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Phenotyping Temperature-Sensitive Coronaviruses

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LOYOLA UNIVERSITY CHICAGO

CHARACTERIZING TEMPERATURE-SENSITIVE CORONAVIRUSES

A THESIS SUBMITTED TO
THE FACULTY OF THE GRADUATE SCHOOL
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MASTER OF SCIENCE

PROGRAM IN MICROBIOLOGY AND IMMUNOLOGY

BY

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LIST OF ABBREVIATIONS

CoV	Coronavirus
ARDS	Acute Respiratory Distress Syndrome
MHV	Murine Hepatitis Virus
TS	Temperature-sensitive
SARS	Severe Acute Respiratory Syndrome
MERS	Middle Eastern Respiratory Syndrome
PEDV	Porcine Epidemic Diarrhea Virus
NSP	Nonstructural Protein
ROS	Reactive oxygen Species
DBT	Delayed Brain Tumor Cells
FCS	Fetal Calf Serum
MEM	Minimum Essential Media
PFU	Plaque Forming Unit
ORF1A	Open Reading Frame

ABSTRACT

Coronaviruses (CoVs) can cause a range of symptoms; from a mild common cold to life threatening acute respiratory distress syndrome (ARDS) upon infection. CoVs provide an example of the importance of studying emerging viruses. These emerging viruses have the ability to be highly pathogenic and detrimental to the human population. Two prime examples of CoV emergence, SARS-CoV (Severe Acute Respiratory Syndrome) and MERS-CoV, (Middle Eastern Respiratory Syndrome), which exhibits the pandemic potential of emerging CoVs that gain human tropism. This human tropism is gained through mutations that allow for cross species and zoonotic transmission. If there was an outbreak of an emerging CoV strain, not only would that be deleterious to human health but could potentially accumulate billions in health care costs to treat infected patients. Given the increasing potential of an emerging CoV outbreak, there needs to be a state of urgency to develop vaccines that will help protect the human population against current and future circulating strains. The Coronaviridae family of viruses are unique because they contain a highly conserved gene arrangement and function within its viral genome. The purpose of this study is to identify a technique that will allow the identification of attenuating mutations that are present within a functionally conserved region. By identifying conserved targets of attenuation, I can identify mutations that can be applied to the development of a CoV vaccine strain for one or more CoVs. Currently, there are many ways in which we can identify attenuating mutations, and one such way is to identify temperature-sensitive (TS) mutants. A TS mutant will be able to confer a wild type phenotype when incubated under permissive conditions and will confer an attenuated phenotype when incubated in non-permissive conditions. By

chemically inducing mutations and then verifying mutations that confer a TS phenotype, I can identify mutants that contain TS mutations in their viral genome. By using genomic sequencing of these TS mutants, I am able to identify novel attenuating mutations in the CoV genome. TS phenotyping allows for the potential application of the attenuating mutation to current strains, and confer protection, but also identifies targets for mutation that may also attenuate future emerging CoVs. The results gained from this study confirm the use of TS phenotyping and sequencing as an advantageous tool to identify sites that confer attenuation. With the proof that CoVs have the capability to mutate to gain human tropism, resulting in deadly disease, we must begin to prepare for potential pandemic outbreak.

CHAPTER ONE

BACKGROUND

Literature Review

There has been an ongoing battle between humans and viruses since both have occupied the earth. As obligate intracellular pathogens, viruses have only two main focuses: replicate and disseminate. Humans, however, have developed methods to counteract these viral infections. Our bodies as living organisms have two main focuses as well: identify the pathogen and eliminate it. Typically, our bodies' constantly adapting immune system has the ability to fight off viral infections by controlling the infection to keep them from causing major health issues. But there have been many examples in history in which viruses have won that battle causing major health issues. Within the last 100 years we have numerous documented examples of such viral success, such as the 1918 influenza outbreak resulting in millions of deaths¹, Human Immunodeficiency Virus (HIV) also killing millions², as well as SARS-CoV and MERS-CoV infections, which combined have killed thousands^{3,4}. Although these RNA viruses are different in their characteristics they harbor, there is one common factor that aided their success to cause so much harm to the human population: un-anticipated emergence. When these viruses emerged from their host species into our naïve human population it resulted in the deaths of many. How can these pandemics be avoided one may wonder? The answer is simple: by studying emerging viruses and making vaccines that can protect against current and potentially emerging strains. One viral group that deserves such attention is coronaviruses, which in the last 15 years have had

two viral strains emerge into the human population with the potential to cause world-wide pandemics.

Coronavirus History and Classification.

CoVs were first isolated in 1965 from human organ cultures from the respiratory tract of an adult with a common cold. *Byone and Tyrell et al.* were able to determine the presence of an infectious agent by inoculating human volunteers with the media from these cultures, which resulted in colds developing in these patients⁵. Simultaneously, another group was able to grow a virus that seemed to have “unusual properties” from samples obtained from medical students who also had colds⁶. This virus was named 229E. In the late 1960’s, *Tyrell et al.* began to work with not only human strains but also many animal viruses, which included 229E, Mouse Hepatitis Virus (MHV) and a gastroenteritis virus of swine, which would later be named PEDV⁵. Looking at the various strains under the electron microscope he noted that the particles were pleomorphic, membrane coated and covered with club-like projections on the surface. This new family of viruses, having a crown-like appearance, was officially named the Coronaviridae. As further studies began to look more in depth at the pathology and the epidemiology of coronaviruses, the number of identified animal CoVs grew at a rapid rate. Researchers were able to isolate CoVs that caused disease in many animal species, which include but are not limited to cats, dogs, rabbits, mice, rats, chickens, turkeys and most importantly bats⁷. Fast forward to current day, using sequence analysis, researchers have been able to identify four subfamilies of CoVs that include, alpha, beta, gamma and delta CoVs (Figure 1). Currently, there are only six CoVs that infect humans: alpha Co’s 229E, NL63 and beta CoV’s OC34, HKU1, SARS-CoV, and MERS-CoV (Figure 1). Of the viruses that infect humans, the latter two listed are the most pathogenic.

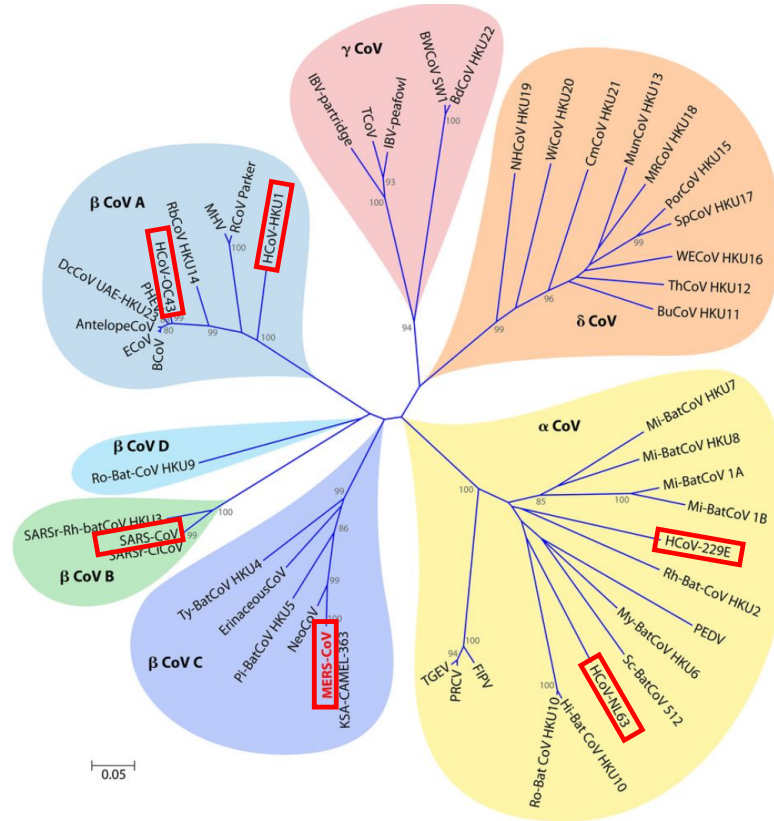


Figure 1. Phylogenetic Tree of Coronavirus Family. Above depicts numerous strains of viruses that have currently been identified to belong to the four CoV subtypes: alpha, beta, gamma, and delta. Highlighted in the red boxes are the current strains that have been identified to infect humans. The phylogenetic tree was comprised of partial nucleotide sequences of RNA-dependent polymerase. Modified from Chan et al.⁸

CoV Structure and Replication.

CoVs are spherical, enveloped viruses, which house a single-stranded, positive sense RNA genome. These enveloped virions are studded with spike proteins on the surface. The surface of CoVs are made up of membrane proteins and a host derived envelope. Some strains also contain a hemagglutinin-esterase protein that is needed for releasing the viral genome during infection. Inside this enveloped virion is the positive strand RNA genome covered in nucleocapsid protein (Figure 2).

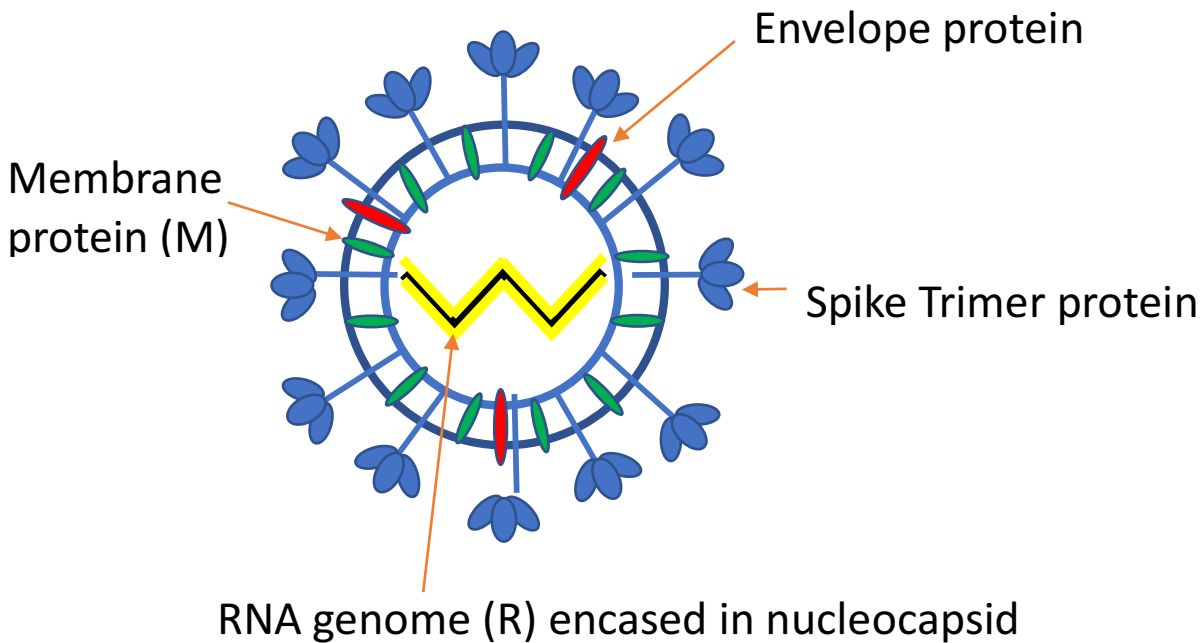


Figure 2. Schematic diagram of the typical virion structure for a Coronavirus. CoVs produce a spherical shaped virion that contains a single stranded RNA genome that is encased in nucleocapsid protein. (S) Spike protein is a transmembrane protein that forms the spike-like projections that interacts with host's surface receptor to allow endocytosis to occur. (M) Membrane houses the viral RNA. (E) Envelope protein that is derived from the host and also serves as a barrier for protection. (R) Viral RNA genome that encodes all of the structural and non-structural proteins used during the viral lifecycle to produce and infectious virion. (N) Nucleocapsid protein covers the viral genome and protects the RNA when injected into the host cell cytoplasm⁹.

Upon viral infection, the virus enters a cell through receptor-mediated endocytosis or fuses directly at the cell membrane for entry into a host cell¹. The genomic RNA, once released into the cytoplasm, is translated into two large polyproteins termed ORF1a/b, which encode the replication machinery needed for viral replication and are processed by the virus-encoded autocatalytic non-structural proteins. The genome also encodes structural and accessory proteins at the 3' end^{10,11}. Although all of the functions of the non-structural proteins (NSPs) that CoV's genome encode have yet to be identified, it is known that some of the NSPs will interact with the host endoplasmic reticulum (ER) allowing the formation of double-membrane vesicles (DMVs).

Inside these DMVs, other NSPs combine to make replication complexes and allow for genomic replication. The structural proteins, viral genome, nucleocapsid and viral envelope are assembled at the ER-Golgi intermediate compartment. Once assembly of the new virion is complete, the newly infectious viral particle is released from the cell ^{12,13} (Figure 3).

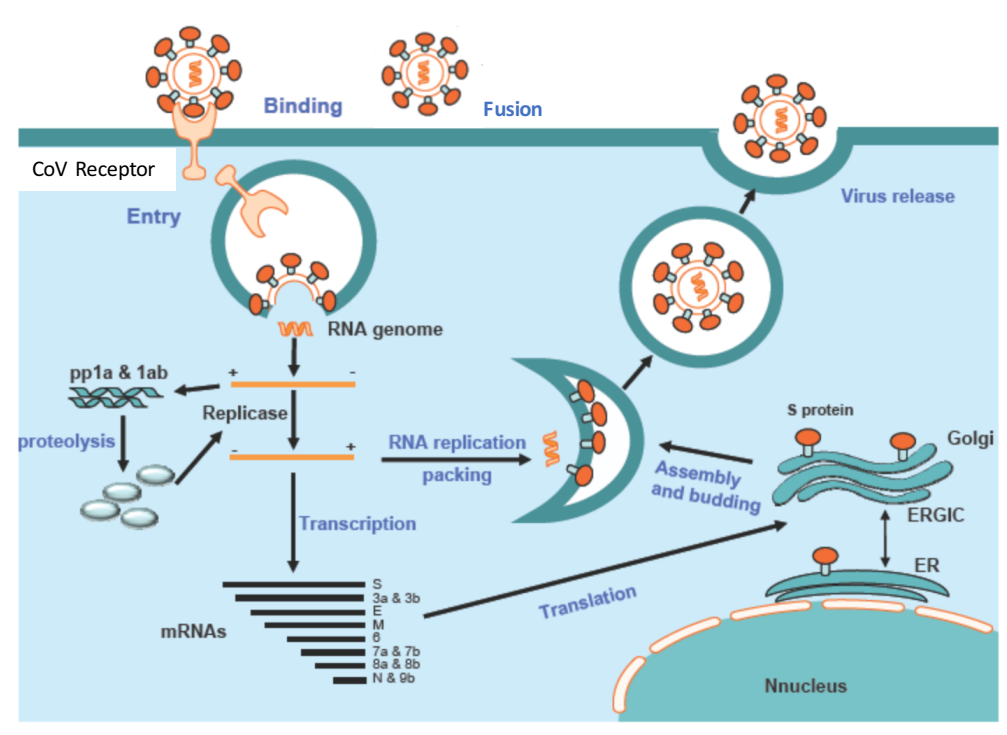


Figure 3. Coronavirus Replication Cycle. Depicted above is the general CoV replication cycle. Replication initiates with receptor mediated endocytosis, or fusing at the cell membrane. Upon entry into the cell the viral genome is released into the cytoplasm where the positive strand genome is translated to make two large polyproteins that encode the viral replicase machinery. Following the production of the replicase machinery, viral transcription occurs in double membrane vesicles derived from the ER-Golgi complex. Virions are packaged and matured within the double membrane vesicles, as they travel towards the host membrane. These vesicles that contain the infectious virion is then released from the cell. Modified from Zhu et al.¹⁴

Coronavirus Genome.

As members of the Nidovirales order, CoVs have a unique coding strategy: a majority of viral RNA is translated into two large polyproteins and the remainder of the viral genome is

transcribed into a nested set of subgenomic mRNAs^{10,13}. The two polyproteins encode 16 non-structural proteins that make up the viral replicase-transcriptase complex¹⁵. Containing a large viral genome is very unique, and this is able to be achieved because CoVs genome encodes an exoribonuclease that functions as a proofreading mechanism and allows for the maintenance of the large viral genome without accumulating deleterious mutations^{16,17}. This large viral genome that is characteristic of CoVs is actually highly conserved amongst the CoV's subtypes (Figure 4). The conservation of gene order and function has been key in studying emerging viruses. This highly conserved gene order and function is the key component in many successful CoV infections. It can be appreciated that it is the accessory proteins and mutations in the viral spike that aid the CoV's ability to have a large range of host tropism¹⁸. However, it is the function of the polyproteins of the viral genome that aids in the efficient replication of these viruses¹⁹. These viruses have a conserved gene order and function because they arose from a common ancestor: the bat.

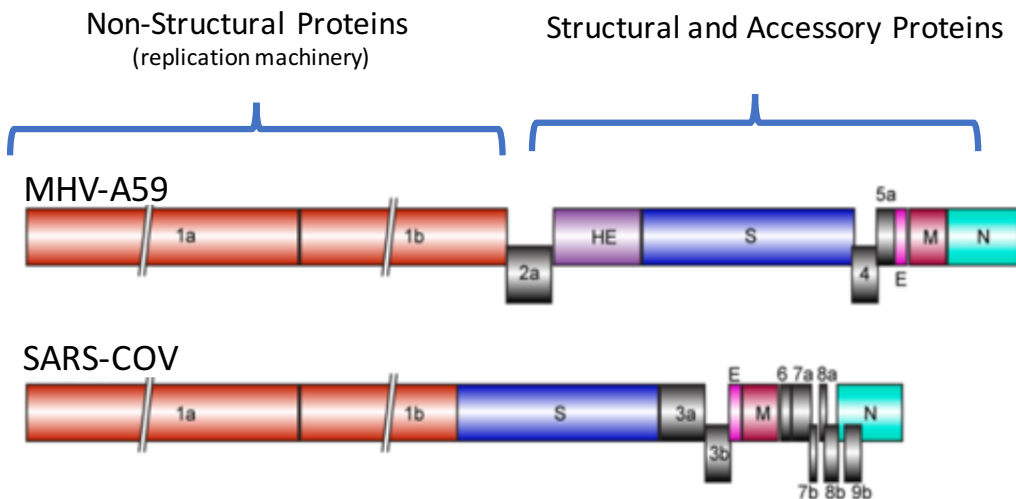


Figure 4. CoVs contain a conserved genome organization. Depicted above are two CoV genomes from two different strains of the virus. MHV is able to infect mice and SARS infects humans, yet they have a very similar genome organization. These two different viruses have very different host tropism but all retain similar replication machinery needed for successful viral infection. Although the other strains of CoVs are not depicted, these are a representation of the

conserved viral genomes organization present in the non-structural protein portion of their genome. Modified from Belouzard et al.⁸

Bats: Coronavirus's Natural Reservoir.

Although CoVs are dangerous due to their pathogenicity, another very important factor that should be considered is their high rate of zoonotic transmission. A study was done to determine which animal species harbored the most novel viral sequences and bats were identified as the number one candidate²⁰. Bats are an advantageous host for viruses for a number of reasons. First, these mammals have the ability to occupy diverse niches, which allows these animals to interact with large colonies of other bats and animals^{18,21}. The interactions with other bats allow for the transmission of different CoV's to co-infect a single bat, resulting in the opportunity for multiple quasi species to maintain a low-level of infection and recombine, resulting in populations of viruses that can infect a broad range of hosts²². Secondly, as humans continue to colonize more of the earth's natural landscape, we begin to force bats to have more interactions with species (i.e. humans and other animals) they may not commonly come into contact with. These interactions aid the transmission of CoVs from bats to other mammals, in which they would not readily infect. A prime example of this gain of host tropism is the emergence of SARS CoV and MERS CoV²². Although these CoVs originated in bats, due to mutations and interactions these viruses were able to gain tropism to allow them to infect an intermediate host (civet cats and camels) and ultimately gain human tropism^{18,23,24} (Figure 5). Aside from these diverse niches, it also has to be taken into consideration that these animals are migratory in nature. This migratory behavior is very advantageous for an emerging virus, giving the virus the opportunity to have a broad geographical area in which these viruses potentially can disseminate.

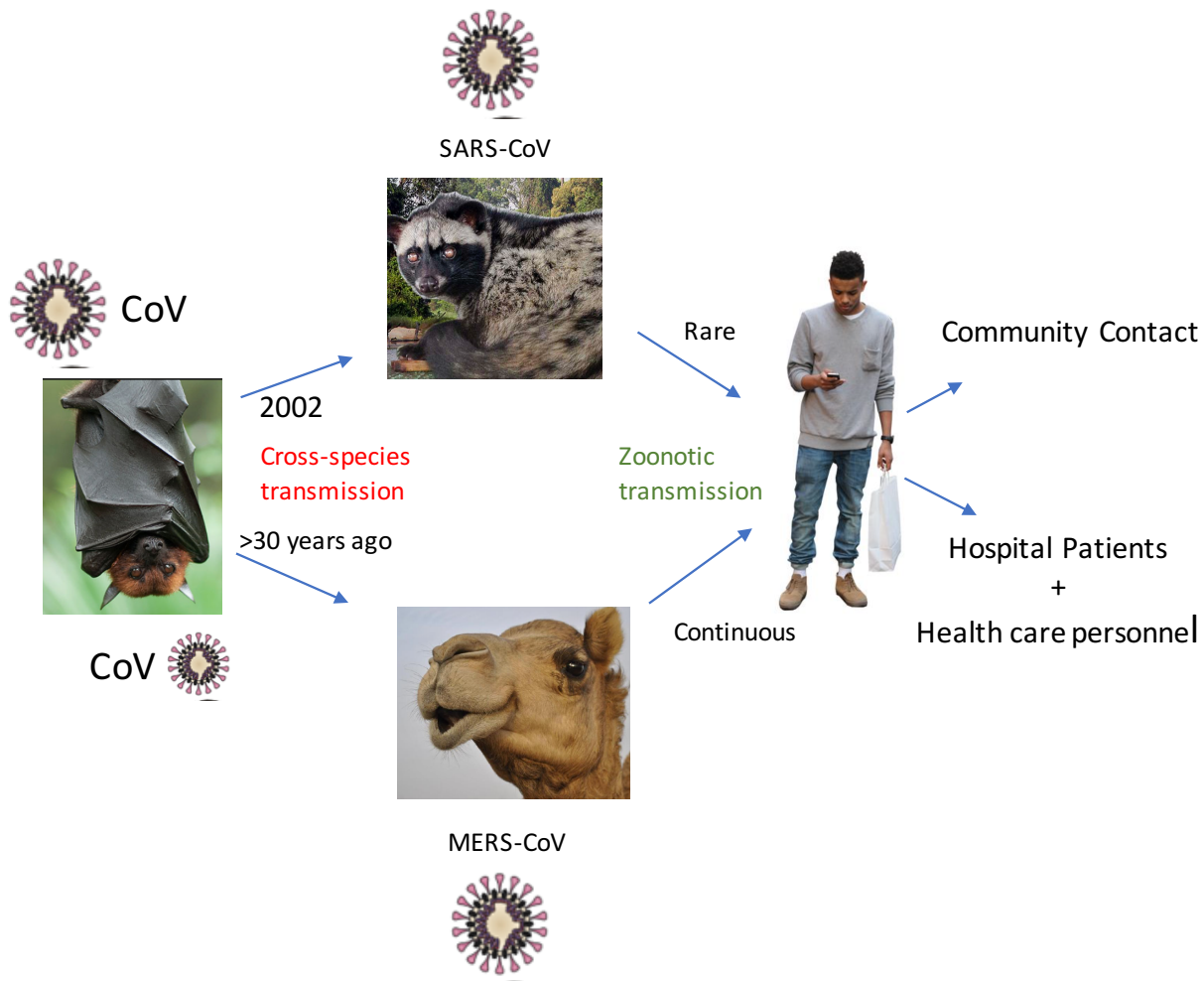


Figure 5. CoVs have the ability to gain human tropism. SARS and MERS to date have been the most pathogenic CoVs resulting in hundreds of deaths combined. These viruses emerged into humans by gaining mutations that allowed the viruses to have cross species transmission and ultimately, use these secondary reservoirs as zoonotic modes of transmission. Depicted above are the routes that SARS and MERS took to become introduced into the human population. Image modified from Wit et al.¹¹

It has yet to be fully elucidated as to why bats have the ability to harbor more than one species of CoVs and result in an asymptomatic infection²⁴. There are several proposed hypotheses as to why multiple CoV infections seem to have no deleterious effects on the bats they infect. First, it has been proposed that bats are able to produce high levels of reactive

oxygen species (ROS) which controls genes that limit oxidative stress, resulting in reduced viral replication and pathogenesis^{25,26}. Also, studies have shown that bats harbor a modified innate immune response that potentially also contributes to the diverse population of CoVs that these mammals harbor. Bats also constitutively express interferon subtypes that rationally could limit disease while permitting low-level viral infection to happen concurrently²⁷.

The Emergence of Potentially Pandemic Strains of CoVs.

In the 21st century, CoVs have proven to be a huge pathogenic threat. In November of 2002, the first known documented case of a novel CoV infection occurred in Foshan, China²⁸. The patient was admitted with symptoms of fever, dry cough, and shortness of breath. These symptoms then resulted in severe respiratory complications, which exhibited symptoms of a deep lung infection. Upon initial diagnoses, medical care workers thought the patient had a novel form of influenza but upon testing the results were negative. By February of 2003 more than 300 individuals had been admitted to the hospital for the same symptoms with an unknown cause¹¹. In March of 2003 the World Health Organization (WHO) established a network of laboratories that were able to identify the causative agent as the emergence of SARS-CoV. By the end of 2003, the SARS emergence resulted in 774 deaths⁴. The SARS CoV outbreak was contained by isolation of infected patients and their contacts.

A decade later in June of 2012 another novel CoV, MERS, was isolated from the sputum of an infected patient in Saudi Arabia²⁹. MERS-CoV continued to emerge and spread outside of the Arabian Peninsula due to infected people traveling out of the country. Since then, there has been a slow spread of infection throughout the Middle East. As of April of 2016, there have been 1,728 confirmed cases of MERS, which resulted in 624 deaths in 27 countries³. Thus, the need to find a vaccine has become of the utmost importance.

Studying CoVs: Animal Model.

In order to study CoVs in a laboratory safe environment, researchers use the model animal CoV Mouse Hepatitis Virus (MHV). MHV is a beta CoV that causes illness in mice with a high mortality rate. Although the pathogenic characteristics differ from that of SARS and MERS, the high mortality is greater in MHV. MHV has more than 25 isolates, which have many different tissue tropisms, but the incidence of enteric infection of MHV strains is most common^{30,31}. Some strains of MHV can cause progressive demyelinating encephalitis in mice, which has also been used as an animal model for multiple sclerosis³². This CoV is readily found in laboratory settings and can be transmitted via fecal-oral, direct contact, aerosols and fomite transmission. Although vertical transmission has been observed in experimental infections, this does not occur in spontaneous infections^{33,34}. In immune competent mice, MHV is very subclinical in its pathology^{30,34}. Expression of disease phenotype is directly dependent upon the virus strain and host factors, which include age, genotype, and immune function³⁴. Upon studying the histopathology of infected mice, the intestinal tracts exhibit syncytia in the mucosal epithelial tissue³⁴. MHV aside from being a murine tropic virus is also a great model because it contains the highly conserved gene order and function that is characteristic of CoVs¹⁹. MHV is the most highly studied CoV in-vivo and in-vitro at the molecular level. The majority of research projects that use MHV as a model, focus on viral pathogenesis and understanding of how CoVs interact and alter host immune functions. With the development of a reverse genetics system for MHV, the isolation and study of individual mutations in certain viral genes can be assessed. I can then identify mutations that specifically effect virus-host interactions resulting in a better outcome for the host³⁵.

Identifying Attenuating Mutations.

Different methods are essential for identifying critical mutations that attenuate the virus. One such method of identifying deleterious mutations, is to induce mutations in the virus and screen for TS mutations. TS mutations are unique because under permissive conditions the mutations are able to confer a normal functioning gene product. In contrast, under non-permissive conditions the mutation will result in a gene product that displays a mutated phenotype. Identifying TS mutations can tell you many things about the pathogen. This method has been used primarily as a genetic tool. In 1965, *Edgar et al.* used TS phenotyping to identify the number of genes in a novel strain of bacteriophage T4D³⁶. By using chemical mutagenesis and screening the mutant progeny for growth under different temperature conditions, this group was able to identify 37 individual genes the phage contained³⁶. These mutations classically aid in the identification of essential genes in an unknown pathogen's genome. However, with the advancement in technology these TS mutations can now be induced and identified by sequencing down to the exact residue conferring the TS phenotype.

Complementation analysis can be used to verify that the mutant progeny observed from chemically inducing TS mutations are unique. Complementation analysis is a special and critical analysis that has been used throughout research in lieu of sequencing to identify not only the unique mutants but to also aid in predicting where in the genome these mutations may be located. *Edgar et al.*, after identifying the chemically induced strains of T4D bacteriophage were TS, used complementation to verify they were unique mutants and to begin to map where these mutations were located^{36,37}. Complementation analysis involves the co-infection of two mutated phage that are grown under non-permissive conditions and assessed for successful phage production. Individually the phage are unable to grow at non-permissive conditions³⁸. Thus, if

the two strains of phage contained the same mutations, they would not be able to complement or “over-come” the attenuating mutations because they are located in the same region. However, if the phage contains different mutations these mutant phage would be able to propagate infectious progeny because the phage were able to complement each other due to the mutations being located in different locations thus allowing the phage to “over-come” the attenuating mutations each phage contains individually.

Phenotyping CoVs: MHV.

In order to design a method to develop a vaccine strain that contains mutations that may help to protect against current and future strains emergence, we first must identify areas of attenuation in conserved regions of the viral genome. As I previously stated, the one common factor that aids in CoVs success in infection is also a chink in the armor, the highly conserved gene order and functions amongst the CoV family. By using different techniques, one may be able to identify key residues that attenuate the virus in an essential gene. For example, currently in vaccine development many attenuated strains contain a mutated structure/surface protein. Although this is typically the most common method, it also has to be taken into account that surface proteins tend to undergo a high rate of mutation to evade the immune response and are typically very tolerable of mutations. In contrast, finding a mutation in a conserved region that does not tolerate mutations presents the opportunity to potentially identify sites for attenuation that are common amongst current and potentially emerging CoV strains.

TS mutants of animal viruses have been very useful for studying many critical functions of individual viral genes^{36,39,40}. These studies have allowed researchers to understand pathogenic, biochemical and pathological characteristics of these viruses with a goal to find an attenuating mutation that can be used to produce a vaccine strain. In 1983, *Koolen et al.* sought

to understand the viral genome of MHV³⁹. Prior to his studies, not much was known about coronaviruses nor its genome, but by using this animal model, they sought to identify different viral genes and their roles in the viral life cycle³⁹. In order to decipher the contents of the viral genome, a chemical mutagenesis was performed on over 1,284 viral clones³⁹. To verify that these mutants were TS, the viruses were allowed to grow under three conditions (33, 37 or 40°C)³⁹. If the mutant viruses showed a defect or reduction in titer at 40°C, these viruses were deemed TS³⁹. Of these clones, they were able to identify 20 TS mutants, that were classified into two categories, RNA + or RNA -. If the virus was RNA-, the virus was unable to synthesize viral RNA at non-permissive temperatures (40°C)³⁹. RNA+ TS mutants were documented to still grow at all three temperatures, but were shown to have a reduction in titer as the temperature increased.

In 1990, *Baric et al.* sought to understand the function of the MHV polymerase genes to better understand how MHV transcription occurs³⁸. Taking a similar approach as Koolen ten years earlier, chemical mutagenesis was performed to identify areas in the viral genome that tolerated mutations under permissive conditions³⁸. Several chemical mutagenesis experiments were performed to induce mutations throughout the genome. 26 mutant viruses containing genetic mutations were isolated. These mutants were assessed for phenotypes that differ to that of Wild Type virus. All 26 mutant strains were reported to have reduced viral titers and defects in RNA synthesis during temperature shift experiments³⁸. Using complementation analysis, this group determined the number of genes or genetic functions that were altered by the chemical mutagenesis. The Baric Lab identified six complementation groups, each representing a hypothesized area of mutation in the viral genome³⁸. The temperature-dependent phenotype paired with the reduction in viral titer led the Baric Lab to hypothesize that the mutations were in

the viral replication machinery. Of these mutants that were derived, LA16 and NC2 stood out as potential candidates that should receive further studies. LA16 and NC2 are both hypothesized to have mutations in the replication machinery, thus giving them their documented TS phenotype. No further analysis was performed to identify the location of these mutations. By identifying the locations of these mutations, potentially I may potentially be able to identify a novel target of attenuation that is conserved amongst many strains of CoVs. This information will be important in the development of a vaccine strain for protection from current and future stains of CoVs.

Aims and Hypothesis

Over the past 15 years, CoVs have exhibited both rapid and highly pathogenic emergences into the human population, eluding to the potential to cause a world-wide pandemic. Prime examples of this emergence were observed by the emergence of SARS-CoV in 2003⁴, which resulted in 774 deaths, followed by the emergence of MERS-CoV, in 2012, which resulted in 624 deaths thus far³. These unanticipated zoonotic jumps into the human population highlight the need to produce common methods or identify conserved targets of attenuation that can be used for generating vaccines against diverse CoV species. Although CoVs are infamous for having diversity in host tropism, one common factor of CoVs is a highly-conserved genome order and function. It is important to identify attenuation mutations in conserved genes or residues because it allows for the development of vaccine strains or direct-acting antivirals that can act on current and future emerging CoVs. The goal of this study is to identify conserved targets of attenuation, with the intention of identifying a strategy to make vaccines that can protect against the current circulating strains but also for future coronavirus outbreaks. For my thesis, I propose to identify the TS phenotype of two previously derived TS mutants of MHV, NC2 and LA16, followed by deep genomic sequencing to identify the location of these mutations within the viral genome. I hypothesize that LA16 and NC2 harbor mutations in the viral polymerase machinery conferring their TS phenotype. In AIM 1, I will characterize LA16 and NC2 by performing plaque assays under three different conditions to verify the TS phenotype⁴⁰. In AIM 2, I will identify the mutations present in the RNA genome of NC2 and LA16 by genomic deep sequencing. By identifying the mutations in the viral genome, I can further hypothesize whether individual or collective mutations confer a TS phenotype.

Significance

By conducting this study, we will gain information on novel mutations that lead to virus attenuation. TS phenotyping has become a key method in identifying novel gene functions of many unknown pathogens^{36,37}. By identifying the mutations that result in a TS phenotype we can begin to investigate how mutations in certain viral genes affect virus-host interactions resulting in a better outcome for the host. In this proposal, we will combine classic genetic phenotyping techniques with current genomic sequencing to identify novel attenuating mutations. By confirming the TS phenotype of these mutant strains of a model CoV MHV, we will be able to confirm the accuracy and reproducibility that chemical mutagenesis can offer as well as establish the stability of the progeny that come from this technique. With the advancement of sequencing we can pin-point mutations that are located in highly conserved regions of the viral genome with much more accuracy than that of classic complementation and gene mapping techniques. Additionally, the information obtained in this study will allow the identification of sites in conserved genes that are important for replication. In the future, this information could be applied to a variety of CoVs to determine if the mutant viruses could be used as vaccines for protection from current and more importantly future strains of CoVs.

CHAPTER TWO

MATERIALS AND METHODS

Virus and Cell lines

Delayed Brain Tumor (DBT) cells were cultured in minimal essential medium (MEM) (Fisher) supplemented with 2.2g NaHCO₃, 5% TPB, 2% Penicillin/Streptomycin, 2% L-Glutamine and 5% heat inactivated Fetal Calf Serum (FCS). Cells were incubated at 37°C in 5% CO₂ enriched environment. Media, used for plaque assays, is made of 2X MEM supplemented with NaHCO₃, 5% TPB, 2% Penicillin/Streptomycin, 2% L-Glutamine and 2% FCS. During plaque assays cells were incubated in 5% CO₂ at either 33, 37, or 40 °C. Typically, cells were passaged 1:3 using trypsin-EDTA to disperse cells from culture plates. Our laboratory stock of WT MHV-A59 has been sequenced and propagated in DBT cells³⁵. LA16 and NC2 viral stocks were graciously obtained from the Baric Lab⁴¹.

Thawing of Viral Stocks

To thaw the frozen viral stocks, vials which contained supernatant from virally infected cells were flash thawed by incubating in the 37 °C water bath until 90% thawed. During the incubation period vials were constantly swirled in bath to ensure even thawing and were placed directly on ice once 90% of contents were no longer frozen. Once fully thawed, vials were vortexed to equally distribute the virions within supernatant.

Performing Plaque Assays

Cells are plated into a six-well tissue culture dish at a 5×10^5 cells/well confluency. These cells are plated in complete MEM supplemented as indicated above. The cells are then placed into the 37°C incubator for at least 18 hours prior to infection to allow cells to evenly form a monolayer on the bottom of the well. A ten-fold dilution was performed as indicated in Figure 6. Dilutions were performed in incomplete MEM on ice. Culturing media was aspirated from each well and cells were washed in PBS. 300 µl of viral dilution is applied to the well. Cells were incubated at 37 °C, 5% CO₂ for one hour, rocking plates gently every 15 minutes. During the absorption step, a 1:1 ratio of 2X-MEM and 0.4% Noble Agar was mixed. After the one hour incubation period the inoculum was removed and 2 ml of the 2X-MEM and Noble agar mix was added to each well. The plates were allowed to sit for ten minutes at room temperature (RT) to solidify prior to being moved to the appropriate incubator. Plates were allowed to incubate at the determined temperature for 48 hours. After 48 hours, 2 ml of 3.7% Formaldehyde-PBS solution was added to each well and incubated for 30 minutes at RT. The Formaldehyde-PBS solution/agar solution was removed and plates were washed with tap water. 1 ml of 0.1% Crystal Violet solution is added and allowed to incubate at RT for 15 mins on a rocker. Crystal violet was removed and plates rinsed and allowed to dry overnight. Plaques were then counted by hand.

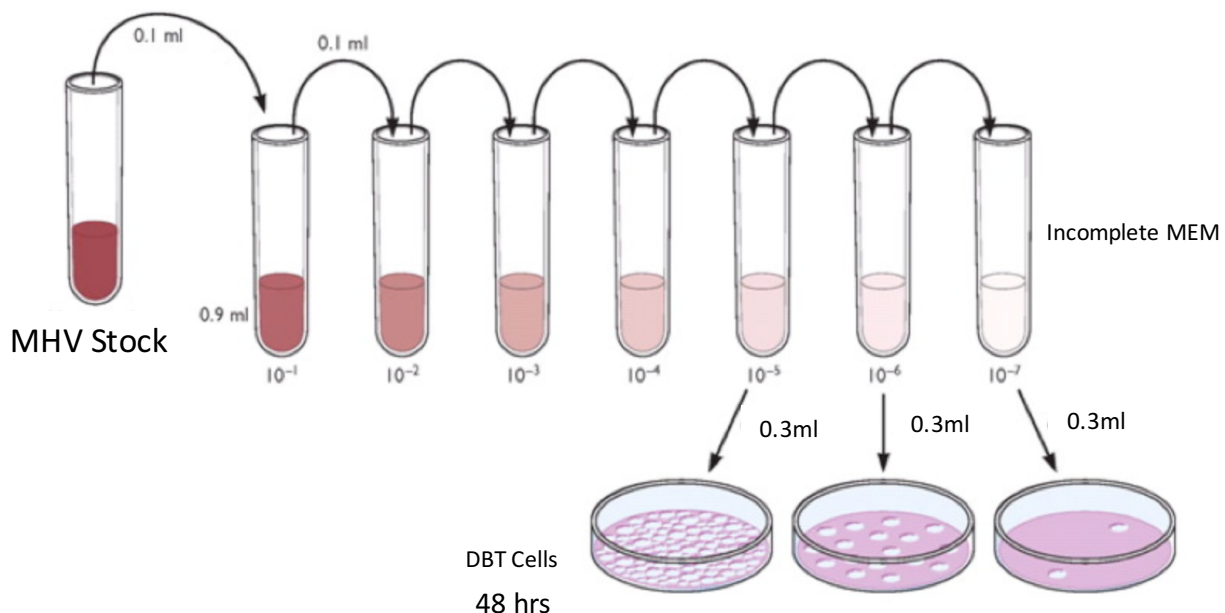


Figure 6. Diluting Viral stock for plaque assay. In order to accurately determine viral titer serial dilutions are performed and applied to DBT cells in sequential order. Viral titer is back calculated based on the number of plaques produced after incubation. One plaque represents the identification of a successful viral infection indicated by the appearance of plaques. Modified from Dulbecco et al^{42,43}.

Calculating Viral Titer

In order to calculate viral titer, individual plaques were hand counted and documented.

Using the following equation, the viral titer was able to be calculated using the amount of inoculum added and the number of plaques produced (Equation 1). By multiplying the number of plaques by the dilution they were formed by 1000ul divided by the amount of inoculum will result in the viral titer.

$$(Eq\ 1) \quad \frac{(\# \text{ Plaques}) \times \frac{1}{\text{dilution}} \times (1000\text{ul/ml})}{\text{volume plated (ml)}} = \text{pfu/ml} = \text{Viral Titer}$$

Imaging and Quantifying Plaques

Plaques were photographed after fixation. Images were taken after the indicated incubation time and temperatures using a consistent magnification with a Zeiss Stemi 2000-C dissecting microscope. Photos were then uploaded to Microsoft Photoshop. Once uploaded the lasso tool was used to outline the clear boarder of the plaques. Once the plaque was outlined the image tab was selected and from the drop-down menu the analysis option was highlighted and the record measurement tab was selected. Upon selection of this option, the number of pixels are calculated within the outlined plaque. These represent the area in which the plaque occupies and is used as the area of the plaque. Five individual plaques were assessed at random for each indicated temperature for each strain.

Genomic Deep Sequencing and Sequencing Analysis

In order to obtain viral genomic sequences, DBT cells were infected with LA16 or NC2. After 48 hours of incubation in 33°C, the cellular supernatant is harvested. Supernatant is centrifuged at 5,000g for ten minutes. The viral supernatant was then added to naïve DBT cells to assess the presence of infectious virus production, verified by plaque formation. 1 ml of the cleared viral supernatant was shipped to Kansas State University's Integrated Genomics Facility in which deep genomic sequencing was performed⁴⁴. The consensus nucleotide sequence was provided in a word processor format which was entered into a genomic sequence file in Clone Manager. Once imputed into Clone Manager, the nucleotide sequence alignment function was applied to compare the sequences of LA16, NC2 and WT MHV (MHV full genome geneID reference accession number: NC_001846). The Blossum 65 Alignment function within Clone

Manager was applied to compare and identify amino acid differences between LA16, NC2 and WT sequences.

CHAPTER THREE

RESULTS

Validation of Temperature-sensitive Phenotype of NC2 and LA16

To determine if the viral stocks of LA16 and NC2 obtained from the Baric lab were TS, plaque assays were performed at 33, 37 and 40°C. DBT cells were infected with serial dilutions of the viral stock. The cells were incubated at different temperatures for 48 hours prior to fixation (Figure 7). Temperature sensitivity was assessed by viral titer and plaque morphology at the different temperatures. As a positive control a WT MHV infection was performed as well. It has been well documented that WT MHV, under all three conditions, is able to maintain the same viral titer, but exhibits an increase in plaque size^{35,40,41,45}. The increase in plaque size is due to the increase in metabolic rate of the cells under these conditions, resulting in an increase in viral replication, i.e. plaque size. WT MHV at 33, 37 and 40°C exhibit normal plaque morphology with a slight increase in plaque size as the temperature increases (Figure 7A). Although the plaque size increases slightly, it can be appreciated that the number of plaques present remains constant. The viral titer was maintained at $6.5 \times 10^6 \pm 0.40$ pfu/ml (Figure 7B). The images of WT MHV at 33, 37 and 40°C were all taken at the 10^5 dilution in which the plaques were able to be visualized individually.

Assessing Temperature-sensitive Phenotype of LA16

When assessing TS mutant LA16 for replication and plaque formation at 33°C, it can be noted that the plaques have the same morphology as that of WT, in which the plaques appear to be the same size and shape (Figure 7A). The representative image of LA16 at 33°C was taken of

a 10^5 dilution allowing the visualization of individual plaques. The viral titer at 33°C was 1.2×10^7 pfu/ml (Figure 7B). The titer of LA16 at 33°C is similar as the literature documented titer, in which *Baric et al.* documented LA16 to have a 4.9×10^7 pfu/ml titer at 33°C (Figure 7B)⁴¹. This conservation of viral titer speaks to the integrity of the samples. When assessing LA16 at 37°C the morphology of the plaques can be appreciated at a 1:1000 dilution (Figure 7A). At this temperature, the plaques have a heterogeneous morphology that appear to range from small to pin-point in size. LA16 has a viral titer of 5.3×10^4 pfu/ml at 37°C (Figure 7B). LA16's titer is similar to the documented titer of 2.7×10^4 pfu/ml when shifted to 37°C ⁴¹. A reduction in titer was observed at 37°C compared to the titer at 33°C . Upon assessing the titer of LA16 at 40°C , I was unable to detect any plaques using our assay, which has the sensitivity to detect 100 pfu/ml. This lack of detection at 40°C as well as the reduction in viral titer further validates that LA16 has retained its TS phenotype as documented in the literature.

Assessing TS Phenotype of NC2

In order to validate that NC2 is TS, as documented in the literature, a plaque assay was performed at different temperatures in which the morphology and viral titer were assessed. At 33°C , NC2 plaque morphology is very similar to that of WT at 33°C . These plaques appeared rather round in shape and the representative image was taken at 10^5 dilution, which was the same as LA16 and WT (Figure 7A). When assessing the viral titer of NC2 at 33°C , the titer was calculated at 1.04×10^7 pfu/ml (Figure 7B). This titer correlates with the viral titer documented in the literature as 5.6×10^7 pfu/ml⁴¹. Upon incubating NC2 at 37°C , the plaques maintained their size and similar titer, resembling that of WT. The representative image of NC2 at 37°C (Figure 7A) was taken at a 10^5 dilution. Although there was a ten-fold decrease in the viral titer, the morphology of the plaques remained constant. At 37°C NC2 has a titer of 10^6 pfu/ml. When NC2

was incubated at 40°C, the plaques uniformly changed to a pin-point morphology (Figure 7A). Upon checking the titer of NC2 at 40°C, the titer was 5.3×10^4 pfu/ml (Figure 7B). This titer was slightly higher than the documented titer which was 4.0×10^3 pfu/ml⁴¹. The reduction of viral titer and change in plaque morphology, upon the increase of incubation temperature validates the integrity of NC2 as TS, as documented in the literature.

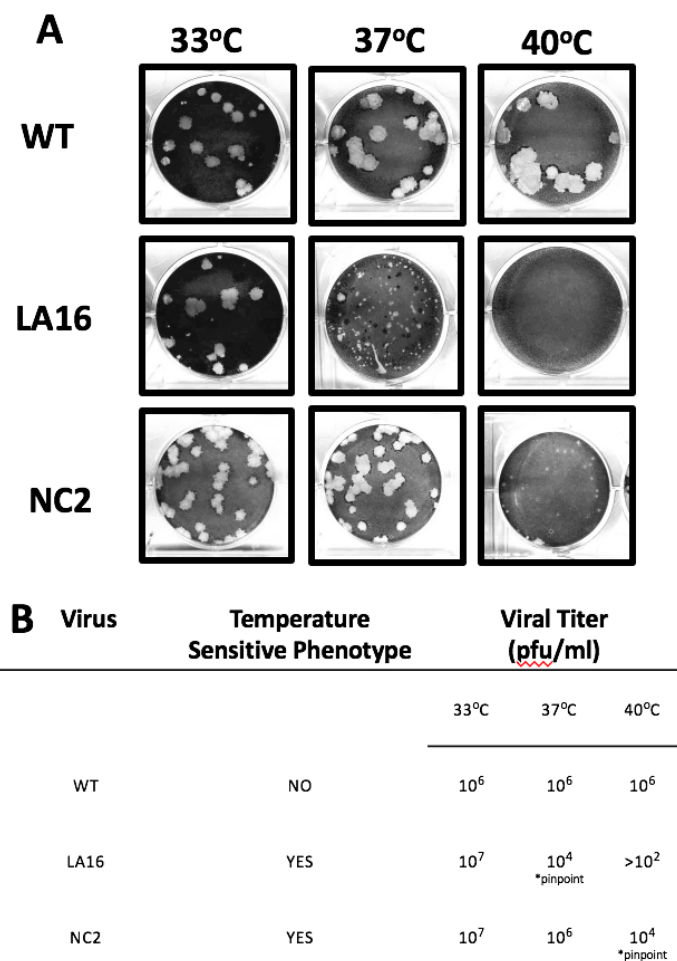


Figure 7. Comparison of Murine Coronavirus strains LA16 and NC2 to assess for Temperature-sensitive defects in replication. (A) Visual representations of plaques that were generated by WT, LA16, and NC2 after incubation in the indicated temperatures. DBT cells were infected with WT, NC2 or LA16 incubated at the indicated temperature and stained 48 hours post infection. These images were representative data from two independent experiments. (B) Summary of the characteristics of WT, LA16, NC2 at different temperatures. Plaque assays

were performed using DBT cell and were allowed to incubate at the indicated temperature (33, 37 or 40°C) for 48 hours.

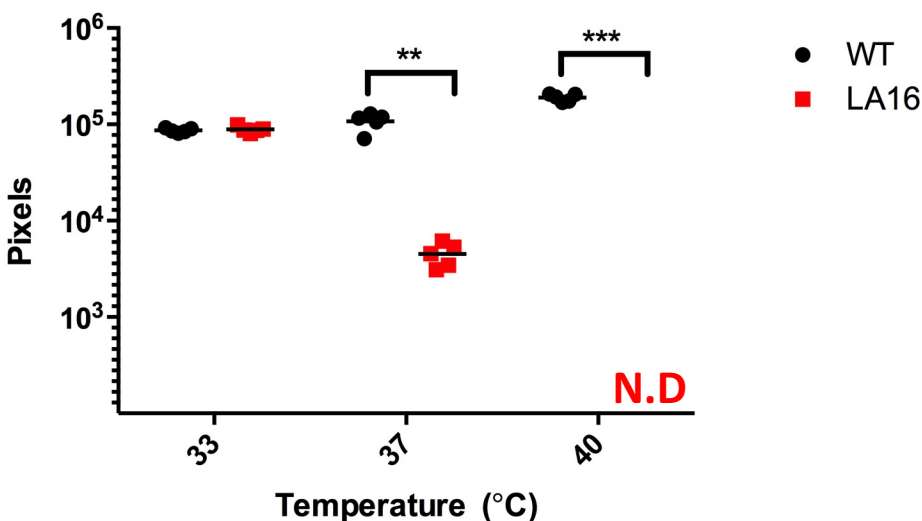


Figure 8. Analysis of WT and LA16 plaque size at different temperatures. Plaque assays were performed using DBT cells. DBT cells were infected with LA16 or WT virus, incubated at the indicated temperature and fixed 48 post-infection. Five plaques were chosen at random and photographed using a fixed camera. These images were analyzed using Adobe Photoshop. Photoshop was used to quantify the number of pixels present in the plaque, which is used to quantify plaque area. Statistical analysis was performed using Student's T test. (**p:>0.005. ***p:>0.0005)

LA16 MHV Exhibits a Reduction in Plaque Size

In order to further assess the TS phenotype of LA16, the plaque areas from the plaque assay shown in Figure 7A were quantified. DBT cells were inoculated with LA16 and WT MHV, and incubated at the indicated temperature for 48 hours. After fixation, images were taken using a camera set at a fixed magnification. These images were then assessed in Adobe Photoshop. Using the lasso tool in Photoshop the outline of plaque was traced. Once the plaque was outlined, Photoshop was able to quantify the amount of pixels within the outlined area corresponding to the area that plaque occupies. Five individual plaques were chosen at random and assessed at each indicated temperature. In order to ensure the plaques were chosen at random, upon fixing the camera at the correct setting the first five plaques that were unobstructed

were selected and assessed. Upon comparing WT and LA16 plaque sizes at 33°C, the plaques were very similar in size (Figure 8). This also correlates with the morphology shown in Figure 7A. When comparing the plaque size of WT and LA16 at 37°C, LA16 has a significant decrease in plaque size. The reduction in plaque size correlates with the change in morphology (Figure 7A) and a decrease in viral titer (Figure 7B). Due to the heterogeneous population of plaques produced during incubation, the small and entirely cleared plaque population were quantified. LA16 failed to produce plaques within the detection limit of the plaque assay when incubated at 40°C. This data further verify that LA16 is TS.

NC2 MHV May Contain Mutations That Confer a Reduction in Plaque Size

To further validate the TS phenotype of NC2, the plaque area from the plaque assay shown in Figure 7A was quantified. DBT cells were inoculated with NC2 and incubated at the indicated temperature for 48 hours. WT was incubated at 40°C for 48 hours as a positive control. These assays were fixed and images were taken using a fixed camera. These images were then assessed in Photoshop. Using the lasso tool in Photoshop the outline of plaque was traced. Once the plaque was outlined, Photoshop was able to quantify the area with the outlined area. Five individual plaques were chosen at random and assessed at each indicated temperature. The average of plaque sizes produced by NC2 are identified at different temperatures as shown in Figure 9A. When assessing the average of the plaques NC2 produces it can be appreciated that the plaque size was maintained from 33 °C to 37 °C. Upon incubating NC2 at 40°C, there was a drastic reduction in plaque size (Figure 9A). When comparing the change in plaque size at 40°C, NC2 had a significant reduction in plaque size compared to WT (Figure 9B). This also correlates with the decrease in titer and change in plaque morphology (Figure 7A). From this preliminary

data, I can further validate NC2 is TS and potentially contains different mutations than that of LA16.

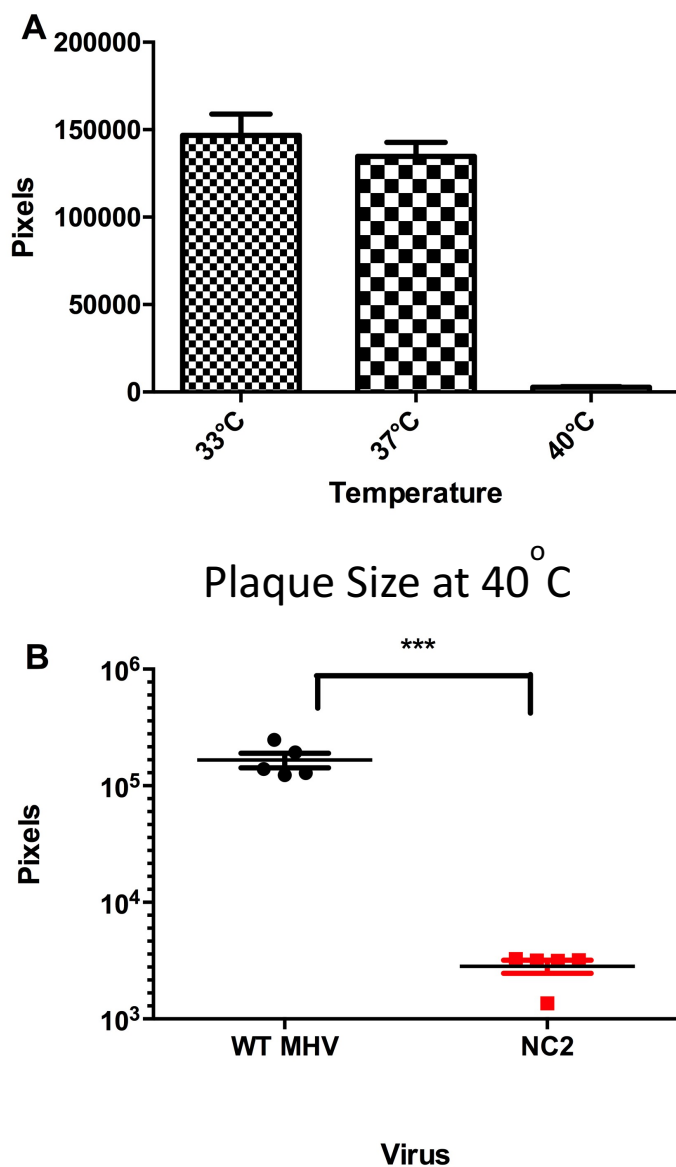


Figure 9. Preliminary Data Quantifying NC2 Plaque Size. (A) Quantification of the average plaque size of five individual plaques of NC2. Plaques size was quantified using Adobe Photoshop. DBT cells were infected with NC2 or WT virus, and were incubated at the indicated temperature and fixed 48 hours post-infection. (B) Quantification of plaque size for NC2 and WT MHV at 40°C. Plaques were incubated for 48 hours prior to fixation and quantification. Statistical Analysis was performed using Students T-test. (p***0.0005)

Deep Sequencing of LA16 and NC2 Identifies Multiple Mutations in ORF1A

Previous data from the Baric lab led to the hypothesis that mutations that conferred the TS phenotype of LA16 and NC2 were located in ORF1A⁴¹. Both mutants are classified in the RNA- group, which has a defect in viral RNA synthesis^{39,41}. The data indicated the RNA synthesis defect further supports the hypothesis that these mutations may be located in ORF1A which contains genes essential for viral replication. Sequencing samples were obtained from the supernatant of DBT cells infected with LA16, NC2 or WT at 33°C and incubated for 48 hours prior to harvesting. These samples were harvested from the infections incubated at 33°C to avoid selecting for mutations that were not originally present in the Baric stock. Selective pressure occurs when growing the viruses at non-permissive conditions. The samples were then cleared of cellular debris by centrifugation and sent to a collaborator for genomic deep sequencing. Upon receiving the sequencing data, the results were analyzed using Clone Manager function which allowed for the alignment of the nucleotide sequence. I also used Blossum 65 to align the three genomic sequences at the amino acid level, allowing the identification of nucleotides that result in amino acid changes (Figure 10).

In analyzing the data, I found that LA16 and NC2 collectively contained 13 nucleotide changes in ORF1A. Although there were 13 changes, only eight of these mutations resulted in amino acid changes. There were two mutations conserved between both strains, which I hypothesize may have been part of the original strain of viruses that these mutants were derived from. LA16 contains two unique mutations that resulted in amino acid changes. These mutations were located in Nsp3 and Nsp10, genes which have been shown to be important in viral replication^{40,45}. The first unique mutation in LA16 was located in Nsp3, the viral protease. This mutation change was in the second position of the codon, which resulted in an “a” nucleotide

substituted for a “g”. This substitution resulted in the change of the amino acid from glycine to glutamic acid. The second unique mutation was located in Nsp10, whose function has been hypothesized to be a regulator of RNA synthesis by controlling polyprotein processing⁴⁶. This mutation resulted in a nucleotide change located in the second nucleotide position for a codon that coded for a cysteine. Additionally, this mutation resulted in an amino acid that was changed from a cysteine to a tryptophan.

In analyzing the data from NC2, it was noted there were four unique mutations that resulted in amino acid changes. These mutations were located in Nsp3, Nsp4 and Nsp5. Of these four unique mutations, three were conservative, resulting in a substitution of amino acids that have conserved properties. However, there was one unique mutation that was located in Nsp3. This mutation occurred in the first position of the codon, resulting in an amino acid change from Lysine to Glutamic Acid. The sequencing data reveal that LA16 and N2 both contain mutations in ORF1A, may be responsible for the TS phenotype observed in each strain.

Figure 10. Genomic Sequence Alignment of WT, LA16 and NC2 of ORF1A. Using the Blossum 65 (clone manager) function the amino acid sequence was determined and was used to identify amino acid changes resulting from a change in the nucleotide sequence. (Black) The WT reference strain nucleotide sequence. (Green) The corresponding amino acids associated with the WT nucleotide sequence directly beneath the WT codon. (Highlighted nucleotide codon) Represents the codon in WT that was mutated in LA16 or NC2. (Red) Represents the mutated nucleotide within the highlighted codon that was changed. (Blue) Indicates a nucleotide mutation that resulted in a silent mutation. (Purple) Nucleotide change that resulted in an amino acid change. (Purple letter) Amino acid change. The sequence starts at the first methionine in ORF1A. This corresponds to nucleotide 210 in the full genomic sequence.

```

WT 1  atg gca aag atg ggc aaa tac ggt ctc ggc ttc aaa tgg gcc cca gaa ttt cca tgg atg ctt ccg aac
    m  a  k  m  g  k  y  g  l  g  f  k  w  a  p  e  f  p  w  m  l  p  n

70  gca tgc gag aag ttg ggt aac cct gag agg tca gag gag gat ggg ttt tgc ccc tct gct gcg caa gaa
    a  s  e  k  l  g  n  p  e  r  s  e  e  d  g  f  c  p  s  a  a  q  e

139 ccg aaa gtt aaa gga aaa act ttg gtt aat cac gtg agg gtg aat tgt agc cgg ctt cca gct ttg gaa
    p  k  v  k  g  k  t  l  v  n  h  v  r  v  n  c  s  r  l  p  a  l  e

208 tgc tgt gtt cag tct gcc ata atc cgt gat att ttt gta gat gag gat ccc cag aag gtg gag gcc tca
    c  c  v  q  s  a  i  i  r  d  i  f  v  d  e  d  p  q  k  v  e  a  s

277 act atg atg gca ttg cag ttc ggt agt gcc gtc ttg gtt aag cca tcc aag cgc ttg tct att cag gca
    t  m  m  a  l  q  f  g  s  a  v  l  v  k  p  s  k  r  l  s  i  q  a

346 tgg act aat ttg ggt gtg ctt ccc aaa aca gct gcc atg ggg ttg ttc aag cgc gtc tgc ctg tgt aac
    w  t  n  l  g  v  l  p  k  t  a  a  m  g  l  f  k  r  v  c  l  c  n

415 acc agg gag tgc tct tgt gac gcc cac gtg gcc ttt cac ctt ttt acg gtc caa ccc gat ggt gta tgc
    t  r  e  c  s  c  d  a  h  v  a  f  h  l  f  t  v  q  p  d  g  v  c

484 ctg ggt aat ggc cgt ttt ata ggc tgg ttc gtt cca gtc aca gcc ata ccg gag tat gcg aag cag tgg
    l  g  n  g  r  f  i  g  w  f  v  p  v  t  a  i  p  e  y  a  k  q  w

553 ttg caa ccc tgg tcc atc ctt ctt cgt aag ggt ggt aac aaa ggg tct gtg aca tcc gcc cac ttc cgc
    l  q  p  w  s  i  l  l  r  k  g  g  n  k  g  s  v  t  s  g  h  f  r

622 cgc gct gtt acc atg cct gtg tat gac ttt aat gta gag gat gct tgt gag gag gtt cat ctt aac ccg
    r  a  v  t  m  p  v  y  d  f  n  v  e  d  a  c  e  e  v  h  l  n  p

691 aag ggt aag tac tcc tgc aag gcg tat gct ctt ctt aag ggc tat cgc ggt gtt aag ccc atc ctg ttt
    k  g  k  y  s  c  k  a  y  a  l  l  k  g  y  r  g  v  k  p  i  l  f

760 gtg gac cag tat ggt tgc gac tat act gga tgt ctc gcc aag ggt ctt gag gac tat gcc gat ctc acc
    v  d  q  y  g  c  d  y  t  g  c  l  a  k  g  l  e  d  y  g  d  l  t

829 ttg agt gag atg aag gag ttg ttc cct gtg tgg cgt gac tcc ttg gat agt gaa gtc ctt gtg gct tgg
    l  s  e  m  k  e  l  f  p  v  w  r  d  s  l  d  s  e  v  l  v  a  w

898 cac gtt gat cga gat cct cgg gct gct atg cgt ctg cag act ctt gct act gta cgt tgc att gat tat
    h  v  d  r  d  p  r  a  a  m  r  l  q  t  l  a  t  v  r  c  i  d  y

967 gtg ggc caa ccg acc gag gat gtg gtg gat gga gat gtg gta gtg cgt gag cct gct cat ctt ctc gca
    v  g  q  p  t  e  d  v  v  d  g  d  v  v  v  r  e  p  a  h  l  l  a

1036 gcc aat gcc att gtt aaa aga ctc ccc cgt ttg gtg gag act atg ctg tat acg gat tcg tcc gtt aca
    a  n  a  i  v  k  r  l  p  r  l  v  e  t  m  l  y  t  d  s  s  v  t

1105 gaa ttc tgt tat aaa acc aag ctg tgt gaa tgc ggt ttt atc acg cag ttt gcc tat gtg gat tgt tgt
    e  f  c  y  k  t  k  l  c  e  c  g  f  i  t  q  f  g  y  v  d  c  c

1174 ggt gac acc tgc gat ttt cgt ggg tgg gtt gcc gcc aat atg atg gat gcc ttt cca tgt cca ggg tgt
    g  d  t  c  d  f  r  g  w  v  a  g  n  m  m  d  g  f  p  c  p  g  c

1243 acc aaa aat tat atg ccc tgg gaa ttg gag gcc cag tca tca ggt gtt ata cca gaa gga ggt gtt cta
    t  k  n  y  m  p  w  e  l  e  a  q  s  s  g  v  i  p  e  g  g  v  l

1312 ttc act cag agc act gat aca gtg aat cgt gag tcc ttt aag ctc tac ggt cat gct gtt gtg cct ttt

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      f t q s t d t v n r e s f k l y g h a v v p f
1381 ggt tct gct gtg tat tgg agc cct tgc cca ggt atg tgg ctt cca gta att tgg tct tct gtt aag tca
      g s a v y w s p c p g m w l p v i w s s v k s
1450 tac tct ggt ttg act tat aca gga gta gtt ggt tgt aag gca att gtt caa gag aca gac gct ata tgt
      y s g l t y t g v v g c k a i v q e t d a i c
1519 cgt tct ctg tat atg gat tat gtc cag cac aag tgt ggc aat ctc gag cag aga gct atc ctt gga ttg
      r s l y m d y v q h k c g n l e q r a i l g l
1588 gac gat gtc tat cat aga cag ttg ctt gtg aat agg ggt gac tat agt ctc ctc ctt gag aat gtg gat
      d d v y h r q l l v n r g d y s l l l e n v d
1657 ttg ttt gtt aag cgg cgc gct gaa ttt gct tgc aaa ttc gcc acc tgt gga gat ggt ctt gta ccc ctc
      l f v k r r a e f a c k f a t c g d g l v p l
1726 cta cta gat ggt tta gtg ccc cgc agt tat tat ttg att aag agt ggt caa gct ttc acc tct atg atg
      l l d g l v p r s y y l i k s g q a f t s m m
1795 gtt aat ttt agc cat gag gtg act gac atg tgt atg gac atg gct tta ttg ttc atg cat gat gtt aaa
      v n f s h e v t d m c m d m a l l f m h d v k
1864 gtg gcc act aag tat gtt aag aag gtt act ggc aaa ctg gcc gtg cgc ttt aaa gcg ttg ggt gta gcc
      v a t k y v k k v t g k l a v r f k a l g v a
1933 gtt gtc aga aaa att act gaa tgg ttt gat tta gcc gtg gac att gct gct agt gcc gct gga tgg ctt
      v v r k i t e w f d l a v d i a a s a a g w l
2002 tgc tac cag ctg gta aat ggc tta ttt gca gtg gcc aat ggt gtt ata acc ttt gta cag gag gtg cct
      c y q l v n g l f a v a n g v i t f v q e v p
2071 gag ctt gtc aag aat ttt gtt gac aag ttc aag gca ttt ttc aag gtt ttg atc gac tct atg tcg gtt
      e l v k n f v d k f k a f f k v l i d s m s v
2140 tct atc ttg tct gga ctt act gtt gtc aag act gcc tca aat agg gtg tgt ctt gct ggc agt aag gtt
      s i l s g l t v v k t a s n r v c l a g s k v
2209 tat gaa gtt gtg cag aaa tct ttg tct gca tat gtt atg cct gtg ggt tgc agt gaa gcc act tgt ttg
      y e v v q k s l s a y v m p v g c s e a t c l
LA16
NC2
2278 gtg ggt gag att gaa cct gca gtt ttt gaa gat gat gtt gtt gat gtg gtt aaa gcc cca tta aca tat
      v g e i e p a v f e d d v v d v v k a p l t y
2347 caa ggc tgt tgt aag cca ccc act tct ttc gag aag att tgt att gtg gat aaa ttg tat atg gcc aag
      q g c c k p p t s f e k i c i v d k l y m a k
2416 tgt ggt gat caa ttt tac cct gtg gtt gtt gat aac gac act gtt ggc gtg tta gat cag tgc tgg agg
      c g d q f y p v v v d n d t v g v l d q c w r
2485 ttt ccc tgt gcg ggc aag aaa gtc gag ttt aac gac aag ccc aaa gtc agg aag ata ccc tcc acc cgt
      f p c a g k k v e f n d k p k v r k i p s t r
2554 aag att aag atc acc ttc gca ctg gat gcg acc ttt gat agt gtt ctt tcg aag gcg tgt tca gag ttt
      k i k i t f a l d a t f d s v l s k a c s e f
2623 gaa gtt gat aaa gat gtt aca ttg gat gag ctg ctt gat gtt gtg ctt gac gca gtt gag agt acg ctc
      e v d k d v t l d e l l d v v l d a v e s t l
2692 agc cct tgt aag gag cat gat gtg ata ggc aca aaa gtt tgt gct tta ctt gat agg ttg gca gga gat
      s p c k e h d v i g t k v c a l l d r l a g d
2761 tat gtc tat ctt ttt gat gag gga ggc gat gaa gtg atc gcc ccg agg atg tat tgt tcc ttt tct gct
      y v y l f d e g g d e v i a p r m y c s f s a
2830 cct gat gat gaa gac tgc gtt gca gcg gat gtt gta gat gca gat gaa aac caa gat gat gat gct gaa
      p d d e d c v a a d v v d a d e n q d d d a e
2899 gac tca gca gtc ctt gtc gct gat acc caa gaa gag gac ggc gtt gcc aag ggg cag gtt gag gcg gat
      d s a v l v a d t q e e d g v a k g q v e a d
2968 tcg gaa att tgc gtt gcg cat act ggt agt caa gaa gaa ttg gct gag cct gat gct gtc gga tct caa
      s e i c v a h t g s q e e l a e p d a v g s q
3037 act ccc atc gcc tct gct gag gaa acc gaa gtc gga gag gca agc gac agg gaa ggg att gct gag gcg

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t p i a s a e e t e v g e a s d r e g i a e a
 3106 aag gca act gtg tgt gct gat gct gta gat gcc tgc ccc gat caa gtg gag gca ttt gaa att gaa aag
 k a t v c a d a v d a c p d q v e a f e i e k
 3175 gtt gaa gac tct atc ttg gat gag ctt caa act gaa ctt aat gcg cca gcg gac aag acc tat gag gat
 v e d s i l d e l q t e l n a p a d k t y e d
 3244 gtc ttg gca ttc gat gcc gta tgc tca gag gcg ttg tct gca ttc tat gct gtg ccg agt gat gag acg
 v l a f d a v c s e a l s a f y a v p s d e t
 3313 cac ttt aaa gtg tgt gga ttc tat tcg cct gct ata gag cgc act aat tgt tgg ctg cgt tct act ttg
 h f k v c g f y s p a i e r t n c w l r s t l
 3382 ata gta atg cag agt cta cct ttg gaa ttt aaa gac ttg gag atg caa aag ctc tgg ttg tct tac aag
 i v m q s l p l e f k d l e m q k l w l s y k
 3451 gcc ggc tat gac caa tgc ttt gtg gac aaa cta gtt aag agc gtg ccc aag tct att atc ctt cca caa
 a g y d q c f v d k l v k s v p k s i i l p q
 3520 ggt ggt tat gtg gca gat ttt gcc tat ttc ttt cta agc cag tgt agc ttt aaa gct tat gct aac tgg
 g g y v a d f a y f f l s q c s f k a y a n w
 3589 cgt tgt tta gag tgt gac atg gag tta aag ctt caa ggc ttg gac gcc atg ttt ttc tat ggg gac gtt
 r c l e c d m e l k l q g l d a m f f y g d v
 3658 gtg tct cat atg tgc aag tgt ggt aat agc atg acc ttg ttg tct gca gat ata ccc tac act ttg cat
 v s h m c k c g n s m t l l s a d i p y t l h
 3727 ttt gga gtg cga gat gat aag ttt tgc gct ttt tac acg cca aga aag gtc ttt agg gct gct tgt gcg
 f g v r d d k f c a f y t p r k v f r a a c a
 3796 gta gat gtt aat gat tgt cac tct atg gct gta gta gag ggc aag caa att gat ggt aaa gtg gtt acc
 v d v n d c h s m a v v e g k q i d g k v v t
 3865 aaa ttt att ggt gac aaa ttt gat ttt atg gtg ggt tac ggg atg aca ttt agt atg tct cct ttt gaa
 k f i g d k f d f m v g y g m t f s m s p f e
 3934 ctc gcc cag tta tat ggt tca tgt ata aca cca aat gtt tgt ttt gtt aaa gga gat gtt ata aag gtt
 l a q l y g s c i t p n v c f v k g d v i k v
 4003 gtt cgc tta gtt aat gct gaa gtc att gtt aac cct gct aat ggg cgt atg gct cat ggt gca ggt gtt
 v r l v n a e v i v n p a n g r m a h g a g v
 4072 gca ggt gct ata gct gaa aag gcg ggc agt gct ttt att aaa gaa acc tcc gat atg gtg aag gct cag
 a g a i a e k a g s a f i k e t s d m v k a q
LA16 ...
NC2 g.. (E)
 4141 ggc gtt tgc cag gtt ggt gaa tgc tat gaa tct gcc ggt ggt aag tta tgt aaa aag gtg ctt aac att
 g v c q v g e c y e s a g g k l c k k v l n i
 4210 gta ggg cca gat gcg cga ggg cat ggc aag caa tgc tat tca ctt tta gag cgt gct tat cag cat att
 v g p d a r g h g k q c y s l l e r a y q h i
 4279 aat aag tgt gac aat gtt gtc act act tta att tcg gct ggt ata ttt agt gtg cct act gat gtc tcc
 n k c d n v v t t l i s a g i f s v p t d v s
 4348 cta act tac tta ctt ggt gta gtg aca aag aat gtc att ctt gtc agt aac aac cag gat gat ttt gat
 l t y l l g v v t k n v i l v s n n q d d f d
 4417 gtg ata gag aag tgt cag gtg acc tcc gtt gct ggt acc aaa gcg cta tca ctt caa ttg gcc aaa aat
 v i e k c q v t s v a g t k a l s l q l a k n
 4486 ttg tgc cgt gat gta aag ttt gtg acg aat gca tgt agt tcg ctt ttt agt gaa tct tgc ttt gtc tca
 l c r d v k f v t n a c s s l f s e s c f v s
 4555 agc tat gat gtg ttg cag gaa gtt gaa gcg ctg cga cat gat ata caa ttg gat gat gat gct cgt gtc
 s y d v l q e v e a l r h d i q l d d d a r v
 4624 ttt gtg cag gct aat atg gac tgt ctg ccc aca gac tgg cgt ctc gtt aac aaa ttt gat agt gtt gat
 f v q a n m d c l p t d w r l v n k f d s v d
 4693 ggt gtt aga acc att aag tat ttt gaa tgc ccg ggc ggg att ttt gta tcc agc cag ggc aaa aag ttt
 g v r t i k y f e c p g g i f v s s q g k k f
 4762 ggt tat gtt cag aat ggt tca ttt aag gag gcg agt gtt agc caa ata agg gct tta ctc gct aat aag

g y v q n g s f k e a s v s q i r a l l a n k
 4831 gtt gat gtc ttg tgt act gtt gat ggt gtt aac ttc cgc tcc tgc tgc gta gca gag ggt gaa gtt ttt
 v d v l c t v d g v n f r s c c v a e g e v f
 4900 ggc aag aca tta ggt tca gtc ttt tgt gat ggc ata aat gtc acc aaa gtt agg tgt agt gcc att tac
 g k t l g s v f c d g i n v t k v r c s a i y
 4969 aag ggt aag gtt ttc ttt cag tac agt gat ttg tcc gag gca gat ctt gtg gct gtt aaa gat gcc ttt
 k g k v f f q y s d l s e a d l v a v k d a f
 5038 ggt ttt gat gaa cca caa ctg ctg aag tac tac act atg ctt ggc atg tgt aag tgg tca gta gtt gtt
 g f d e p q l l k y y t m l g m c k w s v v v
LA16 c..(P)
NC2 c..(P)
 5107 tgt ggc aat tat ttt gct ttc aag cag tca aat aat aat tgc tat ata aat gtg gca tgt tta atg ctg
 c g n y f a f k q s n n n c y i n v a c l m l
 5176 caa cac ttg agt tta aag ttt cct aag tgg caa tgg caa gag gct tgg aac gag ttc cgc tct ggt aaa
 q h l s l k f p k w q w q e a w n e f r s g k
 5245 cca cta agg ttt gtg tcc ttg gta tta gca aag ggc agc ttt aaa ttt aat gaa cct tct gat tct atc
 p l r f v s l v l a k g s f k f n e p s d s i
 5314 gat ttt atg cgt gtg gtg cta cgt gaa gca gat ttg agt ggt gcc acg tgc aat ttg gaa ttt gtt tgt
 d f m r v v l r e a d l s g a t c n l e f v c
 5383 aaa tgt ggt gtg aag caa gag cag cgc aaa ggt gtt gac gct gtt atg cat ttt ggt acg ttg gat aaa
 k c g v k q e q r k g v d a v m h f g t l d k
 5452 ggt gat ctt gtc agg ggt tat aat atc gca tgt acg tgc ggt agt aaa ctt gtg cat tgc acc caa ttt
 g d l v r g y n i a c t c g s k l v h c t q f
 5521 aac gta cca ttt tta att tgc tcc aac aca cca gag ggt agg aaa ctg ccc gac gat gtt gtt gca gct
 n v p f l i c s n t p e g r k l p d d v v a a
 5590 aat att ttt act ggt ggt agt gtg ggc cat tac acg cat gtg aaa tgt aaa ccc aag tac cag ctt tat
 n i f t g g s v g h y t h v k c k p k y q l y
 5659 gat gct tgt aat gtt aat aag gtt tcg gag gct aag ggt aat ttt acc gat tgc ctc tac ctt aaa aat
 d a c n v n k v s e a k g n f t d c l y l k n
 5728 tta aag caa act ttt tcg tct gtg ctg acg act ttt tat tta gat gat gta aag tgt gtg gag tat aag
 l k q t f s s v l t t f y l d d v k c v e y k
 5797 cca gat tta tcg cag tat tac tgt gag tct ggt aaa tat tat aca aaa ccc att att aag gcc caa ttt
 p d l s q y y c e s g k y y t k p i i k a q f
 5866 aga aca ttt gag aag gtt gat ggt gtc tat acc aac ttt aaa ttg gtg gga cat agt att gct gaa aaa
 r t f e k v d g v y t n f k l v g h s i a e k
 5935 ctc aat gct aag ctg gga ttt gat tgt aat tct ccc ttt gtg gag tat aaa att aca gag tgg cca aca
 l n a k l g f d c n s p f v e y k i t e w p t
 6004 gct act gga gat gtg gtg ttg gct agt gat gat ttg tat gta agt cgg tac tca agc ggg tgc att act
 a t g d v v l a s d d l y v s r y s s g c i t
LA16 ..g
NC2 ..g
 6073 ttt ggt aaa ccg gtt gtc tgg ctt ggc cat gag gaa gca tcg ctg aaa tct ctc aca tat ttt aat aga
 f g k p v v w l g h e e a s l k s l t y f n r
 6142 cct agt gtc gtt tgt gaa aat aaa ttt aat gtg ttg ccc gtt gat gtc agt gaa ccc acg gac aag ggg
 p s v v c e n k f n v l p v d v s e p t d k g
 6211 cct gtg cct gct gca gtc ctt gtt acc ggc gtc cct gga gct gat gcg tca gct ggt gcc ggt att gcc
 p v p a a v l v t g v p g a d a s a g a g i a
 6280 aag gag caa aaa gcc tgt gct tct gct agt gtg gag gat cag gtt gtt acg gag gtt cgt caa gag cca
 k e q k a c a s a s v e d q v v t e v r q e p
 6349 tct gtt tca gct gct gat gtc aaa gag gtt aaa ttg aat ggt gtt aaa aag cct gtt aag gtg gaa ggt
 s v s a a d v k e v k l n g v k k p v k v e g
 6418 agt gtg gtt gtt aat gat ccc act agc gaa acc aaa gtt gtt aaa agt ttg tct att gtt gat gtc tat
 s v v v n d p t s e t k v v k s l s i v d v y

6487 gat atg ttc ctg aca ggg tgt aag tat gtg gtt tgg act gct aat gag ttg tct cga cta gta aat tca
d m f l t g c k y v v w t a n e l s r l v n s

6556 ccg act gtt agg gag tat gtg aag tgg ggt aag gga aag att gta aca ccc gct aag ttg ttg ttg tta
p t v r e y v k w g k g k i v t p a k l l l l l
LA16 .t. (M)
NC2 .t. (M)

6625 aga gat gag aag caa gag ttc gta gcg cca aaa gta gtc aag gcg aaa gct att gcc tgc tat tgt gct
r d e k q e f v a p k v v k a k a i a c y c a

6694 gtg aag tgg ttt ctc ctc tat tgt ttt agt tgg ata aag ttt aat act gat aat aag gtt ata tac acc
v k w f l l y c f s w i k f n t d n k v i y t

6763 aca gaa gta gct tca aag ctt act ttc aag ttg tgc tgt ttg gcc ttt aag aat gcc tta cag acg ttt
t e v a s k l t f k l c c l a f k n a l q t f

6832 aat tgg agc gtt gtg tct agg ggc ttt ttc cta gtt gca acg gtc ttt tta tta tgg ttt aac ttt ttg
n w s v v s r g f f l v a t v f l l w f n f l

6901 tat gct aat gtt att ttg agt gac ttc tat ttg cct aat att ggg cct ctc cct acg ttt gtg gga cag
y a n v i l s d f y l p n i g p l p t f v g q

6970 ata gtt gcg tgg ttt aag act aca ttt ggt gtg tca acc atc tgt gat ttc tac cag gtg acg gat ttg
i v a w f k t t f g v s t i c d f y q v t d l

7039 ggc tat aga agt tcg ttt tgt aat gaa agt atg gta tgt gaa cta tgc ttc tca ggt ttt gat atg ctg
g y r s s f c n g s m v c e l c f s g f d m l
LA16 .a. (E)
NC2 ...

7108 gac aac tat gat gct ata aat gtt gtt caa cac gtt gta gat agg cgt ttg tcc ttt gac tat att agc
d n y d a i n v v q h v v d r r l s f d y i s

7177 cta ttt aaa tta gta gtt gag ctt gta atc ggc tac tct ctt tat act gtg tgc ttc tac cca ctg ttt
l f k l v v e l v i g y s l y t v c f y p l f

7246 gtc ctt att gga atg cag ttg ttg acc aca tgg ttg cct gaa ttc ttt atg ctg gag act atg cat tgg
v l i g m q l l t t w l p e f f m l e t m h w

7315 agt gct cgt ttg ttt gtg ttt gtt gcc aat atg ctt cca gct ttt acg tta ctg cga ttt tac atc gtg
s a r l f v f v a n m l p a f t l l r f y i v

7384 gtg aca gct atg tat aag gtc tat tgt ctt tgt aga cat gtt atg tat gga tgt agt aag cct ggt tgc
v t a m y k v y c l c r h v m y g c s k p g c

7453 ttg ttt tgt tat aag aga aac cgt agt gtc cgt gtt aag tgt agc acc gtt gtt ggt ggt tca cta cgc
l f c y k r n r s v r v k c s t v v g g s l r

7522 tat tac gat gta atg gct aac ggc ggc aca ggt ttc tgt aca aag cac cag tgg aac tgt ctt aat tgc
y y d v m a n g g t g f c t k h q w n c l n c

7591 aat tcc tgg aaa cca ggc aat aca ttc ata act cat gaa gca gcg gcg gac ctc tct aag gag ttg aaa
n s w k p g n t f i t h e a a a d l s k e l k

7660 cgc cct gtg aat cca aca gat tct gct tat tac tcg gtc aca gag gtt aag cag gtt ggt tgt tcc atg
r p v n p t d s a y y s v t e v k q v g c s m

7729 cgt ttg ttc tac gag aga gat gga cag cgt gtt tat gat gat gtt aat gct agt ttg ttt gtg gac atg
r l f y e r d g q r v y d d v n a s l f v d m

7798 aat ggt ctg ctg cat tct aaa gtt aaa ggt gtg cct gaa acg cat gtt gtg gtt gtt gag aat gaa gct
n g l l h s k v k g v p e t h v v v v e n e a

7867 gat aaa gct ggt ttt ctc ggc gcc gca gtg ttt tat gca caa tcg ctc tac aga cct atg ttg atg gtg
d k a g f l g a a v f y a q s l y r p m l m v

7936 gaa aag aaa tta ata act acc gcc aac act ggt ttg tct gtt agt cga act atg ttt gac ctt tat gta
e k k l i t t a n t g l s v s r t m f d l y v

8005 gat tca ttg ctg aac gtc ctc gac gtg gat cgc aag agt cta aca agt ttt gta aat gct gcg cac aac
d s l l n v l d v d r k s l t s f v n a a h n

8074 tct cta aag gag ggt gtt cag ctt gaa caa gtt atg gat acc ttt att ggc tgt gcc cga cgt aag tgt
s l k e g v q l e q v m d t f i g c a r r k c

8143 gct ata gat tct gat gtt gaa acc aag tct att acc aag tcc gtc atg tcg gca gta aat gct ggc gtt
a i d s d v e t k s i t k s v m s a v n a g v

8212 gat ttt acg gat gag agt tgt aat aac ttg gtg cct acc tat gtt aaa agt gac act atc gtt gca gcc
d f t d e s c n n l v p t y v k s d t i v a a

8281 gat ttg ggt gtt ctt att cag aat aat gct aag cat gta cag gct aat gtt gct aaa gcc gct aat gtg
d l g v l i q n n a k h v q a n v a k a a n v

8350 gct tgc att tgg tct gtg gat gct ttt aac cag cta tct gct gac tta cag cat agg ctg cga aaa gca
a c i w s v d a f n q l s a d l q h r l r k a

8419 tgt tca aaa act ggc ttg aag att aag ctt act tat aat aag cag gag gca aat gtt cct att tta act
c s k t g l k i k l t y n k q e a n v p i l t

8488 aca ccg ttc tct ctt aaa ggg ggc gct gtt ttt agt aga atg tta caa tgg ttg ttt gtt gct aat ttg
t p f s l k g g a v f s r m l q w l f v a n l

8557 att tgt ttc att gtg ttg tgg gcc ctt atg cca aca tat gca gtg cac aaa tcg gat atg cag ttg cct
i c f i v l w a l m p t y a v h k s d m q l p

8626 tta tat gcc agt ttt aaa gtt ata gat aat ggt gtg cta agg gat gtg tct gtt act gac gca tgc ttc
l y a s f k v i d n g v l r d v s v t d a c f

8695 gca aac aaa ttt aat caa ttt gat caa tgg tat gag tct act ttt ggt ctt gct tat tac cgc aac tct
a n k f n q f d q w y e s t f g l a y y r n s

8764 aag gct tgt cct gtt gtg gtt gct gta ata gat caa gac att ggc cat acc tta ttt aat gtt cct acc
k a c p v v v a v i d q d i g h t l f n v p t

8833 aca gtt tta aga tat gga ttt cat gtg ttg cat ttt ata acc cat gca ttt gct act gat agc gtg cag
t v l r y g f h v l h f i t h a f a t d s v q

8902 tgt tac acg cca cat atg caa atc ccc tat gat aat ttc tat gct agt ggt tgc gtg ttg tca tcc ctc
c y t p h m q i p y d n f y a s g c v l s s l

8971 tgt act atg ctt gcg cat gca gat gga acc ccg cat cct tat tgt tat aca ggg ggt gtt atg cac aat
c t m l a h a d g t p h p y c y t g g v m h n

9040 gcc tct ctg tat agt tct ttg gct cct cat gtc cgt tat aac ctg gct agt tca aat ggt tat ata cgt
a s l y s s l a p h v r y n l a s s n g y i r

9109 ttt ccc gaa gtg gtt agt gaa ggc att gtg cgt gtt gtg cgc act cgc tct atg acc tac tgc agg gtt
f p e v v s e g i v r v v r t r s m t y c r v

9178 ggt tta tgt gag gag gcc gag gag ggt atc tgc ttt aat ttt aat cgt tca tgg gta ttg aac aac ccg
g l c e e a e e g i c f n f n r s w v l n n p

9247 tat tat agg gcc atg cct gga act ttt tgt ggt agg aat gct ttt gat tta ata cat caa gtt tta gga
y y r a m p g t f c g r n a f d l i h q v l g

9316 gga tta gtg cgg cct att gat ttc ttt gcc tta acg gcg agt tca gtg gct ggt gct atc ctt gca att
g l v r p i d f f a l t a s s v a g a i l a i

9385 att gtc gtt ttg gct ttc tat tat tta ata aag ctt aaa cgt gcc ttt ggt gac tac act agt gtt gtg
i v v l a f y y l i k l k r a f g d y t s v v

9454 gtt atc aat gta att gtg tgg tgt ata aat ttt ctg atg ctt ttt gtg ttt cag gtt tat ccc aca ttg
v i n v i v w c i n f l m l f v f q v y p t l

9523 tct tgt tta tat gct tgt ttt tat ttc tac aca acg ctt tat ttc cct tcg gag ata agt gtt gtt atg
s c l y a c f y f y t t l y f p s e i s v v m

9592 cat ttg caa tgg ctt gtc atg tat ggt gct att atg ccc ttg tgg ttt tgc att att tac gtg gca gtc
h l q w l v m y g a i m p l w f c i i y v a v

9661 gtt gtt tca aac cat gca ttg tgg ttg ttc tct tac tgc cgc aaa att ggt acc gag gtt cgt agt gac
v v s n h a l w l f s y c r k i g t e v r s d

9730 ggc aca ttt gag gaa atg gcc ctt act acc ttt atg att act aaa gaa tct tat tgt aag ttg aaa aat
g t f e e m a l t t f m i t k e s y c k l k n

LA16
NC2
9799 tct gtt tct gat gtt gct ttt aac agg tac ttg agt ctt tat aac aag tat cgt tat ttt agt ggc aaa
s v s d v a f n r y l s l y n k y r y f s g k

LA16
NC2
9868 atg gat act gcc gct tat aga gag gct gcc tgt tca caa ctg gca aag gca atg gaa aca ttt aac cat

m d t a a y r e a a c s q l a k a m e t f n h
 9937 aat aat ggt aat gat gtt ctc tat cag cct cca acc gcc tct gtt act aca tca ttt tta cag tct ggt
 n n g n d v l y q p p t a s v t t s f l q s g
 10006 ata gtg aag atg gtg tcg ccc acc tct aaa gtg gag cct tgt att gtt agt gtt act tat ggt aac atg
 i v k m v s p t s k v e p c i v s v t y g n m
 10075 aca ctt aat ggg ttg tgg ttg gat gat aaa gtt tat tgc cca aga cat gtt atc tgt tct tca gct gac
 t l n g l w l d d k v y c p r h v i c s s a d
 10144 atg aca gac cct gat tat cct aat ttg **ctt** tgt aga gtg aca tca agt gat ttt tgt gtt atg tct ggt
 m t d p d y p n l l c r v t s s d f c v m s g
LA16
NC2
 10213 cgt atg agc ctt act gta atg tct tat caa atg cag ggc tgc caa ctt gtt ttg act gtt aca ctg caa
 r m s l t v m s y q m q g c q l v l t v t l q
 10282 aat cct aac acg cct aag tat tcc ttc ggt gtt gtt aag cct ggt gag aca ttt act gta ctg gct gca
 n p n t p k y s f g v v k p g e t f t v l a a
 10351 tac aat ggc aga cct caa gga gcc ttc cat gtt acg ctt cgt agt agc cat acc ata aag ggc tcc ttt
 y n g r p q g a f h v t l r s s h t i k g s f
 10420 cta tgt gga tcc tgc ggt tct gta gga tat gtt tta act ggc gat agt gta cga ttt gtt tat atg cat
 l c g s c g s v g y v l t g d s v r f v y m h
 10489 cag cta gag ttg agt act ggt tgt cat acc ggt act gac ttt agt ggg aac ttt tat ggt ccc tat aga
 q l e l s t g c h t g t d f s g n f y g p y r
 10558 gat gcg caa gtt gta caa ttg cct gtt cag gat tat acg cag act gtt aat gtt gta gct tgg ctt tat
 d a q v v q l p v q d y t q t v n v v a w l y
 10627 gct gct att ttt aac aga tgc aac tgg ttt gtg caa agt gat agt tgt tcc ctg gag gag ttt aat gtt
 a a i f n r c n w f v q s d s c s l e e f n v
 10696 tgg gct atg acc aat ggt ttt agc tca **atc** aaa gcc gat ctt gtc ttg gat gcg ctt gct tct atg aca
 w a m t n g f s s i k a d l v l d a l a s m t
LA16
NC2
 10765 ggc gtt aca gtt gaa cag gtg ttg gcc gct att aag agg ctg cat tct gga ttc cag ggc aaa caa att
 g v t v e q v l a a i k r l h s g f q g k q i
 10834 tta ggt agt tgt gtg ctt gaa gat gag ctg aca cca agt gat gtt tat caa caa cta gct ggt gtc aag
 l g s c v l e d e l t p s d v y q q l a g v k
 10903 cta cag tca aag cgc aca aga gtt ata aaa ggt aca tgt tgc tgg ata ttg gct tca acg ttt ttg ttc
 l q s k r t r v i k g t c c w i l a s t f l f
 10972 tgt agc att atc tca gca ttt gta aaa tgg act atg ttt atg tat gtt act acc cat atg ttg gga gtg
 c s i i s a f v k w t m f m y v t t h m l g v
 11041 aca ttg tgt gca ctt tgt ttt gta agc ttt gct atg ttg ttg atc aag cat aag cat ttg tat tta act
 t l c a l c f v s f a m l l i k h k h l y l t
 11110 atg tat att atg cct gtg tta tgc aca ctg ttt tac acc aac tat ttg gtt gtg tac aaa cag agt ttt
 m y i m p v l c t l f y t n y l v v y k q s f
 11179 aga ggt cta gct tat gct tgg ctt tca cac ttt gtc cct gct gta gat tat aca tat atg gat gaa gtt
 r g l a y a w l s h f v p a v d y t y m d e v
 11248 tta tat ggt gtt gtg ttg cta gta gct atg gtg ttt gtt acc atg cgt agc ata aac cac gac gtc ttt
 l y g v v l l v a m v f v t m r s i n h d v f
 11317 tct att atg ttc ttg gtt ggt aga ctt gtc agc ctg gta tcc atg tgg tat ttt gga gcc aat tta gag
 s i m f l v g r l v s l v s m w y f g a n l e
 11386 gaa gag gta cta ttg ttc ctc aca tcc cta ttt ggc acg tac aca tgg act act atg ttg tca ttg gct
 e e v l l f l t s l f g t y t w t t m l s l a
 11455 acc gct aag gtt att gct aaa tgg ttg gct gtg aat gtc ttg tac ttc aca gac gta ccg caa att aaa
 t a k v i a k w l a v n v l y f t d v p q i k
 11524 tta gtt ctt ttg agc tac ttg tgt att ggt tat gtg tgt tgt tgt tat tgg gga atc ttg tca ctc ctt
 l v l l s y l c i g y v c c c y w g i l s l l

11593 aat agc att ttt agg atg cca ttg ggc gtc tac aat tat aaa atc tcc gtt cag gag tta cgt tat atg
n s i f r m p l g v y n y k i s v q e l r y m
11662 aat gct aat ggc ttg cgc cca cct aga aat agt ttt gag gcc ctg atg ctt aat ttt aag ctg ttg gga
n a n g l r p p r n s f e a l m l n f k l l g
11731 att ggt ggt gtg cca gtc att gaa gta tct caa att caa tca aga ttg acg gat gtt aaa tgt gct aat
i g g v p v i e v s q i q s r l t d v k c a n
11800 gtt gtg ttg ctt aat tgc ctc cag cac ttg cat att gca tct aat tct aag ttg tgg cag tat tgt agt
v v l l n c l q h l h i a s n s k l w q y c s
11869 act ttg cac aat gaa ata ctg gct aca tct gat ttg agc gtg gcc ttc gat aag ttg gct cag ctc tta
t l h n e i l a t s d l s v a f d k l a q l l
11938 gtt gtt tta ttt gct aat cca gca gca gtg gat agc aag tgc ctt gca agt att gaa gaa gtg agc gat
v v l f a n p a a v d s k c l a s i e e v s d
12007 gat tac gtt cgc gac aat act gtc ttg caa gcc tta cag agt gaa ttt gtt aat atg gct agc ttc gtt
d y v r d n t v l q a l q s e f v n m a s f v
12076 gag tat gaa ctt gct aag aag aat cta gat gag gct aag gct agc gcc tct gcc aat caa cag cag att
e y e l a k k n l d e a k a s g s a n q q q i
12145 aag cag cta gag aag gcg tgt aat att gct aag tca gca tat gag cgc gac aga gct gtt gct cgt aag
k q l e k a c n i a k s a y e r d r a v a r k
12214 ctg gaa cgt atg gct gat tta gct ctt aca aac atg tat aaa gaa gct aga att aat gat aag aag agt
l e r m a d l a l t n m y k e a r i n d k k s
12283 aag gta gtg tct gca ttg caa acc atg ctc ttt agt atg gtg cgt aag cta gat aac caa gct ctt aat
k v v s a l q t m l f s m v r k l d n q a l n
12352 tct att tta gat aat gca gtt aag ggt tgt gta cct ttg aat gca ata cca tca ttg act tcg aac act
s i l d n a v k g c v p l n a i p s l t s n t
12421 ctg act ata ata gtg cca gat aag cag gtt ttt gat cag gtt gtg gat aat gtg tat gtc acc tat gct
l t i i v p d k q v f d q v v d n v y v t y a
12490 ggg aat gta tgg cat ata cag ttt att caa gat gct gat ggt gct gtt aaa caa ttg aat gag ata gat
g n v w h i q f i q d a d g a v k q l n e i d
12559 gtt aat tca acc tgg cct cta gtc att gct gca aat agg cat aat gaa gtg tct act gtt gtt ttg cag
v n s t w p l v i a a n r h n e v s t v v l q
12628 aac aat gag ttg atg cct cag aag ttg aga act cag gtt gtc aat agt gcc tca gat atg aat tgt aat
n n e l m p q k l r t q v v n s g s d m n c n
12697 act cct acc cag tgt tac tat aat act act gcc acg ggt aag att gtg tat gct ata ctt agt gac tgt
t p t q c y y n t t g t g k i v y a i l s d c
12766 gat ggt **ctc** aag tac act aag ata gta aaa gaa gat gga aat tgt gtt gtt ttg gaa ttg gat cct ccc
d g l k y t k i v k e d g n c v v l e l d p p
LA16 ...
NC2 ..g
12835 tgt aag ttt tct gtt cag gat gtg aag ggc ctt aaa att aag tac ctt tac ttt gtg aag ggg tgt aat
c k f s v q d v k g l k i k y l y f v k g c n
12904 aca ctg gct aga ggc tgg gtt gta ggc acc tta tcc tcg aca gtg aga ttg cag gcg ggt acg gca act
t l a r g w v v g t l s s t v r l q a g t a t
12973 gag tat gcc tcc aac tct gca ata ctg tcg ctg tgt gcg ttt tct gta gat cct aag aaa acg tac ttg
e y a s n s a i l s l c a f s v d p k k t y l
13042 gat tat ata aaa cag ggt gga gtt ccc gtt act aat tgt gtt aag atg tta **tgt** gac cat gct ggc act
d y i k q g g v p v t n c v k m l c d h a g t
LA16 .a. (Y)
NC2
13111 ggt atg gcc att act att aag ccg gag gca acc act aat cag gat tct tat ggt ggt gct tcc gtt tgt
g m a i t i k p e a t t n q d s y g g a s v c
13180 ata tat tgc cgc tcg cgt gtt gaa cat cca gat gtt gat gga ttg tgc aaa tta cgc gcc aag ttt gtc
i y c r s r v e h p d v d g l c k l r g k f v
13249 caa gtg ccc tta ggc ata aaa gat cct gtg tca tat gtg ttg acg cat gat gtt tgt cag gtt tgt ggc
q v p l g i k d p v s y v l t h d v c q v c g

```

13318 ttt tgg cga gat ggt agc tgt tcc tgt gta ggc aca ggc tcc cag ttt cag tca aaa gac acg aac ttt
      f w r d g s c s c v g t g s q f q s k d t n f
13387 tta aac ggg ttc ggg gta caa gtg taa
      l n g f g v q v -
LA16 ..a
NC2 ..a

```

Comparing Mutations Located in ORF1A from LA16 and NC2

To compare the mutations identified in the viral genome (Figure 10) a table was constructed (Table 1). Table 1 lists the mutated nucleotide position in the viral genome, the amino acid change and the type of mutation that resulted. The nucleotide position that was entered into the table was obtained from the sequence of ORF1A that starts with the first “atg” present in the first open reading frame. This corresponds to nucleotide number 210 in the full viral genome that is located in appendix. In assessing the location of the mutations, LA16 contains mutations in Nsp3 and Nsp10. LA16 has shown to have a more significant TS phenotype, assessed by a reduction in titer and plaque size, indicating further that these mutations in Nsp3 and Nsp10 are important (Figure 7&8). It is interesting that of the six mutations identified in NC2 that resulted in an amino acid change, three of these mutations are conservative. Conservative mutations are defined as mutations that result in an amino acid change which conserves the same amino acid charge but has a slightly different structure (Table 1). These results indicate NC2 and LA16 contain different attenuating mutations. The role of these mutations in conferring the TS phenotype could be evaluated using reverse genetics.

Virus	Nsp mutation location	Mutated Nucleotide Positon	Mutated Amino Acid	
LA16	Nsp3	t 5090 c	S→P	Polar to Nonpolar
	Nsp3	a 6587 t	K→M	Positively Charged to Nonpolar
	Nsp3	g 7064 a	G→E	Polar to Negatively Charged
	Nsp10	g 13094 a	G→Y	Polar to Nonpolar
NC2	Nsp3	a 4090 g	K→E	Positively Charged to Negatively Charged
	Nsp3	t 5090c	S→P	Polar to Nonpolar
	Nsp3	a 6587 t	K→M	Positively Charged to Nonpolar
	Nsp4	c 9770 g	T→S	Conservative
	Nsp4	c 9815g	A→G	Conservative
	Nsp5	c 10171 a	L→I	Conservative

TABLE 1. Table of nucleotide and amino acid changes in the genomic sequences of LA16 and NC2. Genomic sequence from ORF1A was analyzed and the nucleotide changes that resulted in amino acid changes are listed. Silent mutations are documented in Figure 10. Nucleotide position, amino acid position, non-structural protein location and mutation type are classified. The location of the nucleotide changes corresponds to the nucleotide sequence of ORF1A and not to the entire genomic nucleotide sequence.

CHAPTER FOUR

DISCUSSION AND FUTURE DIRECTIONS

Using TS phenotyping has become a staple in virology to better understand many unknown pathogens. TS mutants of pathogens allow for the identification of critical genes or residues which can be identified as targets for potential vaccine development. In assessing the TS phenotype for LA16 and NC2, it was observed that at 33°C, both viruses were able to maintain a WT-like plaque size and viral titer (Figure 7A, B). Upon incubating LA16 at 37°C, I observed a drastic change in plaque morphology (Figure 7A). When assessing the plaque morphology, I found a heterogeneous population of plaques formed. These plaques range from small to pinpoint in size. *Schaad et al.* hypothesized that LA16 may contain two different mutations that confer the TS phenotype documented⁴¹. This heterogeneity does seem to further support why LA16 was placed into two complementation groups indicating multiple mutations in different areas of the viral genome. This change in morphology was also associated with a reduction in viral titer which also helps to support the hypothesis that LA16 confers a TS phenotype. Upon quantifying the plaque size of LA16 at 37°C (Figure 8), there was a significant decrease in plaque size when compared to WT, further supporting that the change in morphology may be due to the mutations identified in ORF1A. LA16 failed to produce any plaques within the detection limit of the plaque assay when incubated at 40°C. When analyzing the sequence of LA16 two unique mutations were identified. The first mutation was observed in Nsp3 which resulted in the substitution of a polar amino acid to a negatively charged amino acid. This could

have an effect on the Nsp3 protein stability or structure, but further analysis is required. The second mutation found was located in Nsp10. Currently the documented function of Nsp10 is to act as a regulator that aides in the efficiency of the polyprotein processing⁴⁵. The amino acid that was mutated has been identified a one of several critical residues involved in Nsp10 stability.

When assessing the TS phenotype of NC2, I saw that NC2 was able to retain WT-like plaques at both 33 °C and 37 °C (Figure 7A). This was obviously different than the morphology depicted by LA16 at 37 °C. It was only when NC2 was incubated at 40 °C was the TS phenotype able to be observed. This reduction in plaque size also correlates with the reduction in titer (Figure 7B). It can be appreciated that although NC2 did present a reduction in plaque size at 40°C, there was a homogenous morphology amongst the plaques formed. They were all pin-point sized plaques (Figure 7A). Upon the quantification of the plaques observed, I noted NC2 produced significantly smaller plaques compared to WT. The genomic sequencing analysis revealed NC2 contained four unique mutations, however, three of the four mutations were conservative. The major mutation observed was located in Nsp3, the viral protease. This mutation conferred a substitution of a positively charged amino acid to a negatively charged amino acid (Table 1). Since the conservative mutations are located around the same region, these mutations could potentially be compensating for the initial Nsp3 mutation. These changes in structure potentially could be to help counter act the deleterious mutation, thus allowing NC2 to not exhibit as drastic of TS phenotype when assessed at 37 °C (Figure 7, 8). To further support my hypothesis that NC2 may have secondary mutations that were induced to stabilize the initial attenuating mutation, it can be seen clearly that half of the mutations found in NC2 were conservative mutation changes. If my hypothesis is true, it may explain why NC2 has much less of a significant TS phenotype than that of LA16.

Interestingly, my data supports the previous studies of *Schaad et al*⁴¹. Using complementation analysis *Schaad et al.* was able to categorize over 20 TS mutants based on the location of TS mutations throughout the viral genome (Table 2). Complementation groups A and B were mapped to contain mutations in ORF1A. ORF1A was the region where I identified the nucleotide changes that are predicted to be responsible for causing the TS phenotype. Over twenty years later it seems that this hypothesis was correct when assessing the genomic sequencing data. NC2 and LA16 both contained important mutations in Nsp3, supporting the rationale for grouping these two mutant strains together.

Complementation Group	Mutants
A	LA3, LA6, LA16, NC8, NC9, NC13
B	LA16, NC2, NC11
C	LA8, LA9, LA14, NC1, NC3, NC10
D	LA10
E	LA18, NC4, NC12
F	LA7, LA12, LA13, NC5, NC6

TABLE 2. Table of TS mutants that have been categorized based on the location of their mutations within the viral genome. Over 2,000 TS mutants were produced following the chemical mutagenesis of WT MHV. Using complementation analysis *Schaad et al.* identified 24 mutants that contained unique mutations⁴¹. Highlighted in red are the two mutants that were further characterized in my study.

It is important to note that LA16 was the only virus that was added to two complementation groups. *Schaad et al.* hypothesized that this mutant strain actually contained two significant mutations in ORF1A. This hypothesis does strongly correlate with the images that were taken of LA16 at 37°C. In assessing the images in Figure 7 you can see that there seem to be two populations of plaques that formed. These two distinct populations may represent viruses that contain one of the two hypothesized mutations in ORF1A. It is important to note that although

this visual representation does seem to further support previous hypothesis, however further analysis will need to be performed.

Temperature-sensitive phenotyping has aided in identifying the function of unknown CoV Nsps. *Donaldson et al.* used TS phenotyping to identify a novel attenuating mutation in another TS mutant that *Schaad et al* identified, LA6^{41,45}. Deep sequencing of the viral genome revealed a mutation in Nsp10. In further assessing the crystal structure of Nsp10, the mutation that conferred the TS phenotype was located in an undefined region of the structure⁴⁵. The amino acids located within the undefined region are thought to be critical to maintaining protein stability⁴⁵. In comparing the location of the mutation in LA16, I found the mutation is located within this undefined region as well. Therefore, it is possible that the mutation in LA16 also affects protein stability.

The sequencing results reported in this study revealed that there are many mutations located within ORF1A of LA16 and NC2. In order to assess the phenotype of the mutations individually, these mutations can be investigated using the MHV reverse genetic system³⁵. A reverse-genetics system allows the study of individual mutations by allowing the manipulation of a RNA viral genome, using classic genetic techniques³⁵. Mutations are introduced into a cDNA version of the RNA genome and using transcription and electroporation, one can produce a “designer virus” that has the desired mutation. The production of this designer virus allows one to study the phenotype that a single mutation may confer. This same system has also been successfully used to identify TS mutation in LA6, as described above⁴⁵. Hopefully, the information obtained in this study will allow the identification of mutations in conserved genes that can be applied to a variety of CoVs resulting in protection from current and more importantly, future strains of CoVs.

APPENDIX:
SUPPLEMENTAL FIGURES

Figure S1. Full Genomic Sequence Alignment of WT, LA16 and NC2. Using Clone Manager I compared the full genomic sequence of LA16, NC2, and WT MHV. Nucleotides that are mutated from the WT reference strain are highlighted in orange. Mutations were found throughout the viral genome however in this study I focused on the mutations located in ORF1A.

MHV IC NC_001846	1	tataagagtgattggcgtccgtacgtaccctctcaactctaaaactctttagtattaaat
LA16 #39	1
NC2 #3	1
MHV IC NC_001846	61	ctaactctaaaactttataaacggcacttcctgcgtgtccatgccgcgggcctggtcttgt
LA16 #39	60
NC2 #3	60
MHV IC NC_001846	121	catagtgtgacattttagtctccttgacttctcggtctctgccagtgacgtgtccattcg
LA16 #39	120
NC2 #3	120
MHV IC NC_001846	181	gcgccagcagcccacccataggttgcataatggcaaagatgggcaaatacggctctcggt
LA16 #39	180
NC2 #3	180
MHV IC NC_001846	241	tcaaattgggccccagaatttccatggatgcttccgaacgcacgagagaagttgggtaacc
LA16 #39	240
NC2 #3	240
MHV IC NC_001846	301	ctgagaggtcagaggaggatgggttttgcccctctgctgcgcaagaaccgaaagttaaag
LA16 #39	300
NC2 #3	300
MHV IC NC_001846	361	gaaaaactttgggtaatacagtgagggtgaattgtagccggcttcagctttggaatgct
LA16 #39	360
NC2 #3	360
MHV IC NC_001846	421	gtgttcagtctgccataatccgtgatattttgtagatgaggatcccagaaggtggagg
LA16 #39	420
NC2 #3	420
MHV IC NC_001846	481	cctcaactatgatggcattgcagttcggtagtgccgtcttggttaagccatccaagcgt
LA16 #39	480
NC2 #3	480
MHV IC NC_001846	541	tgtctattcaggcatggactaatttgggtgtgcttccaaaacagctgccatggggttgt
LA16 #39	540
NC2 #3	540
MHV IC NC_001846	601	tcaagcgcgtctgcctgtgtaacaccagggagtgctcttgtgacgccacgtggccttct
LA16 #39	600
NC2 #3	600

MHV IC NC_001846	661	accttttacggccaacccgatgggtgatgcctgggtaatggccgttttataggctgg
LA16 #39	660
NC2 #3	660
MHV IC NC_001846	721	tcgttccagtcacagccataccggagatgccaagcagtggttgaaccctggccatcc
LA16 #39	720
NC2 #3	720
MHV IC NC_001846	781	ttcttcgtaagggtggtaacaaagggtctgtgacatccggccaactccgccgcgctgta
LA16 #39	780
NC2 #3	780
MHV IC NC_001846	841	ccatgcctgtgatgactttaatgtagaggatgcttgtgaggagggttcattcctaaccgga
LA16 #39	840
NC2 #3	840
MHV IC NC_001846	901	agggtaagtactcctgcaaggcgtatgctcttctaagggtatcgcggtgtaagccca
LA16 #39	900
NC2 #3	900
MHV IC NC_001846	961	tcctgtttgtggaccagatgggtgagactatactggatgtctcgccaagggtcttgagg
LA16 #39	960
NC2 #3	960
MHV IC NC_001846	1021	actatggcgatctcaccttgagtgagatgaaggagttgtccctgtgtggcgtgactcct
LA16 #39	1020
NC2 #3	1020
MHV IC NC_001846	1081	tggatagtgaagtccttgtggctggcacggtgatcgagatcctcgggctgctatgcgtc
LA16 #39	1080
NC2 #3	1080
MHV IC NC_001846	1141	tcgagactcttgctactgtacgttgattgattatgtgggccaaccgaccgaggatgtgg
LA16 #39	1140
NC2 #3	1140
MHV IC NC_001846	1201	tggatggagatgtggtagtgctgagcctgctcatcttctcgagccaatgccattgta
LA16 #39	1200
NC2 #3	1200
MHV IC NC_001846	1261	aaagactccccggttggtggagactatgctgtatacggattcgtccggttacagaattct
LA16 #39	1260
NC2 #3	1260
MHV IC NC_001846	1321	gttataaaaccaagctgtgtgaatgcggttttatcacgcagtttggtatgtggattgtt
LA16 #39	1320
NC2 #3	1320
MHV IC NC_001846	1381	gtggtgacacctgcgattttcgtgggtgggttgcggcaatatgatggatggcttccat
LA16 #39	1380
NC2 #3	1380
MHV IC NC_001846	1441	gtccagggtgtacaaaaattatatgcctgggaattggaggcccagtcattcagggtgta
LA16 #39	1440
NC2 #3	1440
MHV IC NC_001846	1501	taccagaaggaggtgttctattcactcagagcactgatacagtgaatcgtgagtccttta
LA16 #39	1500
NC2 #3	1500

MHV IC NC_001846	2461	tgggttgacagtgaagccacttgttggtgggtgagattgaacctgcagttttgaagatg
LA16 #39	2460c.....
NC2 #3	2460c.....
MHV IC NC_001846	2521	atgttggtgatgtggttaaagccccattaacatatcaaggctggtgtaagccaccactt
LA16 #39	2520
NC2 #3	2520
MHV IC NC_001846	2581	ctttcgagaagatttgattgtggataaattgtatatggccaagtgtggtgatcaat
LA16 #39	2580
NC2 #3	2580
MHV IC NC_001846	2641	accctgtggtggtgataacgacactggtggcgtgtagatcagtgctggaggttccct
LA16 #39	2640
NC2 #3	2640
MHV IC NC_001846	2701	gtgcgggcaagaaagtcgagtttaacgacaagcccaaagtcaggaagataccctccacc
LA16 #39	2700
NC2 #3	2700
MHV IC NC_001846	2761	gtaagattaagatcaccttcgactggatgacaccttgatagtggtctttcgaaggcgt
LA16 #39	2760
NC2 #3	2760
MHV IC NC_001846	2821	gttcagagtttgaagttgataaagatgttacattggatgagctgcttgatggtgtgcttg
LA16 #39	2820
NC2 #3	2820
MHV IC NC_001846	2881	acgcagttgagagtacgctcagcccttgtaaggagcatgatgtgataggcacaaaagttt
LA16 #39	2880
NC2 #3	2880
MHV IC NC_001846	2941	gtgctttacttgataggtggcaggagattatgtctatctttttgatgagggaggcgatg
LA16 #39	2940
NC2 #3	2940
MHV IC NC_001846	3001	aagtgatcgccccgaggatgtattgttccttttctgctcctgatgatgaagactgcgttg
LA16 #39	3000
NC2 #3	3000
MHV IC NC_001846	3061	cagcggatggtgtagatgcagatgaaaaccaagatgatgatgctgaagactcagcagtcc
LA16 #39	3060
NC2 #3	3060
MHV IC NC_001846	3121	ttgtcgctgatacccaagaagaggacggcgttgccaaggggaggttgaggcggattcgg
LA16 #39	3120
NC2 #3	3120
MHV IC NC_001846	3181	aaatttgcgttgcgcatactggtagtcaagaagaattggctgagcctgatgctgtcggat
LA16 #39	3180
NC2 #3	3180
MHV IC NC_001846	3241	ctcaactcccacgctctgctgaggaaaccgaagtggagaggcaagcgacagggag
LA16 #39	3240
NC2 #3	3240
MHV IC NC_001846	3301	ggattgctgaggcgaaggcaactgtgtgtgctgatgctgtagatgcctgccccgatcaag
LA16 #39	3300
NC2 #3	3300

MHV IC NC_001846	3361	tggaggcatttgaattgaaaaggttgaagactctatcttggatgagcttcaaactgaac
LA16 #39	3360
NC2 #3	3360
MHV IC NC_001846	3421	ttaatgcgccagcggacaagacctatgaggatgtcttggcattcgatgccgtatgctcag
LA16 #39	3420
NC2 #3	3420
MHV IC NC_001846	3481	aggcgttgtctgcattctatgctgtgccgagtgatgagacgcactttaaagtgtgtggat
LA16 #39	3480
NC2 #3	3480
MHV IC NC_001846	3541	tctattcgctgctatagagcgcactaattggtggctgcgcttctactttgatagtaatgc
LA16 #39	3540
NC2 #3	3540
MHV IC NC_001846	3601	agagtctacctttggaatttaaagacttggagatgcaaaagctctggttgtcttacaagg
LA16 #39	3600
NC2 #3	3600
MHV IC NC_001846	3661	ccggctatgaccaatgcttgtggacaaactagttaagagcgtgcccaagtctattatcc
LA16 #39	3660
NC2 #3	3660
MHV IC NC_001846	3721	ttccacaaggtggttatgtggcagatcttgcctatttcttcttaagccagtgtagcttta
LA16 #39	3720
NC2 #3	3720
MHV IC NC_001846	3781	aagcttatgctaactggcgttgttttagagtgtgacatggagttaaagcttcaaggcttgg
LA16 #39	3780
NC2 #3	3780
MHV IC NC_001846	3841	acgccatgttttctatggggacggttgtgtctcatatgtgcaagtgtggtaatagcatga
LA16 #39	3840
NC2 #3	3840
MHV IC NC_001846	3901	ccttgttgtctgcagatataacctacactttgcattttggagtgcgagatgataagtttt
LA16 #39	3900
NC2 #3	3900
MHV IC NC_001846	3961	gcgctttttacacgccaaagaaggtctttagggctgcttgtgctggtatagttaatgatt
LA16 #39	3960
NC2 #3	3960
MHV IC NC_001846	4021	gtcactctatggctgtagtagagggcaagcaaattgatggtaaagtggttaccaaattta
LA16 #39	4020
NC2 #3	4020
MHV IC NC_001846	4081	ttggtgacaaatttgattttatggtgggttacgggatgacatttagtatgtctccttttg
LA16 #39	4080
NC2 #3	4080
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LA16 #39	4140
NC2 #3	4140
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NC2 #3	4200

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LA16 #39	4260
NC2 #3	4260g.....
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NC2 #3	4320
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LA16 #39	4380
NC2 #3	4380
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LA16 #39	4440
NC2 #3	4440
MHV IC NC_001846	4501	atgttgtcactactttaatttcggctggtatatttagtgtgcctactgatgtctccctaa
LA16 #39	4500
NC2 #3	4500
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LA16 #39	4560
NC2 #3	4560
MHV IC NC_001846	4621	ttgatgtgatagagaagtgtcagggtgacctccggttgctggtaccaaagcgctatcacttc
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NC2 #3	4620
MHV IC NC_001846	4681	aattggccaaaaatttgtgccgtgatgtaaagtttgtgacgaatgcatgtagttcgcttt
LA16 #39	4680
NC2 #3	4680
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LA16 #39	4740
NC2 #3	4740
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NC2 #3	4800
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LA16 #39	4860
NC2 #3	4860
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LA16 #39	4920
NC2 #3	4920
MHV IC NC_001846	4981	agaatggttcatttaaggaggcgagtgttagccaaataagggcttactcgctaataagg
LA16 #39	4980
NC2 #3	4980
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LA16 #39	5040
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LA16 #39	5100
NC2 #3	5100

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LA16 #39	5160
NC2 #3	5160
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LA16 #39	5220
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LA16 #39	5280C.....
NC2 #3	5280C.....
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NC2 #3	5340
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LA16 #39	5400
NC2 #3	5400
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LA16 #39	5520
NC2 #3	5520
MHV IC NC_001846	5581	aatttGtttgTaaatgtggTgtgaagcaagagcagcgcaaaggTgtgacgctgttatgc
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LA16 #39	5640
NC2 #3	5640
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LA16 #39	5700
NC2 #3	5700
MHV IC NC_001846	5761	cagagggtaggaaactgcccGacgatgttGttgcagctaataTTttactggtggtagtg
LA16 #39	5760
NC2 #3	5760
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LA16 #39	5820
NC2 #3	5820
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LA16 #39	5880
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LA16 #39	5940
NC2 #3	5940
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NC2 #3	6000

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LA16 #39	6120
NC2 #3	6120
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LA16 #39	6180
NC2 #3	6180
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NC2 #3	6240g.....
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NC2 #3	6300
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LA16 #39	6360
NC2 #3	6360
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LA16 #39	6420
NC2 #3	6420
MHV IC NC_001846	6481	gtattgccaaggagcaaaaagcctgtgcttctgctagtgtggaggatcaggttgttacgg
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NC2 #3	6480
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LA16 #39	6540
NC2 #3	6540
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LA16 #39	6600
NC2 #3	6600
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LA16 #39	6660
NC2 #3	6660
MHV IC NC_001846	6721	atgtggtttggactgctaagtgattgtctcgactagtaaattcaccgactgttagggagt
LA16 #39	6720
NC2 #3	6720
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NC2 #3	6780t.....
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LA16 #39	6840
NC2 #3	6840
MHV IC NC_001846	6901	ctgtgaagtggtttctcctctattgttttagttggataaagtttaatactgataataagg
LA16 #39	6900
NC2 #3	6900

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LA16 #39	6960
NC2 #3	6960
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LA16 #39	7020
NC2 #3	7020
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LA16 #39	7080
NC2 #3	7080
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LA16 #39	7140
NC2 #3	7140
MHV IC NC_001846	7201	catttggtgtgtcaaccatctgtgatttctaccagggtgacggatttgggctatagaagtt
LA16 #39	7200
NC2 #3	7200
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LA16 #39	7260a.....
NC2 #3	7260
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LA16 #39	7320
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LA16 #39	7380
NC2 #3	7380
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LA16 #39	7440
NC2 #3	7440
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NC2 #3	7500
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LA16 #39	7560
NC2 #3	7560
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LA16 #39	7620
NC2 #3	7620
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LA16 #39	7680
NC2 #3	7680
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LA16 #39	7740
NC2 #3	7740
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LA16 #39	7800
NC2 #3	7800

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NC2 #3	7860
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LA16 #39	7920
NC2 #3	7920
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LA16 #39	7980
NC2 #3	7980
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LA16 #39	8040
NC2 #3	8040
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LA16 #39	8100
NC2 #3	8100
MHV IC NC_001846	8161	ctaccgccaacactggtttgtctgttagtcgaactatgtttgaccttatgtagattcat
LA16 #39	8160
NC2 #3	8160
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LA16 #39	8220
NC2 #3	8220
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NC2 #3	8280
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LA16 #39	8340
NC2 #3	8340
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LA16 #39	8400
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NC2 #3	8460
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LA16 #39	8520
NC2 #3	8520
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LA16 #39	8580
NC2 #3	8580
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LA16 #39	8640
NC2 #3	8640
MHV IC NC_001846	8701	cgttctctcttaaagggggcgctgttttttagtagaatgttacaatggttgtttgttgcta
LA16 #39	8700
NC2 #3	8700

MHV IC NC_001846	8761	at ttgattt gtttcattgtgtt gttg gggcccttatgccacatatgcagtgcaaaaatcgg
LA16 #39	8760
NC2 #3	8760
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LA16 #39	8820
NC2 #3	8820
MHV IC NC_001846	8881	tgtctgttactgacgcatgcttcgcaacaaatttaataatcaatttgatcaatgggatgagt
LA16 #39	8880
NC2 #3	8880
MHV IC NC_001846	8941	ctacttttggctttgcttattaccgcaactctaaggcttgtcctggttggttgctgtaa
LA16 #39	8940
NC2 #3	8940
MHV IC NC_001846	9001	tagatcaagacattggccataccttatttaaatgttcctaccacagttttaagatatggat
LA16 #39	9000
NC2 #3	9000
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LA16 #39	9060
NC2 #3	9060
MHV IC NC_001846	9121	cacatatgcaaatcccctatgataatttctatgctagtggttgcgtggttgcacccctct
LA16 #39	9120
NC2 #3	9120
MHV IC NC_001846	9181	gtactatgcttgcgcatgcagatggaaccccgcatccttattgttatacagggggtgta
LA16 #39	9180
NC2 #3	9180
MHV IC NC_001846	9241	tgcacaatgcctctctgtatagttctttggctcctcatgtccgttataacctggctagtt
LA16 #39	9240
NC2 #3	9240
MHV IC NC_001846	9301	caaatggttatatacgttttcccgaagtggtagtgaaggcattgtgcgtggttgcgca
LA16 #39	9300
NC2 #3	9300
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LA16 #39	9360
NC2 #3	9360
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LA16 #39	9420
NC2 #3	9420
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LA16 #39	9480
NC2 #3	9480
MHV IC NC_001846	9541	ttgatttctttgccttaacggcgagttcagtggtggtgctatccttgcaattattgtcg
LA16 #39	9540
NC2 #3	9540
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LA16 #39	9600
NC2 #3	9600

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LA16 #39	9660
NC2 #3	9660
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LA16 #39	9720
NC2 #3	9720
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NC2 #3	9780
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LA16 #39	9840
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NC2 #3	9900
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NC2 #3	9960g.....
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NC2 #3	10020	...g.....
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NC2 #3	10080
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NC2 #3	10140
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LA16 #39	10200
NC2 #3	10200
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LA16 #39	10260
NC2 #3	10260
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LA16 #39	10320
NC2 #3	10320a
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LA16 #39	10380
NC2 #3	10380
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LA16 #39	10440
NC2 #3	10440
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LA16 #39	10500
NC2 #3	10500

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LA16 #39	10560
NC2 #3	10560
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LA16 #39	10620
NC2 #3	10620
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NC2 #3	10680
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NC2 #3	10740
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LA16 #39	10800
NC2 #3	10800
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LA16 #39	10860
NC2 #3	10860
MHV IC NC_001846	10921	gttttagctcaatcaaagccgatcttgtcttgatgcgcttgcttctatgacagggcgta
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NC2 #3	10920t.....
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LA16 #39	10980
NC2 #3	10980
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LA16 #39	11040
NC2 #3	11040
MHV IC NC_001846	11101	ctgggtgcaagctacagtcaaagcgcacaagagttataaaagggtacatggtgctggatat
LA16 #39	11100
NC2 #3	11100
MHV IC NC_001846	11161	tggcttcaacgttttgttctgtagcattatctcagcatttgtaaaatggactatgttta
LA16 #39	11160
NC2 #3	11160
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LA16 #39	11220
NC2 #3	11220
MHV IC NC_001846	11281	ctatggtggtgatcaagcataagcatttgtatttaactatgtatattatgctgtgttat
LA16 #39	11280
NC2 #3	11280
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LA16 #39	11340
NC2 #3	11340
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LA16 #39	11400
NC2 #3	11400

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NC2 #3	11460
MHV IC NC_001846	11521	tcttttctattatgttcttgggtgtagacttgtcagcctgggatccatgtggatatttg
LA16 #39	11520
NC2 #3	11520
MHV IC NC_001846	11581	gagccaatttagaggaagaggtactattgttcctcacatccctatttggcacgtacacat
LA16 #39	11580
NC2 #3	11580
MHV IC NC_001846	11641	ggactactatggtgtcattggctaccgctaaggttattgctaaatggttggctgtgaatg
LA16 #39	11640
NC2 #3	11640
MHV IC NC_001846	11701	tcttgtacttcacagacgtaccgcaaattaaattagttcttttgagctacttgtgtattg
LA16 #39	11700
NC2 #3	11700
MHV IC NC_001846	11761	gttatgtgtgttgttattggggaatcttgtcactccttaatagcatttttaggatgc
LA16 #39	11760
NC2 #3	11760
MHV IC NC_001846	11821	cattgggcgtctacaattataaaaatctccgttcaggagttacgttatatgaatgctaag
LA16 #39	11820
NC2 #3	11820
MHV IC NC_001846	11881	gcttgcgccacctagaaatagttttgaggccctgatgcttaattttaagctgttgggaa
LA16 #39	11880
NC2 #3	11880
MHV IC NC_001846	11941	ttggtgggtgtgccagtcattgaagtatctcaaattcaatcaagattgacggatgttaaat
LA16 #39	11940
NC2 #3	11940
MHV IC NC_001846	12001	gtgctaattgtgtgttgccttaattgcctccagcacttgcatattgcatctaattctaagt
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NC2 #3	12120
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LA16 #39	12180
NC2 #3	12180
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NC2 #3	12240
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LA16 #39	12300
NC2 #3	12300

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LA16 #39	12420
NC2 #3	12420
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NC2 #3	12480
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LA16 #39	12540
NC2 #3	12540
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LA16 #39	12600
NC2 #3	12600
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NC2 #3	12720
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LA16 #39	12900
NC2 #3	12900
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LA16 #39	12960
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LA16 #39	13080
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NC2 #3	13200

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LA16 #39	13440
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NC2 #3	13500
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NC2 #3	13620
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NC2 #3	13920
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NC2 #3	14220
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LA16 #39	14340
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LA16 #39	14400
NC2 #3	14400
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LA16 #39	14640
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LA16 #39	14760
NC2 #3	14760
MHV IC NC_001846	14821	ttatgagthttatthttgagtaaaaggcctgctthaaagaggggagctccgthttgatttgaagca
LA16 #39	14820
NC2 #3	14820
MHV IC NC_001846	14881	cttcttctttacgcaggatgthtaagctgcttactgattataattattacaagtataa
LA16 #39	14880
NC2 #3	14880
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NC2 #3	15000

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NC2 #3	15060
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NC2 #3	15300
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LA16 #39	15360
NC2 #3	15360
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LA16 #39	15420
NC2 #3	15420
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LA16 #39	15480
NC2 #3	15480
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NC2 #3	15660
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LA16 #39	15720
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LA16 #39	16020
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NC2 #3	16260
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NC2 #3	16380
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LA16 #39	16440
NC2 #3	16440
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LA16 #39	16500
NC2 #3	16500
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LA16 #39	16560
NC2 #3	16560
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LA16 #39	16620
NC2 #3	16620
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LA16 #39	16740
NC2 #3	16740
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NC2 #3	16860
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LA16 #39	16920
NC2 #3	16920
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LA16 #39	17040
NC2 #3	17040
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LA16 #39	17100
NC2 #3	17100
MHV IC NC_001846	17161	ttatcagcacattggaatgaagcgctattgtactgtacagggaccgcctggtagtggtaa
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NC2 #3	17160
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LA16 #39	17220
NC2 #3	17220
MHV IC NC_001846	17281	tgctagccatgctgcagttgacgcgctgtgtgaaaaggcacataaatttttaaatattaa
LA16 #39	17280
NC2 #3	17280
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LA16 #39	17340
NC2 #3	17340
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LA16 #39	17400
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LA16 #39	17460
NC2 #3	17460
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LA16 #39	17640
NC2 #3	17640
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LA16 #39	17880
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NC2 #3	18120
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LA16 #39	18180
NC2 #3	18180
MHV IC NC_001846	18241	tgatgacaaatataaggtaggcggtgatttagccgtttgacctaatggtgctgattctgc
LA16 #39	18240
NC2 #3	18240
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LA16 #39	18300
NC2 #3	18300
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LA16 #39	18360
NC2 #3	18360
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LA16 #39	18420
NC2 #3	18420
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LA16 #39	18480
NC2 #3	18480
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LA16 #39	18540
NC2 #3	18540
MHV IC NC_001846	18601	ccttatcccacttatgtcaagagggcagaaatgggatgtgggttcgaattagaatagtaca
LA16 #39	18600
NC2 #3	18600

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NC2 #3	18660t.....
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LA16 #39	18720
NC2 #3	18720
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NC2 #3	18780
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NC2 #3	18960
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NC2 #3	19080
MHV IC NC_001846	19141	gtgttatgacattggcaaccctaaaggcttgcctgtgtcaaaggatatgattttaagtt
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NC2 #3	19140
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LA16 #39	19200
NC2 #3	19200
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NC2 #3	19260
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NC2 #3	19320
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LA16 #39	19380
NC2 #3	19380
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LA16 #39	19440
NC2 #3	19440
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NC2 #3	19500

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NC2 #3	19560
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LA16 #39	19620
NC2 #3	19620
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LA16 #39	19680
NC2 #3	19680
MHV IC NC_001846	19741	gtataatttggccaatgctggacactttgatggccggggggggaactgccttgctgtgt
LA16 #39	19740
NC2 #3	19740
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NC2 #3	19800
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LA16 #39	19860
NC2 #3	19860
MHV IC NC_001846	19921	ccccgagcttaagctctttagaaatttgaatattgacgtgtgctggagtcacgtccttg
LA16 #39	19920
NC2 #3	19920
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LA16 #39	20220
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NC2 #3	20400

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NC2 #3	20820
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LA16 #39	20940
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LA16 #39	21000
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LA16 #39	21300
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LA16 #39	21540
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LA16 #39	21720
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LA16 #39	22200
NC2 #3	22200

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LA16 #39	22380
NC2 #3	22380
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LA16 #39	22440
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LA16 #39	22560
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LA16 #39	22620
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NC2 #3	22800
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LA16 #39	22920
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NC2 #3	22980
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NC2 #3	23362
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NC2 #3	23542
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NC2 #3	23962c

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LA16 #39	24259
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NC2 #3	24382
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LA16 #39	24439
NC2 #3	24442
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NC2 #3	24502
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NC2 #3	24562
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NC2 #3	24622
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NC2 #3	24682
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NC2 #3	24742
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NC2 #3	24802
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LA16 #39	24979
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NC2 #3	25102
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NC2 #3	25222
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NC2 #3	25402
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LA16 #39	25459
NC2 #3	25462
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NC2 #3	25522
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LA16 #39	25579
NC2 #3	25582
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LA16 #39	25639
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NC2 #3	26062
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LA16 #39	26479
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NC2 #3	26602
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NC2 #3	26662

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NC2 #3	26722
MHV IC NC_001846	26820	tgtgcttagtgagaaccaaagatgattgctagtgttttaacaatgcgctgggtgctat
LA16 #39	26779
NC2 #3	26782
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NC2 #3	26842
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NC2 #3	27022
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NC2 #3	27082
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NC2 #3	27142
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NC2 #3	27202
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NC2 #3	27262
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NC2 #3	27322
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NC2 #3	27382
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NC2 #3	27442
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NC2 #3	27502
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NC2 #3	27562

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NC2 #3	27622
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LA16 #39	27679
NC2 #3	27682
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LA16 #39	27739
NC2 #3	27742
MHV IC NC_001846	27840	tgatgagtatggaggacaccaggacagtattgtgatacataatatttcctctcatgagga
LA16 #39	27799
NC2 #3	27802
MHV IC NC_001846	27900	ttgactatcacagcctctcctggaagacagaaaatctaacaatttatagcattctcat
LA16 #39	27859
NC2 #3	27862
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LA16 #39	27919t.....
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LA16 #39	27979
NC2 #3	27982
MHV IC NC_001846	28080	at ttattgcaattgcaagttcaaatttttcatgttaaggataccatacgtgtgactggca
LA16 #39	28039
NC2 #3	28042
MHV IC NC_001846	28140	agccagccactgtgtcttatactacaagtacaccagtaacaccgagcgcgacgacgctcg
LA16 #39	28099
NC2 #3	28102
MHV IC NC_001846	28200	atggactacgtatactttaattagaccactagctcttatacaagagtttatcttggtg
LA16 #39	28159
NC2 #3	28162
MHV IC NC_001846	28260	ctccaagagggttttgattatagtacatttgggcctaagaccctagattatgttactaatc
LA16 #39	28219
NC2 #3	28222
MHV IC NC_001846	28320	taaacctcatcttaattctggtcgtccatatacttttaaggcattgtccaggcatatgag
LA16 #39	28279
NC2 #3	28282
MHV IC NC_001846	28380	accaacagccacatggatttggcatgtgagtgatgcatggttacgccgcacgcgggactt
LA16 #39	28339
NC2 #3	28342
MHV IC NC_001846	28440	tggtgctattcgccctagaagatttttggtttcaatttaattatagccaaccccagttgg
LA16 #39	28399
NC2 #3	28402
MHV IC NC_001846	28500	ttattgtagagttcctttaaggcttgggtgtagcaaccagggtaaatttgcagcgcagtt
LA16 #39	28459
NC2 #3	28462

MHV IC NC_001846	28560	taccctaaaaagtgcgaaaaaccagggtcacgaaaaatttactagcttcacggccta
LA16 #39	28519
NC2 #3	28522
MHV IC NC_001846	28620	cggcagaactgtccaacaggccgtagcaagttagtagaagaagctggtgattttattct
LA16 #39	28579
NC2 #3	28582
MHV IC NC_001846	28680	ttttagggccacgcagctcgaaagaaatgtttaatttattccttacagacacagtatggt
LA16 #39	28639
NC2 #3	28642
MHV IC NC_001846	28740	atgtggggcagattatTTTTatattcgagtggttgatgggtcaccataattgtgggtg
LA16 #39	28699
NC2 #3	28702
MHV IC NC_001846	28800	ccttccttgctctatcaaactttgtattcaactttgcggttatgtaatactttggtgc
LA16 #39	28759
NC2 #3	28762
MHV IC NC_001846	28860	tgtccccttctatttatttgtatgataggagtaagcagctttataagtattataatgaag
LA16 #39	28819
NC2 #3	28822
MHV IC NC_001846	28920	aaatgagactgccctattagagggtggatgatataatcctaaacattatgagtagtact
LA16 #39	28879c.....
NC2 #3	28882c.....
MHV IC NC_001846	28980	actcaggccccagagcccgctctatcaatggacggccgacgaggcagttcaattccttaag
LA16 #39	28939
NC2 #3	28942
MHV IC NC_001846	29040	gaatggaacttctcgttgggcattatactactctttattactatcatactacagttcgggt
LA16 #39	28999
NC2 #3	29002
MHV IC NC_001846	29100	tacacgagccgtagcatgtttatttatggttgaaaaatgataatcttggtggttaatgtgg
LA16 #39	29059
NC2 #3	29062
MHV IC NC_001846	29160	ccactgactattgtttgtgtattttcaattgcgtgatgcgctaaataatgtgtatcct
LA16 #39	29119
NC2 #3	29122
MHV IC NC_001846	29220	ggattttctatagtgttactatagtgtccattgtaatctggattatgtattttgtaat
LA16 #39	29179
NC2 #3	29182
MHV IC NC_001846	29280	agcataaggttgtttatcaggactggttagctggtggagcttcaacccccgaaacaaacaac
LA16 #39	29239
NC2 #3	29242
MHV IC NC_001846	29340	cttatgtgtatagatatgaaaggtagcgtgtatgtagaccattattgaggattacat
LA16 #39	29299
NC2 #3	29302
MHV IC NC_001846	29400	acactaacagccactattattcgtggccacctctacatgcaaggtgtaagctaggcacc
LA16 #39	29359
NC2 #3	29362

MHV IC NC_001846	29460	ggtttctctttgtctgacttgcccgttatgttacagttgctaaggtgtcacacctttgc
LA16 #39	29419
NC2 #3	29422
MHV IC NC_001846	29520	acttataagcgcgcatctcttagacaaggtagacggtgtagcggttttgcgtttatgtg
LA16 #39	29479
NC2 #3	29482
MHV IC NC_001846	29580	aagtccaaggtcggaaattaccgactgccctcaaacaaaccgagtggcgcggacaccgca
LA16 #39	29539
NC2 #3	29542
MHV IC NC_001846	29640	ttgttgagaatctaataactttaaggatgtctttgttcctgggcaagaaaatgccg
LA16 #39	29599c.....
NC2 #3	29602c.....
MHV IC NC_001846	29700	gtggcagaagctcctctgtaaaccgcgctggtaatggaatcctcaagaagaccacttggg
LA16 #39	29659
NC2 #3	29662
MHV IC NC_001846	29760	ctgaccaaaccgagcgtggaccaaataatcaaatagaggcagaaggaatcagccaaagc
LA16 #39	29719
NC2 #3	29722
MHV IC NC_001846	29820	agactgcaactactcaacccaactccgggagtgtggttccccattactcctggtttctg
LA16 #39	29779
NC2 #3	29782
MHV IC NC_001846	29880	gcattaccagttccaaaagggaaaggagtttcagtttgagaaggacaaggagtgccta
LA16 #39	29839
NC2 #3	29842
MHV IC NC_001846	29940	ttgccaatggaatccccgcttcagagcaaaagggatattggtatagacacaaccgccgtt
LA16 #39	29899
NC2 #3	29902
MHV IC NC_001846	30000	cttttaaacacctgatgggcagcagaagcaattactgccagatgggtattttactatc
LA16 #39	29959
NC2 #3	29962
MHV IC NC_001846	30060	ttggcacagggccccatgctggagccagttatggagacagcattgaaggtgtcttctggg
LA16 #39	30019a.....
NC2 #3	30022a.....
MHV IC NC_001846	30120	ttgcaaacagccaagcggacaccaatacccgctctgatattgtcgaaagggaccaagca
LA16 #39	30079
NC2 #3	30082
MHV IC NC_001846	30180	gtcatgaggctattcctactaggttgcgcccggcacggattgcctcagggttttatg
LA16 #39	30139
NC2 #3	30142
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LA16 #39	30199
NC2 #3	30202g.....
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LA16 #39	30259
NC2 #3	30262

MHV IC NC_001846	30360	ctgatatggccgaagaaattgctgctcttgttttgctaagctcggtaaagatgccggcc
LA16 #39	30319
NC2 #3	30322
MHV IC NC_001846	30420	agcccaagcaagtaacgaagcaaagtgccaaagaagtcaggcagaaaattttaacaagc
LA16 #39	30379
NC2 #3	30382
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LA16 #39	30439
NC2 #3	30442
MHV IC NC_001846	30540	gccccaatcagaattttgaggctctgaaatgttaaaacttggaaactagtgatccacagt
LA16 #39	30499
NC2 #3	30502	.t.....
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LA16 #39	30559
NC2 #3	30562
MHV IC NC_001846	30660	aattgggtcaaaaagaattctgggtggtgctgatgaaccaccaagatgtgtatgagctgc
LA16 #39	30619
NC2 #3	30622
MHV IC NC_001846	30720	aatattcaggtgcagttagatttgatagtagtactctacctggttttgagactatcatgaaag
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NC2 #3	30682
MHV IC NC_001846	30780	tgttgaatgagaatttgaatgcctaccagaaggatgggtgggtgcagatgtgggtgagcccaa
LA16 #39	30739
NC2 #3	30742
MHV IC NC_001846	30840	agccccaagaaaagggcgtagacaggctcaggaaaagaaagatgaagtagataatgtaa
LA16 #39	30799
NC2 #3	30802
MHV IC NC_001846	30900	gcggtgcaaagcccaaaagctctgtgacgcaaatgtaagtagagaattaaccccagagg
LA16 #39	30859
NC2 #3	30862
MHV IC NC_001846	30960	atagaagtctgttggctcagatccttgatgatggcgtagtgccagatgggttagaagatg
LA16 #39	30919
NC2 #3	30922
MHV IC NC_001846	31020	actctaattgtgaaagagaatgaatcctatgtcggcgctcggtggtaaccctcgcgaga
LA16 #39	30979
NC2 #3	30982
MHV IC NC_001846	31080	aagtcgggataggacactctctatcagaatggatgtcttgctgtcataacagatagagaa
LA16 #39	31039
NC2 #3	31042
MHV IC NC_001846	31140	ggttgtggcagaccctgtatcaattagttgaaagagattgcaaatagagaatgtgtgag
LA16 #39	31099
NC2 #3	31102
MHV IC NC_001846	31200	agaagttagcaaggtcctacgtctaaccataagaacggcgataggcgccccctgggaaga
LA16 #39	31159
NC2 #3	31162

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MHV IC NC_001846 31260 gctcacatcagggtactattcctgcaatgccctagtaaataaatgaatgaagttgatcatggcc
LA16 #39         31219 .....
NC2 #3          31222 .....

MHV IC NC_001846 31320 aattggaaga-atcacaaaaaaaaaaaaaaaaaaaaaaaa-----
LA16 #39         31279 .....t.....aaaaaaaaaaaaaaaaaaaaaaaa
NC2 #3          31282 .....t.....aaaaaaaaaaaaaaaaaaaaaaaa

MHV IC NC_001846 -----
LA16 #39         31339 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaa-
NC2 #3          31342 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
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REFERENCE LIST

1. Taubenberger, J. K. & Morens, D. M. 1918 Influenza: the Mother of All Pandemics. *Emerg. Infect. Dis.* **12**, 15–22 (2006).
2. WHO | Number of deaths due to HIV. *WHO* (2017).
3. WHO | Middle East respiratory syndrome coronavirus (MERS-CoV) – Saudi Arabia. *WHO* (2016).
4. WHO | Summary of probable SARS cases with onset of illness from 1 November 2002 to 31 July 2003. *WHO* (2015).
5. Bradburne, A. F., Bynoe, M. L. & Tyrrell, D. A. Effects of a ‘new’ human respiratory virus in volunteers. *Br. Med. J.* **3**, 767–9 (1967).
6. Hamre, D. & Procknow, J. J. A new virus isolated from the human respiratory tract. *Proc. Soc. Exp. Biol. Med.* **121**, 190–3 (1966).
7. Monto, A. S. Medical reviews. Coronaviruses. *Yale J. Biol. Med.* **47**, 234–51 (1974).
8. Chan, J. F. W. *et al.* Middle East respiratory syndrome coronavirus: another zoonotic betacoronavirus causing SARS-like disease. *Clin. Microbiol. Rev.* **28**, 465–522 (2015).
9. Yang, D. & Leibowitz, J. L. The structure and functions of coronavirus genomic 3’ and 5’ ends. *Virus Res.* **206**, 120–33 (2015).
10. Pasternak, A. O., Spaan, W. J. M. & Snijder, E. J. Nidovirus transcription: how to make sense...? *J. Gen. Virol.* **87**, 1403–21 (2006).
11. de Wit, E., van Doremalen, N., Falzarano, D. & Munster, V. J. SARS and MERS: recent insights into emerging coronaviruses. *Nat. Rev. Microbiol.* **14**, 523–534 (2016).
12. Fehr, A. R. & Perlman, S. Coronaviruses: an overview of their replication and pathogenesis. *Methods Mol. Biol.* **1282**, 1–23 (2015).
13. Perlman, S. & Netland, J. Coronaviruses post-SARS: update on replication and pathogenesis. *Nat. Rev. Microbiol.* **7**, 439–50 (2009).
14. Zhu, X., Liu, Q., Du, L., Lu, L. & Jiang, S. Receptor-binding domain as a target for developing SARS vaccines. *J. Thorac. Dis.* **5 Suppl 2**, S142-8 (2013).
15. Calisher, C. H., Childs, J. E., Field, H. E., Holmes, K. V & Schountz, T. Bats: important reservoir hosts of emerging viruses. *Clin. Microbiol. Rev.* **19**, 531–45 (2006).
16. Eckerle, L. D. *et al.* Infidelity of SARS-CoV Nsp14-exonuclease mutant virus replication

- is revealed by complete genome sequencing. *PLoS Pathog.* **6**, e1000896 (2010).
17. Snijder, E. J. *et al.* Unique and conserved features of genome and proteome of SARS-coronavirus, an early split-off from the coronavirus group 2 lineage. *J. Mol. Biol.* **331**, 991–1004 (2003).
 18. Menachery, V. D., Graham, R. L. & Baric, R. S. Jumping species—a mechanism for coronavirus persistence and survival. *Curr. Opin. Virol.* **23**, 1–7 (2017).
 19. Fong, I. W. Emerging Animal Coronaviruses: First SARS and Now MERS. in *Emerging Zoonoses* 63–80 (Springer International Publishing, 2017). doi:10.1007/978-3-319-50890-0_4
 20. Anthony, S. J. *et al.* A strategy to estimate unknown viral diversity in mammals. *MBio* **4**, e00598-13 (2013).
 21. Luis, A. D. *et al.* A comparison of bats and rodents as reservoirs of zoonotic viruses: are bats special? *Proc. R. Soc. B Biol. Sci.* **280**, 20122753–20122753 (2013).
 22. Wynne, J. W., Wang, L.-F., Cui, J., Field, H. & Holmes, E. Bats and Viruses: Friend or Foe? *PLoS Pathog.* **9**, e1003651 (2013).
 23. Mandl, J. N. *et al.* Reservoir Host Immune Responses to Emerging Zoonotic Viruses. *Cell* **160**, 20–35 (2015).
 24. Fong, I. W. *Emerging Zoonoses*. (Springer International Publishing, 2017). doi:10.1007/978-3-319-50890-0
 25. Reshi, M. L., Su, Y.-C. & Hong, J.-R. RNA Viruses: ROS-Mediated Cell Death. *Int. J. Cell Biol.* **2014**, 1–16 (2014).
 26. Zhang, G. *et al.* Comparative Analysis of Bat Genomes Provides Insight into the Evolution of Flight and Immunity. *Science (80-.)*. **339**, (2013).
 27. Zhou, P. *et al.* Contraction of the type I IFN locus and unusual constitutive expression of IFN- α in bats. *Proc. Natl. Acad. Sci. U. S. A.* **113**, 2696–701 (2016).
 28. Zhong, N. S. *et al.* Epidemiology and cause of severe acute respiratory syndrome (SARS) in Guangdong, People's Republic of China, in February, 2003. *Lancet (London, England)* **362**, 1353–8 (2003).
 29. Zaki, A. M., van Boheemen, S., Bestebroer, T. M., Osterhaus, A. D. M. E. & Fouchier, R. A. M. Isolation of a Novel Coronavirus from a Man with Pneumonia in Saudi Arabia. *N. Engl. J. Med.* **367**, 1814–1820 (2012).
 30. Mouse Hepatitis Virus.

31. Boot, R. & Bisgaard, M. Reclassification of 30 *Pasteurellaceae* strains isolated from rodents. *Lab. Anim.* **29**, 314–319 (1995).
32. Barthold, S. W. & Smith, A. L. Viremic dissemination of mouse hepatitis virus-JHM following intranasal inoculation of mice. *Arch. Virol.* **122**, 35–44 (1992).
33. Baker, D. G. Natural pathogens of laboratory mice, rats, and rabbits and their effects on research. *Clin. Microbiol. Rev.* **11**, 231–66 (1998).
34. University of Missouri-Comparative Medicine Program and IDEXX-BioReaeasrch. Mouse Hepatitis Virus (MHV). (2013). Available at: <http://dora.missouri.edu/mouse/mouse-hepatitis-virus-mhv/>. (Accessed: 17th August 2017)
35. Coley, S. E. *et al.* Recombinant mouse hepatitis virus strain A59 from cloned, full-length cDNA replicates to high titers in vitro and is fully pathogenic in vivo. *J. Virol.* **79**, 3097–106 (2005).
36. Edgar, R. S. & Lielausis, I. Temperature-sensitive Mutants of Bacteriophage T4D: Their Isolation and Genetic Characterization. *HGenetics* **49**, 649–62 (1964).
37. Edgar, R. S., Denhardt, G. H. & Epstein, R. H. A Comparative Genetic Study of Conditional Lethal Mutations of Bacteriophage T4D. *Genetics* **49**, 635–48 (1964).
38. Complementation and Recombination - Biology LibreTexts. (2016). Available at: [https://bio.libretexts.org/TextMaps/Map%3A_Working_with_Molecular_Genetics_\(Hardison\)/Unit_I%3A_Genes%2C_Nucleic_Acids%2C_Genomes_and_Chromosomes/1%3A_Fundamental_Properties_of_Genes/Complementation_and_Recombination](https://bio.libretexts.org/TextMaps/Map%3A_Working_with_Molecular_Genetics_(Hardison)/Unit_I%3A_Genes%2C_Nucleic_Acids%2C_Genomes_and_Chromosomes/1%3A_Fundamental_Properties_of_Genes/Complementation_and_Recombination). (Accessed: 28th August 2017)
39. Koolen, M. J., Osterhaus, A. D., Van Steenis, G., Horzinek, M. C. & Van der Zeijst, B. A. Temperature-sensitive mutants of mouse hepatitis virus strain A59: isolation, characterization and neuropathogenic properties. *Virology* **125**, 393–402 (1983).
40. Mielech, A. M. *et al.* Murine coronavirus ubiquitin-like domain is important for papain-like protease stability and viral pathogenesis. *J. Virol.* **89**, 4907–17 (2015).
41. Schaad, M. C. *et al.* Genetics of mouse hepatitis virus transcription: identification of cistrons which may function in positive and negative strand RNA synthesis. *Virology* **177**, 634–45 (1990).
42. Dulbecco, R. & Vogt, M. Some problems of animal virology as studied by the plaque technique. *Cold Spring Harb. Symp. Quant. Biol.* **18**, (1953).
43. Hirano, N., Murakami, T., Fujiwara, K. & Matsumoto, M. Utility of mouse cell line DBT

- for propagation and assay of mouse hepatitis virus. *Jpn. J. Exp. Med.* **48**, 71–5 (1978).
44. Padmanabhan, A. Genomic Deep Sequencing of LA16 and NC2. *Kansas State University Integrated Genomics Facility* (2017).
 45. Donaldson, E. F., Graham, R. L., Sims, A. C., Denison, M. R. & Baric, R. S. Analysis of murine hepatitis virus strain A59 temperature-sensitive mutant TS-LA6 suggests that nsp10 plays a critical role in polyprotein processing. *J. Virol.* **81**, 7086–98 (2007).
 46. Smith, E. C. *et al.* Mutations in coronavirus nonstructural protein 10 decrease virus replication fidelity. *J. Virol.* **89**, 6418–26 (2015).

VITA

The author, Amani T. Eddins, was born in Dekalb, IL on August 10, 1992 to Trevell and Brenda Eddins. She attended Hampton University in Hampton, Virginia where she earned her Bachelor's of Science, *cum laude*, in Cellular and Molecular Biology in May 2014. After graduation Amani participated in a post-baccalaureate program at the University of Chicago in Chicago, IL. While attending the University of Chicago, Amani worked in the virology lab of Glenn Randall, PhD. where she participated in Hepatitis C and Dengue Virus research. It was there under the mentorship of Dr. Randall and a Loyola University alumni Dr. Anna Shulla that urged Amani to pursue an advanced degree in Microbiology and Immunology.

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