGIYFKQNPIEDEYNVEILLWTKESPESWDKIIKDIKTELLVNFTRNIKISSWGKNSVNIKMKLDRLYQVNILYNLEEPKLNITISYPKIINESAY
DNFL

complement(54942..55895) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00060; phage(gi100119) 0.0
MNTSTLYNDKGKVVLQWVKNVPKSIPSEEVIESIKLASKKFKKYPFKNVSKLKSLNTNSLTLYNISDMHFGMLALKEETNDSDWNLDIALKTLDQLSTELINGADK
TEECIICNLGDLIDINDFTHKTPRSGNVLDVDKKFPQILSVAYNSIINMIYKALGKHKYVYYYINIPGNHDILPSMAVQYIIKEHFAGNKRVICDESLMNIKYHSFGNVL
MAFTHGDNIKMKDVGQIIAFDNKENFVHSKHVYAYFGHYHVDKVIDTPLCRCESFRNLAPLNKWASNSGFRRGIGTISSITIHKSYGEISRRTYNMDMVNGN

complement(55917..57239) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00061; phage(gi100171) 0.0
MLVNIINNLKNENTDAGKIAIIKNNKDNQNFIKLLDIVYNPKTRLGITDFELPSETGNDILDNIISSLDYLQNGIYRGNDAETFIIKLAKQLDYENQLLLQKVIRKNLQA
DLGIKTINSAIPNFVKKPPYMRCALLNEKTSSKIKYPAYIQEKLDGQFCNVIVTKNSIQFVSRAGTEYKFKRDFSKLQQLIYYTLGECVIMGELLCTENGNILPREIGN
GIINKSSETNQTITEEESNKVILKAWDCIPYSDYLERKCNIPYETRFNNIRKITETPNGFIYPVVYNIVNNMEEIMEHYKNLVSQDQEGVIVKNRFATWGDKTSNDQLK

LKIKFQVDLRIKGYQCGKSGTSFEDTLGALICESDEGSLEVCVGTGFKESDRDFFWNNNMIGKIVTVEAHRAMEKNGKYSLILPVFIELRQDKDEADGIEKILEQEKS
AKYK

complement(57285..57413) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00062; phage(gi100010) 9.38e-21
MTTSGDIATTPSRLTLKRGKIKPKVIKYKQTKTLTLKKLSKN

complement(57410..57709) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00063; phage(gi100122) 8.28e-63
MYTKYLYESSLDLQFEVTDQDFDESFLNFNKELPVSLSETLKLKYNIKLSLKFQSKYDDIGILVKLNDNGKYVVYSNSIENIDKFIIFVDTLNQNKGNL

complement(57699..58199) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00064; phage(gi100012) 3.95e-117
MANKSKSKGNTFERTVAKMLSDNYADVFNVAQSFQRNISSGSMFGGSNSYRGMNVLDEHTFYAGDIICPSEFKYTVECKHYATAPSFNSLIIQECAQWDKWILQV
EADCEISNKLPMLVVKYDNIKPFVFIKHNFEGFIFKYRDYYAYNFEMFIKEYKKELINNVY

complement(58216..58593) PHAGE_Campyl_PC14_NC_031909: cytosine-specific methyltransferase; PP_00065; phage(gi100124) 1.45e-84
MKVQFINSKELSANVVSTKNLHKLNRKILVPGVVDISGTIYLASPSKELPTIRVEMDAVFKCGECSSFKIKHYVVNKKVYGSNSEIYDGISKFLRKYAKLILVSKDEI
MFFNYTYTGFAKYFKNK

complement(58710..59489) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00066; phage(gi100125) 2.16e-175
MKKSTTLNEAIKRKAKNMNKGKSITLNEAAKKGYFKYIKRKISINESEINGLKDALENMEEFSDENIMGSVVGKDYVISIFEKVCIILVNGTTPFLIEREDITEDEQTLI
DDIFETLNLELDDDLDNVDDNQGDDGLDDLDDDLEDDDLDDNSMNESRKIDKKIGLYFYNSKPIKDGNTVVSVDDKGNTEVKLHGNLIAVKNKNGDEKYSLAGY
NSQTTRARLNGLGFNVVQRKGKLFVDNNEINADDWYDIFGNKVSW

complement(59500..60081) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00067; phage(gi100126) 2.28e-137
MVTYEEIQQLIRNCLDVGIKAPASAYSKLLRHGYCVMYGGDAKFNKLEELEDNFDVKQFDRDTWVIKEYKKELTPEEWKDVNSQALYNGGTPDQIAKDIEDGEK
NPILENAFNKLDEAKLKQISKDDLKNIWNENDLETKREKTLKLISELKYKSPSLEKIIDIIKTTKDKNKIDQIITNIMFVGTGDKVIKI

60177..61259 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00068; phage(gi100164) 0.0
MDKIEYLKSLGYNLLSVEGSYVKVECKNKHVFRRAFASFKIRNTPCPECEIENRKQFLDSINYSLISVKGRKVEVKCKTCNTIFSKEYCNFKQGKITCNYCETNNKIE
YIQSLGYNIVDFESRGYVKIQCKYNHIFSRAYNSLKNGFISCPYCEHEQRETFFKFINLELITFDKGKITAKCKKNHIFNRTYGSFKRGSILCPICYPKSSSFEKEVKNILP
RNVIINDRTVLDGKELDFYLPEYNLAIECNGDYWHSEQMGKDKNYHLGKSLKCINKGIYLIHIFESKWRSNKQFYINLIKNHINGTIKRYPNKVISDISCENQLIFPKL
GYKLVDNVEPNFEIFQNTLKVYNCGYNIWLK

complement(61280..62662) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00069; phage(gi100128) 0.0
MNEINVVKTYTNGEIALCNLASINLHEYDQLSDTEKYNLVYDIINTMDNTIDLAYYMVKDAQTANKKYRYLGIGVSNLAVLLAKHKIIIDSQESLEFQAKLFDELLY
NCVKASMQLAIEKGRAEGFSETKWAKGLYPYLIGNEKAKKLIQFKPDENKWNKLMEDVKKYGMRNCALTAIAPTACVTKETKIKTENGIKSYKDIMKEQGINFNE
IENYGIPSWIDFKVPFKVQTRHGLKEVNRIWFNGKQPTKTITFEDNTILTLTYNHKLLVKLDSGIEEWIEARDLKKGMEIVSITNNIKIKSISNNTDVLFNTWDIEVPDV
HEYLLENGCISHNTSGRSINASESIEPIQKLLYKEDGNINVKTLAPMFKEYNKYYKLAQECDPMMLIKAAAVRQLFLDQSQSVNMYSYTFNGELNYIQKSSHKLSLL
HMYAHQLGLKTLYYFKSEKDNGVEHECESCS

complement(62700..64586) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00070; phage(gi100129) 0.0
MDKIKYLKSLGYTPVSSNLTNNLEVLCHKCNNTFKRSFYTFKNGSVDCPNCQNIERLNYLKSIGFEAVDLYNVKCLKGHIFKRRFSEFKNGATACPICIDNEKQEFIK
GLGYVIKDIKGDNFTVECQKGHIFNRVYSSFRSKNITFCPECKNNEKTLFLNSVGLKQIKSDGDKMTLQCSKGHTFVRRYCDIKRGSINCPECIIHMKEEYLKSIGFTL
IKTNVVKCSKGHIFNRSYSDFVNGSIACPTCQKENILNFIESNGLQLVSLGKSIKLKCQSDHIFTRAFNTLKVNTTCPICDKEKRKLFIESFGIKLLKDGNRLQLQCSKG
HVFEREYCNFKKCTLCPVCNPSTSSFEKEISELLTNYNKNDRNILDGKELDFYLPEYNLAIECNGDYWHSESNGKDKNYHLNKTNKCLERGIQLLHIFESSWIEKKDI

WKSIINNKLGKSNKIMARKCVLREVPKTEEKEFLDTNHLQGFTGSTVCYGLYCRDELVCLMSFGKPRFTDKYDWELIRLCTKMDHNIIGGASKLLKHFHKNHPGSLISYSDRLYSDGSIYLRLGFTFSHYSKPGYYYFKNGTKYSRQQFMKHKLKDKLEKFDPNLTELENMSINGYHKIWDCGQGVWVKGNLS

complement(64635..65942) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00071; phage(gi100130) 0.0
MDKIEYLKSLGYIPVSSNLAGNLEVQCKNGHKFKRSLGNFQRGTIHCPECEKQEKISFLNSLGYTPISSNLGNNLEVMCKNGHIFKRRYEHFKNGISTCIMCDEQNKSNYLDDIGFSIISDNTADDLEVICKNGHIIKRSYHNFKKGAKICPVCSPSTSSFEKEVSKLLDNYIENDYSVLGDKELDFYIPNYKLAIECNGVYWHSDKFKDKNYHLNKTEKCKEKDIQLLHIFEHSWAEKKDIWKSIINNKLGKSEKIMARKCVIKEVPKIEEKEFLDTNHLQGFTGSSICYGLYYQDKLVCLMSFGKPRFTNKYDWELIRLCTKMGLNVIGGASKLLSYFHKHNKGSLISYSDRLYSDGEIYKQLGFEFSHYSEPGYFYFKNNQVYSRQQFMKHKLKDKLEKFDPNLTESENMNINGYSRIWDCGQGVWVKLSIP

complement(66037..67434) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00072; phage(gi100131) 0.0
MADKYLLDESTKEKFITSNLYPNLNESEKNIMRTVLENQGKEVKMLMESTVTGDIAQFTPILVPVIRRALPTLIGTEIAGVQALKTPTAYLYAMVPHYVGDGNNSVSPTKNAIVLKLKTESANKDDFNYTGTPIEVSFKTATTVKGKIVYSEKQAGTDNIVNVLLRLESNSTGSVTIGDEVDKAATFATKKATIEAVYTNEALWLKVLKNYTGPYATATGEKLGKDMKEMGISVQRVLAEAKTRKVKGTYTIEMLQDLKAQHGINAEKELADILSAEVALEIDRTIIEKANEVATVCTDFDVNSADGRWFIEKARGLSMRISNEAREIGRQTRKGGGNKLIVSPKVATILDEIGSFVLSPAGSKINAIDSGIKPNVGKFDNRYDVIVDNFAEFDYCTVAYKGASNFDAGIFFAPYNITLQQNLTDPVSGQPAMILNNRYDVVGAPLHPEAFIRTFVVNLNNYIIS

complement(67466..68212) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: DNA helicase; PP_00073; phage(gi100021) 5.68e-156
MEELLSKLDKNIFTPEVVDEIKGLFEAAVDNKVEAALKIADIHAIEVDKHYEKQVKMLKESAEMYKQQVNKNNQKVIHNAITKIKKDYNKLVEGIIKGKVDEFVKKGSMNLEMLVESSNKKVVDACIKTADKIHGPVNALKRINESVKKEKNVKKLEEKNKKLQMKLEEAQKNNIYNNIRNTVSIGNRDMFDTLAESVAYTGDISYESNLKSIANKIALKSKTISRKSTGRKQQLSESQNNTTYGNFL

complement(68223..68852) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00074; phage(gi100159) 9.26e-153
MKLIIEEPVKIKGSVELNESKGEKNYYIQGIFATINQQNINGRVYPRPIWESAVNSYQHHITTPTTSSLMEYQHPNRQYVDPLEAVAKIVDLRIEGDYVMGKAKLLDNPKANQLKNLIDEGISIGVSSRGCGELMNGTVTEYELITFDIVPNPSDRNAHTKGLNESFDNGILKDKNYIKDKNGILVEADESNINNKSITSQFVDLFSQL

complement(68849..69016) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00075; phage(gi100158) 1.84e-30
MYNYIKYAERKDMNGLSNVIQKKLQQEYNNHPKVVNHIETIKKNEALIKVLKEYK

complement(69017..70723) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00076; phage(gi100136) 0.0
MANMFNGLVESVKKTFLKIENQEGSIKSDDPHKEANLTRDDIVLGYFDEGNYRYNNFETDTINDVSKQASLIKEYRRIAAYPEVADAIDEITNEMSFVPNNIDCCYLGFKDNILSDNLKEAFQSLFDMSCEILQLNENIDVLCRRFYIDGQLVIGLSYDDNNSILDAVIMNPSGLYFNKSTNKWQYFNNSNNYGVADDTSEVYDPEEIIRIDSGLYSDNLILSHLHSVIKIVNQLQTLEDLMIPLRYSRSVSRRVFNIDVGNLGYEKAIAAVEDIKNKFKYKKYYNTETGSISNGASIQSMVEDYYFPNRGGTKGTQVDVLDETGNLGETGDLDYFKNKLYNALKVPTSRLMGDNKTVFDFSSTSIESTEIKFFAFVNRLRQRFNVLLIEIMKRYAITNNILTEDEFDNYSKYIFIGWEKESNFLERQNLDILKQRLDLYTEFKEYEGDIFSRSYLLKNVLKMTDEEIDQMREEILQEGSQTTPGEDEFGNEITDDEDITDDEDNFNNDIEDESEDNSLDNIENKDLKIKDDISNNKRNIVKKATKLGIPKNIIKRKISKATKLIKGE

70768..71469 PHAGE_Campyl_vB_CjeM_Los1_NC_041896: DNA primase subunit; PP_00077; phage(gi100025) 1.41e-165
MTNIPKQNKFAYTEDKPKYIDINGTTNYILPGFEYPSDVAVKFPQFFGGKDNVFYPDLQVTLTPDSLTFENSKKSQAITYTATDGSSITSAVVTIEPSDLATWNEGDK

TFTGNEEGSGKAIFELTDDKGRTAIKELPLTVTKAAVVTTLTLSPDNLTFANASAAMQEVTVTTNASDFMLEFNNQNIQAVKSGNKIQVTPKTGKTGSFTITVKAQA
SGGNQVSKTLNITVNAGG

complement(71498..71818) hypothetical; PP_00078 N/A
MLKLPCTVPPNSIACISVGVITKPPGILNPKKPPPLGYIRNVITSEILESNLIFLTPLGRSINSVPFNLPYIANSENFCIVKLIFSSIWKSVSSTVITGEPNIPKI

71817..72203 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00079; phage(gi100155) 1.42e-89
MQNVYSVLANMSILDTYFTIIPNYAFNPFTNMLEFFEDITSEKVLLEVRYKYIPEEEDGIYEQPWVKEYALNLCKRTWGSNIGKYDAPLIGGIKANYERIIQEANTELE
RLETVLLENYCEPLPLLRG

72233..73561 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00080; phage(gi100139) 0.0
MYEVLTPNGFSSFDDISREKKDVYKVITEDDFIKVTKGHKFETPNGFKQLKYLKINDLIKYKNKFSKIVSIDYIGVEYVYDLINVHKNNEYYTNNFVSHNCAFIDKWS
EFSNSVIPTISASKKSQIIAASTPVGLNHWYKMWSDAVEGKSSYKPFKVEWWKVPGRDENYKELMIKTLEGGIRTWNQEYACEFIGSSDTLVDMTVLSNIKFGNTL
REPNFGETIRVYEAPQENHKYMVLADAAKGAIDGFVFHVIDVTNIPFKQVASGKIPESYLMAPPIFYNILRTYNEAMFVCENNEGAGTSVVDLLFQMYEYENIYQEP
DKKWLGVRTTKSNRSKNLSNMKLFIENNKLILQDEPTVKELLTFCNVNGKYQAQNSKAHDDYVMALSLLFVPLLDLNNIVDYDVFLNKINSDSETTDGDVKYLQ
MGFFDDGTSSFYGIFDD

73590..73811 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00081; phage(gi100153) 8.05e-44
MPPIKHMSVADRIAQKRYRKQPKVKRKLKIRAKKNAKAPSENMSWSSKKRGYVRKDPKLRRTMKLVAKLRRKS

73814..74545 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00082; phage(gi100152) 2.67e-173
MGLNKFDSVDYILSSGQRPFRYKVSLILPTKIAKISGALYDNAVNILCKGATLPAPSILTTPIGLDGRNINIPTLMKLDNTTNMTFFIDEKSSVRRILEYWHFCIDSGITA
NEETPSVPGAGVANIVGSVANIGAGFISDITSDIPIIGNAVNSFLGINKGVSGNTDINMTGELKLTLLNYSGNAVGSYTYKNIFPIDVTGSDMQDDQTETINEFSVTFGY
THYVYKKETESIIDAVTGLVGL

complement(74540..75949) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00083; phage(gi100151) 0.0
MLKEWGFTPISSNLNYGLEVKCDKCGSNIKRSWNQMLKYNKCLSCDDNKLLLELNNLGYTVTDIRLSKLEIQCRNNHIFNRNKADFKRGVISCPECDELEKLEFIKS
CGFTKIDVNHMRCNKCNNIVKKSYPTLKSGITFCKFCDENNKKSLLDNINLEMVDKNIFKCNKGHTFYRTYDNLIKSNNLCPECYPNNTMFEKELKEILPKCIENDY
SVLGDKELDFYLPGYNLAIECNGVYWHSDKFKDKNYHLNKTEKCNGKGIQLLQIFESSWIEKKDIWKSIINNKLGKSEKIMARKCIIKQVPKTEEKEFLENNHLQGF
AGSSICYGLYFNDGLVCLMSFGKPRFTDKCNWELIRLCTKMGLNVVGGASKLLSYFHKNHPGSLISYSDRLYSDGSIYKQLGFKFSHFSKPGYMYTKNGRTLNRQQ
FMKHKLKDKLEKFDPNLTESENMSINGYYKIWDCGQGVWVKL

complement(75957..76724) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00084; phage(gi100143) 0.0
MAKSLREWYRTHVKSMADNFEDFEIFRTQFYRNPHRAIVKNSSAFKSPADGVIINQTQVNDIDDEVLKIKGKKYTLRNALGNNEEMLDLIKERGGALVIDVFMTYY

DVHYNRIPTDGFLTYEKLLPTESYNNESMLAVEEGLFANNFKKAVTELGYMFCNERLLNIIYSPVLQEKYAVVQIADEQINCIQTAWVPARGEPNTHLYQQGDIFGN
IRKGSQCTIVIPFSKKWNYIPILEPSFHVEAGIDELVRVEPK

complement(76735..77031) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00085; phage(gi100144) 8.84e-65
MDNFDVNSFKIVHPHDVLLEVAYPSEIKSESGIIVTVHPSLIDDRQTQGKVLQIGSEVKDIEIGDTVVFGKQHGIDLHKNDKVKYMLIRDESLMGILR

complement(77087..77596) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00086; phage(gi100145) 1.27e-115
MAKLILQRNKEYKDIKWQNSDKIEDSTIGELSLLDDNDNVIFKCASCENIGPSTDESGTDKRIVAREYKLKWCNSSKNGLLSKKYPEWKADNGSNIAIWVVSDEVE
GFNNRLIRIHTGNAPQHTEGCILPGSDLNNGTVGSSVDITHKLFTKIKELGIENIVFEIKEID

complement(77599..78096) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00087; phage(gi100146) 5.63e-113
MYYSNVVFPLNEVIPGFTYNVKKSKSNIYIRFVAYGYSVDDLEIVYNNSIITISTIKDYHEVKTDPKFSNNFPQQDKFYIQFWCPKISGINAEYSGNFIKLNCSLGDTSV
NLGVVPIKFINEDNDIDILENTSDDTMNIIQLNGFMDKLEDTKDDFDSEITNNKD

complement(78131..78274) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00088; phage(gi100146) 5.64e-25
MVEIIASFFVGGLIGFIAGYFVYHNNKKKASEIGDKIESVKDEIIKK

complement(78306..80669) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00089; phage(gi100145) 0.0
MKYIFTVIDNTSKTKVLKTDIDNKVNFRNVICPSINSFAQLIESNFILSRPIHSNGLFERKRENMDYLHDCGYIILDLDKVTKGNFQKIIDYFKNTKWECLICNSRSYNF
VDNFNLKVICKIDYKSTDENIRNTLLFFKEQLKGLCSIDESATRHSSYQAPSLKISVFYKNENNIGIPFSILPKSQSKTTLINCSNKQVEWCLNYVKTKLKGNIKEYVG
YYSINLPSEKKSKYSYCLYETNPFVIFHPNPSKNINILQEYLKTKDGKAFLQEKQSKIILSSLKYTPDIHINQKFLKNVDIPDTRVVCIKSPMGSGKSNIINQYIKDKSKIL
FISVRQTLAKDISLKYGCKYYLEDKKILYGENYVCQINSLHKINLDYFDYVVLDEFETLLMYIVTSIEDSPYALNILRKFYNILNSKYLLILDAFLSDHSDILSDVCRIK
NHYKDQTNVSLYTKKNTFFSVLEYVCKNKNKNEVVTMSFSTLSEFKTVESLLIKSNLKVISINSNTNRFIRDNIFTEYFKKKYVNYDCILFSPSITVGVSIMNNISHHF
HFDNSASIDAITSIQMVKRSRLASNIHIFVEGSTNMITPLEVEKNIIDSFEIDDLEYLSEFYNKLCYYYETIELNHKMSFCLLLQDQFNNINTVDSIVNYNIVQADIPKEIE
LNEFENSKIKDELIYAIKKDKNYLNYIRNFKFYTLNKNKNEFLENYLLNNPSNLLELSYRAKFLKYCVTYPDIRLKDIFTYNDIQNIKYTTDYFSFSNFLKELGYKKM
NGNYYLPLQYIKHLSKI

complement(80726..82246) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00090; phage(gi100149) 0.0
LIKIEKINESAYKIVSETQLYLDEIKQLCSAKIPNAQFLPAVRMGYSDGVKYFYKDCGDYLIVPKGFIKGIIKRLNEKYKLELSFDDEIEKITEEEFNKFVKSLKLPFEPY
DFQLKAAFDSINTGNNICVMATGSGKSLTIYILCRWFIEKYKNTDDKILIIVPSVVLLNQMYSDFKEYGFTDIDKYVDRLGGDFKVVSFVKKLNISTWQSLYRNVSLF
KDITVIIEDECHTAASDVHESIIFPSATNAKYRFGFTGTLPQNYCDKLSLMAVLGTAKTYVTPRELIDMGLATEMEIKPIILKYNDATSSIVRTVKNYQQEVSFFLGIPE
RDNIIAKLICKVSQKGNSIVLFTRVSNGENLARKVCKLKHGVDVEISELRKLNKYNIFFVSGETKASDREAIRQIMESCDDAIIFGTTSIMSTGVNIRKLKNLVSTMPG
KSYIKINQSIGRMLRKHETKNNIVYLYDIVDDARGRYAKKNYMFKHYEERLKYYNENQYVIDEVVVNI

complement(82287..82706) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00091; phage(gi100038) 4.38e-96
MTIDDLKSFHKKIIEEYDMDSNWNPSTIKHHLTTLSGTIAKYLNYWSRLKHIIIQIDEEYNEKYMILYSHYRENSNINYTVTEIKDLISKDNELCNIRVKKSTAILIMEYI
EKCVDNLNKTRYDLSNYIEIEKFLNGKG

complement(82708..83436) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00092; phage(gi100151) 2.73e-170
MLKKLCFIVTLASSLFAYNYIDSTVIEDKGNNIVIELSFCTKDLDSEKEYIIDHFNNQIDGLEQQQVKSEVYQYRGKQYVFNKGKNVKYNKPIITFVPTSTNGCYIATA
LYKIKHDDIKTSVNNKYESYFNGFITKNTSTKNEVENEIRQNLENEIKENIIIKPEQIKNSHETFVEVPKYLYAQTKENYYINIICEVTNSDNEFIYNFEIKDYKRPLIVK
GKIWGDLTPYFNTNCKVELVGK

complement(83609..84991) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00093; phage(gi100141) 0.0
MKFVNSLSNLSYTENGALTLSSSLNVALDLFFIIGTTNENNIDNVFEKVKESFNIDKELTSRILLWTRDAREGAGRREIFKRFLDFIAENNKEIYKRIIRKVPELGRFDD
LITYKQLDLVGNELIKILDFNNQLCAKWMPREKSSKSKLAKKLMKLLKLNAKDYRKLLSSNTCVVENKMCSKEWNLIEYEKIPSKAMTKYNDAFERNDKERFGN

YQESLIKGESKVNTSAIYPYEIIKLMFKNDILANEMWKNQKDWMEDSKKTLFPIIDVSGSMYTAVQGSTTALNIAISLGMYLSERNDKDFKDYFITFSANPEMVKIEG
NDLKEKYHSIKISNWGMNTNLAKTFDLILNRAKADNLSQEDLPDALVVLSDMEFDEAQQGKTNFEYIRDSFKNSGYKMPELIFWNIYGRSGNIPVRKDENGTCLIS
GFSPSIVKGLLTNDLNPEKIMFETINKERYDF

complement(85755..86399) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00094; phage(gi100134) 2.20e-149
MILTFDPYYDIKESNEFIKNLKENKINFNTYILSKSPYYWFYEVADKYKPVFLKFNEANSTDLRFMLPKLKELTPSDENYLRRIPKTPSDFERYVSPNIFKKAKYAEYF
CVFRYKNISEINKITETLGIKIYILPKKVKEWNIAFTFNKMIRNFVFGHYILLEKTKKTQFNKVGEIELYLNNKVFVTDKMKFKTRELPFSEDGTYYPLKFQIKQ

complement(86383..87561) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00095; phage(gi100154) 0.0
MNININKNYLIKGDNLEVMNSILPFYKGKVKLIYIDPPYNTGNKNFQYNDNFESIDLIIKYFNVDEEEAKKIRSQDKFIGSKVWLKFMKERLEVAREFLRDDGVIFVQCD
DNEQAYLKVLMDEIFGRENFVNCIVVKMNESKGLKNANCHKKLPKNKEYILLYKKQDNKSILKQIRLKKTQNELSSYIKYYNKYITNIENDYKEWEIKYFDPKLNK
QDYLKNLIYLVKPDNNININMEEGTFEKIINSKGKTNYYYMNNGVIMKVLFLHENLDYSLGDLWTNISTIGICKEGLKTTFKNGQKPEYLLKIILDLSTNENDLVMDF
FAGSGTTLAVAHKMKRKWIGIEQMDYIETITKERLKKVIEGEQGGISKEVQWQGGGDFEYLNKEHDDTNI

complement(87567..88298) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00096; phage(gi100155) 1.11e-177
VKYRYSYSRLECFRQCKLKFKYSYIDKISVPKDQTALIKGSYIHWLIEQSFKEEPIEVSKSYHNPLINADQYKEYNEIFEKFKETEKYKNIKDLPALGNEVNWALDSK
LNPTNYYGNDYVIRGTIDYIAIKNRCAIIIDWKTGKTKDKKYIPDANQLALYAIWAEKVLNVDKIICQFVYVETNDFHTYTYTSDDLVPLKKQFAQDIMSIENEKAFI
ANPSILCNWCEFKSMCDSFKNSSYNRE

complement(88308..88652) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00097; phage(gi100130) 2.13e-71
MENIDEFIELKSQKLNVTDFIEKNSINEDELVKNAIKQIFDLEKQKREIDVEIRDIKTKLSKDGINITEFNRVLSTLKNELKMSIDSLSANISMYNSIVSDKELLQNLKDQ
IND

complement(88709..89323) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00098; phage(gi100157) 5.27e-142
MKLFEKLEEWLKERHLDKKEYDHLTLLGYLHEEIDEGIKKRDSEHESIDWRCDCIVFLINSLYQDGYNPKICMDECLKEIEERTGEYSESERKFKKHMGAYTYKEA
LDEIIKNYNCRKEDITLHGDHREFWYFLVNGKQIKVKKWYKADYSKSIRDDISNERYITKAYKLGKKIMFRQLNTKNRWKLLRDENLNFKEFDYKVVD

complement(89698..92361) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: rnaseH; PP_00099; phage(gi100048) 0.0
MFKYEYVFEHNFKLYARLYDEVTKNSIIKEYKSTEYVPELFIRTNEKTEYKDFYTHGYLKKKTFKATYEIYQYLKNVSPSTPLYGNINRPQKYIRENFKDIDCNHEFR
TQYLDIETRAINGYAKPSNPTEEISLIQVYDNYLNKFIIFGAKDLNISLESDIGEVIYKKCDNEIQMLKKYLTFVVKTNPTIIAGFNSNLFDIPYIVNRMIHLGIDDYIELS
PIKAITHKKMKTNDDIEYDGVKIEGIIQLDLRDLYIKYTTQKPSRFSLDEISKLELGDTKVNYDGSIEDLYKDFNKFVSYGLKDVELLIKLERKLKLLKVCQLVAYKC
GVNADEVSGTLMQWASLMYNYALSKNVILPLRQLKIINYDPPYPGGWVRVIEGLHKNVCSYDFTSLYPNIIIEFKIGLDNYIPVSNIPYEKAKILEENRARFINEEPNE
VISTSLPEDLKDMLNKYFYFYSETYDKTNNDSMEEFYYFKNIIDNKDEIKQICKKYGVNVTPNGCLYFSNGTSLFAELIESFFKDRLNHKSFLKNDNLTASEIDYHDL
MQYMFKILMNSAYGSTSLAINPFSFGKKMSESITTTGRFLNMWVSYKVNKFCNETYNLNIDVNSRPLSIQCDTDSNYFEFKFLETPKDLQENAKFLKSYCETTISPVI
DDAISEAVTAINGLDKNSNLGMEQETICDRLISCARKRYVGRYFNKKKSDKGFKITGLPMIDKTTPKWTKLKLNECLDLILDSDLHGLRQFINNIKNEFKQQLLSDIC

MNKSVSSLSYIISNGKWVSSINGNPCPIQSRGSIHYNNLTNKYKLKKIMEGEKVYIVYLKTPNTITCDNVICIPDDEIVREIPSINEFVDYETMFEKYFIQKLDIMSKHIG
FDYKNIFANTLDEWL

complement(92501..92890) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00100; phage(gi100161) 5.90e-82
MKFIECIQILLENNSIGSLSLENDYIKIYKDNDKLKIVDSKDNNVLLSSEHINNENWELNNKLFELILGSMWINDSDIVTKVEDNSFYNNIQYTTFRNMLTNEISILESD
KYYTNYCKNKWFQPEPLKV

complement(92887..93327) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00101; phage(gi100162) 2.30e-102
MENISKDLITIYRYGNNFELYNDFYFIFDFDVTSKGFKLEKYLVGNNIIRIPKGFRTDFGSIPQLFQSIISPVGKPTKAYVLHDFLCGKSNKGDIPRALADELFLDAMKL
LGVNVVKRYVVWAWVRVYGIIYKPLAKFFKDIWNKL

complement(93329..93832) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: recombination endonuclease subunit; PP_00102; phage(gi100052) 2.97e-114
MIKLIIGPMRSGKSLELLREAEKLHFGRKKYILIRPEIDDREFISRSYKTLHNLNVIKTNNINTIVNEYDYILLDEFQFFDNSITNIIIDNISKNWILCGLNINYESKLFENII
NILPYADRICKLSSICEKCGSEYGNHNISNTGEICIGDDYTILCSTCKLQLKG

complement(93829..94038) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00103; phage(gi100121) 1.26e-33
MQIEDVVIDTFKSILILLISAIMLKVYVILFLIISLGVLYYDLTIGIPVTATLMFISIYLANKFEKFIS

complement(94017..94961) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00104; phage(gi100165) 0.0
MLNPINVKYWEIIHNKEDLGIKKSDDYNCKCDVCGDSKYKNKKRLHLYRKDSYTDDSIKCFNCGYTATMYSYIKTFHPMYLNNYLNEIGEKYIDDLNIQNITLTKK
EPQKPKEFFSLNLPKASEIKEAKEYILKRGGNPDDFYYCKESFVINDKTFKLPNFIIYLNTVNDNAFSFYSRSINDKIFYIFNSDDGFKVMNYFNIDPLKEVYVFEGLFD
MLCTPFKNKIAMLGATLPKGMKVIPYIIWCCDNDETGRKEMLKHTNNPNHKFVVWCDDEKFKKYKDINEIYQSGVNIENFIKEHTFDGLIAECKLRMW

complement(94945..95451) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00105; phage(gi100166) 2.51e-115
MKKVLCSAVMVAGLMFVGCSTTTPQQFAKPMLEKYDDLPSWVKEYGDIDTAVGSAMYMGQNYIQQQTEAIAVAKMNLTQKLSSKVDSMIKQYYQNKGVVKTN
NSQVSVQVSSSLVKNVKVVDTYVADDGELFVKIEAYSTNLLETIKNDDSKSLFDELDRRVGNVKSN

complement(95538..95864) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00106; phage(gi100167) 1.23e-72
MYFSLKETLEFLSTNSKNGVWEYDDISEADTTVFCSYFSDNSDENDIYIILSNPTGKSDIDLQGNVTDTDSEDGIPDRFSTCIMKVNLAKLNISNFDELGNAIKKYRL

95950..96405 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00107; phage(gi100117) 2.54e-105
MNFRNIALNSNIVFRTLLFSDDTQYYCQKVKLPRISLEGQKVGHSTGTLTLGGEVAKFDSITLTLLVDENLEVWKNFVNLINKYNKISTNTGCGIEATSWLEIHDSKN
KYLFKVEFYKSKLDEVSELEYSTTDNNIITLDITLNFDYMKII

complement(96406..96687) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00108; phage(gi100058) 3.41e-60
MNYLLELSPIFIVGLICGLSNYLSDEEDTCAGKHIKCILKYIFNSAVLCTIIYCILTSLELPYLTKIGVAGAITYLGIDKAMSLIKEFIHLKK

complement(96873..97535) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00109; phage(gi100059) 1.12e-155
MIISKKTLADQGQLNKNVILWAIDIGSELALLNRPMTVRKNSENMMVEYVDDITPEEIEAGKQAIKEYCISNNIMDIYYNFLIATTQESNKLDILKEKKRYEIQSNRD
KALENGIVYNGHTFQTREKDKLNINGAVTNLMLDIQSGTNSVSEIIWIDINDEKVTFNPQEFLKFTSMVAYNTQEITFKANVLKAKIEAAKTIEELEKIQWDDSVKTT
QKKR

complement(97571..98275) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00110; phage(gi100171) 2.21e-153
MKTYGQTKFKDIIDNTPELAYNLEFTIGNGGNFTNILDALNHCKRYINYPYYTITLKLLNNLTIDYTINIANTDFRNLIFDGNGFTISKNCKSQYDTVFHSDMSIYPWI

KNLTVENTNNRSFGIAFTNYHGSIFASHANVENNLTIKNFWNGIRHACSYLFVPGLTLDNCEYGLYAFRKSDTCLDAFVNIKNCGTGIAVYHGSEVVAQGVTFAGN
TTDCNISYNTPTTNGTIWK

complement(98452..99060) PHAGE_Campyl_PC14_NC_031909: protector from prophage-induced early lysis; PP_00111; phage(gi100001) 2.05e-127
LQTAINEANKYINYSNKSITIKLISDLVINEYINIVNIHSPFLNIDFNDYSIILNNASYDIGFSMYNSILGHINKLKINCNNKSINTAILLQKNSFCCFYYMKGILNCLGNAF
ALSTNSEAFVSDSTCELSAGSSGYYSKGILSVGSRLLFHTCKFTQNSGTLSQSVETSGIIDNFYTTFSGSVTGKSQVVGTWTKNGYISA

complement(99045..99170) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: ribonucleotide reductase A subunit; PP_00112; phage(gi100062) 3.96e-14
MLEYGRSSIKDIIDNSAKLLTSNLEWTVGTGGASSKTCKLL

complement(99215..100012) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: aerobic ribonucleotide reductase B subunit; PP_00113; phage(gi100063) 0.0
LSDALAKALEYISVKNNCNINIILKSGYKLNEQIILRNALANHINILSEDDEVLLNNFDTQDYIFMFYGCKAPNIKIMINAVGTRARGWYFRESSVTMVPSTSNAYKY
GIKNCYKNAVLSLSSKILISKYSFINNGNNLDGTQEQSLLYCNDQGELTGFDLKLDNNGSENCNGWLYYCGYGSKMTLTNSSITNNKSAANILNNNNSYMNLQYPN
FTGSKAANLLLCYNGAHTNITGRNVTNCTWSKYEFPFATNTITANGIIHAP

complement(99997..100119) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: aerobic ribonucleotide reductase B subunit; PP_00114; phage(gi100063) 1.88e-13
MINYGNSNIKEIINGSVKILTESKTYTVGRGGGSPNCQML

complement(100137..101474) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00115; phage(gi100064) 0.0
MAYGIDNVWSFVNDSQTGIDKVPVNKIILLKSENKLYLKKQEGGLTATSTVNEAILNNSIVSLSSDGNLGAVDSSIKVINDPEFTTTDNISKGKKMFKIAIEPDTIIQVL
GLYIENAANSSIDAVPFDYIIKNNNVVIYTDNDTIPIKKIIYSKTKSSQLSLSSLPKLLTENLEWTVGANGTFSNLADALQEASKYISVTNYKITITMKSSYKLTESLHIN
NANLGHVVLTSEDDYVDFDGTMTPNPSFINQYATTPIAVSFTFGISPTISFKLRFSSIPTMFSMAFGFLQTNFKLNNSGVYNAKWGVGSVGCIGLVQNSTFENCTKSG
VVADNGSILNVLENNTFKTCSGNILWSADSSKIYAGSVTFDGTYNNVAANCGVSHIASELGFNIPIFKNISNSNSYALFASYGGKITCGSNIVVSGFNKTNITANVFSS
SGCIFLY

complement(101498..103144) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: endonuclease II; PP_00116; phage(gi100065) 0.0
LNNINFKSITLQNFMKYGNKKTKFEFTNGIHLVTGKNGAGKSSLFLALHYCLFGKTYNGKTIGSLVNNINKKGMYVEVEMNINGDEFTIKRGTNPSIFEIYKNNELIP
LLSTNSAYQEFLENNILKFTEQAFRNLIYLGGDLLSQSFVRLSKKEKEDVFAILSDTATFLELTEKIKLLKKEKTTVQTNTLFKINTLQDVISKAKIKYEYDLKAYNDY
IENKNNNINEIENKIKEESGKVEKLKELKTQYDSILTQDPSNKINDLLKIINEQKSALQLMEKYKMCKGCEKLKQIIPSNIDVSNHDDLLKQLEVLQNENEVYIKNKD
DIYTKMLELKPSIENKKIYEDLLEKSKIEHIEKPSNDDIISNEKELQEVSNEYNEINTYISNLNQLEILLNNNNLKGAFLNMHLPFINKTINKYINMFDEFNFTFLLDSNL
KETITKDNKPFEYKSMSNGEALRLTFSIMLAFLDICRNKFDVKCNLLILDEVLDSSLDSVGKNELLKILTKNTDLMSMYVISHNSEIKNQLDYFTSTVNIINDGKFSEIE
YK

complement(103186..103506) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: RNA ligase 1; PP_00117; phage(gi100066) 1.74e-64
MIINVDKNMFQERMQKQGLSYGASDVLFDYIEQLEDDIGEQIEFDPIAIMSDFSVAEGEDELKDQLETLGYFDMEGDDSDLDDAKQRAINDGVLVYEDDDYYVFKS

complement(103564..104559) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00118; phage(gi100007) 0.0
MGKLIALIGDLHFGCKNFDHDILEVQLNSLEKYRDILKEKNCSTIYQLGDMFDNRKLIDLKLLHTLSTRFRNIFEGFNFYTFAGNHDMYNRDNRDIVSSELFADLLGI
KYIKEPSYHIFGKYKIGISPWLCGDEELLKECDILLGHAELKGFKYNHTSIAEEGLNIDNSKYKKVYMGHYHFNQNNVYIGTPYQMTFNEINSVPGIILLNENLEEEFI
ENTWDRRYFTVTVLKDKIILQYKDEPELFTGNLPDFCKVGKIVLKEKNEKEDKILEYFGARARISRIFYKYEEEKLYESVNLNNSVAESLDFIKEYILKEHKHLESVL
NDVINN

complement(104547..105416) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00119; phage(gi100008) 0.0
MDYLKEEDLRDEIIKLQKVEKLKELLKIEDKTDDDIQQIEKLREEGISEHYKKTKFGEMCLLLIKRILTMPKFSGYTYKDDFYSNATEKLMLYVIPNFDANKVSKISK

EPVKAFAYCTQIIVNSILQVINERKAEQELLKNYYTDYTELELRLEQKEYTCCYKTDDENIEYDVEIYPIVVIDDKLYIVEDINKKVETDLNLDISKRYFIVNEDIIQSN
TLWDILKNIDNNKTVRMIYHHDYLLKTDEYNKITGKNFKTLDIMKFRNTYIPSFPKKEKKTVESELDIWEN

105509..106471 PHAGE_Campyl_CP81_NC_042112: baseplate subunit; PP_00120; phage(gi100104) 0.0
MSKVINESTTTVDIAGVELKLAKLIYRIYTESLLNRIGARINVAVPNGSIFAFKGKYLTDYTGTDKSSTPYATILPDFAGNRDNNQETDVKAEMNYKIVKRTINCQTK
KIRSKWSIEAITDLVALTGKTTVEDILEKELLTEIIQEIDFSALKMMTTKATKTQLTLKAPNDPLVGIELFNAAQKKILEMAASTKRAITMCITAPYETCAKLMSHPNF
KANEDFTNSYFMGSIGATEIYCDYYNSLNKEYMLISYKHRNKEVEIADGSTCFAFYSYNITKAFDATSGAESYFHFLRYDVVQHPLDNTNDGQSIFLHCIEIQ

106479..107126 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00121; phage(gi100010) 6.98e-158
MAWNLNNRQNEYQLFGTLSAEIIDMYGFQLTYIKTTRLGHDKVLDDIVNYGTEATYQIFALPENAEMFDERGDILNKFGIFTMDSMNLFVSANTMKRIFQDDSKIPS
AVGDLLLLPSGKYIEITSIEHQVPGANNQFTYSNSKNVYMLRCKSFNYNHDNIPTLEEVNNEEVNESLDEIFNLVGSAENSKDKIKEEQDKESPLVKGTDSVFGYLDS

complement(107111..108889) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00122; phage(gi100071) 0.0
MDNDNKIDYLNNLGYEVISKNLSVNLEVRCSKGHTFKRAFSVFEKGCTTCPKCKDEAKMQFLHSLGYKIISKDKSDYFEVECKHGHVFKRALSVFKKGTHSCPKCE
LESKINHLHNLGFKYKSDNLVECPSGHTFKRQFSKFTDGHIICPDCNKQNKLDFLRKCGYETVSDDLTYNLMVKCPKGHIFKRTYYTFEKGIVTCPECDKNKKEIYL
SNLGFTIQSESLGHSLEVKCPKGHIFQRSFSNFFGKNVTYCPKCKDDEKMLIINEIGYKITSENLAKYLTVECPEGHIFQRSFGHFKRGNILCPICNPSTSSFEKEVSNLL
DNYIENDYSVLGDKELDFYLPEHNLAIECNGDYWHSESNGKDKNYHLNKTEKCKEKGIQLLHIFESSWIEKKDIWKSIINNKLGKSERIFARKCVLREVPKIEEKEFL
ENNHLQGFTGSSVCYGLYFNNELVCLMSFGKPRFTDKYDWELIRLCTKKNTNVIGGASKLLKYFEKENEGSLISYSDRLYSDGSIYKQLGFIFSHYSEPGYFYIKGNN
KYSRQQFMKHKLKDKLEKFDPSLTEYENMFLNGYNRVWDCGQGVWVKDQLSK

108998..110029 PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00123; phage(gi100012) 0.0
MEFFFFETTKKYCKGLLDIFNSIQVKKKIDEKTDKYVTVPISFGSKDAASVFNDTELDQLLSGNFNILPRMSLALMSMERDDQRATSRFQIPIKDIDGKNITFQHNCVP
YSFDFVLSIATRSLTDLTSILEQILPFFNPNINLRVRELEWLTEPTTIQVELISVDYELPDENDGADIRVCSANVTMRLHGNIYPPIKNGAVIQQVKLYLSPVVDFSEDSK

EIVHKFNVNENTHMMDIDSFVRIDYGEEWNKVKPVIDGVKGEVKNLPIQENIKYRILYTDDTDDNIKFIINVLEDNGVNPIISKQLNYFTVFAKNKGTLKLSIQAVNS
FDLQSNIYEMELEFQ

110026..110481 PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00124; phage(gi100100) 1.55e-102
MKEKAEALGKKLDKINDIFNITEKTIVEVEKSDLVKSNPEENLKFTYLKEDFNLMRESLVNTIKRGQDILEVISNNILADPLSSNQAVMAYSTLVDTINNSTKLLTDIY
KNIVDIQIKIAPKEAEKGSGKQEIMTIAQITKMISKNQQSQN

complement(110478..111029) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00125; phage(gi100099) 4.96e-112
MADLKKIEELIALAYGYEYGISHIDESDIDVFIKGFDEKNAEQQLKKADIDLESLLSNNFDKNALIMINYKKYYPIKLYGFNNLIKEFPSLNNINFYGALSGASTIIIKD
DEIMCLVDPNDYEKFKESFDSMLIELMKFIANSNSAEKAMDYLVSNDVGVGSYYNENKELTQMIFNAIELNKA

complement(111022..111213) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00126; phage(gi100098) 7.00e-26
MFKKLLNWFMNNFCACILLLYLILLLVIIDGEISLSNVITVIVITGCYIVERIENTIKGNKNG

complement(111237..111536) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00127; phage(gi100097) 2.60e-62
MKSSNFKTCKINKKYHCINTKSALVQENYKMEKSKYSVVKEFINLNYNIPIEKIDKETELFFFSIKLLCDIIELCPKHKKEIEDKVGELCDFREYQLES

complement(111523..111690) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00128; phage(gi100016) 1.02e-29
MLEYFNCYTSKKELYNYEKLKQELNEHGLNIKDDENSIKEDIDENILKRKNNEIK

complement(111684..112106) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00129; phage(gi100017) 2.94e-79
MTNRCFIGILENNNNVKYSFCMYDGNIELAGRILLQNYNKLCELLNIGKDIRFLSNRIDLCNFFEYEYNYNHDVKMNLETFKNIVFDDHYCDIKYIYLFKDGKYYFA
DRNNYKNLLENALEDFICYSMNNEDNLIEEIKC

complement(112199..112636) PHAGE_Campyl_PC14_NC_031909: exonuclease A; PP_00130; phage(gi100018) 3.71e-86
MENYKSVYNDCLLLFLELQKSDDNKKLQIYDLMLKCIKLKLPEITTKENIKKVQEVLKNYKEIETLDKDKTYGTISWYYLLYYIGNVYNIGYKVVFYGTNGRYSYN
DDYFEDIINLYSTITFLKEKLQKGCPDNVSLAVFNKEGN

complement(112760..113353) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00131; phage(gi100019) 1.36e-72
MTEIQFNKIKERLTQWREERHLTYENQQAEFFGNVFEKVSEYFRAKDDLEKIDAICDIVIYFFNAFDFKYIAVSSNMYCYTFSDVVVYNIYSLFGARTDNLCVVENE
NDFINLEKNLNLTMFEIEQLYENLDFDFYKCMLEKIKEIESRTGYYDEKLKKFIKDTSDEAKAKWYKADYESCMFEGWEIISKLIKEFKK

complement(113334..113675) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00132; phage(gi100091) 1.47e-63
MVSTVFENDYVEVVTRKDAESIVENFIKTCDCDWNDDENCDKCASIDNLKFHLEANRDCNIFVRFKFNKDDKTNLRWSGNLCVNSISEYVENELENDIKVVKYNR
RLNDRNTI

complement(113719..113922) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00133; phage(gi100022) 1.67e-42
MNKIKQWTIELMCMFYPIKIKSTAKDNYYISYKFKFNKYYVFGDKGGALFAENYKDALRIVEWMDDN

complement(113925..114074) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00134; phage(gi100023) 4.33e-28
MKIEITRDISNVVKKSPEIILNDEFYKLYVKYIGPSEELLFYKNCNKGR

complement(114301..114777) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00135; phage(gi100084) 5.29e-110
MYSKFINEAVSDDMLKAINVANWKTGLDFRKDYEEIESHGKKALEILDKLAKGGYNSKQYYNIYSDLRDELWNIHDRLLSYKNKMPWFRDELQSPELKRYREIIK
DYIYEVNQAMKDLKSDYAVVSHISNRNLESIIKAIIDEYERLYEIVEKIALSQ

complement(114904..115035) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00136; phage(gi100085) 6.33e-18
VKLKSFNFRIYDENTTINLLVDHKYDLFETLCGEFEPDKCEYC

complement(115047..115328) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00137; phage(gi100080) 3.56e-57
MALYKFSVKLYDDKHENIQKFCLIDGKHWHLLKDFRNCLISPDNVYFYDEKDLISISDYEDALKVFKKPIHRRMFIEYGSSYQEPDDKFITEY

complement(115448..115900) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00138; phage(gi100091) 2.26e-98
MLLEVVFENFKFCRQDRVEINFDKLYSPDYFKKTFRKVKCKCNPLKSLFFVDCDLPKYILKAIKRDKSLCNEITKDYGVITLTYRQDDFLIDYILKITESEIIQTTDLVY
LDLYLKDENSDCAKTINENTKLKPSEKKALEKVKQFEKIQ

complement(116011..116325) PHAGE_Campyl_CP30A_NC_018861: hypothetical protein; PP_00139; phage(gi410493054) 1.39e-68
MRITFNFEKEYTSTPYARNAEHDKEKNGEDFEKNYLSKWIDEKQETLIKVDNLELPFSDSFVDASFCKLIRQNKKLFYKYIKIDDKTDDEKDLLNTIKEVLARK

complement(116481..116669) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00140; phage(gi100076) 4.00e-10
MDKKCRDSYGQIDYLDAYGNYVKTIFESNTERHRNYSGENIRRGNGTKRLEESIKKCKGAKM

complement(116675..117289) PHAGE_Campyl_CP81_NC_042112: co-chaperonin for GroEL; PP_00141; phage(gi100075) 6.32e-107
MIESKFIIKRKLNFKNMEFGYKLFDVSGYFEFVEKPIYPRILEEFKKLDPTMKNKTILNRLRYIDRVRYDLLYDFTFTLAYSKSKLDKTIKNGKDLCEYDLYDLKPDW
LLKMVSDIIDEKTLLKYLPDIFEYMDDIIKSINDNFDLSNNAIFKWFQNVRNYIKLLLDGKIDYKNYCINIDLVIKSNMENALLFEKEVIEELNRC

complement(117450..117836) PHAGE_Campyl_PC14_NC_031909: membrane-associated initiation of head vertex; PP_00142; phage(gi100034) 5.89e-75
MAMILSQEEIDALLECDSRPTNLGIRSIVDKKISELREEHSKLSIKMKAIQGLNLLAHTDDFTIKDYMSIINDLIDCLKYKISHCQSFRDNISNKEAEKEFLKELGSFKLT
LLDFELNMNTGEENGEI

complement(117915..118070) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00143; phage(gi100072) 2.42e-27
MRELRGIVFNFYKKYFCKCESCNFREFGKLFKNYFIYLNLFQLYKITDEGI

complement(118258..118659) PHAGE_Campyl_CP81_NC_042112: 3'phosphatase, 5'polynucleotide kinase; PP_00144; phage(gi100070) 9.18e-90
MNNATVISFKFETEQLAFLNNCICYYDDEFYNVKYMCNLSDDEFKRITNFISCMKNNIKYLEINDKNVDIETLINRLGTHIFRYAHTDTPKEHKDTEYMLLKDYLLL
HIKDYGDNELVKQILKKSEELNSKYL

complement(118710..119153) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00145; phage(gi100038) 2.47e-103
MPEFKQGFYKPINPEKYIDDVTNIIYRSSWEYKFMLWCDNNAGVLKWASESIVIPYEFLGKKHRYFPDFYIEVKDKDNNIKKYIIEIKPQKDAIFKKPKIITEKNKKRV
VEQALTVSKNQAKWEAAREFCRINNMEFMVLTENELFK

complement(119153..119536) PHAGE_Campyl_PC14_NC_031909: RegA; PP_00146; phage(gi100039) 2.74e-74
MNESLADYGLDVNGFYKHIDGKESIVETDDFKIKITYDSVNSEFDGDNEELLLKMHCNIELRYIAGIEDAMRVSDEINNKIVEIIEEDLKKYDDVSKYLILVDSGVFID
PDDPDYIQNAYIIIQPKY

complement(119533..119856) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00147; phage(gi100099) 5.69e-60
MNIYSIFLNEEVEPQKDLAKKSLDFLGEKLNATHSVSEKGNTLIATYKDKNGNKLCDVNITVNDNNIKVTKVTDNKGKPKQIDLVIHRINDIIGSRMMSYINKVKKQ

complement(120157..120432) PHAGE_Weisse_WCP30_NC_031101: DCTP pyrophosphatase; PP_00148; phage(gi100024) 4.39e-05
MNNKRKNNGTRRFTGYFDKNGNKIYKDDIIIFNDIVHDTNRIGVIIKRQHSGEFRLEFSKDDTLGLKILDESKLLVIGNINENAELLEAKE

complement(120592..120834) hypothetical; PP_00149 N/A
MKIGTDKNGKEIKIGDVLFCLELVATEVEDEGDEVEYEEFEHYIQVLEKDNEIIVCDLDSDEWWFLHQFSFADYKIVSDY

complement(120831..121298) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00150; phage(gi100087) 8.74e-13
MKLKDFDFRIWDDTNKGYIEEIEIHKFQNYPIEAGYTFMETDRIGEVEFIKNKNDLEIELFTGLYDKNGTKIYEGDIVCCSTSQGKTLFYFITTNKNINTFQIFVISDLEK
FKICNEIDINSLLYCDLSNLEDMKLNSEVIGNIHNREGISKELK

complement(121295..121501) hypothetical; PP_00151 N/A
MKEKVQNISIDVNVEELLEQVETEYLLHELSRRPLLYVDITSLIWDTLDEDELKILKKEVHQMIKEKQ

complement(121836..122006) PHAGE_Campyl_CP81_NC_042112: aerobic ribonucleotide reductase B subunit; PP_00152; phage(gi100063) 1.03e-30
MDIKKLKESLEGKDNGKYFCEIFNTNVDILVVDNGMKKSEAIIQVLEDVKELYKND

complement(122052..122333) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: baseplate subunit; PP_00153; phage(gi100104) 6.97e-53
MEKVIHKESGKEYSYFKPVLNKTTNEVMICYTDGVNFYVRTKNDFFDKFEILETPEKYDTIKYFHDLVNNKLWALKRQEELLDKVSKFDLSLI

complement(122340..122582) PHAGE_Campyl_PC14_NC_031909: ssDNA binding protein; PP_00154; phage(gi100044) 1.85e-46
MKLIISLLILASMAFSIEVCSFKEPLKRGFFSIDNSIVFLCIDKKLFVRNFPGETDYSYSVTQVFEEGMKPQACSCQAEE

complement(122579..122746) PHAGE_Campyl_PC14_NC_031909: loader of DNA helicase; PP_00155; phage(gi100045) 4.14e-21
MTPKKIQKIFEKVLKEKEKEYTDGRLEEIRKEREYVESIVNEGIQKANNMLKEFK

complement(123104..124144) PHAGE_Campyl_PC14_NC_031909: dsDNA binding protein; PP_00156; phage(gi100047) 0.0
MINKKALINHMYSEMLHKCLNGTETVDNPYHLEKTVLDHTIMVLNKVEDLFKNDKDYKVLMFGAALHDLGKIFTREVITKDNRTVKVRFINHENVGVYYACDVL
SKFDLSEEEIIKIIKIVAYHDIYKYNIDELKRKFTYDDLQLLYKFSICDLLGRITHTPKPTDIYKQIKSLEYYETKGIDSSKPTITMLIGVPGVGKSILCNQYENVVSRDDV
LMSYGKNKFNLETYSEIWSKLSQDDQKEIDNIFKFKLNRLLQQGKDIIIDKTNTSIKSRKSLLNSSSLIKSYNKVAIVVLCPYNTILERIEKRSLETGKEISKNIVDDFIKS
MRLPTLEEFDEISFKWSI

complement(124347..125720) PHAGE_Campyl_PC14_NC_031909: rnaseH; PP_00157; phage(gi100048) 0.0
MLPVKTLTELNDININVIKRNGTVEKYSPDKMYKFLLKVCDNKESYAINILSKSKIKLRDNIKIQDLYDEILSTTVNEISMLYPMYEKFAAKLYIIKYRKNIGDEISLSS
VLKLGLSSGVYSSDFVNSFSEDEIQELDRYIDNNRDYLFQNYKAISMFYTKYCLNRTKTIKLETPQITYMRVAMFICMNESNRVEKIKRIYDLISTHKFTYATPIMLNS
GINKGQLSSCVLAKMGDDSHSILATNDNLAIYSKNKGGTACDVSALRATGSIIDGVGVSSGPIPFIKLLDSTISAWNQGSTRKGSCCVYYPTWHMDVQNLIMLKDN
GGTESTRARNLQYAIKIDDVFVKRWYNNENYTLFDPKDTPKLLDTFGDDFEKYYLEYEQKSNIRKKSINARELFDEILKYRVETGNIYIFFIDNVNKQGMLNRIVTQS
NLCCEIVLPTSAPYKKDEKIVHYM

complement(125707..126843) PHAGE_Campyl_CP81_NC_042112: hypothetical protein; PP_00158; phage(gi100055) 0.0
MLLSKKNLVTDKSKEKFFFGEYSGFQRYDWYSHNQLESLDRKQQAQLWFPEEISMIHEPKSFIELPEHNQKQIKANLTFQTLMDSGQNRGLDNILIPLVTSSGLEGC
LKTQAYFEYIHSRSYSHIIKSVFPNPTDVFDEYCEYPEIKTRINDEIDTYESLEGSLEENDENKLKILEACLRIQFLEGVKFYVSFLTTYMINKYSAGGNKIPNLTKIIKLI
NNDEDIHLIIFSFIIKTLRSEQHQGFSHLFDDSLSRKARKIAKKVYQDELEWAKYLLSMGPIPGLTIENIDGFLKFFVDDRLKKCGFQPIWNAQKTDLVKEFQEIKNISS
ENQMLQEVDSITYSKGVMKKDTKLEIYNGETLENELEKILNGEIGNVAS

complement(126856..127074) PHAGE_Campyl_CP81_NC_042112: recombination endonuclease subunit; PP_00160; phage(gi100054) 1.92e-41
MLFETYTDMLIWSFIIICCMLLLVTNKYTTKLYNIVVSLSVVYIMYNFISNCIELYSLYNLIYVEQFFDVNE

127043..127180 hypothetical; PP_00159 N/A
MSISVYVSNNIVTYSFGFSKCTPTLSNTSKATGKLIKLMIIESTQ

complement(127208..127579) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00161; phage(gi100111) 6.26e-83
MKLLVAGSRDFNDYNLLKNKIFELNIQPSTIVCGMTRGADMLGYQYGIDNSLKIEKYKPNWNLYGKSAGPIRNKLMADSLNKETDMAIIFWDGISKGTKNMISILD
DKKINYKIIYYKEKENE

complement(127576..127782) PHAGE_Campyl_PC14_NC_031909: recombination endonuclease subunit; PP_00162; phage(gi100052) 4.52e-41
MFVKIKELICKFVNFKTLQKFITTDRQFIIEGQNGMKYSGDFFFVDEDGCICKISDGSYVGTMVKSSK

complement(127816..129291) PHAGE_Campyl_PC14_NC_031909: hypothetical protein; PP_00163; phage(gi100053) 0.0
MTNHEKIIFLNNLGYKAISENLSKNLKVECKSGHVFGRMFDDFKRGSVNCPECDRLGKLNYLNNLGYKVASENLADSLHVECPKGHIFKRAFGDFKNGKINCPKC

NIQSKLDYLNSLGYEVISENLSKGLEVRCSNGHIFKRAFGKFKDGFTTCPKCKDTNKVNYINNLGYEIISNNLADELKVRCIQGHIFNRTYGNFKQGKIICPICNPSTSS
FEKEVSDLLDNYIENDYSILGDKELDFYLPEHNLAIECNGDYWHSESNGKDKNYHLDKTLKCESKGIHLLHVFEHSWYSKKNIWTSIINNKLGKSNKIMARKCVLR
EVPKTEEKEFLDENHLQGFTGSSICYGLYYQDKLVCLMSFGKPRFTGKYDWELIRLCTKMDHNIIGGASKLLKHFHKNHPGSLISYSDRLYSDGSIYLRLGFTFSHYS
KPGYYYFKNGTKYSRQQFMKHKLKDKLEKFDPNLTESENMVENGYHKVWDCGQGVWVKGNL

complement(129324..130370) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00164; phage(gi100114) 0.0
MSLIDKLLKSSTLGNRTSVLKESKYFGKDEFVETPIPMLNLALSGKLNGGLTSGLTVIAGPSKHFKSNYALVMMASYLKKYPDSVCIFYDSEFGITPDYMQNFGVDT
TRVIHTPVANVEELKFDIANQLENIGDNDKVIIVLDSLGNLASKAEIENAINEKSVVDMQRSKHIKSLFRIVTPYLSMKKIPMVVVNHTYDDIGSLWGGQVVSGGTG
VIYSADTIFVIGKAQEKDSKKNLQGWQFTINVEKSRFIKEKSKIPILVTFDNGINKWSGLADLGLELGFLQKQGDSHFNPFTEKKLYLKGAPQEQLDEFFSELLSNKD
FVDALEYKYSLLNITPNNNETTENNV

complement(130426..130719) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00165; phage(gi100116) 1.92e-53
MKRNILLLIFSSFLFIGCSTATKTVTITKKEYLKYPLDEKYIPHKLDVKIMKQKLNGKDYLLILPNDFITIYNQYKHLELNYNNLYDSVEKFNLQIK

complement(130688..131026) PHAGE_Campyl_vB_CjeM_Los1_NC_041896: hypothetical protein; PP_00166; phage(gi100117) 1.44e-49
MFNIILSVIKSNIVYIIFGCLLVAITYRYISLEKSNAVLIENEKQLTQNLNESKKELEVLDKYNKITVEIFKEKETKYKEVLRNIKNIETKIKNLQPIGKDKNETQYIIIN

Appendix 3 – Abstract – conference presentation

– Invited presentation at the international conference "Tropical Agriculture" held in Brisbane 11 – 13th November 2019

A biocontrol option to control a foodborne pathogen; using *Campylobacter* bacteriophages to control *Campylobacter* in poultry

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Campylobacter is a leading cause of foodborne illnesses both in Australia and internationally and is a commensal in poultry. There is a need for environmentally friendly options to support the current farm management strategies that address food-safety. The use of bacteriophages provides a safe biocontrol option. A collaborative study by the Department of Agriculture and Fisheries (QLD), the University of Nottingham (UK) and the Institute of Environmental Science and Research (NZ) is in progress. *Campylobacter* bacteriophages were sourced from Queensland poultry farms and following extensive screening, suitable candidates to be used in cocktails were identified. This followed an on-farm proof of concept study on a small sample of chickens, using selected cocktail candidates, to provide an understanding for practical application. The trial demonstrated a 2-log reduction of *Campylobacter* in the caeca of treated birds (compared to control) ($P < 0.05$). Another important finding of this study was the absence of bacteriophage resistance, a concern with phage therapy. Work at ESR has addressed approaches to select and adapt bacteriophage cocktails to particular hosts, which included screening against NZ and Australian hosts. This approach enabling the formulation of high performing bacteriophage cocktails for Australian and international markets. Work in the UK is exploring the understanding of the host-bacteriophage relationships to ensure safety to meet regulatory requirements and support potential scale-up options. In summary, the work in progress via international collaborations is aimed at delivering a safe biocontrol option that can meet both commercial and regulatory needs aiming at controlling on-farm *Campylobacter*.

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Project Summary	*Campylobacter* naturally colonises the chicken gut, where it can reach high numbers and potentially contaminate the marketed product. A low number of organisms can cause human illness. This study explored a biocontrol option using bacteriophages (phages) to reduce *Campylobacter* numbers in chickens. Bacteriophages are viruses that infect and kill the target bacteria. These specific, *Campylobacter*-killing phages occur naturally in farm chickens, where they are already in a 'predator–prey relationship' with *Campylobacter*. The aim of this study is to better the outcome of this natural phenomenon. The study builds upon data from previous studies to progress the option of using *Campylobacter* bacteriophages to control *Campylobacter* levels in poultry. *Campylobacter* phages sourced during a previous study were narrowed down to a 23-member cocktail candidate panel by screening against farm campylobacters. The outcomes of the laboratory studies undertaken provided a detailed understanding of the phage candidates. Some phages were subjected to detailed molecular analysis. With an understanding, the selected candidates were mixed as cocktails, which included all Australian phages or Australian candidates with the inclusion of New Zealand phages. The combined Australian and New Zealand phages cocktails performed the best against farm campylobacters from both countries. The work undertaken provided a detailed understanding of phages, the approaches adopted demonstrated the potential progressing to a more advanced stage in working with these phages to develop a biocontrol option to control *Campylobacter* in poultry. In summary: • Poultry are a major source of *Campylobacter*, with the most important single source of campylobacteriosis considered to be broiler meat. • Modelling indicates that on-farm poultry interventions can be very effective in reducing human infections. • Development and validation of on-farm control options for reducing *Campylobacter* levels by 1.0 to 2.0 logs can realistically result in a 90% reduction of human infections. • This study is progressing towards delivering an environmentally compatible option for the industry to achieve these reductions in *Campylobacter* on-farm There is need to formulate and address selection of cocktails from a scale up perspective to ensure a viable commercialisation pathway to market There is need to seek potential commercial entities to understand the way forward in providing a Australian regulatory frame work for the use of phages as bio-control agents by the Australian Poultry Industry

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Moving from concept to control; use of phages for Campylobacter reduction

by H.N. Chinivasagam, Estella, W, Cockerill, S, Maddock, L, Mayer, D, Billington, C, Premaratne, A, Liang, L, Connerton, P. L, Connerton, I. F.
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