GENERATION of NOVEL RANDOM MUTAGENESIS LIPASE LIBRARIES via DIRECTED EVOLUTION

by

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via
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Abstract

Lipases (triacylglycerol acylhydrolases, EC 3.1.1.3) function as significant biocatalysts in biotechnological applications. The fact that their mechanism, selectivity and structure is well known make lipases a suitable candidate for studies of protein engineering and directed evolution. Using the merits of DNA shuffling method, directed evolution and random mutagenesis,libraries of mutant lipases are constructed with improved features and functionality of pre-existing ones, which in turn encourages the use of industrial lipases in applications such as biosensors, pharmaceuticals, agrochemicals, bioremediation, etc. With increasing demand on lipase production for commercial use, it has thus become crucial to identify and isolate novel and target-specific lipases, as well as optimizing existing ones for acquisition of desired functionality. The aim of this study is to generate mutant lipase libraries using directed evolution and to screen for a candidate biocatalyst. There are two lipases of interest, the mesophilic *Aspergillus niger* lipase (ANL) and the thermophilic *Bacillus thermocatenulatus* lipase (BTL), which were shuffled in order to obtain a mutant library that would have the desired features such as increased thermostability, pH stability and a broader range of substrate specificity.

Yönlendirilmiş evrim metodu ile yeni, rastgele mutasyona uğratılmış lipaz kütüphanelerinin oluşturulması.

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Anahtar Kelimeler : DNA karma metodu, Yönlendirilmiş evrim, Endüstriyel lipazlar, Rastgele Mutasyon Yöntemi

Özet

Lipazlar (triasilgliserol asilhidrolaz EC 3.1.1.3), biyoteknolojik uygulamalarda etkili rol oynayan biyokatalizörlerdir. Mekanizmaları, seçicilikleri ve yapıları bilindiği için, protein mühendisliği ve yönlendirilmiş evrim metodlarına uygun adaylardır. DNA karma metodu, yönlendirilmiş evrim ve rastgele mutajenez tekniklerinin bir arada kullanılabilmesi, istenilen özelliklere sahip mutant lipaz kütüphanelerinin oluşturulabilmesine imkan tanımıştır. Bu durum, lipazlarin aynı zamanda biyosensör, ilaç, tarım endüstrilerinde kullanılmasına olanak sağlamıştır. Lipazların ticari kullanımına karşı artan talep sonucu yeni ve hedefe özgün lipazların tanımlanması ve izole edilmesi kritik önem taşımaktadır. Bu tez, yönlendirilmiş evrim tekniğiyle mutant lipaz kütüphanelerinin oluşturulmasını hedef almakla beraber, aday biyokatalizörlerin analizini yapmayı amaçlamaktadır. Bunun için, fungal ve mezofilik bir lipaz olan *Aspergillus niger* lipazı (ANL) ile bakteriyel ve termofilik bir lipaz olan *Bacillus thermocatenulatus* lipazı (BTL) DNA karma metodu ile karıtırılmıştır. Rastgele mutajene olacak olan enzimlerin, termostabilite, pH stabilite ve sübstrat seçiciliğinde artı göstermesi ve endüstriyel ve biyokteknolojik uygulamalarda önemli bir lipaz olması öngörülmektedir. Elde edilen klonlarda, sübstrat seçiciliği değişikliği görülmemekle beraber, enzimlerin genel aktivitelerinde belirli değişiklikler saptanmış, ve bu özellikler yapısal boyutta tartışılmıştır.

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To ones who are close to the heart.

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1 Introduction

1 .1 Lipases

Lipases are metabolic enzymes which are involved in every domain of life. Animals, plants and microorganisms are all producing various types of lipases. Lipases were discovered by Eijkmann in 1900s. This discovery was simply the observation of several bacteria that can produce and secrete lipases and the degradation of lipids via these produced enzymes. Microbial enzymes are one of the largest enzyme class due to the large variety of known microbes and therefore lipases are one of the most studied enzyme class as well. Since lipases have been studied sweepingly, their mechanism of action, selectivity and structure are already well known [1, 2].

Lipases (triacylglycerol acylhydrolases; EC 3.1.1.3) function as biocatalysts to hydrolyze triglycerides into glycerol and fatty acids on water-insoluble substrates [3].They actively have a role on the digestion, transportation and processing of triglycerides. It is well known fact that bacteria, yeast and fungi share a high potential on the production of lipases. Since lipases which are produced from different types of microorganisms have specific features in terms of substrate specificity, heat resistance thresholds and wide pH range, these features make them efficient in terms of selectivity through many industrial

applications such as biosensors, pharmaceuticals, cosmetics, agrochemicals, bioremediation etc. Lipases have been used on numerous studies, ranging from industrial production and immobilization techniques, to the analysis of pure enzymes and their biocatalytical features [4]. For instance, lipase-detergent compounds are used to clean surface fatty residues and clogged drains [5].

As well as being lipolytic, lipases have the capability to perform esterification. This combined feature enables them to be effective under wide substrate range [6]. With increasing demand on lipase production for commercial use, it has become crucial to identify and isolate novel and target-specific lipases, as well as optimizing existing ones for acquisition of desired functionality. Nowadays, this can be achieved by directed evolution techniques, and it is heavily relied upon [7]. By means of directed evolution, it is aimed to improve features and functionality of pre-existing lipases, both with time and cost efficiency. DNA shuffling is a widely used technique, serving as a fundamental method for studies in directed evolution.

Since properties of lipases are mainly strain-dependent, the catalytic properties and functional parameters are crucial for design and application procedures, including thermostability, specificity, optimum pH and enantioselectivity. For instance, *Aspergillus niger* lipase (ANL) is one of the significant biocatalysts used in industrial food processing and production, utilized as food and detergent additive, as well as in cellulose acetylation [8]. ANL shows regio-selectivity on its first and third position, towards glycerol binding site. Because of this, this lipase has proven to be safe for utilization in food and pharmaceutical industry [9]. The thermoalkalophilic lipase, *Bacillus thermocatenulatus* lipase 2 (BTL2), on the other hand, is an enantioselective biocatalyst which shows considerably high resistance and stability at elevated temperatures and organic solvents, making it a hub for industrial and biotechnological applications [10]. Quyen *et.al*, (2002) have successfully produced the recombinant BTL lipase out of both *Pichia pastoris* and *E.coli* and performed enzyme characterization [11].

1 .2 Reaction

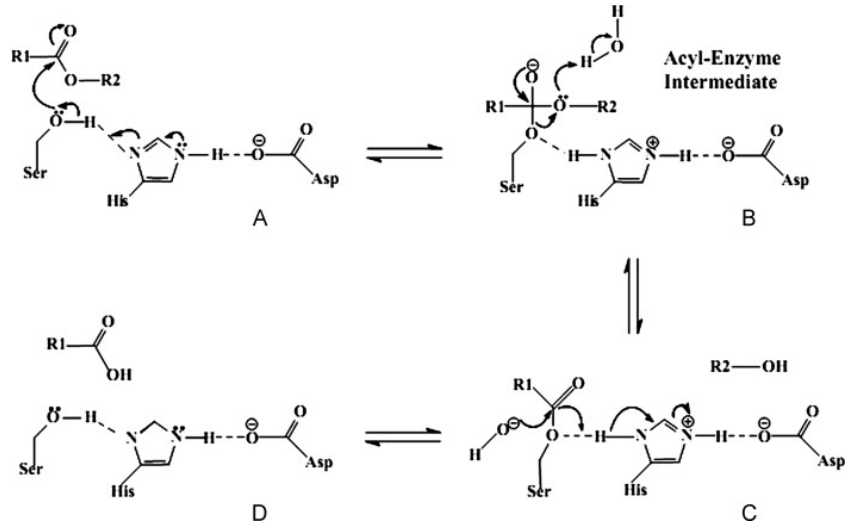
The hydrolysis of triacylglycerols to free fatty acids, diacylglycerols, monoacylglycerols and glycerol is catalyzed by lipases. This breakdown reaction is an equilibrium reaction, which can be disturbed by changing the concentration of substrates or products. One of the reactants of hydrolysis reaction is water. Therefore, changing the hydrolytic conditions of the hydrolysis causes a shift of the equilibrium [12].

Either by breaking as in hydrolysis or by forming as in esterification, lipases act on carboxylic ester bonds. The acyl transfer reactions through esterification are also catalyzed by lipases. Triacylglycerols are commonly their natural substrates, depending on the chemical properties of the reactants and the amount of water in the medium [13].Under low water conditions, a carboxyl/thiolester or amide can also be formed. An ester group, serving as an acyl donor, can form an acyl-enzyme intermediate by either releasing an acid, in this case acyl acceptor would be water, or by forming a new ester and in that case acyl acceptor would be alcohol/thiol/amine. In addition, acidolysis, alcoholysis, aminolysis and interesterification can be given as examples to transesterification.

1 .3 Mechanism

Although lipases catalyze many versatile reactions, the reaction mechanisms are distinctive. In all lipases, the catalytic machinery is conserved and it is composed of three residues, which are serine, histidine and aspartate/glutamate [14]. Two residues (histidine and aspartate/glutamate) are aligned in order to lower the pKa of the serine hydroxyl, so that serine can carry out a nucleophilic attack on the ester bond. The acyl donor, the substrate, interacts with the active site of the lipase, forming the enzyme-substrate (ES) complex. The hydroxyl group of serine is activated by the histidine in the catalytic triad. Serine carries out a nucleophilic attack on the carbonyl carbon of the substrate, so that the first tetrahedral intermediate is formed. The main-chain amide groups of two residues generate a hole and the negative charge on the oxyanion is stabilized. The aspartate or glutamate stabilize the positive charge on the histidine. The tetrahedral intermediate is

then decomposed into another intermediate which is determined by the first leaving group of the substrate (an alcohol or an acyl enzyme intermediate). A second tetrahedral intermediate is formed right after the formation of the acyl enzyme intermediate. Newly formed intermediate corresponds to the highest energy barrier in the reaction. In order to yield the deacylated-free form of the enzyme and the hydrolysis of the second substrate, an acid, this intermediate is also collapsed. A proton is transfered from the substrate to histidine during the deacylation step.



Scheme 1: Mechanism of hydrolysis by lipases. During Step A, His residue acts as a general base and removes a proton from the active site of Ser. In Step B, an acyl-enzyme intermediate is formed, followed by the deacetylation (Step C). With a nucleophile attacking the acetylated enzyme, the catalytic site is regenerated and a long-chain fatty acid is formed as a product (Step D). [15]

1 .4 Selectivity

Lipase selectivity towards Triacylglycerols (TAGs) is generally categorized as regio-selectivity, stereo-selectivity and substrate selectivity [16, 17]. Regio-selectivity is related to the position of the ester bond in TAG, whereas stereo-selectivity is related to the chiral center. Substrate selectivity is related to the type and chain-length.

1 .4.1 Substrate Selectivity

Lipases show selectivity regarding to the type and the chain-length of the acyl groups in their substrates. They can differ in terms of certain fatty acids or groups of fatty acids. For instance, porcine is a lipase with specificity to cis-2 over cis-7 octadecenoyl moiety [2]. Moreover, the lipases most preferred substrate is primary alcohols and the least preferred is tertiary alcohols [5]. Lipases are also able to accommodate cyclic esters, thioesters and amines apart from triacylglycerols and aliphatic esters [18–20]. The chain-length selectivity of lipases has been the subject of many studies [21–24]. Lipases mostly prefer a range of medium (C6) to long (C16) chain-length with respect to the chain-length of fatty acids [2]. However, there are some exceptions to this generalization such as *Penicillum roquefortti* and *Bacillus thermocatenulatus* lipases and they hydrolyze only short chains of C4.

1 .5 Structure

In 1990, the first lipase structure was crystallized by Brady [14]. In protein data bank, there are more than one hundred 3D lipase structures available. According to these studies, some common features of all lipases are determined. One of the common features is that all lipases are among the members of α-β (hydolase fold so that lipase structures are composed of central sheets and surrounding helices [25–28]. Another one is that, in a hairpin turn between an -helix and -helix or -sheet is placed the catalytic serine in lipases. A highly conserved penta-peptide sequence of G-X-S-X-G is also found in this region. This sequence forms a characteristic turn, which is referred as the nucleophilic elbow [9, 26, 27]. Moreover, the active sites in lipases consist of three amino acids, ser-

ine, histidine and aspartic/glutamic acid, which is common to another class of hydrolases, serine-protease [14,29]. Compared to proteases, the structural arrangement of the residues in active site is oriented to invert the stereochemistry of the catalytic triad in lipases, although they have the same chemistry for their active sites [30]. There is an amphiphilic lid found covering the active site of lipases [31, 32]. The composition and size of the lid structure differs from lipase to lipase. The lid from the lipase of guinea pig has only five amino acids where the lid from *Bacillus thermocatenulatus* lipase has two -helices which corresponds to 20% of the whole lipase structure [28, 33].

In addition to the given features of lipase structures, the catalytic cleft in lipases are attributed to specificity. The lipase clefts, fatty acid binding sites in particular, have been investigated and it came out that there are three different geometry that lipase structures may exhibit; crevice-like, funnel-like and tunnel-like [34]. These differences in the binding pockets is related to the diverse substrate specificities in lipases. Additionally, stereoselectivity depends on the steric interaction of the cleft with the substrate, so lipase structure is also critical for understanding the stereoselectivity [35].

1 .6 Lipase in Industry

Enzymes are generally produced from bio-based elements by fermentation so that the enzymes are entirely biodegradable and are able to be revitalized [38]. Lately, there has been many improvements made in the production processes. These have led us that delivering enzyme concentrates at relatively low costs [39] is possible – encouraging enzyme applications in the bulk industrial process.

Since the hydrolysis or production of many esters can be catalyzed by naturally occurring fats and oils, they are the generally favored substrates of lipases [40–43]. With their far-scaled spectrum of substrates, lipases are among the largest class of biocatalysts considering the two coercing enzyme markets which are food processing and detergent industry, are the mainly operations of lipases [42].

Since lipases are able to catalyze reactions in aqueous and in organic media, they are especially tempting for solving challenging synthesis of organic reactions [44]. Lipases are particularly attractive for protein engineering applications because of their broad use in industry consequent to their important products. The extracellular nature of microbial lipases enables them to be produced easily at large quantities and to be isolated and they are the favored source for many industrial applications. Being stable in organic solvents, at high temperatures and ionic strengths, not requiring cofactors and having a wide substrate selectivity and high enantioselectivity are among the main reasons for the high

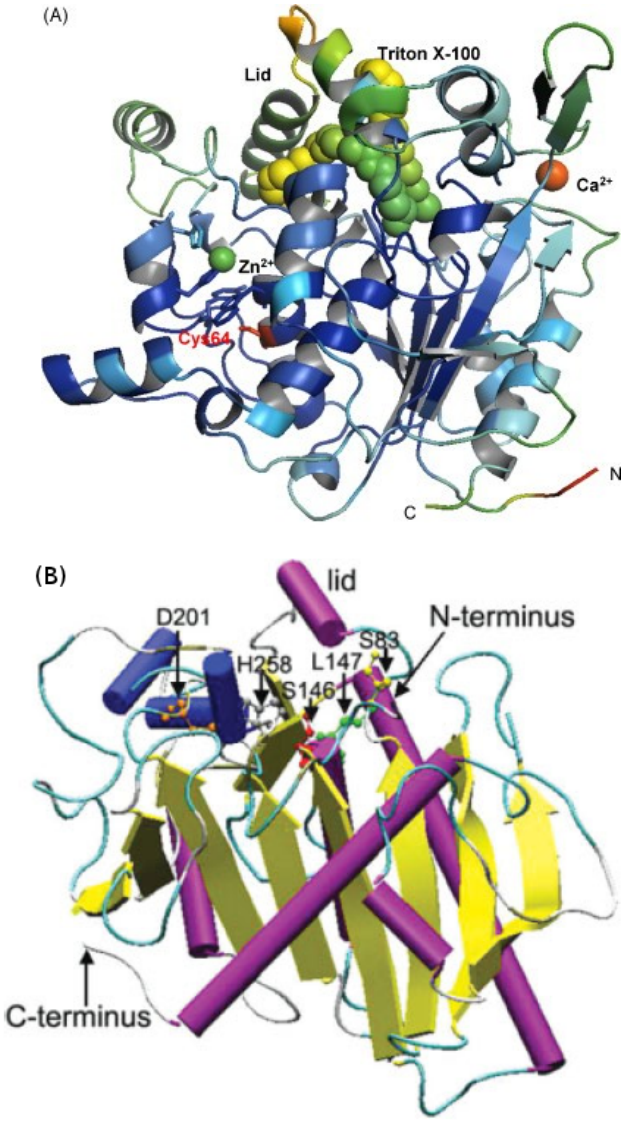


Figure 1: (A) – Structure of mature *Bacillus thermocatenulatus* lipase 2, on which amino and carboxyl termini, Zn^{2+}, Ca^{2+} and cysteine 64 is labeled. [36] (B) – Structure of *Aspergillus niger* lipase by homology modeling [37].

industrial potential of microbial lipases [45]. Large number of articles and reviews studied in the molecular biology, biochemical and structural properties of lipases and their biotechnological applications reflect the tempt in microbial lipases.

Removal of the pitch in pulp industry is also among the known applications of lipases. The hydrophobic component of wood is called pitch and it must be removed before processing. At low costs, the enzymatic removal of pitch is achieved via *C. rugosa* lipase [46]. Lipases are also used in the textile industry in order to bypass a process called stoning, especially for denim production [47]. Abbreviated exposure to toxic chemicals used in chemical process, which requires asbestos, is among the numerous advantages of this enzymatic bypass mentioned above. Pharmaceutical industry also uses lipases because of their ability to synthesize enantio-pure drugs [48–50]. Ibuprofen for pain, Taxol for cancer and Diltiazem for high blood pressure medications are examples to enantiopure drugs. The costs and drug toxiticy in pharmaceutical industry are reduced by the use of lipases in enantioselective production of drugs.

1 .7 Protein engineering and Directed Evolution

Directed evolution is an *in vitro* process, where genetic mutations are generated and inserted into a microorganism's genome to analyze specific functional patterns and properties on molecular level. Directed evolution performs under the same fundamental principles as natural evolution: the offsprings vary from the predecessor and selection critera is the survival of the fittest. In nature, random mutation and recombination lead to genetic diversification. Directed evolution requires a mechanism, for introducing those genetic variations such as error prone PCR, nucleoside analogs [51], degenerate oligonucleotides [52], propagation in strains that lack DNA repair capabilities, growth in the presence of chemical mutagens and DNA shuffling for recombination [53].

Mimicking the evolution *in vitro* would provide a better understanding of natural evolution as well as allow the development of new enzyme activities. Since there is a considerable interest in new biocatalysts, directed evolution became more widely used in

industrial and academic laboratories in order to generate and modify enzymes [54].

Directed evolution in laboratory, necessitates a precise selection of a suitable starting genes. A suitable candidate for molecular evolution is the class of α/β- barrel class of proteins due to their wide spectrum of catalytic functions [54]. Evolution did its job by evolving α/β- barrel to have a substrate binding sites within the barrel and the catalytic residues within the connecting loop regions. These distinct regions, which are responsible for specificity and catalysis, are suitable tools for their semi-autonomous evolution. And this will lead to generate diversity in a combinatorial manner.

Protein engineering has been used as a key concept for producing biotechnologically functional and novel biocatalysts. It has been applied on numerous fields such as oil recovery enhancement, in which cellulosic ethanol has been produced [55], as well as detergents, in which proteases are used [56], and polyester production via enzyme modeling and engineering [57].

Since rational design introduces mutation(s) specifically for the desired properties of certain protein sites and acquires numerous structural and functional parameters, as well as characteristic information about the enzymes, itself and molecular evolution are the fundamental approaches held for protein engineering. Despite the fact that molecular evolution does not necessarily need any structural or functional information of the enzymes, randomly generated mutants need additional screening for establishing desired properties.

To choose a best approach, limitations of both approaches should be considered thoroughly, such as methods for mutagenesis, information intensity that includes further details of structural and functional information, and selection and screening methods for directed evolution techniques. Thereby, various strategies may result in a different outcome, all having their certain advantages or disadvantages. The trade-off between rational design efforts and screening can be given as an example. If X-ray crystal structures are used for the rational design of a well-characterized and understood enzyme, it may limit

screening to a few number of amino acid substitutions. On the contrary, if a powerful screening method is applied, it may disregard the rational design altogether [58]. As a result, choosing the optimal method depends on detailed information about the locations for amino acid substitution, as well as the screening methods, group wise.

Another common target for protein engineering is to increase thermostability of a protein. A rigid and stable enzyme can be engineered, specifically functional at high temperatures, using the X-ray structure as one approach, following a design of stability interactions such as disulfide bonds and/or salt bridges, as well as inserting Proline or removing Glycine for stabilizing loops and focusing specifically on mutagenesis at flexible regions of the desired enzyme [58].

Another improvement can be made on the catalytic activity and the enantioselectivity of the enzyme, by substituting certain amino acid residues on the catalytic site of a target protein that are closely located [57]. Certain strategies for introducing substitution includes shuffling, simultaneous mutagenesis (for multiple amino acid substitution), Error-prone PCR, saturation mutagenesis (single amino acid substitution), and gene synthesis for specific modifications [59]. While establishing multiple amino acid substitutions provides numerous possibilities and design parameters for a target protein, it may lead to a loss in cooperative interactions and create a large library that has many idle variants. To overcome this problem with cooperative interactions of multiple amino acid substitutions, F.H. Arnold has suggested a stepwise accretion of single amino acid substitutions that has each variant superior than the previous one [60].

To be able to locate paths for a specific derivative of a protein with desired properties, all available paths should be tested beforehand. As an example, for an amino acid substitution that has five positions, there are 120 possible paths that leads to a final decisive variant. In a study, the resistance of β-lactamase was enhanced with 18 paths at each stage [61]. Thermostability of the enzyme phytase has been enhanced. After following 9 rounds of optimization, Tyr277Asp mutation has been resulted as the only single base exchange,

while the other was double-base (three mutations) and three-base exchanges [62]. A prior mutation earlier than the final variant being developed may lead to a dead end, as well as random mutations at several sites. Nevertheless, this may cause further screening efforts, therefore a well-designed selection method can be applied beforehand, as well as eliminating unfolded or unstable proteins by reductionist assumptions [63, 64] to diminish the number of variants that needs to be screened [65].

It is probable to detect which mutations are more functionally beneficial for a particular given characteristic by manipulating the data manually, if it's a small dataset. However, as more mutations are evaluated and screened for functional variance through each library, the analysis of the data by hand becomes too complicated as it increases in size. Statistical analysis introduced by ProSar uniquely analyzes the biological evolutionary relationship between protein structure and activity and it compares the data for each variant that has same or similar substitutionary information which in turn provides a clear understanding about whether the particular substitution is functionally significant or non-functional at all [66, 67]. In his study, G.W. Fox has used this statistical approach to successfully observe the evolutionary path of a halohydrin dehalogenase [68].

As easily may be anticipated, there are numerous screening strategies, most of them being either time or labor intensive. Most of the time, a final target variant can be missed out due to a lack of a suitable and efficient screening-selection strategy. However, some limited calorimetric screening methods can be developed for a limited number of enzymes to overcome this complication. To be concise, the best protein engineering approach may be defined as the one that brings the optimal solution with the least amount of effort and with a time efficiency. Because of this reason, certain individual approaches should be combined in order to produce the optimum outcome. For instance, due to the lack of a suitable screening methodology for industrial enzymes used in directed evolution applications, and the difficulty of hitting the optimal substitution for an enzyme with desired functionality in rational design, using these approaches individually is not a unique protein engineering approach. Instead, a combination of both strategies is crucial to provide a

novel and efficient path for enhancing the functional and structural properties of enzymes and thereby leading to rapid improvements in protein engineering.

1 .7.1 DNA shuffling

Stemmer had introduced DNA shuffling as a technique for *in vitro* recombination of homologous genes, for accelerating evolution rate of certain genes to perform directed evolution. The technology is highly used in applications such as gene therapy, vaccines, small molecule pharmaceuticals, and so on [7]. DNA shuffling techniques mimic diversity due to the merits of meiotic recombination. It is noted that libraries as large as 10^{15} molecules can be constructed by directed evolution. This may be considered as a drawback in terms of challenges at screening procedures; however, it is more of an advantage in terms of obtaining more recombinations that facilitates the production of a targeted enzyme, which is aimed to be utilized in industrial applications. As well as recombining DNA fragments, point mutations are also introduced to the sequence with a low rate, naturally propose a high-throughput methodology – both accelerating rate of evolution and obtaining the desired features for functionality, which leads to a novel advancement in industrial applications [7].

The classical DNA shuffling method is basically performed by digesting specific genes by DNAse I enzyme and attaining pieces of different types of genes shuffled together and reassembled under optimized PCR protocol, followed by integration into vectors and transformation into the target organisms [69, 70].One of the advantages of DNA shuffling is that, after the gene to be improved is introduced with a point mutation, there is a variety of beneficial mutations which are low on frequency relative to deleterious mutations, which then can be added to the cycle one at a time, building more beneficial mutations that eventually give out the best mutant from that given cycle [7]. Suen *et al*. (2004), have used DNA shuffling method on *Candida antartica* lipase (CALB) to obtain chimeric lipase B. The obtained lipase have shown 20 fold increase in activity and 11 fold increase in the 45^oC half life towards the diethyl 3-(3',4'-dichlorophenyl) glutarate (DDG) substrate, compared to it's wild type [71]. Yu *et al.* (2012) have also used DNA shuffling method

to increase heat resistance of *Rhizopus chinernsis* lipases. The half life of the obtained mutant at 60^oC and 65^oC have increased by 46 and 23 fold, respectively [72].

Directed evolution has played a significant role in improving the performance of an enzyme (or create one) through introducing new features that natural selection normally would not necessarily provide [73], as well as enhancing the selection criteria to yield targeted properties for that specific enzyme or microorganism, through custom schemes. A lead enzyme is picked and mutagenized, followed by selection or screening which results in improved variants that contains the target evolved enzyme. Protein molecules can be altered due to their structural and functional properties, which in turn can increase their thermal stability or introduce a new functionality (enzyme engineering), as well as changing the topology or structure, and altering the existing properties for improvement. While creating new enzymes improved for applications in industry and biotechnology, directed evolution methods can also be applied to improve limitations of certain functions of proteins, via accumulating beneficial mutations that lead to an augmentation of the enzyme's activity. In a study, it has been noted that the improved enzyme previously containing 10 amino acid substitution is enhanced by 157-fold [73].

2 Materials and Methods

2 .1 Molecular Cloning

Bacillus thermacatenulatus lipase gene(*BTL2*), which is 1,167 bp DNA fragment, and *Aspergillus niger* lipase gene(*ANL*), which is 891 bp, are amplified from the mature lipase clones (pMCSG7 - BTL2 and ANL). Primer sets are containing ligation independent cloning (LIC) sites; for forward (F_BTL2_LIC : 5'- TACTTCCAATCCAATGCCGCGGCATCCCCACGC - 3' and F_ANL_LIC: 5' - TACTTCCAATCCAATGAAATGTTCTCTGGACGGTTTG - 3') and for reverse (R_BTL2_LIC: 5' - TTATCCACTTCCAATGTTAAGGCCGCAAACTCGCC - 3' and R_ANL_LIC: 5' - TTATCCACTTCCAATGAATAGCAGGCACTCGGAAA - 3'). PCR conditions are the following: 5 min at 94 ^{o}C, 35 cycles of 30 sec at 94 ^{o}C, 30 sec at 53 ^{o}C, 1 min at 72 ^{o}C, 10 min at 72 ^{o}C. After DNA shuffling procedures, 4μg of expression vector, pMCSG7, is linearized using SspI restriction enzyme (see Appendix A.1 for vector map). Linear vector and insert are elecroporated at 135 V in 1.5% agarose gels using tris borate EDTA (TBE) buffer system for 20 minutes. Both fragments are extracted from agarose gel and treated with T4 DNA Polymerase. The exonuclease activity is restricted using excess amount of dGTP for vector and dCTP for the inserts according to the given LIC sequences. The reaction is carried on for 50 minutes at 20^{o}C followed by heat-activation at 70^{o}C for 20 minutes. Phenol/chloroform extraction and ethanol precipitation procedures are applied to the T4 DNA polymerase treated DNA samples. Vector (in 5 μl) and shuffled lipase genes(in 3μl) solubilized in distilled water and annealed at 23^{o}C for 16 hours. *E.coli* Shuffle chemically competent cells are prepared according to Maniatis *et al* [74]. All the annealing reaction after 16 hours are transformed into *E.coli* Shuffle cells by using a chemical transformation method [75]. For colony PCR , ANL_LIC and BTL2_LIC primer pairs are used in the given PCR cycle profile for the selected colonies. PCR products, which are amplified by Colony PCR reaction, are run in 1.5% agarose gel using GeneRuler 1kb DNA Ladder SM0311(Fermentas). To the colony PCR positive clones, plasmid purifications are applied. The plasmid purifications are done using Qiagen Plasmid Purification kit .

Plasmids are sequenced using the primer set combinations which are used at the DNA shuffling process by Molecular Cloning Laboratories (MCLAB).

2 .2 DNA Shuffling

PCR products of ANL and BTL2 genes, which are amplified with the PCR cycle mentioned above, are purified using Qiagen PCR Purification Kit. 1.2μg DNA from ANL and BTL2 is mixed in a tube and digested with 0.05 U DNase(Roche,10 U/μl) in 10X digestion buffer with $MnCl_2$ for 75, 90 and 120 min at room temperature. The reaction is inactivated with 2.5 mM EDTA and incubation at 85^{o}C for 5 minutes. The mixtures are run in 2% agarose gel. Fragments that are lower than 50 base pairs in size and between 50 and 100 base pairs are extracted from the gel by using QIAEX II gel extraction kit. Extracted fragments are reassembled by the previous PCR cycles but without the primers. Amplification of the reassembled fragments are made through the same PCR reaction using the assembled fragments as the template but the primer combinations of ANL and BTL2 were added. Amplified reassembled fragments are cloned to pMCSG7 expression vector by ligation independent cloning.

2 .3 Lipase Expression

Shuffled genes are transformed to Shuffle *E.coli* by chemical transformation. Transformed cells are plated on LB-Agar plates with Ampicillin. Colonies, which survived, inoculated on LB- Rhodamine, which has IPTG (isopropyl-β -D-thiogalactopyranoside), plates to check the qualitatively check the lipase activity. All possible mutants are also expressed in suspension culture using 1mM IPTG in LB broth. The expressions are lasted out for eight hours and sampled once at fourth hour. The cells are harvested by centrifugation (for 5 min at top speed) and lysed by using B-PER(Thermoscientific). After centrifugation at maximum speed for 10 min, lipase activity of soluble fractions is determined using fluorescent substrates, 4MU-C8 in 0.1M Tris at pH 7.25. SDS-PAGE gel is run to analyze the soluble fractions and visualized by coommassie staining.

2 .4 Lipase Assays

Lipase activity is determined in two different ways:

2 .4.1 Rhodamine plate assays

Selected colonies are inoculated on to the Rhodamine-LB agar plates which are containing IPTG (for expression), oil (as substrate), Rhodamine(dye that interacts with free fatty acids) and LB agar. When the expression starts at the inoculated colonies, expressed recombinant lipases start to hydrolyze oil. Fatty acids which yielded from the hydrolysis reaction interacts with the Rhodamine dye and gives light under UV. Preliminary detection of active recombinant enzymes is achieved by this screening technique.

2 .4.2 Fluorescence assay

For more quantitative measurement, lipase activity is measured with fluorescent assay methods. For fluorescent assays, lipase activity measured in a 96-well black micro titer plate using 4MU - caprylate as the substrate. Expression medium, which do not contain any cell, assayed in reaction medium of 100 mM Tris-Cl at pH 7.25. 4MU fluorescence is measured by using Gemini XS (Molecular Devices) using wavelength of 355 nm for excitation and an emission wavelength of 460 nm. For one hour, in every minutes, measurements are taken. All assays are made in duplicates and initial velocities are calculated using SoftMax Pro Software (Molecular Devices). Relative Fluorescent Unit obtained from fluorometer is converted to 4MU units with respect to the linear relationship obtained from 4MU standard curve.

2 .5 Lipase Characterization

2 .5.1 Thermostability

Soluble fractions of the clones that do have expressions, are used in fluorescent assays to profile thermostability by quantifying the residual activity of lipases after 30 minutes of incubation at temperatures 30^{o}C, 40^{o}C, 50^{o}C, 60^{o}C, 70^{o}C, and 80^{o}C is set to 100% activity for calculating the percent activity.

2 .5.2 Substrate specificity

Chain length specificity of the mutated lipases are screened by fluorescent enzyme assays using reaction medium of 100 mM Tris-Cl at pH 7.25 as the reaction buffer. From the chain lengths of 2C to 16C the following lipids are used; Acetate(2C), propionate(3C), butyrate(4), caproate(6C), enatiothe(7C), caprylate(8), and palmitate(16C).

3 Results

In this study, DNA shuffling method has been successfully performed on ANL and BTL2 genes in order to generate randomly mutated novel lipases. The reason ANL and BTL was chosen as candidates due to their evolutionary distance, in which they share 42% identity. Furthermore, the fact that *Bacillus thermocatenulatus* lipase is thermophilic and *Aspergillus niger* lipase is mesophilic, DNA shuffling on these candidate lipases could lead to obtain the expected features such as wide range of temperature, pH, which remarkably appeals to industrial and biotechnological applications.

Due to the fact that DNA shuffling introduces random mutagenesis, numerous mutants can be produced in a single run, which in turn enables an increase in the shuffled gene library size. In our experimentation, multiple optimization experiments have been held for DNase digestion to obtain the desired fragment size (50bp), using time, temperature and DNA concentration as parameters. Using regular cloning methodology, randomly mutated library has been transformed into Shuffle type *E.coli* cells. For screening, only qualitative plate assay has been performed, and for sequencing, sequencing data have been obtained and analyzed from libraries to detect random mutations.

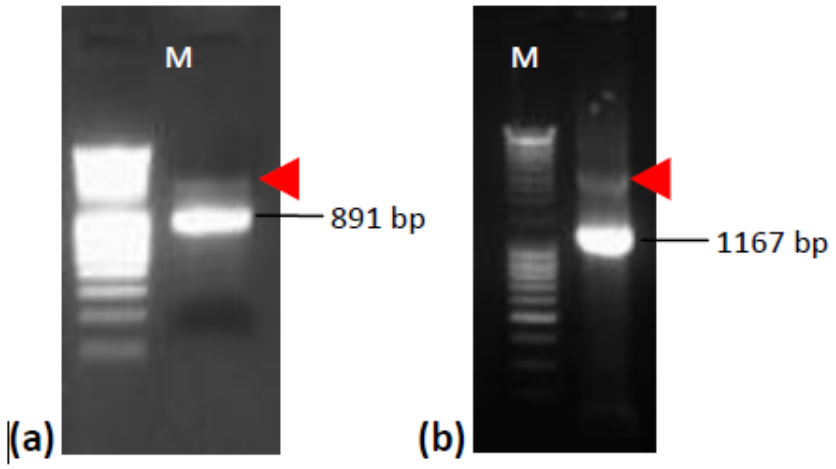


Figure 2: PCR amplifications of (a) ANL (891bp), and, (b) BTL2 (1167bp). Arrowheads show the plasmids. M: MassRuler DNA Ladder Mix (Fermentas).

ANL and BTL2 genes were amplified from the mature lipase clones, pMCSG7-ANL and BTL2 , by using their specific primers. PCR conditions are the following: 5 min at 94 C, 35 cycles of 30 sec at 94 ^{o}C, 30 sec at 53 ^{o}C, 1 min at 72 ^{o}C, 10 min at 72 ^{o}C. In Figure 2, the bands that appeared above the PCR product indicates presence of the plasmid which is used as the template. This plasmid would spoil the DNase digestion.

In order to eliminate plasmid interference, Dpn2 digestion applied to the PCR products at 37C for overnight. In Figure 3 , digested plasmid fragments are shown with arrow heads. PCR products were extracted from the agarose gel.

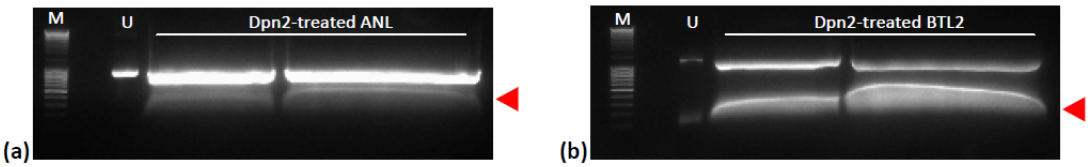


Figure 3: Dpn2 digestion of the plasmids carrying (a) ANL, and (b) BTL2. Arrowheads show the digested plasmid fragments. U: Uncut PCR products for (a) ANL, and (b) BTL2. M: MassRuler DNA Ladder Mix (Fermentas).

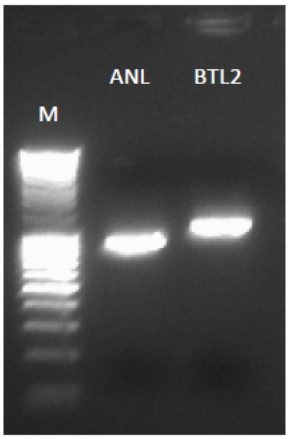


Figure 4: Purified PCR products for ANL and BTL2, excised and extracted from the agarose gel shown in Figure 2. M: MassRuler DNA Ladder Mix (Fermentas).

Extracted PCR products are run on 1.2% agarose gel in order to confirm that there is no plasmid left in the mixture. So Figure 4 indicates that the PCR products are plasmid-free and ready to DNase digestion.

DNase digestion is applied to PCR products. 2 μg DNA from ANL and BTL were digested separately with 0.05 unit of DNase I (Roche). As the reaction buffer, 10X digestion buffer which is 500mM Tris-HCl pH 7.4 and 100mM $MnCl_2$ is used. The digestion was done at room temperature until it is terminated after 20 minutes by heating at 85^{o}C with the presence of 2.5mM EDTA. Mixture is run on 2% agarose gel. Smear on Figure 5 shows the digested fragments of the particular genes. Fragments from 150 to 300bp are excised and extracted from the gel.

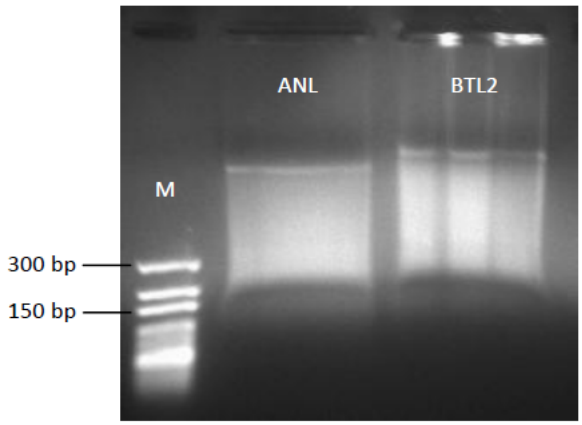


Figure 5: DnaseI digestion of ANL and BTL2 PCR Products. DNA smears indicative of digestion products of varying lengths, as low as 200bp, are evident. M: GeneRuler Ultra Low Range DNA Ladder (Fermentas).

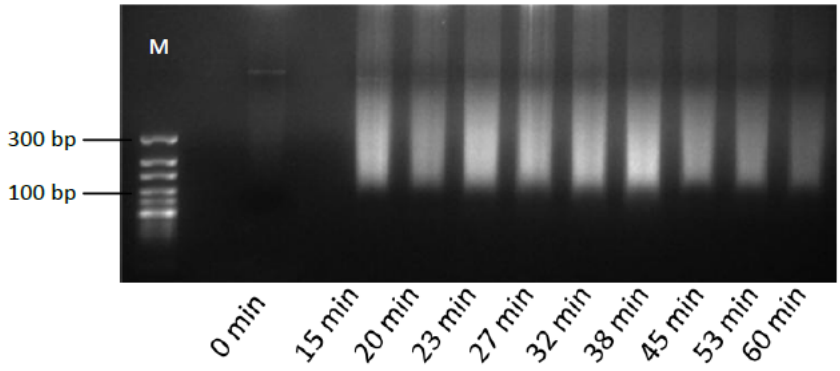


Figure 6: Digest products from DnaseI-treated ANL and BTL2 mixtures at different time points as given at the bottom. M: GeneRuler Ultra Low Range DNA Ladder (Fermentas).

20 minutes of digestion was not sufficient for obtaining the desired fragment size which is smaller than 100 base pair. So DNase digestion is applied to PCR products. This time 1,2 μg of each gene from were mixed and digested in a tube with 0.05 unit of DNase I (Roche). As the reaction buffer, 10X digestion buffer which is 500mM Tris-HCl pH 7.4 and 100mM $MnCl_2$ is used. The digestion was done at room temperature. 15, 20, 23, 27, 32, 38, 45, 53, 60 minutes of digestion was done in order to find out the most efficient digestion time point. Inactivation is done by heating the samples at 85C with the presence of 2.5mM EDTA. Mixture is run on 2% agarose gel. Smears on Figure 7 show the digested fragments of the particular genes.

Same protocol used at Figure 5 was applied for 75 minutes, 90 minutes and 120 minutes in order to obtain smaller fragments(smaller than 50bp). Inactivation is done by heating the samples at 85C with the presence of 2.5 mM EDTA. Mixture is run on 2% agarose gel. Smears on Figure 8 show the digested fragments which are in the range of desired fragment size. Fragments below 50bp and between 50 -100bp are excised and extracted from the gel followed by the reassembly PCR.

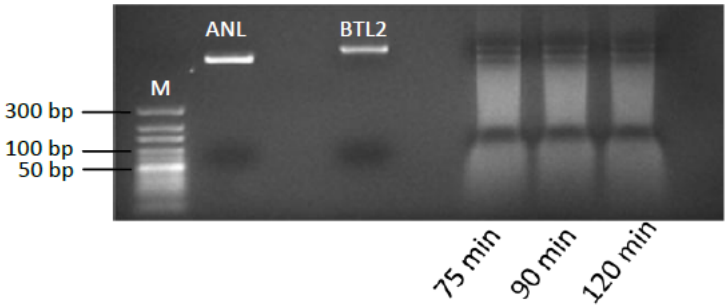


Figure 7: Digest products from DnaseI-treated ANL and BTL2 mixtures at different time points as given at the bottom. M: GeneRuler Ultra Low Range DNA Ladder (Fermentas).

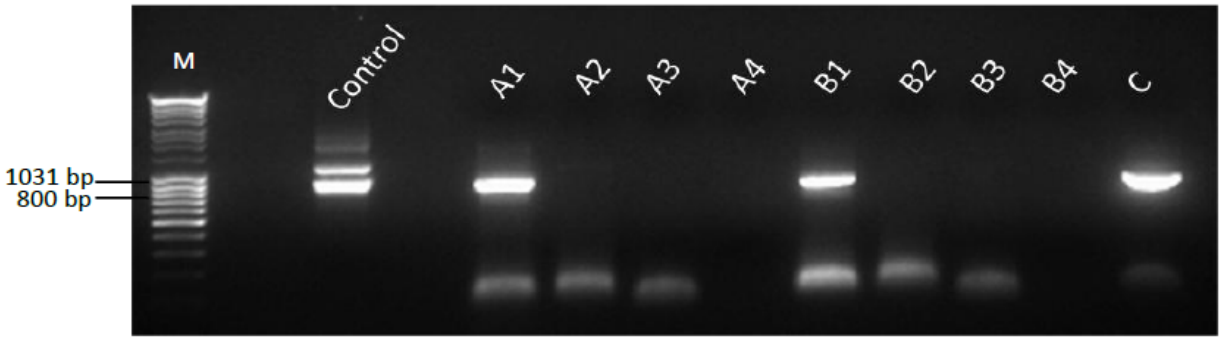


Figure 8: Amplification PCR with the primer combinations. M: MassRuler DNA Ladder Mix (Fermentas).

In figure 7, Group A indicates the reassembled 50bp and below fragments, while Group B indicates the reassembled fragments in the range of 50-100 bp. Lastly, Group C indicates the reassembled ANL fragments which are 150-300 bp in length. The primer combinations are; (1) F_ANL - R_ANL, (2) F_BTL, R_BTL, (3) F_ANL, R_BTL, and (4) F_BTL, R_ANL. A1, B1 and C1 labeled samples, which are produced by using ANL primer sets, are detected on 1,2% agarose gel. The amplified fragments were excised and extracted from the gel.

Extracted shuffled genes are cloned to expression vector pMCSG7 by ligation independent cloning and transformed into Shuffle *E.coli* competent cells by chemical transformation. As a result of the transformation, 75 colonies (37 colonies from A1, 18 colonies from B1, 20 colonies from C1) were obtained on LB-agar plates. Colony PCR was performed to check the insertion of the shuffled genes into the transformed vectors. It is confirmed that all colonies had the insert, shown in Figure 9.

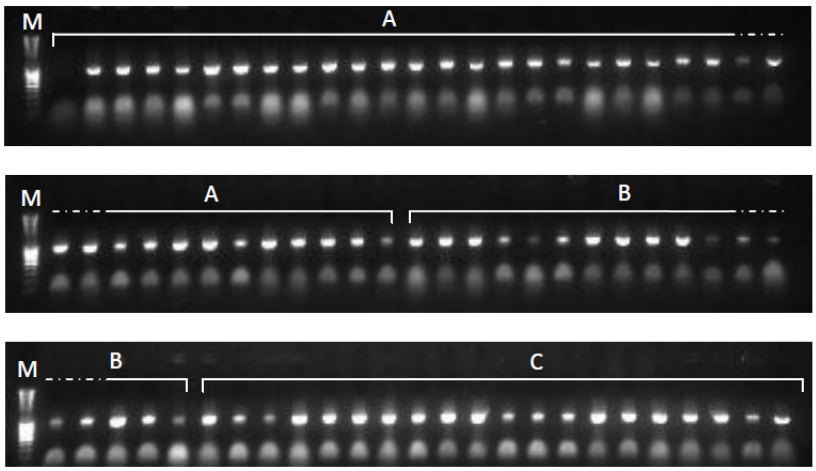


Figure 9: Colony PCR of obtained colonies.

Obtained A1 colonies are inoculated to LB - rhodamine activity plates to decide the activity of the possible mutants qualitatively. All the colonies except colony 33 had the lipase activity (Figure 10).

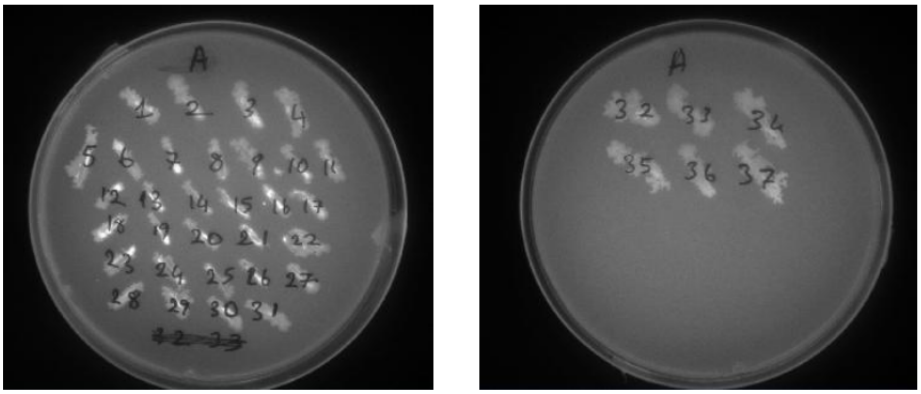


Figure 10: LB-Rhodamine activity plates of A colonies.

Obtained B1 colonies are inoculated to LB - rhodamine activity plates to decide the activity of the possible mutants qualitatively. The LB- rhodamine plate of B1 combination showed that most of the colonies have the lipase activity (Figure 11).

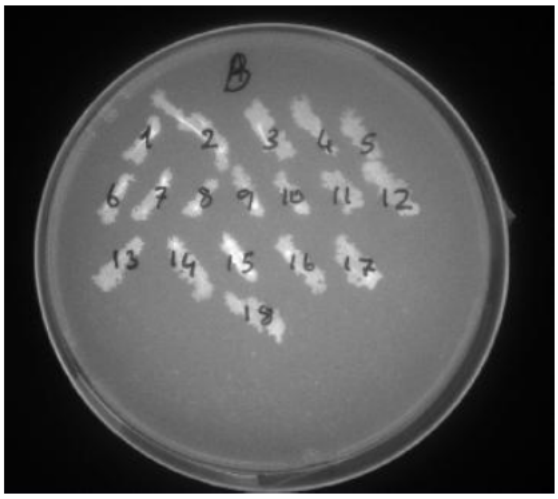


Figure 11: LB-Rhodamine activity plates of B colonies.

Obtained C1 colonies are inoculated to LB - rhodamine activity plates to decide the activity of the possible mutants qualitatively. Inoculated 14 C1 colonies out 20 have the lipase activity on LB-rhodamine plates (Figure 12).

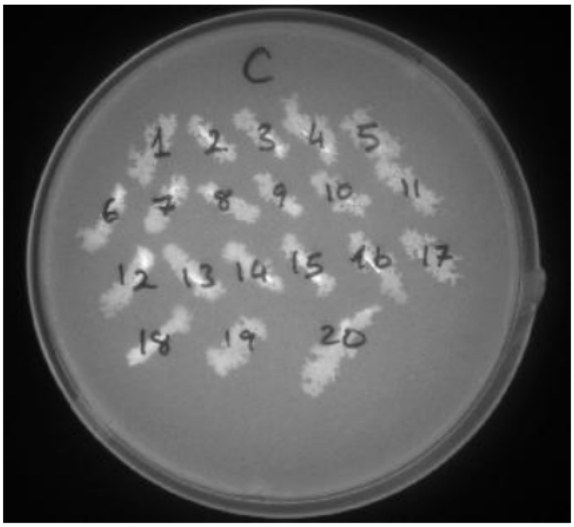


Figure 12: LB-Rhodamine activity plates of C colonies.

To screen the mutations which occurred by DNA shuffling, plasmid isolation is applied to all 75 colonies and the purified plasmids are sent to sequencing with R_ANL primer. Alignment of the samples with ANL and BTL2 native genes shows that samples have similarity more than 90% with ANL gene. Although, samples mostly similar to ANL, eight of the samples have point mutations which may lead to the activity change. In fact, colony A33 has 10 point mutations which lead to the loss of activity. Point mutations at these eight samples are listed at Table 1. There are point mutations in these samples that would normally lead to activity loss but didn't caused any activity loss such as Asp to Gly mutation at colony B15 or Gly to Ser mutation at colony C15 or Thr to Ala at colony C15.

Clone	**Location of the Mutation**	**Amino acid Substitution**	**Activity**
A33	60^{th} amino acid	GUG (Val) → GUA (Val).	
A33	64^{th} amino acid	GCC (Ala) → ACC (Thr)	
A33	68^{th} amino acid	CCU (Pro) → GCU (Ala)	
A33	95^{th} amino acid	GCC (Ala) → GUC (Val)	
A33	106^{th} amino acid	GCC (Ala) → UCC (Ser)	(-)
A33	124^{th} amino acid	CUC (Leu) → CUU (Leu)	
A33	160^{th} amino acid	GCC (Ala) → GAC (Asp)	
A33	184^{th} amino acid	AGC (Ser) → AAC (Asn)	
A33	214^{th} amino acid	ACG (Thr) → GAG (Glu)	
A33	250^{th} amino acid	AGC (Ser) → AAC (Asn)	
B2	3^{rd} amino acid	UCU (Ser) → UAU (Tyr)	
B2	44^{th} amino acid	UCU (Ser) → UCC (Ser)	(+)
B2	46^{th} amino acid	GCA (Ala) → GCG (Ala)	
B8	188^{th} amino acid	AAU (Asn) → AAC (Asn)	(+)
B15	65^{th} amino acid	GAC(Asp) → GGC(Gly)	
B15	61^{st} amino acid	AAU(Asn) → AGU(Ser)	(+)
C6	61^{th} amino acid	ACA(Thr) → GCA(Ala)	
C6	275^{th} amino acid	GGU(Gly) → GAU(Asp)	(+)
C12	137^{th} amino acid	CAC(His) → CGC(Arg)	(+)
C14	86^{th} amino acid	AAC(Asn) → GAC(Asp)	(+)
C15	31^{th} amino acid	ACU(Thr) → GCU(Ala)	
C15	151^{th} amino acid	CUG(Leu) → CCG (Pro)	
C15	176^{th} amino acid	GGC(Gly) → AGC (Ser)	(+)
C15	223^{th} amino acid	GUU(Val) → GCU(Ala)	

Table 1 : Types of point mutations and their locations on the sequence.

The locations of the mutations of particular colonies given in table 1 were investigated. Since the colonies have more than 90% identity with ANL, homology model of ANL is used to locate the point mutations which are detected. Homology model of ANL is made by using *Thermomyces lanuginosa* lipase structure as the template. They have 51% sequence similarity with the query coverage of 99%.

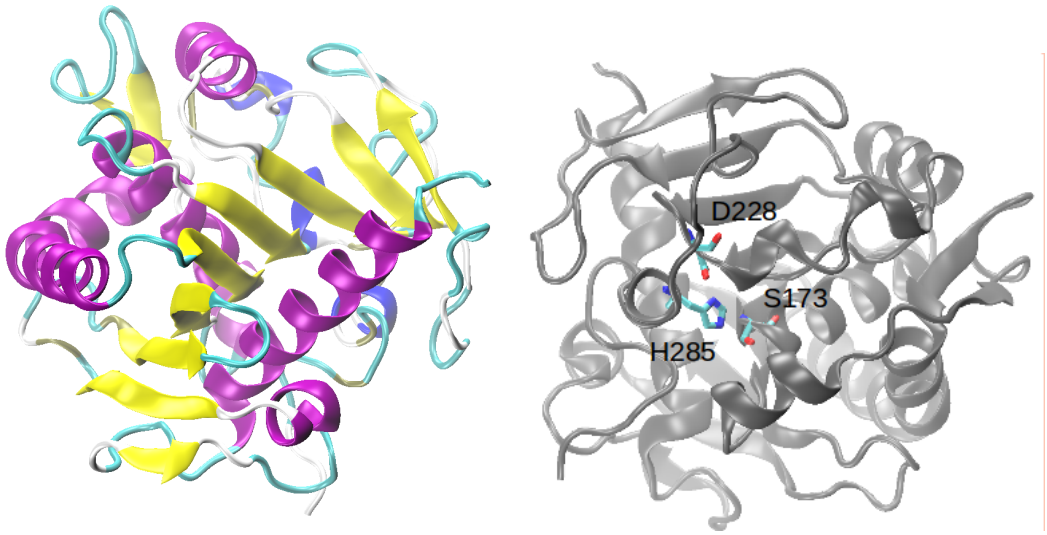


Figure 13: Homology modeling of *Aspergillus niger* lipase, using 1dt3 (*Thermomyces lanuginosa* lipase) as the template.

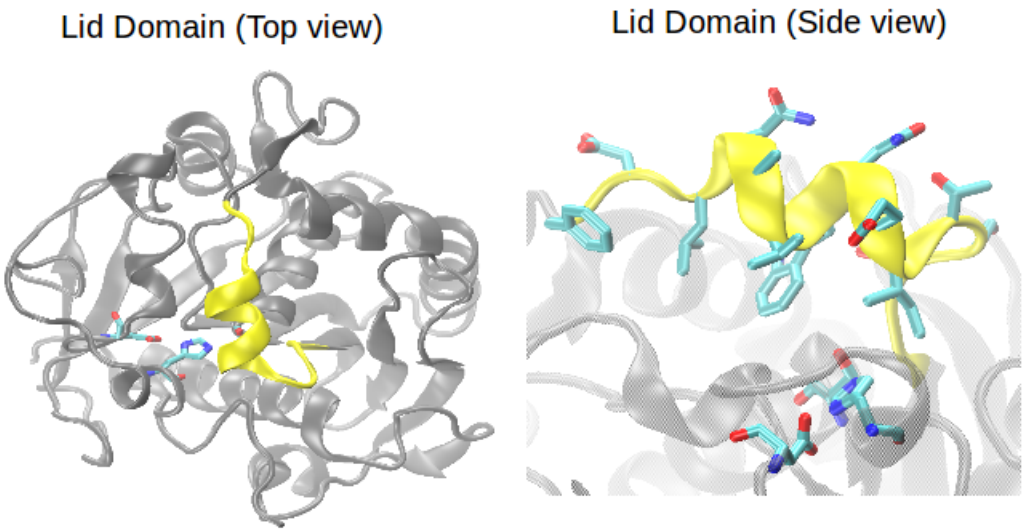


Figure 14: The Lid domain has been shown from top and side view, respectively. The predicted model corresponds to the inactive lipase form where the lid is in its closed conformation.

The best candidate for the Lid domain is shown in Figure 14 in yellow. The reason for chosen as best candidate is because the catalytic Serine has also been covered. Also, the amino acid content of the lid explains the interfacial properties of the lipase. In the closed conformation, the polar residues like, N, D and T are exposed to solvent. In the open conformation, the non-polar residues like W, I and V should be exposed to the lipid-interface.

Multiple sequence alignment is applied to all mutants (see Appendix A.2), which are obtained from sequencing, with native ANL. Afterwards, locations of the point mutations, which are detected from sequencing data, pointed with arrows (Red = ”deadly” mutations, Blue = ”compensating” mutations, Grey = ”silent” mutations) and in addition, only ”deadly” mutations which indicates non polar amino acid - polar amino acid change, are shown on the homology model of ANL by using VMD (Visual Molecular Dynamics).

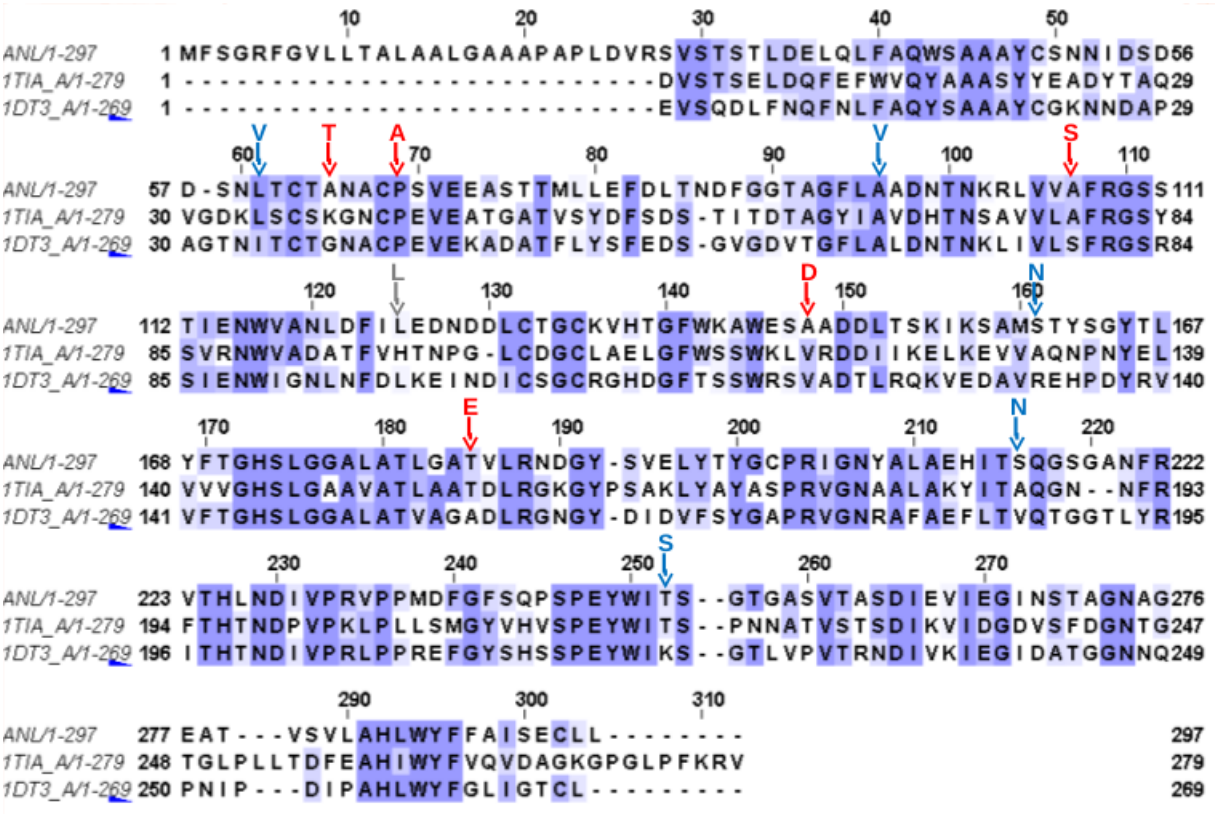


Figure 15: Multiple sequence alignment of Colony A33.

Colony 33 had 5 “deadly”, 5 “compensating” and 1 “silent” mutations. As it can be seen from Figure 15, 2 out of 5 deadly mutations are located at core of the protein. In fact, T184E mutation located on the nucleophilic elbow (in Magenta color) which carries the catalytic serine residue. And the A146D mutation is located at the adjacent β-sheet to the nucleophilic elbow. Locations of these 2 mutations make them important due to their closeness to the catalytic site.

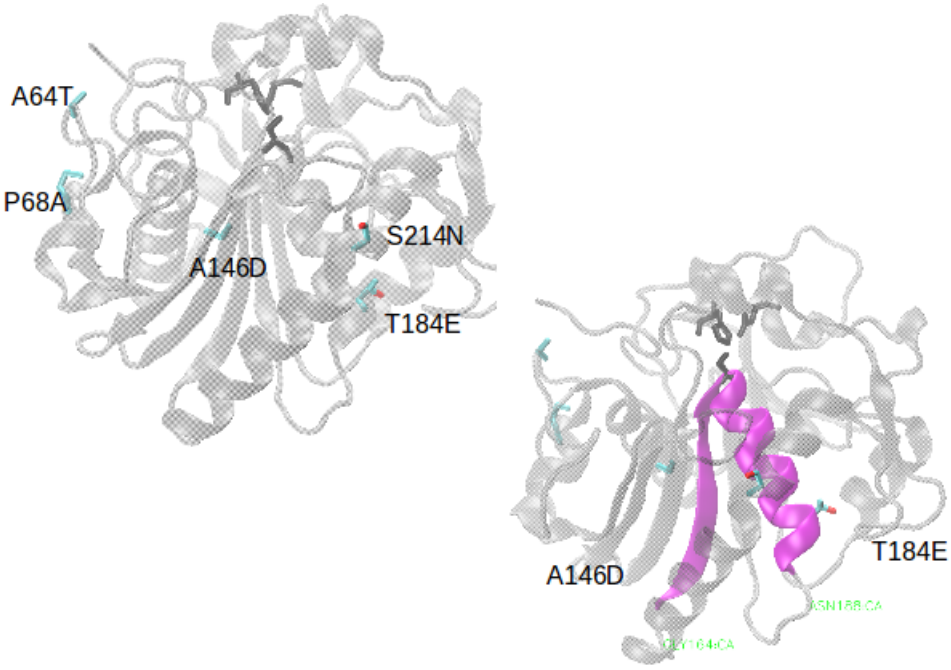


Figure 16: Locations of the mutations for Colony A33. The nucleophilic elbow that carries the catalytic serine is shown in magenta.

For the mutations at the colonies B2, B8, B15, C12 and C14, they are either “deadly” but surface exposed or silent mutations which are unlikely to cause a change in activity of the enzyme. At the colony B2, three codon changes have occurred, two of them being silent mutations (Serine to Tyrosine on the 3^{rd} amino acid, Serine to Serine on the 44^{th} amino acid, and Alanine to Alanine on the 46^{th} amino acid, respectively). At the colony B8, Asparagine to Asparagine change has occurred on the 188^{th} amino acid. At the colony B15, two codon changes have occurred, an Aspartic acid to Glycine on the 65^{th} amino acid, and an Asparagine to Serine on the 61^{st} amino acid. At the colony C12, a Histidine to Arginine substitution has occurred on the 137^{th} amino acid, and at the colony C14, an Asparagine to Aspartic acid substitution on the 86^{th} amino acid.

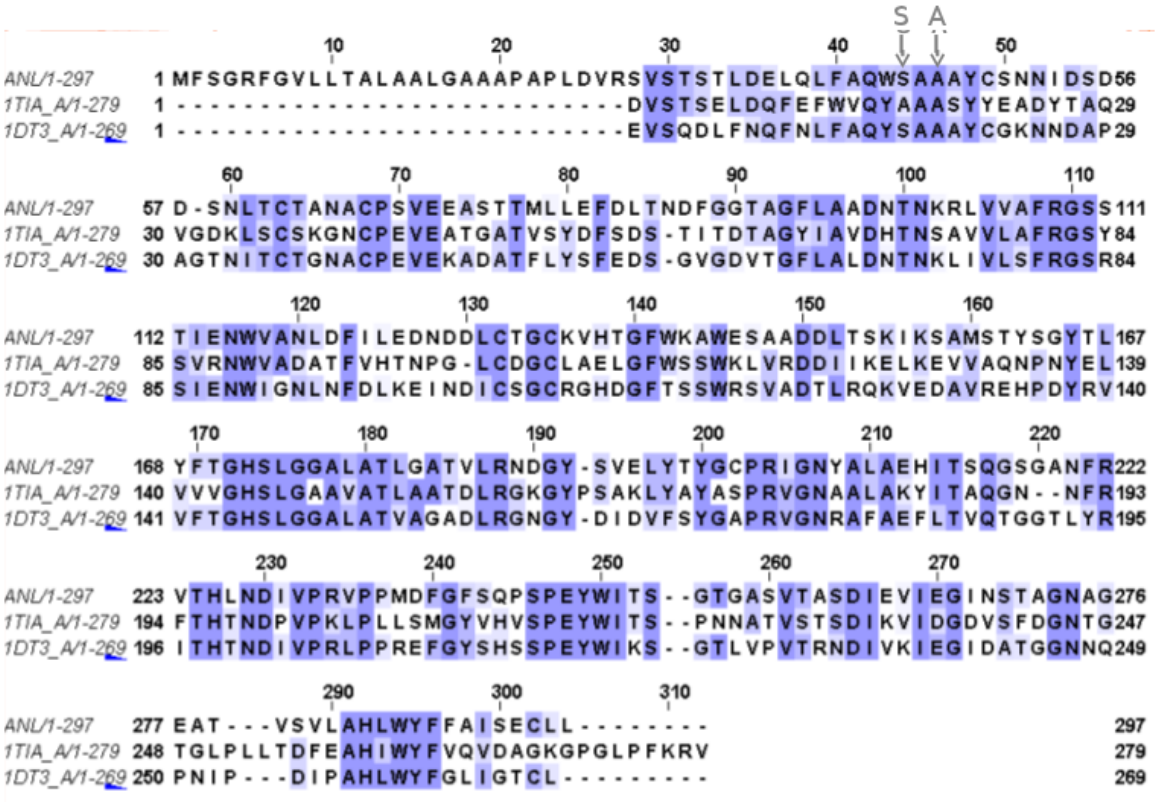


Figure 17: Multiple sequence alignment of Colony 39 (B2).

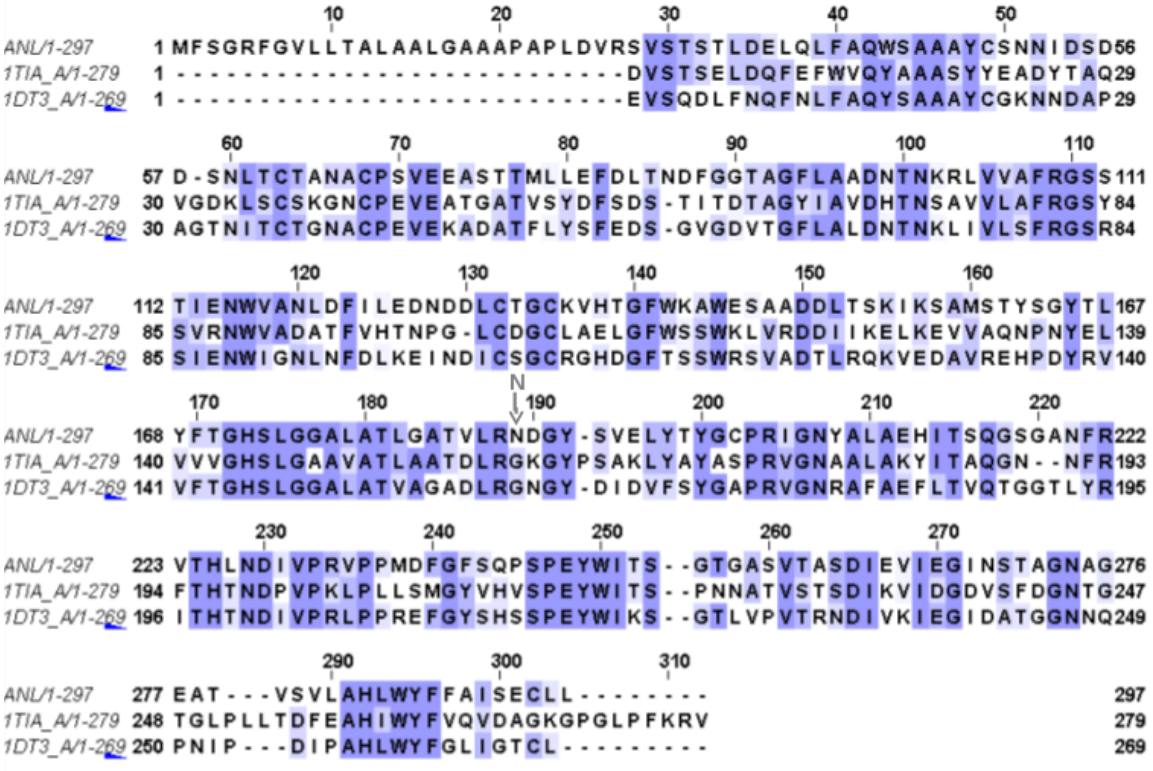


Figure 18: Multiple sequence alignment of Colony 45 (B8).

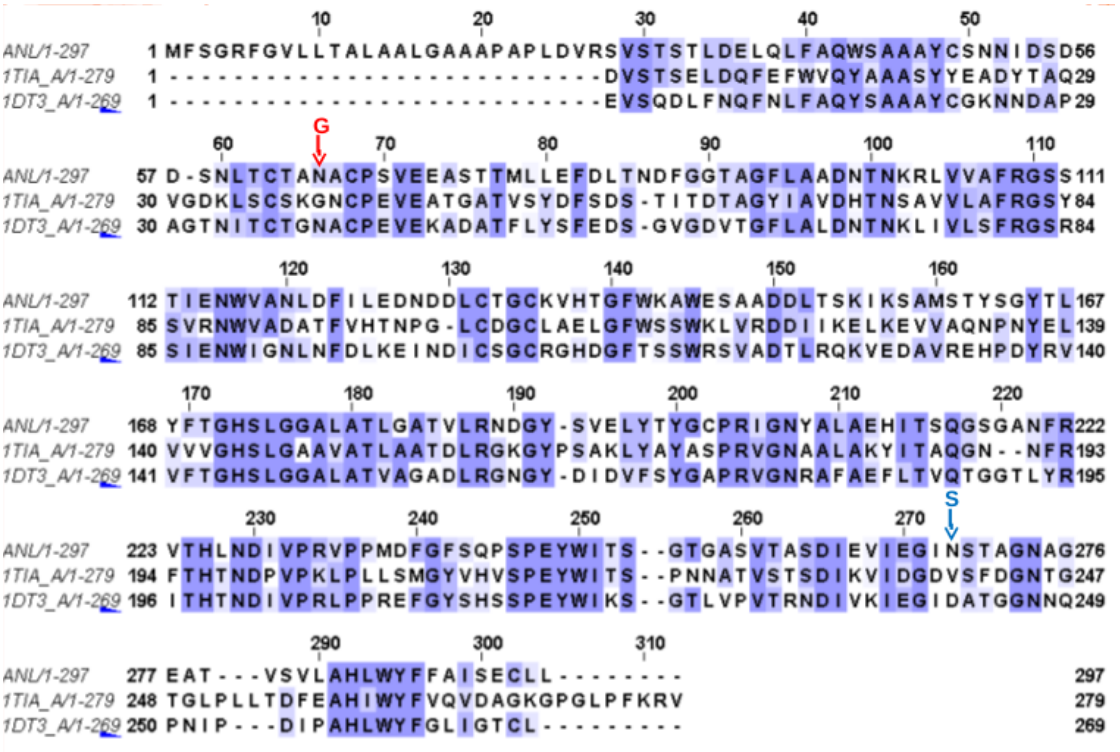


Figure 19: Multiple sequence alignment of Colony 52 (B15).

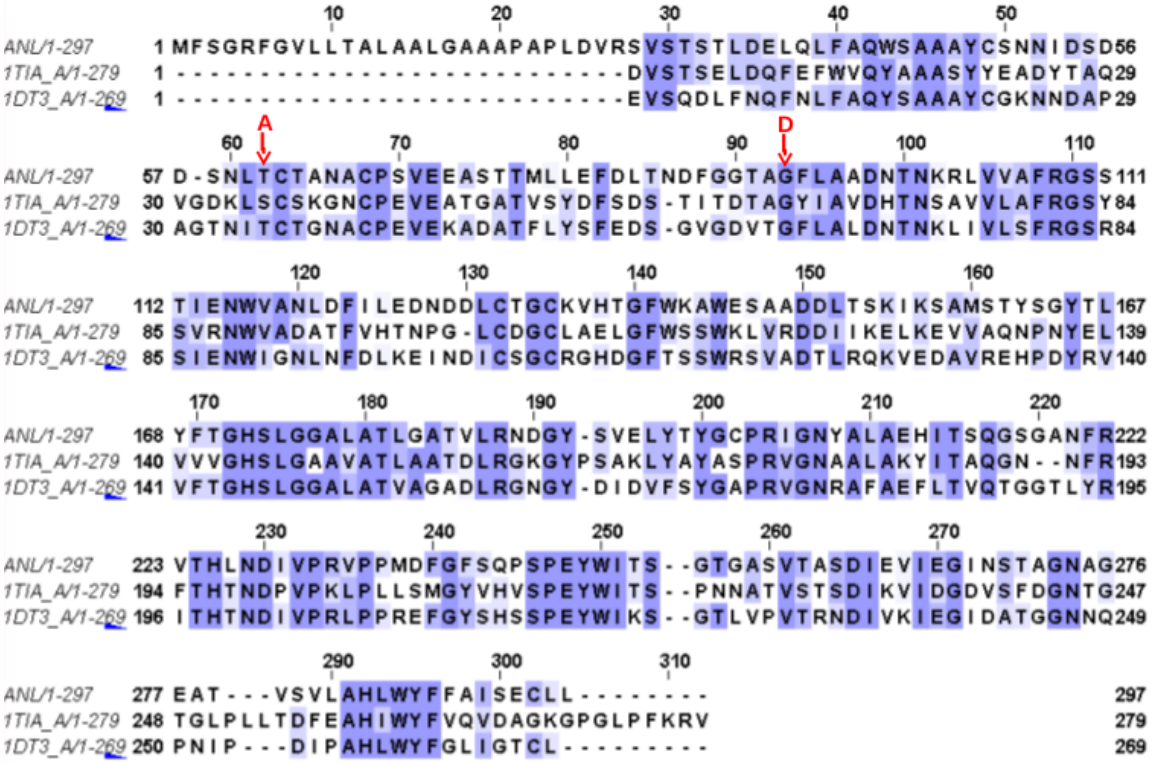


Figure 20: Multiple sequence alignment of Colony 61 (C6).

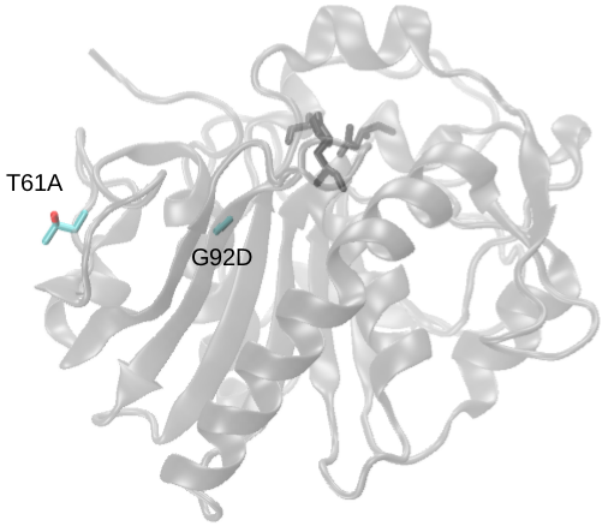


Figure 21: Locations of the mutations for Colony 61 (C6)

Colony C6 has 2 “deadly” mutations which are Threonine to Alanine substitution at 61st amino acid which is surface exposed and far away from the catalytic site. The other one is the Glycine to Asparagine substitution at the 275^{th} amino acid which is located more closely to the catalytic site (Figure 20). Since this is also a non polar to polar substitution, the mutation has a role in changing the activity.

Figure 22: Multiple sequence alignment of Colony 67 (C12).

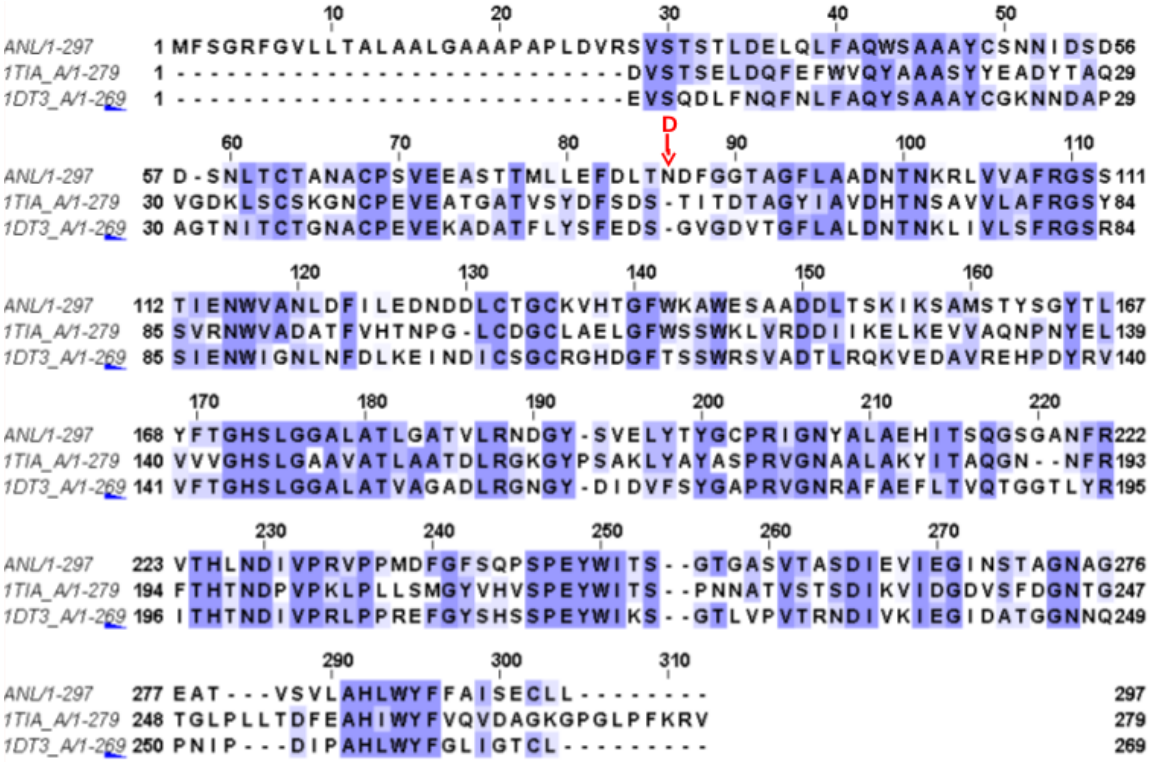


Figure 23: Multiple sequence alignment of Colony 69 (C14).

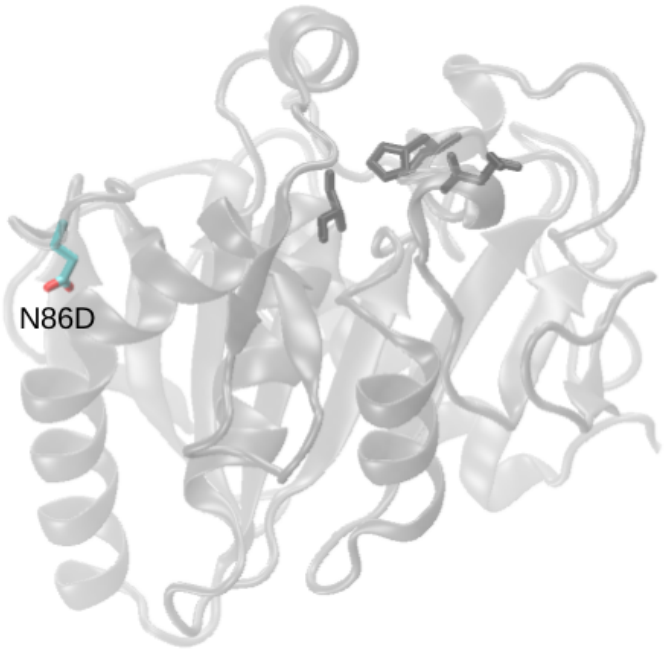


Figure 24: Locations of the mutations for Colony 69 (C14).

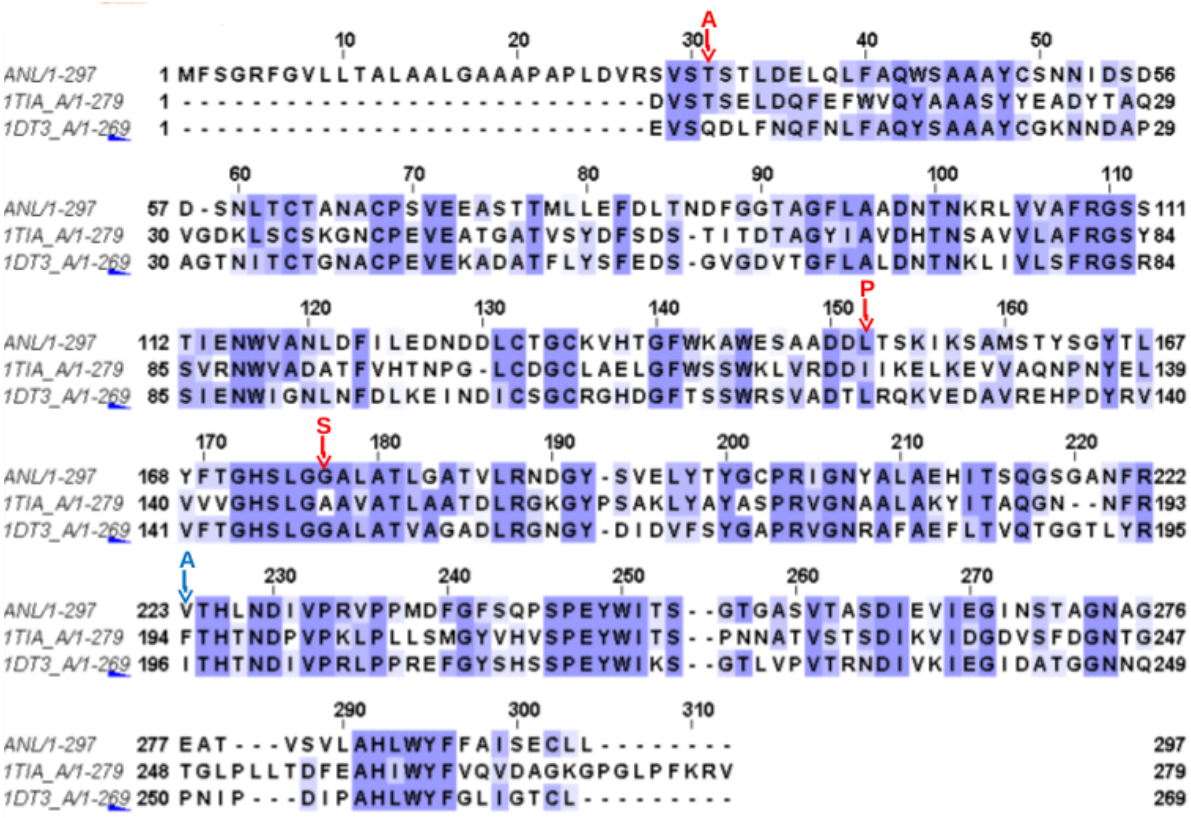


Figure 25: Multiple sequence alignment of Colony 70 (C15).

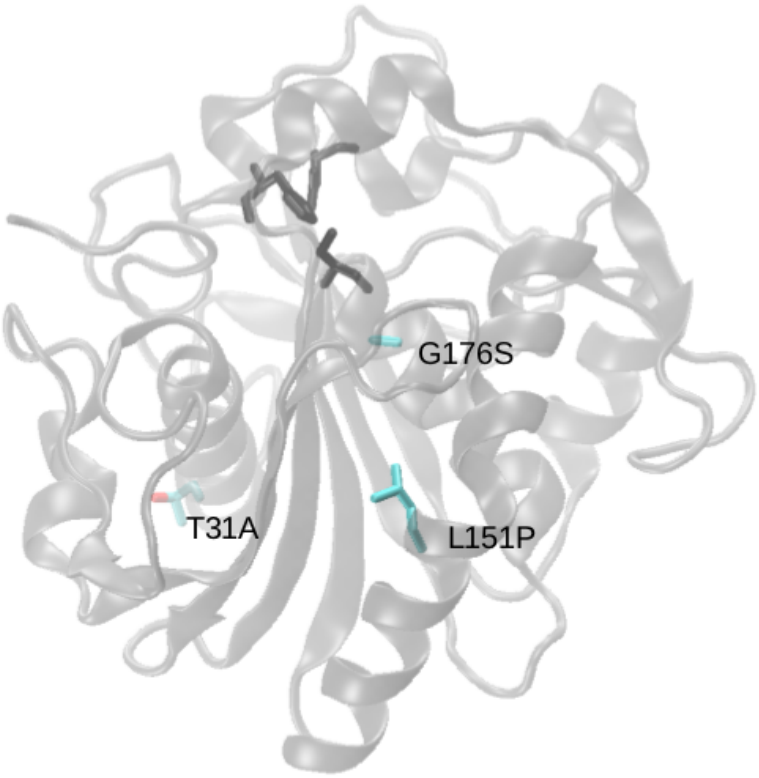


Figure 26: Locations of the mutations for Colony 70 (C15).

Colony C15 has 3 "deadly" mutations which are Threonine to Alanine substitution at 31st amino acid Leucine to Proline substitution at 151^{st} amino acid, Glycine to Serine substitution at 176^{th} amino acid (Figure 25). 2 out of these 3 "deadly" mutations are likely to effect the activity of the enzyme. G176S mutation is very much at the core of the protein and is significantly close to the catalytic site. This kind of mutation (non-polar to polar) would be significant since there will be a presentation of a polar amino acid at the core of the protein. Another significant "deadly" mutation would be L151P because a presentation a Proline in to a existing α-helix would cause rupture the α helical structure which is also likely to change the activity of an enzyme.

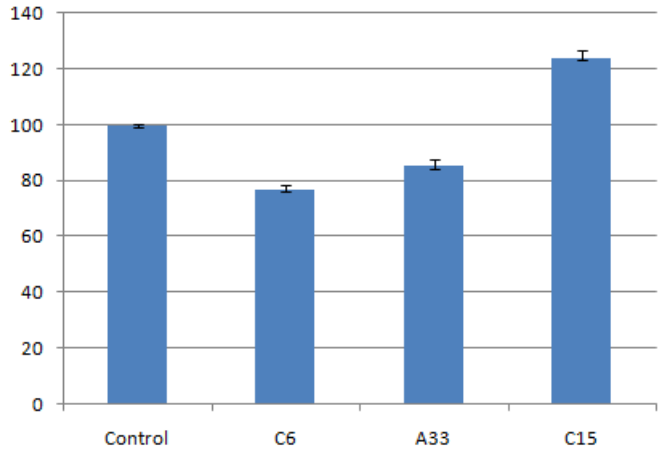


Figure 27: The relative activity plot of the colonies, using fluorescence enzyme assays. As a substrate, 4MU-caprylate has been used to detect the activity of lipase from the soluble fraction.

For quantitatively determining the lipase activity, fluorescent lipase assay methodology is applied. 5 micro liters of the soluble fraction from the cultured cells are assayed by using 4MU - caprylate as the substrate. Soluble fraction of the cultured cells, which do not contain any cell, assayed in reaction medium of 100 mM Tris-Cl at pH 7.25. 4MU fluorescence is measured by using Gemini XS (Molecular Devices) using wavelength of 355 nm for excitation and an emission wavelength of 460 nm. As it is shown in Figure 26 the mutations caused a decrease on the lipase activity at clones A33 and C6, as well as increase in activity of clone C15 by 25%. These activity changes may be due to the "deadly" mutations that are presented near the catalytic site. To investigate whether the mutations caused a change in substrate selectivity and due to that the activity loss against caprylate has occurred or it is the general activity loss, a substrate selectivity assay is made. From the chain lengths of 2C to 16C the following lipids are used; Acetate(2C), propinate(3C), butyrate(4), caproate(6C), enatiothe(7C), caprylate(8), and palmitate(16C) for the investigation of the substrate selectivity. As it is shown in Figures 27, 28, 29 and 30, there is no detectable change in the substrate selectivity trend with respect to the control group which is the native ANL.

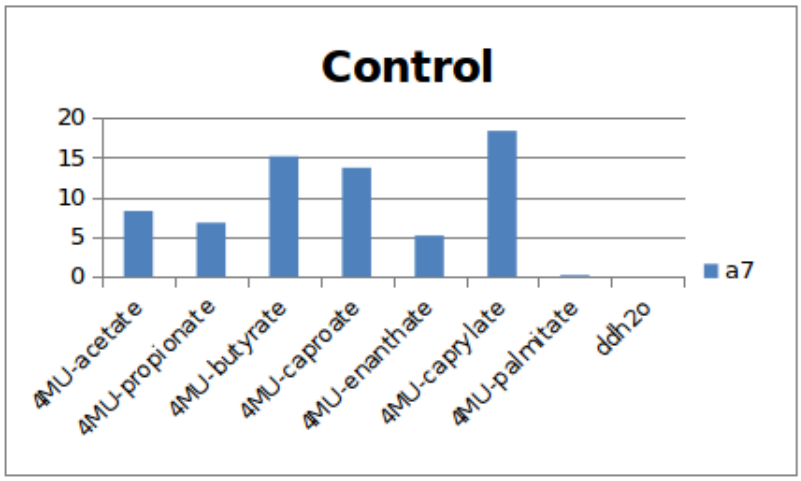


Figure 28: Substrate selectivity assay of native ANL. From the chain lengths of 2C to 16C the following lipids are used; Acetate(2C), propinate(3C), butyrate(4), caproate(6C), enatiothe(7C), caprylate(8), and palmitate (16C).

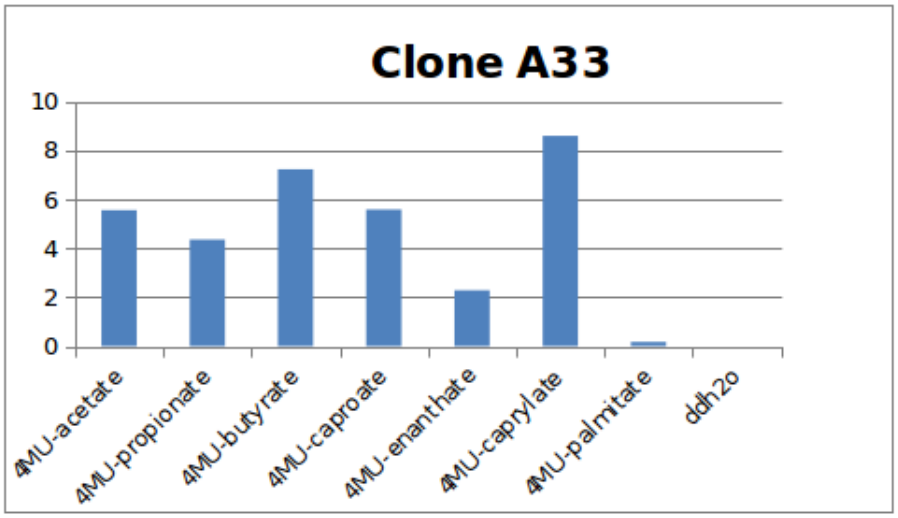


Figure 29: Substrate selectivity assay of clone A33. From the chain lengths of 2C to 16C the following lipids are used; Acetate(2C), propinate(3C), butyrate(4), caproate(6C), enatiothe(7C), caprylate(8), and palmitate (16C).

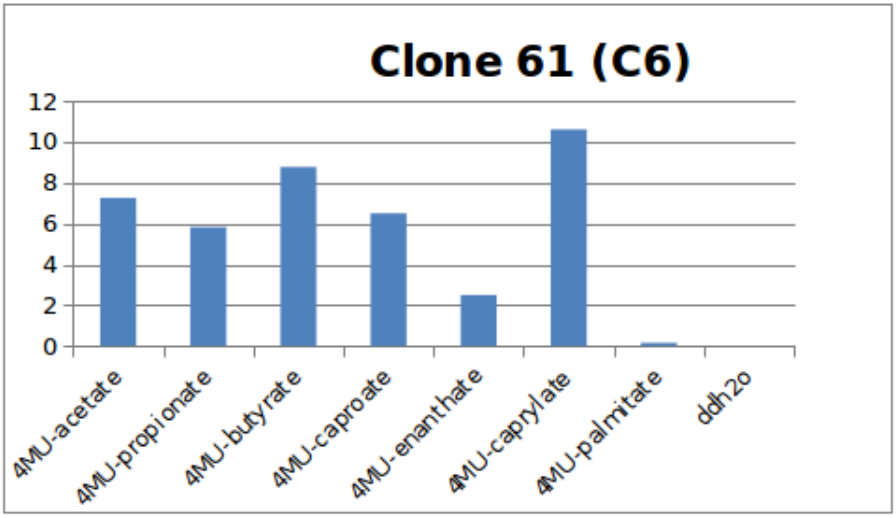


Figure 30: Substrate selectivity assay of clone 61 (C6). From the chain lengths of 2C to 16C the following lipids are used; Acetate(2C), propinate(3C), butyrate(4), caproate(6C), enatiothe(7C), caprylate(8), and palmitate (16C).

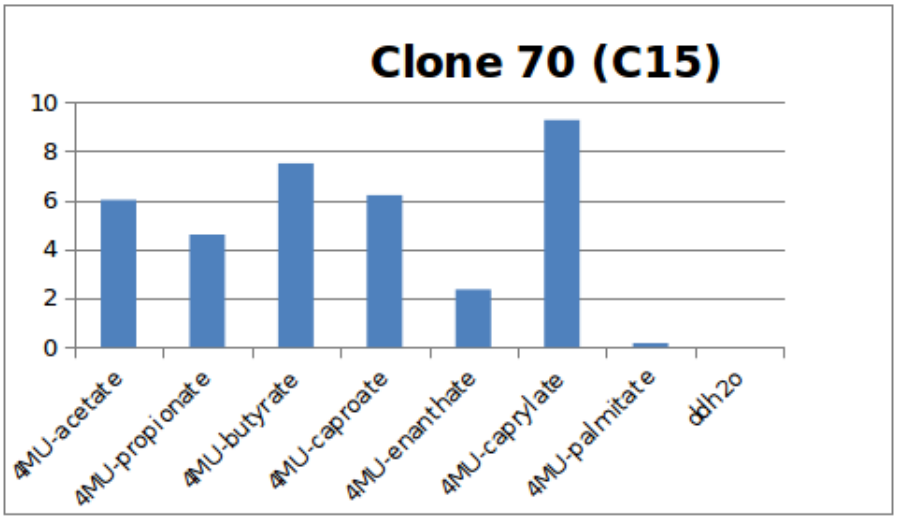


Figure 31: Substrate selectivity assay of clone 70 (C15). From the chain lengths of 2C to 16C the following lipids are used; Acetate(2C), propinate(3C), butyrate(4), caproate(6C), enatiothe(7C), caprylate(8), and palmitate (16C).

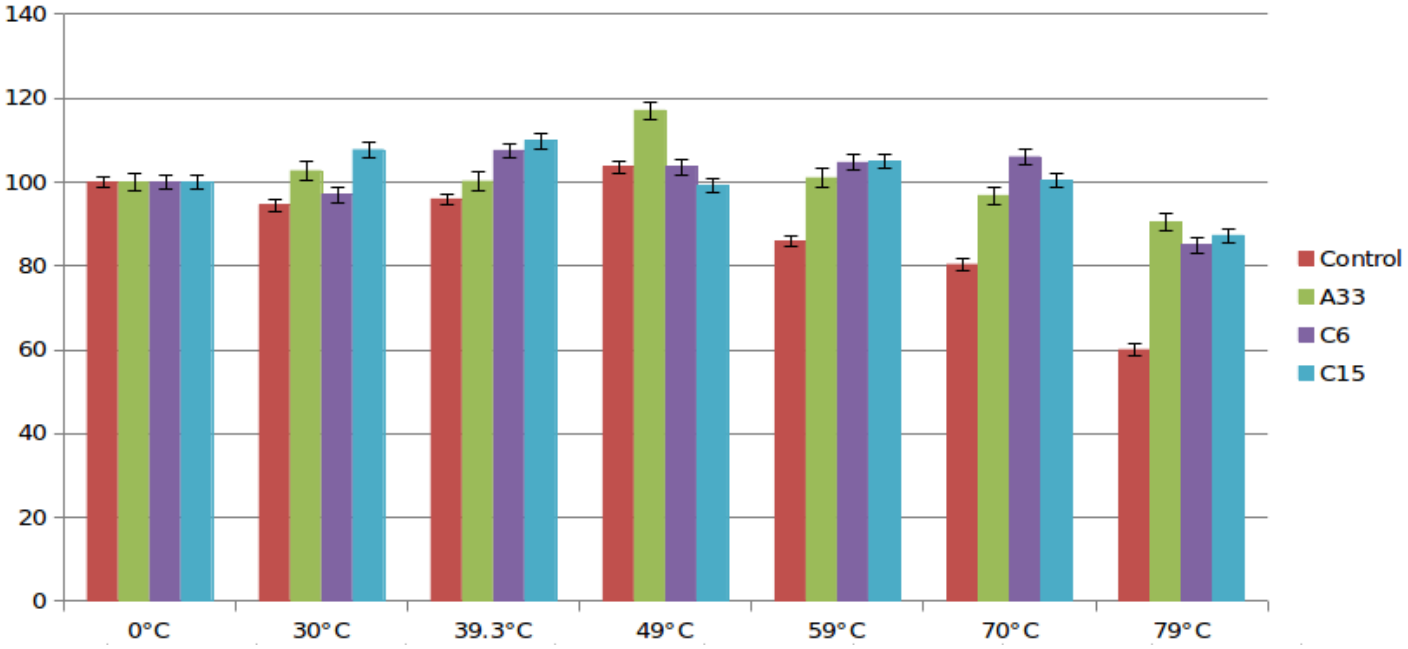


Figure 32: Thermostability assay of clone 33 (A33), 61 (C6), and 70 (C15).

Soluble fractions of the clones that do have expressions, are used in fluorescent assays to profile thermostability by quantifying the residual activity of lipases after 30 minutes of incubation at temperatures 30^{o}C, 40^{o}C, 50^{o}C, 60^{o}C, 70^{o}C, and 80^{o}C is set to 100% activity for calculating the percent activity. As it is shown at the results, C6's and C15's activity peak shifted to around 40^{o}C whereas A33's has peaked at the same with control but has higher activity on the particular temperatures. This may due to the various mutations located at the different places at the structure. Although, the activity of A33 is decreased 20% , it's thermostability is slightly better.

4 Discussion and Conclusion

Here, it is reported that DNA shuffling is a suitable methodology for generating randomly mutated lipase libraries for industrial usage. In this study, instead of family shuffling, which is a common preferred method for random mutagenesis of an enzyme, non-family shuffling has been tried. ANL, which is a fungal lipase, and BTL2, which is a bacterial lipase, were shuffled in order to obtain a mutant library which would have the desired features such as increased thermostability, and broader substrate specificity.

To the best of our knowledge, this study describes the first application of DNA-shuffling of lipases from *B. thermocatenulatus* and *Aspergillus niger*. As it can be seen from multiple alignments, the clones which are obtained from this study are not chimeric proteins. Multiple sequence alignments of the clones do not produce hits for BTL sequence and moreover, they all have at least 99% sequence identity to ANL sequence. This may due to the usage of genes from different families. Although ANL and BTL have 41% sequence homology, they didn't shuffle, as can be deduced from the results. It can be speculated that the reason for not seeing any chimeric proteins would be the slight difference in their codon usage. Due to this, the chimeric proteins couldn't have survived during the cloning selection. The reason of not seeing any BTL self-shuffled proteins would be the evolutionary difference between fungi and bacteria, since their codon usage is related to their evolutionary path as well. Evolution of synonymous codon usage is reported to be decided by a balance between mutation, genetic drift and natural selection. However, natural selection on codon usage is considered to be a weak evolutionary force and selection on codon usage is expected to be the strongest force [76]. Reported point mutations may come from self shuffling of ANL fragments which could lead to point mutations as well or it may come from the errors of the DNA polymerase. The second case is not likely since Pfu DNA polymerase is used and Pfu has high fidelity. Therefore, it can be reported that these mutations are coming from the self shuffling of the ANL fragments. There are also studies which indicate that using single genes and random point mutations which are generated by shuffling of the single gene is also a source of diversity [53, 77]. Self

shuffling or family shuffling utilizes naturally occurring nucleotide substitutions as the driving force for the evolution *in vitro*. It is also reported that multiple rounds of shuffling would increase the recombination and the mutations yield [77]. Thereby, in further studies, shuffling of the clones which are obtained from this study can be used to generate different mutations and more evolved clones.

From a single round of DNA-shuffling with these two parent lipases, three mutants (A33, C6, C15) with various point mutations have occurred, which could normally cause an activity loss (non polar - polar /charged amino acid substitution). In this case, only A33 and C6 clones show activity loss around 20% due to the point mutations. Activity loss of these clones may occur due to the mutations that are located at a close proximity to catalytic site. In A33 clone, T184E mutation which is located on the nucleophilic elbow is likely to cause the activity loss and the C6 G92D mutation may be the responsible of the activity loss due to the fact that they are close to the catalytic triad and also located at the core of the protein.

Since the aim of this project was to generate the library that could be investigated on further studies, the mutant proteins are not purified. However, substrate selectivity and thermostability assays are effectuated, with the soluble fraction of the cells to shed light on the features of the lipases as a preliminary examination. As it is mentioned at the results section, there are no changes in the substrate selectivity trend with respect to the control's substrate selectivity trend. In this case, this is expected, since the point mutations are not in close proximity with amphiphilic lid of the lipases. All three clones and the control have the highest activity against caprylate (8C) and the lowest activity against palmitate (16C).

Their thermostability features are more diverse than their substrate selectivity. As it is shown in the results, C6's and C15's activity peak shifted to around 40^oC whereas A33's has peaked at the same with control but has higher activity on the particular temperatures. This may be due to the various mutations located at the different places at the structure.

These mutations may have lead to decreased flexibility of A33 clone and therefore it might cause an increase in thermostability. Although the activity of A33 has decreased by 20% , it's thermostability is slightly better. Again this may due to synergistic effect of all point mutations but the A146D and T184E mutations could have a crucial effect on both flexibility and the activity of the protein. The reason for the thermostability shift of clone may again be caused by the G92D mutation because this mutation would lead an increase on flexibility of the protein therefore decrease in thermostability. In clone C15, there is a G176S mutation at the core of the protein and a L151P mutation at a helical structure which would break the helix and would turn it to loop or multiple helices. As it can be seen from the bar graph of thermostability, thermostability trend of clone C15 is shifted around 40^{o}C and it is more likely that this shift is caused by the L151P mutation because since proline mutation breaks the α helical structure, the flexibility of the protein would increase and therefore again it would lead to a decrease in thermostability. Although the thermostability trend is shifted in C6 and C15, their activity is not dead even in 80^{o}C. It may be caused by the other proteins in the soluble fraction of the cells. To find out the real stability of these enzymes further studies like purification and same characterization experiments should be performed.

These point mutations may affect substrate binding and/or regulate the reaction rate for the hydrolysis of the covalent reaction intermediate. Therefore, it could affect the activity change. Also, synergistic effects of mutations may occur and lead up to the getting the desired functions for the industrial applications.

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A Appendix A

A.1 DNA ladders and Experimental Protocols

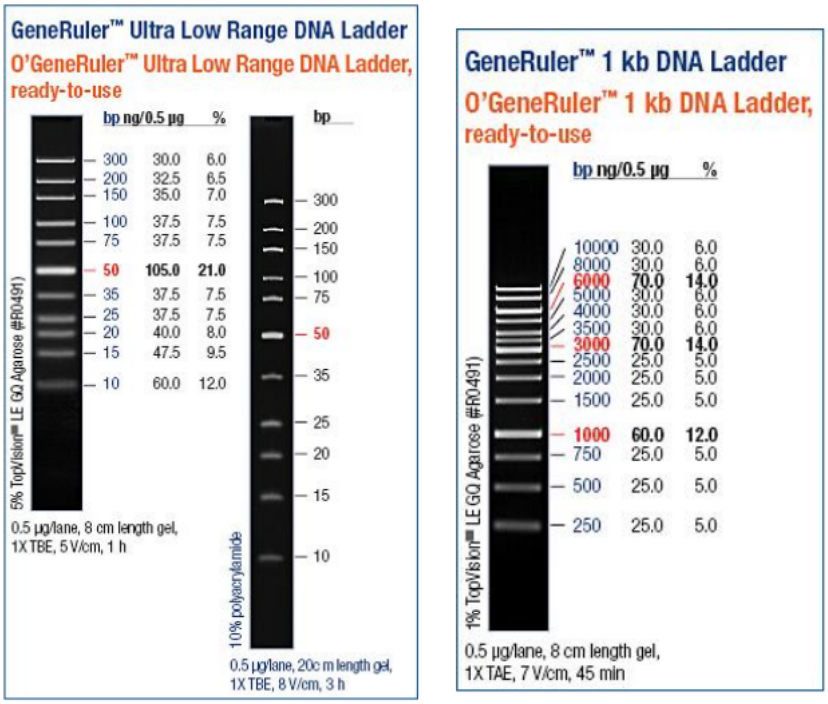

Figure A.1 : DNA molecular weight markers, Ultra low range and 1kb ladders, respectively.

A.1.1 Vector (pMCSG-7) Overnight Digest with Ssp1

pMCSG-7 (his-tagged bacterial expression vector) is a vector that is transformed into *E.coli* and expressed as 6 x His-tagged-protein complex. This vector was digested by restriction enzyme digestion. The restriction enzyme was chosen as Ssp1.

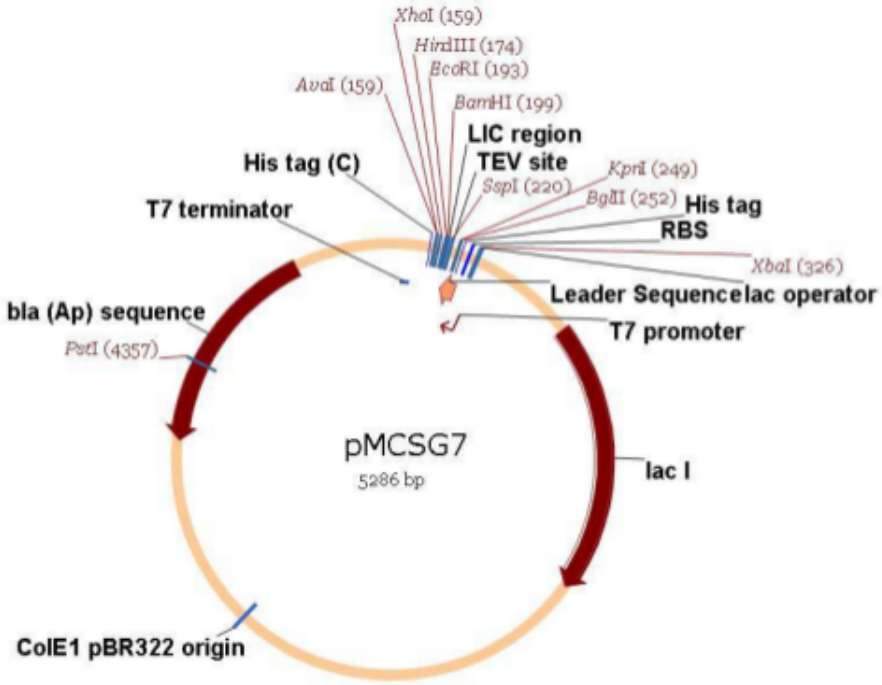

Figure A.2 : pMCSG -7 (his-tagged bacterial expression vector)

The restriction enzyme digestion of pMCSG-7 was performed according to the table below:

pMCSG-7	50μl
Ssp1	2μl
Green Buffer	6μl
ddH_20	2μl

Table A.1 : Procedure for the restriction enzyme digestion of pMCSG-7

A.1.2 Gel Electrophoresis Procedure

For the gel electrophoresis the general protocol was applied as indicated below.

- Take 50X TAE buffer, dilute it to 1X by adding 10 ml to 490 ml water.
- Weight 1 gr agarose; dissolve it in 100 ml 1X TAE buffer.
- Heat the solution until full homogeneity is obtained.
- Cool the solution; add 2 l EtBr; mix the solution to solve EtBr.
- Pour solution to the rack; place comb; wait till polymerization.
- Place the rack onto the container; fill the container with 1X TAE buffer.
- Place the samples to the wells.
- Run the machine for 30 min; later on, check the gel under UV light.
- If necessary run for additional minutes.

Gel Extraction

After the agarose gel electrophoresis of PCR products and pMCSG-7 overnight digest with Ssp1, the samples are extracted from the gel for obtaining pure reaction products.

QIAGEN- QIAquick Gel Extraction Kit Protocol was performed as listed.

1. Excise the DNA fragment from the agarose gel with a clean, sharp scalpel.
2. Weigh the gel slice in a colorless tube. Add 3 volumes Buffer QG to 1 volume gel (100 mg 100 μl). For $>$ 2% agarose gels, add 6 volumes Buffer QG.
3. Incubate at 50^{o}C for 10 min (or until the gel slice has completely dissolved). Vortex the tube every 2–3 min to help dissolve gel.
4. After the gel slice has dissolved completely, check that the color of the mixture is yellow (similar to Buffer QG without dissolved agarose). If the color of the mixture is orange or violet, add 10 μl 3 M sodium acetate, pH 5.0, and mix. The color of the mixture will turn yellow.
5. Add 1 gel volume of isopropanol to the sample and mix.
6. Place a QIAquick spin column in a provided 2 ml collection tube or into a vacuum manifold.
7. To bind DNA, apply the sample to the QIAquick column and centrifuge for 1 min or apply vacuum to the manifold until all the samples have passed through the column. Discard flow- through and place the QIAquick column back into the same tube. For sample volumes of $>$ 800 μl, load and spin/apply vacuum again.

8. If the DNA will subsequently be used for sequencing, *in vitro* transcription, or micro injection, add 0.5 ml Buffer QG to the QIAquick column and centrifuge for 1 min or apply vacuum. Discard flow-through and place the QIAquick column back into the same tube.

9. To wash, add 0.75 ml Buffer PE to QIAquick column and centrifuge for 1 min or apply vacuum. Discard flow-through and place the QIAquick column back into the same tube.
   Note: If the DNA will be used for salt-sensitive applications (e.g., sequencing, blunt-ended ligation), let the column stand 2–5 min after addition of Buffer PE.

10. Centrifuge the QIAquick column once more in the provided 2 ml collection tube for 1 min at 17,900 x *g* (13,000 rpm) to remove residual wash buffer.

11. Place QIAquick column into a clean 1.5 ml micro centrifuge tube.

12. To elute DNA, add 50 μl Buffer EB (10 mM Tris · Cl, pH 8.5) or water to the center of the QIAquick membrane and centrifuge the column for 1 min. For increased DNA concentration, add 30 μl Buffer EB to the center of the QIAquick Membrane, let the column stand for 1 min, and then centrifuge for 1 min. After the addition of Buffer EB to the QIAquick membrane, increasing the incubation time to up to 4 min can increase the yield of purified DNA.

13. If the purified DNA is to be analyzed on a gel, add 1 volume of Loading Dye to 5 volumes of purified DNA. Mix the solution by pipetting up and down before loading the gel.

A.1.3 T4 DNA Polymerase Reaction

For ligation independent cloning vector and insert were modified according to T4 DNA Polymerase reaction which creates guanine overhangs for vector and cytosine overhangs for insert.

Vector	Volume	Insert	Volume
ddH_2O	-	ddH_2O	1 µL
5X Buffer	16 µL	5X Buffer	14 µL
T4 Polymerase	3 µL	T4 Polymerase	3 µL
dGTP	2 µL	dCTP	2 µL
DNA	60 µL	DNA	50 µL
V_{final}	80 µL	V_{Final}	70 µL

Reaction Condition	20°C	60'
Inactivation Condition	75°C	20'

Table A.2 : T4 DNA Polymerase Reaction Program

A.1.4 Phenol/Chloroform Extraction and Ethanol Precipitation

Phenol/Chloroform extraction and ethanol precipitation is carried out for both vector and insert in separate tubes based on the following procedure.

- Product of T4 DNA polymerase reaction for vector (80 μl) was completed up to 100 μl with ddH_2O
- Product of T4 DNA polymerase reaction for insert (70 μl) was completed up to 100 μl with ddH_2O.
- Addition of 1:1 ratio phenol/chloroform (100 μl) into both tubes.
- Vortex
- 5' of top speed centrifuge (13.2 rpm)
- Take supernatant
- Addition of 4 μl NaOAc, 10 μl LPA and 250 μl EtOH (%100)
- Keep the tubes at-80^{o}C for 20'
- 15' Top speed centrifuge (13,2 rpm)
- Discard the supernatant
- Addition of 250 μl EtOH (%70) onto the pellet
- 10' Top speed centrifuge
- Discard the supernatant
- Re-suspend the pellet with 10 μl of ddH_2

A.1.5 Annealing Reaction

Purified vector and insert were combined together by annealing reaction at 22^{o}C for 45'– 60'.

	Control	Sample
Vector	150 ng	150 ng
Insert	-------	100 ng

Table A.3 : Annealing reaction

A.1.6 Transformation to Shuffle Competent Cells

For the transformation of plasmid into the competent cell, the following procedure was carried out.

- Mix 2 μL product of annealing reaction with 200 μL of each competent cells
- Keep on ice for 20'
- Heat shock for 1' at strictly at 42^{o}C
- Keep on ice for 10'
- Addition of 800 μL SOC
- Incubation at 37^{o}C for 60'
- Centrifuge at 7000 rpm for 2'
- Discard the supernatant until 100 μL of supernatant remains
- Re-suspend the pellet in 100 μL of supernatant
- Spread on LB agar plate with beads.
- Incubation at 37^{o}C for 24–48 hours.

A.1.7 Colony PCR and Mini-prep Protocol

Taq Polymerase MM	7,5 µL
Reverse Primer	0,75 µL
Forward Primer	0,75 µL
ddH2O	6 µL
V_{final}	15 µL

Table A.4 : Colony PCR

Positive colonies are taken from the previously streaked plate and inoculated into 5 mL of LB broth. Overnight incubation was performed at 37^oC shaker. The 5 mL of cultures were centrifuged for 5' at the top speed. The supernatants were discarded and QIAGEN-Plasmid DNA Purification Kit was performed on pellets.

QIAGEN - Plasmid DNA Purification Kit Protocol:

1. Re-suspend pelleted bacterial cells in 250 μl Buffer P1 and transfer to a 1.7ml micro-centrifuge tube. No cell clumps should be visible after resuspension of the pellet. The bacteria should be resuspended completely by vortexing or pipetting up and down until no cell clumps remain.

2. Add 250 μl Buffer P2 and mix thoroughly by inverting the tube 4–6 times. Do not vortex, as this will result in shearing of genomic DNA. If necessary, continue inverting the tube until the solution becomes viscous and slightly clear. Do not allow the lysis reaction to proceed for more than 5 min. If LyseBlue has been added to Buffer P1, the cell suspension will turn blue after addition of Buffer P2. Mixing should result in a homogeneously colored suspension. If the suspension contains localized colorless regions or if brownish cell clumps are still visible, continue mixing the solution until a homogeneously colored suspension is achieved.

3. Add 350 μl Buffer N3; mix immediately and thoroughly by inverting the tube 4–6 times. Keep on ice for 10 mins. To avoid localized precipitation, mix the solution thoroughly, immediately after addition of Buffer N3. The solution should become cloudy. If LyseBlue reagent has been used, the suspension should be mixed until all trace of blue has gone and the suspension is colorless.

4. Centrifuge for 10 min at 13,000 rpm (17,900 x g) in a table-top micro-centrifuge. A compact white pellet will form.

5. Apply the supernatants from step 4 to the QIAprep spin column by decanting or pipetting.

6. Centrifuge for 30 – 60 sec. Discard the flow-through.

7. Wash QIAprep spin column by adding 0.75 ml Buffer PE and centrifuging for 30 – 60 sec.

8. Discard the flow-through, and centrifuge for an additional 1 min to remove residual wash buffer.
   Important: Residual wash buffer will not be completely removed unless the flow-through is discarded before this additional centrifugation. Residual ethanol from Buffer PE may inhibit subsequent enzymatic reactions.

9. Place the QIAprep column in a clean 1.5 ml micro-centrifuge tube. To elute DNA, add 50 μl Buffer EB (10 mM Tris·Cl, pH 8.5) or water to the center of each QIAprep spin column, let stand for 1 min, and centrifuge for 1 min.

A.1.8 Expression

- Take positive clones from each transformation plates (Shuffle) by tips.
- Add them to 5 ml LB Broth with 5 μl Ampicillin (1000X)
- After overnight growth at 37^{o}C, take glycerol stocks of each cell culture (200 μl 60% Glycerol + 600 μl cell culture)
- Transfer cell cultures to 30 ml LB Broth with 30 μl Ampicillin (1000X)
- Take 1 ml sample from each of the cultures and label them as t_0
- Add IPTG when efficient optimal density is reached.
- For expression of the proteins wait for 8 hours.
- Centrifuge samples for 15 minutes at 4000 rpm.
- Add sufficient amount of B-PER according to the pellet amount (between 100 μl -250 μl)
- Centrifuge samples for 5 minutes at 13.2 rpm.
- Take 20 μl sample from supernatant and mix with 4 μl dye mix (loading dye + DTT)
- Load the samples and run SDS-PAGE electrophoresis and carry out the characterization step.

A.2 Multiple Sequence Alignments

	01	02	03	04	05	06	07	08	09	10	11	12
A	Strip .. 864/869..	Strip .. 862/864..	Strip .. 861/863..	Strip .. 862/863..	Strip .. 677/712..	Strip .. 0/0/895	Strip .. 20/20/894	Strip .. 859/863..	Strip .. 0/0/895	Strip .. 857/859..		
B	2 Rever.. 865/867..	10 Reve.. 858/858..	18 Reve.. 858/859..	26 Reve.. 858/858..	34 Reve.. 855/858..	42 Reve.. 0/0/895	50 Reve.. 0/0/895	58 Reve.. 858/858..	66 Reve.. 0/0/895	74 Reve.. 0/0/895		
C	3 Rever.. 862/862..	11 Reve.. 862/867..	19 Reve.. 859/860..	27 Reve.. 859/860..	35 Reve.. 864/865..	43 Reve.. 859/860..	51 Reve.. 860/865..	59 Reve.. 0/0/895	67 Reve.. 855/862..	75 Reve.. 849/859..		
D	4 Rever.. 854/857..	12 Reve.. 853/866..	20 Reve.. 855/857..	28 Reve.. 817/824..	36 Reve.. 0/0/895	44 Reve.. 778/789..	52 Reve.. 860/863..	60 Reve.. 860/860..	68 Reve.. 851/863..			
E	5 Rever.. 861/863..	13 Reve.. 863/863..	21 Reve.. 865/865..	29 Reve.. 0/0/895	37 Reve.. 833/836..	45 Reve.. 857/859..	53 Reve.. 0/0/895	61 Reve.. 859/863..	69 Reve.. 850/857..			
F	6 Rever.. 860/862..	14 Reve.. 790/797..	22 Reve.. 860/862..	30 Reve.. 858/860..	38 Reve.. 862/863..	46 Reve.. 857/858..	54 Reve.. 860/860..	62 Reve.. 858/859..	70 Reve.. 860/864..			
G	7 Rever.. 860/860..	15 Reve.. 0/0/895	23 Reve.. 854/858..	31 Reve.. 0/0/895	39 Reve.. 856/860..	47 Reve.. 0/0/895	55 Reve.. 0/0/895	63 Reve.. 862/863..	71 Reve.. 859/860..			
H	8 Rever.. 857/858..	16 Reve.. 861/862..	24 Reve.. 0/0/895	32 Reve.. 863/864..	40 Reve.. 0/0/895	48 Reve.. 0/0/895	56 Reve.. 0/0/895	64 Reve.. 853/859..	72 Reve.. 0/0/895			

Color Overview (Alignment Percentage)	Identities >= 90%	90% > Identities >= 75%	75% > Identities >= 60%	Identities < 60%

Figure A.2: The scheme of multiple sequence alignments of the clones against native ANL.

```
 Score = 1673 bits (844), Expect = 0.0
 Identities = 864/869 (99%), Gaps = 2/869 (0%)
 Strand = Plus / Minus

Query: 12  aaagtncnacaagtgagccanaacgtccaccgttgcttcgcctgcattccccgccgtcga 71
           ||||| | ||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct: 867 aaagtaccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcga 808

Query: 72  attgattccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggt 131
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 807 attgattccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggt 748

Query: 132 gatccagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggac 191
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 747 gatccagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggac 688

Query: 192 gatgtcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctc 251
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 687 gatgtcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctc 628

Query: 252 ggccagcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataacc 311
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 627 ggccagcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataacc 568

Query: 312 gtcatttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggt 371
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 567 gtcatttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggt 508

Query: 372 gaagtagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagatt 431
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 507 gaagtagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagatt 448

Query: 432 gtctgcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagag 491
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 447 gtctgcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagag 388

Query: 492 gtcatcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctact 551
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 387 gtcatcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctact 328

Query: 552 gcctcggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgt 611
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 327 gcctcggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgt 268

Query: 612 gcctccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgac 671
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 267 gcctccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgac 208

Query: 672 tgatggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcga 731
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Sbjct: 207 tgatggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcga 148

Query: 732 gcaataagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcga 791
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Sbjct: 147 gcaataagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcga 88

Query: 792 gacactccgcacatcaagttggtgtcggtgccgcagcactcagcgcagcgtgcgccgttc 851
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Sbjct: 87  gacactccgcacatcaag-tggtgtcggtgccgcagcactcagcgcagcgtgcgccg-tc 30

Query: 852 aaaagcactccaaaccgtccagagaacat 880
           |||||||||||||||||||||||||||||
Sbjct: 29  aaaagcactccaaaccgtccagagaacat 1
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Figure A.3: Clone A1

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 Score = 1707 bits (861), Expect = 0.0
 Identities = 865/867 (99%)
 Strand = Plus / Minus

Query: 15  aaagnacnacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcga 74
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Sbjct: 867 aaagtaccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcga 808

Query: 75  attgattccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggt 134
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 807 attgattccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggt 748

Query: 135 gatccagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggac 194
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 747 gatccagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggac 688

Query: 195 gatgtcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctc 254
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 687 gatgtcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctc 628

Query: 255 ggccagcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataacc 314
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 627 ggccagcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataacc 568

Query: 315 gtcatttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggt 374
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 567 gtcatttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggt 508

Query: 375 gaagtagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagatt 434
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 507 gaagtagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagatt 448

Query: 435 gtctgcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagag 494
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Sbjct: 447 gtctgcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagag 388

Query: 495 gtcatcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctact 554
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Sbjct: 387 gtcatcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctact 328

Query: 555 gcctcggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgt 614
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Sbjct: 327 gcctcggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgt 268

Query: 615 gcctccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgac 674
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Sbjct: 267 gcctccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgac 208

Query: 675 tgatggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcga 734
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Sbjct: 207 tgatggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcga 148

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Sbjct: 147 gcaataagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcga 88

Query: 795 gacactccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaa 854
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Sbjct: 87  gacactccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaa 28

Query: 855 aagcactccaaaccgtccagagaacat 881
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Sbjct: 27  aagcactccaaaccgtccagagaacat 1
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Figure A.4: Clone A2

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 Score = 1709 bits (862), Expect = 0.0
 Identities = 862/862 (100%)
 Strand = Plus / Minus

Query: 18  accacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattga 77
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Sbjct: 862 accacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattga 803


Query: 78  ttccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatcc 137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 802 ttccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatcc 743


Query: 138 agtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgt 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 742 agtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgt 683


Query: 198 cgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcca 257
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Sbjct: 682 cgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcca 623


Query: 258 gcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcat 317
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Query: 318 ttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagt 377
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Query: 378 agagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctg 437
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Sbjct: 442 cagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcat 383


Query: 498 cgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctc 557
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Sbjct: 382 cgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctc 323


Query: 558 ggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctc 617
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Sbjct: 322 ggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctc 263


Query: 618 caaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatg 677
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Sbjct: 262 caaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatg 203


Query: 678 gacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaat 737
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Query: 738 aagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacac 797
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Sbjct: 142 aagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacac 83


Query: 798 tccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagca 857
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Sbjct: 82  tccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagca 23


Query: 858 ctccaaaccgtccagagaacat 879
           ||||||||||||||||||||||
Sbjct: 22  ctccaaaccgtccagagaacat 1
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Figure A.5: Clone A3

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 Score = 1671 bits (843), Expect = 0.0
 Identities = 854/857 (99%), Gaps = 1/857 (0%)
 Strand = Plus / Minus

Query: 22  agtgngccaaaacgnccaccgttgcttcgcctgcattccccgccgtcgaattgattccct 81
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Sbjct: 856 agtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattccct 797

Query: 82  cgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagtatt 141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 796 cgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagtatt 737

Query: 142 ctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgttca 201
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 736 ctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgttca 677

Query: 202 agtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgcat 261
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 676 agtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgcat 617

Query: 262 agtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcgca 321
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 616 agtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcgca 557

Query: 322 agaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagaggg 381
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 556 agaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagaggg 497

Query: 382 tatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagcgg 441
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 496 tatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagcgg 437

Query: 442 cttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgttat 501
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 436 cttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgttat 377

Query: 502 cttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaagg 561
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 376 cttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaagg 317

Query: 562 cgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaagt 621
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 316 cgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaagt 257

Query: 622 tatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggacagg 681
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 256 tatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggacagg 197

Query: 682 cgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagctg 741
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 196 cgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagctg 137

Query: 742 cggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccgca 801
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 136 cggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccgca 77

Query: 802 catcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaaagcactcca 861
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct: 76  catcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtc-aaaagcactcca 18

Query: 862 aaccgtccagagaacat 878
           |||||||||||||||||
Sbjct: 17  aaccgtccagagaacat 1
```

Figure A.6: Clone A4

```
 Score = 1699 bits (857), Expect = 0.0
 Identities = 861/863 (99%)
 Strand = Plus / Minus


Query: 16  tacnacaagtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattg 75
           ||| ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 863 taccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattg 804


Query: 76  attccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatc 135
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 803 attccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatc 744


Query: 136 cagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatg 195
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 743 cagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatg 684


Query: 196 tcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcc 255
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 683 tcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcc 624


Query: 256 agcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtca 315
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 623 agcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtca 564


Query: 316 tttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaag 375
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 563 tttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaag 504


Query: 376 tagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtct 435
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 503 tagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtct 444


Query: 436 gcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtca 495
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 443 gcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtca 384


Query: 496 tcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcct 555
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 383 tcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcct 324


Query: 556 cggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcct 615
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 323 cggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcct 264


Query: 616 ccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgat 675
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 263 ccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgat 204


Query: 676 ggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaa 735
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 203 ggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaa 144


Query: 736 taagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagaca 795
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 143 taagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagaca 84


Query: 796 ctccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagc 855
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 83  ctccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagc 24


Query: 856 actccaaaccgtccagagaacat 878
           |||||||||||||||||||||||
Sbjct: 23  actccaaaccgtccagagaacat 1
```

Figure A.7: Clone A5

```
 Score = 1697 bits (856), Expect = 0.0
 Identities = 860/862 (99%)
 Strand = Plus / Minus

Query: 18  accacaagtgngccanaacgtccaccgttgcttcgcctgcattccccgccgtcgaattga 77
           |||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 862 accacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattga 803

Query: 78  ttccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatcc 137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 802 ttccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatcc 743

Query: 138 agtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgt 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 742 agtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgt 683

Query: 198 cgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcca 257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 682 cgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcca 623

Query: 258 gcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcat 317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 622 gcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcat 563

Query: 318 ttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagt 377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 562 ttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagt 503

Query: 378 agagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctg 437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 502 agagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctg 443

Query: 438 cagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcat 497
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 442 cagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcat 383

Query: 498 cgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctc 557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 382 cgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctc 323

Query: 558 ggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctc 617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 322 ggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctc 263

Query: 618 caaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatg 677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 262 caaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatg 203

Query: 678 gacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaat 737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 202 gacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaat 143

Query: 738 aagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacac 797
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 142 aagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacac 83

Query: 798 tccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagca 857
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 82  tccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagca 23

Query: 858 ctccaaaccgtccagagaacat 879
           ||||||||||||||||||||||
Sbjct: 22  ctccaaaccgtccagagaacat 1
```

Figure A.8: Clone A6

```
 Score = 1705 bits (860), Expect = 0.0
 Identities = 860/860 (100%)
 Strand = Plus / Minus

Query: 20  cacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgatt 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 860 cacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgatt 801


Query: 80  ccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccag 139
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 800 ccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccag 741


Query: 140 tattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcg 199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 740 tattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcg 681


Query: 200 ttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagc 259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 680 ttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagc 621


Query: 260 gcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcattt 319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 620 gcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcattt 561


Query: 320 cgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtag 379
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 560 cgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtag 501


Query: 380 agggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgca 439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 500 agggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgca 441


Query: 440 gcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcg 499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 440 gcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcg 381


Query: 500 ttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgg 559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 380 ttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgg 321


Query: 560 aaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcca 619
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 320 aaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcca 261


Query: 620 aagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgga 679
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 260 aagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgga 201


Query: 680 caggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataa 739
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 200 caggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataa 141


Query: 740 gctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactc 799
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 140 gctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactc 81


Query: 800 cgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcact 859
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 80  cgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcact 21


Query: 860 ccaaaccgtccagagaacat 879
           ||||||||||||||||||||
Sbjct: 20  ccaaaccgtccagagaacat 1
```

Figure A.9: Clone A7

```
 Score = 1695 bits (855), Expect = 0.0
 Identities = 857/858 (99%)
 Strand = Plus / Minus

Query: 22  caagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 81
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 858 caagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 799

Query: 82  ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 798 ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 739

Query: 142 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 201
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 738 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 679

Query: 202 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 261
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 678 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 619

Query: 262 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 321
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 618 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 559

Query: 322 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 381
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 558 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 499

Query: 382 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 441
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 498 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 439

Query: 442 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 501
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 438 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 379

Query: 502 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 561
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 378 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 319

Query: 562 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 621
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 318 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 259

Query: 622 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 681
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 258 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 199

Query: 682 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 741
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 198 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 139

Query: 742 tgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccg 801
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 138 tgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccg 79

Query: 802 cacatcaagtggtgtcggtgccgcagcactcagcgcagngtgcgccgtcaaaagcactcc 861
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct: 78  cacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcactcc 19

Query: 862 aaaccgtccagagaacat 879
           ||||||||||||||||||
Sbjct: 18  aaaccgtccagagaacat 1
```

Figure A.10: Clone A8

```
 Score = 1681 bits (848), Expect = 0.0
 Identities = 862/864 (99%), Gaps = 2/864 (0%)
 Strand = Plus / Minus

Query: 18  accacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattga 77
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 862 accacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattga 803

Query: 78  ttccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatcc 137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 802 ttccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatcc 743

Query: 138 agtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgt 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 742 agtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgt 683

Query: 198 cgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcca 257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 682 cgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcca 623

Query: 258 gcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcat 317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 622 gcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcat 563

Query: 318 ttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagt 377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 562 ttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagt 503

Query: 378 agagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctg 437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 502 agagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctg 443

Query: 438 cagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcat 497
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 442 cagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcat 383

Query: 498 cgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctc 557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 382 cgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctc 323

Query: 558 ggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctc 617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 322 ggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctc 263

Query: 618 caaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatg 677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 262 caaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatg 203

Query: 678 gacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaat 737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 202 gacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaat 143

Query: 738 aagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacac 797
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 142 aagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacac 83

Query: 798 tccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcn 857
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 82  tccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagc- 24

Query: 858 actccaaaccgtcccagagaacat 881
           |||||||||||| ||||||||||
Sbjct: 23  actccaaaccgt-ccagagaacat 1
```

Figure A.11: Clone A9

```
 Score = 1701 bits (858), Expect = 0.0
 Identities = 858/858 (100%)
 Strand = Plus / Minus

Query: 20  caagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 858 caagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 799

Query: 80  ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 139
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 798 ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 739

Query: 140 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 738 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 679

Query: 200 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 678 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 619

Query: 260 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 618 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 559

Query: 320 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 379
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 558 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 499

Query: 380 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 498 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 439

Query: 440 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 438 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 379

Query: 500 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 378 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 319

Query: 560 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 619
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 318 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 259

Query: 620 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 679
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 258 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 199

Query: 680 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 739
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 198 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 139

Query: 740 tgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccg 799
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 138 tgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccg 79

Query: 800 cacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcactcc 859
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 78  cacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcactcc 19

Query: 860 aaaccgtccagagaacat 877
           ||||||||||||||||||
Sbjct: 18  aaaccgtccagagaacat 1
```

Figure A.12: Clone A10

```
 Score = 1649 bits (832), Expect = 0.0
 Identities = 862/867 (99%), Gaps = 4/867 (0%)
 Strand = Plus / Minus


Query: 14  taccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattg 73
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 863 taccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattg 804


Query: 74  attccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatc 133
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 803 attccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatc 744


Query: 134 cagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatg 193
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 743 cagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatg 684


Query: 194 tcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcc 253
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 683 tcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcc 624


Query: 254 agcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtca 313
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 623 agcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtca 564


Query: 314 tttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaag 373
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 563 tttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaag 504


Query: 374 tagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtct 433
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 503 tagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtct 444


Query: 434 gcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtca 493
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 443 gcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtca 384


Query: 494 tcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcct 553
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 383 tcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcct 324


Query: 554 cggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcct 613
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 323 cggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcct 264


Query: 614 ccaaagttatttgtcaggtcaaactccagcagnatcttggtgctcgcctcctcgactgat 673
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct: 263 ccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgat 204


Query: 674 ggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaa 733
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 203 ggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaa 144


Query: 734 taagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagaca 793
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 143 taagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagaca 84


Query: 794 ctccgcacatcaagtggtgtcggtgccgcagcactcaggcgcagcgtgcgccgtcaaana 853
           |||||||||||||||||||||||||||||||||| |||||||||||||||||||| |
Sbjct: 83  ctccgcacatcaagtggtgtcggtgccgcagcactca-gcgcagcgtgcgccgtcaaa-a 26


Query: 854 gcactcccaaaccgttccagagaacat 880
           ||||| |||||||| ||||||||||||
Sbjct: 25  gcact-ccaaaccg-tccagagaacat 1
```

Figure A.13: Clone A11

```
 Score = 1540 bits (777), Expect = 0.0
 Identities = 853/866 (98%), Gaps = 10/866 (1%)
 Strand = Plus / Minus


Query: 23  agtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattccct 82
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 856 agtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattccct 797


Query: 83  cgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagtatt 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 796 cgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagtatt 737


Query: 143 ctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgttca 202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 736 ctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgttca 677


Query: 203 agtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgcat 262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 676 agtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgcat 617


Query: 263 agtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcgca 322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 616 agtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcgca 557


Query: 323 agaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagaggg 382
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 556 agaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagaggg 497


Query: 383 tatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagcgg 442
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 496 tatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagcgg 437


Query: 443 cttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgttat 502
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 436 cttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgttat 377


Query: 503 cttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaagg 562
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 376 cttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaagg 317


Query: 563 cgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaaag 622
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct: 316 cgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcc-aaag 258


Query: 623 ttattttgtcaggtcaaactccagcagcatcttggtgctcgccctcctcgactgatggac 682
           ||| ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct: 257 tta-tttgtcaggtcaaactccagcagcatcttggtgctcg-cctcctcgactgatggac 200


Query: 683 aggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgntcgagcaataag 742
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct: 199 aggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataag 140


Query: 743 ctgcggcagaccattgcgagaacaatttgcagctcatccaacgtggaagtcgagacactc 802
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct: 139 ctgcggcagaccattgcgagaacaa-ttgcagctcatccaacgtggaagtcgagacactc 81


Query: 803 cgccacatctaagtggtgtcggtgcccgcagcactcagngcagcgtgcgcccgtcaaaag 862
           || |||||| |||||||||||||| |||||||||||||| |||||||||| ||||||||||
Sbjct: 80  cg-cacatc-aagtggtgtcggtg-ccgcagcactcagcgcagcgtgcg-ccgtcaaaag 25


Query: 863 ccactcccaaaccgtccagagaacat 888
            |||| ||||||||||||||||||||
Sbjct: 24  -cact-ccaaaccgtccagagaacat 1
```

Figure A.14: Clone A12

```
 Score = 1711 bits (863), Expect = 0.0
 Identities = 863/863 (100%)
 Strand = Plus / Minus

Query: 16  taccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattg 75
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 863 taccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattg 804

Query: 76  attccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatc 135
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 803 attccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatc 744

Query: 136 cagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatg 195
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 743 cagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatg 684

Query: 196 tcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcc 255
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 683 tcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcc 624

Query: 256 agcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtca 315
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 623 agcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtca 564

Query: 316 tttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaag 375
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 563 tttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaag 504

Query: 376 tagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtct 435
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 503 tagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtct 444

Query: 436 gcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtca 495
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 443 gcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtca 384

Query: 496 tcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcct 555
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 383 tcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcct 324

Query: 556 cggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcct 615
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 323 cggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcct 264

Query: 616 ccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgat 675
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 263 ccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgat 204

Query: 676 ggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaa 735
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 203 ggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaa 144

Query: 736 taagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagaca 795
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 143 taagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagaca 84

Query: 796 ctccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagc 855
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 83  ctccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagc 24

Query: 856 actccaaaccgtccagagaacat 878
           ||||||||||||||||||||||
Sbjct: 23  actccaaaccgtccagagaacat 1
```

Figure A.15: Clone A13

```
 Score = 1509 bits (761), Expect = 0.0
 Identities = 790/797 (99%), Gaps = 3/797 (0%)
 Strand = Plus / Minus


Query: 22  caagtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 81
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 858 caagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 799


Query: 82  ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 798 ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 739


Query: 142 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 201
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 738 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 679


Query: 202 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 261
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 678 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 619


Query: 262 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 321
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 618 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 559


Query: 322 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 381
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 558 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 499


Query: 382 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 441
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 498 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 439


Query: 442 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 501
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 438 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 379


Query: 502 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 561
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 378 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 319


Query: 562 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 621
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 318 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 259


Query: 622 gttatttgtcaggtcaaactccagcagnatcttggtgctcgcctcctcgactgatggaca 681
           |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct: 258 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 199


Query: 682 ggtcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataag 741
           || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 198 gg-cgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataag 140


Query: 742 ctgcggcagaccattgcgagaacaattgcagctcatcccnacgtgggaagtcgagacact 801
           |||||||||||||||||||||||||||||||||| || |||| ||||||||||||||||
Sbjct: 139 ctgcggcagaccattgcgagaacaattgcagctcat-ccaacgt-ggaagtcgagacact 82


Query: 802 ccgcacatcaagnggtg 818
           |||||||||||| ||||
Sbjct: 81  ccgcacatcaagtggtg 65
```

Figure A.16: Clone A14

```
 Score = 1703 bits (859), Expect = 0.0
 Identities = 861/862 (99%)
 Strand = Plus / Minus

Query: 18  accacaagtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattga 77
           |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 862 accacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattga 803

Query: 78  ttccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatcc 137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 802 ttccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatcc 743

Query: 138 agtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgt 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 742 agtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgt 683

Query: 198 cgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcca 257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 682 cgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcca 623

Query: 258 gcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcat 317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 622 gcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcat 563

Query: 318 ttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagt 377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 562 ttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagt 503

Query: 378 agagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctg 437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 502 agagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctg 443

Query: 438 cagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcat 497
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 442 cagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcat 383

Query: 498 cgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctc 557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 382 cgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctc 323

Query: 558 ggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctc 617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 322 ggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctc 263

Query: 618 caaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatg 677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 262 caaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatg 203

Query: 678 gacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaat 737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 202 gacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaat 143

Query: 738 aagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacac 797
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 142 aagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacac 83

Query: 798 tccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagca 857
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 82  tccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagca 23

Query: 858 ctccaaaccgtccagagaacat 879
           ||||||||||||||||||||||
Sbjct: 22  ctccaaaccgtccagagaacat 1
```

Figure A.17: Clone A16

```
 Score = 1699 bits (857), Expect = 0.0
 Identities = 861/863 (99%)
 Strand = Plus / Minus

Query: 16  tacnacaagtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattg 75
           ||| ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 863 taccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattg 804

Query: 76  attccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatc 135
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 803 attccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatc 744

Query: 136 cagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatg 195
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 743 cagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatg 684

Query: 196 tcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcc 255
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 683 tcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcc 624

Query: 256 agcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtca 315
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 623 agcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtca 564

Query: 316 tttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaag 375
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 563 tttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaag 504

Query: 376 tagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtct 435
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 503 tagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtct 444

Query: 436 gcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtca 495
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 443 gcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtca 384

Query: 496 tcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcct 555
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 383 tcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcct 324

Query: 556 cggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcct 615
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 323 cggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcct 264

Query: 616 ccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgat 675
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 263 ccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgat 204

Query: 676 ggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaa 735
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 203 ggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaa 144

Query: 736 taagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagaca 795
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 143 taagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagaca 84

Query: 796 ctccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagc 855
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 83  ctccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagc 24

Query: 856 actccaaaccgtccagagaacat 878
           |||||||||||||||||||||||
Sbjct: 23  actccaaaccgtccagagaacat 1
```

Figure A.18: Clone A17

```
 Score = 1697 bits (856), Expect = 0.0
 Identities = 858/859 (99%)
 Strand = Plus / Minus

Query: 18  acaagtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattc 77
           ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 859 acaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattc 800


Query: 78  cctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagt 137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 799 cctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagt 740


Query: 138 attctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgt 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 739 attctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgt 680


Query: 198 tcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcg 257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 679 tcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcg 620


Query: 258 catagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttc 317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 619 catagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttc 560


Query: 318 gcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtaga 377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 559 gcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtaga 500


Query: 378 gggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcag 437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 499 gggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcag 440


Query: 438 cggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgt 497
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 439 cggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgt 380


Query: 498 tatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgga 557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 379 tatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgga 320


Query: 558 aggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaa 617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 319 aggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaa 260


Query: 618 agttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggac 677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 259 agttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggac 200


Query: 678 aggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataag 737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 199 aggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataag 140


Query: 738 ctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactcc 797
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 139 ctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactcc 80


Query: 798 gcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcactc 857
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 79  gcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcactc 20


Query: 858 caaaccgtccagagaacat 876
           ||||||||||||||||||
Sbjct: 19  caaaccgtccagagaacat 1
```

Figure A.19: Clone A18

```
 Score = 1699 bits (857), Expect = 0.0
 Identities = 859/860 (99%)
 Strand = Plus / Minus

Query: 15  cacaagtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgatt 74
           |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 860 cacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgatt 801

Query: 75  ccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccag 134
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 800 ccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccag 741

Query: 135 tattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcg 194
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 740 tattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcg 681

Query: 195 ttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagc 254
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 680 ttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagc 621

Query: 255 gcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcattt 314
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 620 gcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcattt 561

Query: 315 cgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtag 374
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 560 cgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtag 501

Query: 375 agggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgca 434
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 500 agggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgca 441

Query: 435 gcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcg 494
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 440 gcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcg 381


Query: 495 ttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgg 554
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 380 ttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgg 321

Query: 555 aaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcca 614
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 320 aaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcca 261

Query: 615 aagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgga 674
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 260 aagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgga 201

Query: 675 caggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataa 734
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 200 caggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataa 141

Query: 735 gctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactc 794
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 140 gctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactc 81

Query: 795 cgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcact 854
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 80  cgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcact 21

Query: 855 ccaaaccgtccagagaacat 874
           ||||||||||||||||||||
Sbjct: 20  ccaaaccgtccagagaacat 1
```

Figure A.20: Clone A19

```
 Score = 1677 bits (846), Expect = 0.0
 Identities = 855/857 (99%), Gaps = 1/857 (0%)
 Strand = Plus / Minus

Query: 20  caagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 858 caagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 799

Query: 80  ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 139
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 798 ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 739

Query: 140 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 738 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 679

Query: 200 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 678 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 619

Query: 260 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 618 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 559

Query: 320 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 379
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 558 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 499

Query: 380 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 498 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 439

Query: 440 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 438 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 379

Query: 500 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 378 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 319

Query: 560 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 619
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 318 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 259

Query: 620 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 679
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 258 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 199

Query: 680 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 739
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 198 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 139

Query: 740 tgcggcagaccattgcgagaacaattgcagctcatccaacgtgnaagtcgagacactccg 799
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct: 138 tgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccg 79

Query: 800 cacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcactcc 859
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 78  cacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcactcc 19

Query: 860 aaaaccgtccagagaac 876
            ||||||||||||||||
Sbjct: 18  -aaaccgtccagagaac 3
```

Figure A.21: Clone A20

```
 Score = 1715 bits (865), Expect = 0.0
 Identities = 865/865 (100%)
 Strand = Plus / Minus

Query: 13  agtaccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaat 72
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 865 agtaccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaat 806

Query: 73  tgattccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtga 132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 805 tgattccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtga 746

Query: 133 tccagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacga 192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 745 tccagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacga 686

Query: 193 tgtcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcgg 252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 685 tgtcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcgg 626

Query: 253 ccagcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgt 312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 625 ccagcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgt 566

Query: 313 catttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtga 372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 565 catttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtga 506

Query: 373 agtagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgt 432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 505 agtagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgt 446

Query: 433 ctgcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggt 492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 445 ctgcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggt 386

Query: 493 catcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgc 552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 385 catcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgc 326

Query: 553 ctcggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgc 612
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 325 ctcggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgc 266

Query: 613 ctccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactg 672
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 265 ctccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactg 206

Query: 673 atggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagc 732
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 205 atggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagc 146

Query: 733 aataagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgaga 792
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 145 aataagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgaga 86

Query: 793 cactccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaa 852
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85  cactccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaa 26

Query: 853 gcactccaaaccgtccagagaacat 877
           |||||||||||||||||||||||||
Sbjct: 25  gcactccaaaccgtccagagaacat 1
```

Figure A.22: Clone A21

```
 Score = 1695 bits (855), Expect = 0.0
 Identities = 860/862 (99%)
 Strand = Plus / Minus

Query: 18  accacaagtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattga 77
           |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 862 accacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattga 803

Query: 78  ttccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatcc 137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 802 ttccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatcc 743

Query: 138 agtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgt 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 742 agtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgt 683

Query: 198 cgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcca 257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 682 cgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcca 623

Query: 258 gcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcat 317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 622 gcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcat 563

Query: 318 ttcgcaagaccgttgcttccagtgtagccaatgcgccgcccaagctgtgcccggtgaagt 377
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct: 562 ttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagt 503

Query: 378 agagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctg 437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 502 agagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctg 443

Query: 438 cagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcat 497
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 442 cagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcat 383

Query: 498 cgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctc 557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 382 cgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctc 323

Query: 558 ggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctc 617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 322 ggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctc 263

Query: 618 caaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatg 677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 262 caaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatg 203

Query: 678 gacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaat 737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 202 gacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaat 143

Query: 738 aagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacac 797
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 142 aagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacac 83

Query: 798 tccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagca 857
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 82  tccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagca 23

Query: 858 ctccaaaccgtccagagaacat 879
           ||||||||||||||||||||||
Sbjct: 22  ctccaaaccgtccagagaacat 1
```

Figure A.23: Clone A22

```
 Score = 1677 bits (846), Expect = 0.0
 Identities = 854/858 (99%)
 Strand = Plus / Minus

Query: 18  caagtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 77
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 858 caagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 799

Query: 78  ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 798 ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 739

Query: 138 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 738 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 679

Query: 198 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 678 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 619

Query: 258 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 618 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 559

Query: 318 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 558 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 499

Query: 378 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 498 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 439

Query: 438 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 497
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 438 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 379


Query: 498 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 378 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 319

Query: 558 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 318 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 259

Query: 618 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 258 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 199

Query: 678 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 198 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 139

Query: 738 tgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccg 797
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 138 tgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccg 79

Query: 798 cacatcaagtggtgtcggtgccgcagcactcagcgcanngngcgccgtcaaaagcactcc 857
           |||||||||||||||||||||||||||||||||||  | ||||||||||||||||||
Sbjct: 78  cacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcactcc 19

Query: 858 aaaccgtccagagaacat 875
           ||||||||||||||||||
Sbjct: 18  aaaccgtccagagaacat 1
```

Figure A.24: Clone A23

```
 Score = 1705 bits (860), Expect = 0.0
 Identities = 862/863 (99%)
 Strand = Plus / Minus

Query: 15  taccacaagtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattg 74
           |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 863 taccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattg 804


Query: 75  attccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatc 134
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 803 attccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatc 744


Query: 135 cagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatg 194
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 743 cagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatg 684


Query: 195 tcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcc 254
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 683 tcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcc 624


Query: 255 agcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtca 314
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 623 agcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtca 564


Query: 315 tttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaag 374
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 563 tttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaag 504


Query: 375 tagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtct 434
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 503 tagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtct 444


Query: 435 gcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtca 494
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 443 gcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtca 384


Query: 495 tcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcct 554
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 383 tcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcct 324


Query: 555 cggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcct 614
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 323 cggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcct 264


Query: 615 ccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgat 674
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 263 ccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgat 204


Query: 675 ggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaa 734
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 203 ggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaa 144


Query: 735 taagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagaca 794
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 143 taagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagaca 84


Query: 795 ctccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagc 854
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 83  ctccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagc 24


Query: 855 actccaaaccgtccagagaacat 877
           |||||||||||||||||||||||
Sbjct: 23  actccaaaccgtccagagaacat 1
```

Figure A.25: Clone A25

```
 Score = 1701 bits (858), Expect = 0.0
 Identities = 858/858 (100%)
 Strand = Plus / Minus

Query: 19  caagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 78
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 858 caagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 799


Query: 79  ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 138
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 798 ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 739


Query: 139 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 198
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 738 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 679


Query: 199 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 678 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 619


Query: 259 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 318
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 618 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 559


Query: 319 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 378
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 558 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 499


Query: 379 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 438
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 498 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 439


Query: 439 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 498
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 438 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 379


Query: 499 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 558
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 378 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 319


Query: 559 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 618
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 318 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 259


Query: 619 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 678
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 258 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 199


Query: 679 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 738
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 198 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 139


Query: 739 tgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccg 798
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 138 tgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccg 79


Query: 799 cacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcactcc 858
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 78  cacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcactcc 19


Query: 859 aaaccgtccagagaacat 876
           ||||||||||||||||||
Sbjct: 18  aaaccgtccagagaacat 1
```

Figure A.26: Clone A26

```
 Score = 1699 bits (857), Expect = 0.0
 Identities = 859/860 (99%)
 Strand = Plus / Minus

Query: 18  cacaagtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgatt 77
           |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 860 cacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgatt 801

Query: 78  ccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccag 137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 800 ccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccag 741

Query: 138 tattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcg 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 740 tattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcg 681

Query: 198 ttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagc 257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 680 ttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagc 621

Query: 258 gcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcattt 317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 620 gcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcattt 561

Query: 318 cgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtag 377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 560 cgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtag 501

Query: 378 agggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgca 437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 500 agggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgca 441

Query: 438 gcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcg 497
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 440 gcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcg 381

Query: 498 ttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgg 557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 380 ttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgg 321

Query: 558 aaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcca 617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 320 aaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcca 261

Query: 618 aagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgga 677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 260 aagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgga 201

Query: 678 caggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataa 737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 200 caggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataa 141

Query: 738 gctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactc 797
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 140 gctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactc 81

Query: 798 cgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcact 857
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 80  cgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcact 21

Query: 858 ccaaaccgtccagagaacat 877
           ||||||||||||||||||||
Sbjct: 20  ccaaaccgtccagagaacat 1
```

Figure A.27: Clone A27

```
 Score = 1550 bits (782), Expect = 0.0
 Identities = 817/824 (99%), Gaps = 5/824 (0%)
 Strand = Plus / Minus

Query: 29  aaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattccctcgatgagt 88
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 848 aaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattccctcgatgagt 789


Query: 89  tcaatatccgacgccgtgacactggctccggtgccactggtgatccagtattctggactt 148
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 788 tcaatatccgacgccgtgacactggctccggtgccactggtgatccagtattctggactt 729


Query: 149 ggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgttcaagtgtgta 208
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 728 ggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgttcaagtgtgta 669


Query: 209 acgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgcatagtttccg 268
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 668 acgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgcatagtttccg 609


Query: 269 actcgaggacatccataggtgtacagttcaacgctataaccgtcatttcgcaagaccgtt 328
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 608 actcgaggacatccataggtgtacagttcaacgctataaccgtcatttcgcaagaccgtt 549


Query: 329 gctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagagggtatagccc 388
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 548 gctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagagggtatagccc 489


Query: 389 gaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagcggcttcccat 448
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 488 gaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagcggcttcccat 429


Query: 449 gccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgttatcttgcagg 508
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 428 gccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgttatcttgcagg 369


Query: 509 atgaagtcgagatcagcaatccagtttcttgatggtgctactgcctcggaaggcgaccac 568
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct: 368 atgaagtcgagatcagcaatccag-ttcttgatggtgctactgcctcggaaggcgaccac 310


Query: 569 gagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaagttatttgt 628
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 309 gagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaagttatttgt 250


Query: 629 caggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggacaggcgtcggc 688
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 249 caggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggacaggcgtcggc 190


Query: 689 cgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagctgcggcaga 748
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 189 cgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagctgcggcaga 130


Query: 749 ccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactcccgccacatca 808
           ||||||||||||||||||||||||||||||||||||||||||||||||||   |||||||
Sbjct: 129 ccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactcc--gcacatca 72


Query: 809 agtggtgtcggtgcccgcagcactcagcgcagncgngcgccgtc 852
           |||||||||||||| |||||||||||||||||| || ||||||||
Sbjct: 71  agtggtgtcggtg-ccgcagcactcagcgcag-cgtgcgccgtc 30
```

Figure A.28: Clone A28

```
 Score = 1683 bits (849), Expect = 0.0
 Identities = 858/860 (99%), Gaps = 1/860 (0%)
 Strand = Plus / Minus

Query: 22  acaagtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattc 81
           ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 859 acaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattc 800

Query: 82  cctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagt 141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 799 cctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagt 740

Query: 142 attctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgt 201
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 739 attctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgt 680

Query: 202 tcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcg 261
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 679 tcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcg 620

Query: 262 catagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttc 321
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 619 catagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttc 560

Query: 322 gcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtaga 381
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 559 gcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtaga 500

Query: 382 gggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcag 441
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 499 gggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcag 440

Query: 442 cggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgt 501
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 439 cggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgt 380

Query: 502 tatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgga 561
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 379 tatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgga 320

Query: 562 aggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaa 621
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 319 aggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaa 260

Query: 622 agttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggac 681
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 259 agttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggac 200

Query: 682 aggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataag 741
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 199 aggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataag 140

Query: 742 ctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactcc 801
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 139 ctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactcc 80

Query: 802 gcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgttcaaaagcact 861
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct: 79  gcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccg-tcaaaagcact 21

Query: 862 ccaaaccgtccagagaacat 881
           ||||||||||||||||||||
Sbjct: 20  ccaaaccgtccagagaacat 1
```

Figure A.29: Clone A30

```
 Score = 1707 bits (861), Expect = 0.0
 Identities = 863/864 (99%)
 Strand = Plus / Minus

Query: 15  gtaccacaagtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaatt 74
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 864 gtaccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaatt 805

Query: 75  gattccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgat 134
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 804 gattccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgat 745

Query: 135 ccagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgat 194
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 744 ccagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgat 685

Query: 195 gtcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggc 254
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 684 gtcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggc 625

Query: 255 cagcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtc 314
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 624 cagcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtc 565

Query: 315 atttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaa 374
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 564 atttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaa 505

Query: 375 gtagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtc 434
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 504 gtagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtc 445

Query: 435 tgcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtc 494
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 444 tgcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtc 385

Query: 495 atcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcc 554
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 384 atcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcc 325

Query: 555 tcggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcc 614
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 324 tcggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcc 265

Query: 615 tccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactga 674
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 264 tccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactga 205

Query: 675 tggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagca 734
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 204 tggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagca 145

Query: 735 ataagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagac 794
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 144 ataagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagac 85

Query: 795 actccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaag 854
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 84  actccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaag 25

Query: 855 cactccaaaccgtccagagaacat 878
           |||||||||||||||||||||||
Sbjct: 24  cactccaaaccgtccagagaacat 1
```

Figure A.30: Clone A32

```
 Score = 1128 bits (569), Expect = 0.0
 Identities = 677/712 (95%), Gaps = 5/712 (0%)
 Strand = Plus / Minus

Query: 32  gccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattccctcgnng 91
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Sbjct: 851 gccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattccctcgatg 792


Query: 92  nnnn-annnnncgncgccgtgacactggctccggtgccactncngntccagtattctgga 150
                |     || |||||||||||||||||||||||||||   | |||||||||||||
Sbjct: 791 agttcaatatccgacgccgtgacactggctccggtgccactggtgatccagtattctgga 732


Query: 151 cttggctggntgaatccaaagtccatgggtggcaaccgggggacgatgtcgttcaagtgt 210
           ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 731 cttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgttcaagtgt 672


Query: 211 gtaacgcggaagttcgctccagatccctggttggtgatgtgctcggccagcgcatagtttt 270
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct: 671 gtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgcatagtttt 612


Query: 271 ccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcgcaagacc 330
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 611 ccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcgcaagacc 552


Query: 331 tctgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagagggtatag 390
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 551 gttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagagggtatag 492


Query: 391 cccgaatacgtgttcatcgcggacttgatcttgctcgtcagattgtctgcagcgtcttcc 450
           |||||||||||| ||||||||||||||||||||||||||||||||||||||| |||||
Sbjct: 491 cccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagcggcttcc 432


Query: 451 catgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgttatcttgt 510
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 431 catgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgttatcttgc 372


Query: 511 aggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaaggtgacc 570
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct: 371 aggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaaggcgacc 312


Query: 571 acgagccgcttgtt-gtgttgtccgcgtccaggaaaccggctgtgcctccaaagttattt 629
           ||||||||||||| |||||||||||| |||||||||||||||||||||||||||||||
Sbjct: 311 acgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaagttattt 252


Query: 630 gtcaggtcaaactcccagcagcatcttggtgctcgcctcctcgactgatgcacaggcgtc 689
           |||||||||||||| ||||||||||||||||||||||||||||||||||| |||||||||
Sbjct: 251 gtcaggtcaaact-ccagcagcatcttggtgctcgcctcctcgactgatggacaggcgtc 193


Query: 690 gntcgtgcatgttacgctagagtcgtccgagtccgatattgtttcgagcaat 741
           |  ||||||||| ||| |||||||||||||| |||||||| ||||||||||
Sbjct: 192 ggccgtgcatgtcacgttagagtcgtccgagt-cgatattg-ttcgagcaat 143
```

Figure A.31: Clone A33

```
 Score = 1673 bits (844), Expect = 0.0
 Identities = 855/858 (99%), Gaps = 1/858 (0%)
 Strand = Plus / Minus

Query: 19  ccacaagtgngccanaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgat 78
           ||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 861 ccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgat 802

Query: 79  tccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatcca 138
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 801 tccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatcca 742

Query: 139 gtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtc 198
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 741 gtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtc 682

Query: 199 gttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccag 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 681 gttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccag 622

Query: 259 cgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatt 318
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 621 cgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatt 562

Query: 319 tcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagta 378
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 561 tcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagta 502

Query: 379 gagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgc 438
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 501 gagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgc 442

Query: 439 agcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatc 498
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 441 agcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatc 382

Query: 499 gttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcg 558
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 381 gttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcg 322

Query: 559 gaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcc 618
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 321 gaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcc 262

Query: 619 aaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgg 678
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 261 aaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgg 202

Query: 679 acaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaata 738
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 201 acaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaata 142

Query: 739 agctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacact 798
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 141 agctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacact 82

Query: 799 ccgcacatcaaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagca 858
           ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 81  ccgcacatc-aagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagca 23

Query: 859 ctccaaaccgtccagaga 876
           ||||||||||||||||||
Sbjct: 22  ctccaaaccgtccagaga 5
```

Figure A.32: Clone A34

```
 Score = 1709 bits (862), Expect = 0.0
 Identities = 864/865 (99%)
 Strand = Plus / Minus


Query: 18  agtaccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaat 77
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 865 agtaccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaat 806


Query: 78  tgattccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtga 137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 805 tgattccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtga 746


Query: 138 tccagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacga 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 745 tccagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacga 686


Query: 198 tgtcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcgg 257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 685 tgtcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcgg 626


Query: 258 ccagcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgt 317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 625 ccagcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgt 566


Query: 318 catttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtga 377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 565 catttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtga 506


Query: 378 agtagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgt 437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 505 agtagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgt 446


Query: 438 ctgcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggt 497
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 445 ctgcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggt 386


Query: 498 catcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgc 557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 385 catcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgc 326


Query: 558 ctcggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgc 617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 325 ctcggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgc 266


Query: 618 ctccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactg 677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 265 ctccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactg 206


Query: 678 atggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagc 737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 205 atggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagc 146


Query: 738 aataagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgaga 797
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 145 aataagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgaga 86


Query: 798 cactccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgncgtcaaaa 857
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct: 85  cactccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaa 26


Query: 858 gcactccaaaccgtccagagaacat 882
           |||||||||||||||||||||||||
Sbjct: 25  gcactccaaaccgtccagagaacat 1
```

Figure A.33: Clone A35

```
 Score = 1629 bits (822), Expect = 0.0
 Identities = 833/836 (99%), Gaps = 1/836 (0%)
 Strand = Plus / Minus

Query: 19  cacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgatt 78
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 860 cacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgatt 801


Query: 79  ccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccag 138
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 800 ccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccag 741


Query: 139 tattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcg 198
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 740 tattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcg 681


Query: 199 ttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagc 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 680 ttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagc 621


Query: 259 gcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcattt 318
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 620 gcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcattt 561


Query: 319 cgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtag 378
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 560 cgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtag 501


Query: 379 agggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgca 438
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 500 agggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgca 441


Query: 439 gcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcg 498
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 440 gcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcg 381


Query: 499 ttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgg 558
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 380 ttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgg 321


Query: 559 aaggcgaccacgagccgcttgttggngttgtccgcggccaggaaaccggctgtgcctcca 618
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct: 320 aaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcca 261


Query: 619 aagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgga 678
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 260 aagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgga 201


Query: 679 caggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataa 738
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 200 caggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataa 141


Query: 739 gctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactc 798
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 140 gctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactc 81


Query: 799 cgcacatcaagtgggtgtcggtgncgcagcactcagcgcagcgtgcgccgtcaaaa 854
           |||||||||||| |||||||||| ||||||||||||||||||||||||||||||
Sbjct: 80  cgcacatcaagt-ggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaa 26
```

Figure A.34: Clone A37

```
 Score = 1705 bits (860), Expect = 0.0
 Identities = 862/863 (99%)
 Strand = Plus / Minus

Query: 17  tacnacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattg 76
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 863 taccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattg 804

Query: 77  attccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatc 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 803 attccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatc 744

Query: 137 cagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatg 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 743 cagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatg 684

Query: 197 tcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcc 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 683 tcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcc 624

Query: 257 agcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtca 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 623 agcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtca 564

Query: 317 tttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaag 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 563 tttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaag 504

Query: 377 tagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtct 436
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 503 tagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtct 444

Query: 437 gcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtca 496
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 443 gcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtca 384

Query: 497 tcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcct 556
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 383 tcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcct 324

Query: 557 cggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcct 616
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 323 cggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcct 264

Query: 617 ccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgat 676
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 263 ccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgat 204

Query: 677 ggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaa 736
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 203 ggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaa 144

Query: 737 taagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagaca 796
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 143 taagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagaca 84

Query: 797 ctccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagc 856
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 83  ctccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagc 24

Query: 857 actccaaaccgtccagagaacat 879
           |||||||||||||||||||||||
Sbjct: 23  actccaaaccgtccagagaacat 1
```

Figure A.35: Clone B1

```
 Score = 1675 bits (845), Expect = 0.0
 Identities = 856/860 (99%)
 Strand = Plus / Minus

Query: 18  cacaagtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgatt 77
           |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 860 cacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgatt 801


Query: 78  ccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccag 137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 800 ccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccag 741


Query: 138 tattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcg 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 740 tattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcg 681


Query: 198 ttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagc 257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 680 ttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagc 621


Query: 258 gcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcattt 317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 620 gcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcattt 561


Query: 318 cgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtag 377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 560 cgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtag 501


Query: 378 agggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgca 437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 500 agggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgca 441


Query: 438 gcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcg 497
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 440 gcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcg 381


Query: 498 ttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgg 557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 380 ttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgg 321


Query: 558 aaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcca 617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 320 aaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcca 261


Query: 618 aagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgga 677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 260 aagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgga 201


Query: 678 caggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataa 737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 200 caggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataa 141


Query: 738 gccgcggcggaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactc 797
           || ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 140 gctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactc 81


Query: 798 cgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcact 857
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 80  cgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcact 21


Query: 858 ccaaaccgtccatagaacat 877
           |||||||||||| |||||||
Sbjct: 20  ccaaaccgtccagagaacat 1
```

Figure A.36: Clone B2

```
 Score = 1699 bits (857), Expect = 0.0
 Identities = 859/860 (99%)
 Strand = Plus / Minus

Query: 19  cacaagtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgatt 78
           |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 860 cacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgatt 801

Query: 79  ccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccag 138
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 800 ccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccag 741

Query: 139 tattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcg 198
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 740 tattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcg 681

Query: 199 ttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagc 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 680 ttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagc 621

Query: 259 gcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcattt 318
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 620 gcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcattt 561

Query: 319 cgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtag 378
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 560 cgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtag 501

Query: 379 agggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgca 438
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 500 agggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgca 441

Query: 439 gcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcg 498
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 440 gcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcg 381

Query: 499 ttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgg 558
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 380 ttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgg 321

Query: 559 aaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcca 618
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 320 aaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcca 261

Query: 619 aagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgga 678
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 260 aagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgga 201

Query: 679 caggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataa 738
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 200 caggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataa 141

Query: 739 gctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactc 798
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 140 gctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactc 81

Query: 799 cgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcact 858
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 80  cgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcact 21

Query: 859 ccaaaccgtccagagaacat 878
           ||||||||||||||||||||
Sbjct: 20  ccaaaccgtccagagaacat 1
```

Figure A.37: Clone B6

```
 Score = 1455 bits (734), Expect = 0.0
 Identities = 778/789 (98%), Gaps = 4/789 (0%)
 Strand = Plus / Minus


Query: 31  gccaaaacgncnaccgttgcttcgcctgcattccccgccgtcgaattgnttccctcgatg 90
           ||||||||| | ||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct: 851 gccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattccctcgatg 792


Query: 91  agttcaatatccgacgccgtgacactggctccggtgccactggtgatccagttattctgg 150
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct: 791 agttcaatatccgacgccgtgacactggctccggtgccactggtgatccagt-attctgg 733


Query: 151 acttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgttcaagtg 210
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 732 acttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgttcaagtg 673


Query: 211 tgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgcatagtt 270
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 672 tgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgcatagtt 613


Query: 271 tccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcgcaagac 330
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 612 tccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcgcaagac 553


Query: 331 cgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagagggtata 390
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 552 cgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagagggtata 493


Query: 391 gcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagcggcttc 450
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 492 gcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagcggcttc 433


Query: 451 ccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgttatcttg 510
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 432 ccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgttatcttg 373


Query: 511 caggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaaggcgac 570
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 372 caggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaaggcgac 313


Query: 571 cacgagccgcntgttggtgttgtccgcggncaggaaaccggttgtgcctccaaagttatt 630
           |||||||||| |||||||||||||||||| |||||||||| ||||||||||||||||||
Sbjct: 312 cacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaagttatt 253


Query: 631 tgtcaggtcaaactccagcagcatccttggtgctcgcctcctcgactgatggacaggcgt 690
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct: 252 tgtcaggtcaaactccagcagcat-cttggtgctcgcctcctcgactgatggacaggcgt 194


Query: 691 cggccgtgcatgttcacgtttagagtcgtccgagtcgatattgttcgagcaataagctgc 750
           |||||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct: 193 cggccgtgcatg-tcacg-ttagagtcgtccgagtcgatattgttcgagcaataagctgc 136


Query: 751 ggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagactctccgcac 810
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct: 135 ggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccgcac 76


Query: 811 atcaagtgg 819
           |||||||||
Sbjct: 75  atcaagtgg 67
```

Figure A.38: Clone B7

```
 Score = 1679 bits (847), Expect = 0.0
 Identities = 857/859 (99%), Gaps = 1/859 (0%)
 Strand = Plus / Minus

Query: 21  caagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 858 caagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 799


Query: 81  ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 798 ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 739


Query: 141 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 738 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 679


Query: 201 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 678 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 619


Query: 261 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcgtttcg 320
           |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct: 618 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 559


Query: 321 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 558 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 499


Query: 381 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 498 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 439


Query: 441 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 438 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 379


Query: 501 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 378 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 319


Query: 561 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 318 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 259


Query: 621 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 258 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 199


Query: 681 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 198 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 139


Query: 741 tgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccg 800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 138 tgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccg 79


Query: 801 cacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcactcc 860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 78  cacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcactcc 19


Query: 861 aaacccgtccagagaacat 879
           ||| ||||||||||||||
Sbjct: 18  aaa-ccgtccagagaacat 1
```

Figure A.39: Clone B8

```
 Score = 1695 bits (855), Expect = 0.0
 Identities = 857/858 (99%)
 Strand = Plus / Minus


Query: 21  caagtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 80
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 858 caagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 799


Query: 81  ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 798 ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 739


Query: 141 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 738 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 679


Query: 201 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 678 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 619


Query: 261 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 618 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 559


Query: 321 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 558 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 499


Query: 381 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 498 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 439


Query: 441 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 438 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 379


Query: 501 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 378 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 319


Query: 561 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 318 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 259


Query: 621 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 258 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 199


Query: 681 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 198 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 139


Query: 741 tgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccg 800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 138 tgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccg 79


Query: 801 cacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcactcc 860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 78  cacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcactcc 19


Query: 861 aaaccgtccagagaacat 878
           ||||||||||||||||||
Sbjct: 18  aaaccgtccagagaacat 1
```

Figure A.40: Clone B9

```
 Score = 1655 bits (835), Expect = 0.0
 Identities = 860/865 (99%), Gaps = 3/865 (0%)
 Strand = Plus / Minus


Query: 17  accacaagtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattga 76
           |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 862 accacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattga 803


Query: 77  ttccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatcc 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 802 ttccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatcc 743


Query: 137 agtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgt 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 742 agtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgt 683


Query: 197 cgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcca 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 682 cgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcca 623


Query: 257 gcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcat 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 622 gcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcat 563


Query: 317 ttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagt 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 562 ttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagt 503


Query: 377 agagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctg 436
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 502 agagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctg 443


Query: 437 cagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcat 496
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 442 cagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcat 383


Query: 497 cgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctc 556
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 382 cgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctc 323


Query: 557 ggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctc 616
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 322 ggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctc 263


Query: 617 caaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatg 676
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 262 caaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatg 203


Query: 677 gacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaat 736
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 202 gacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaat 143


Query: 737 aagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacac 796
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 142 aagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacac 83


Query: 797 tccgcacatccaagtggtgtcgggngccgcagcactcagcgcagcgtgcgccgtccaaaa 856
           ||||||||| |||||||||| || ||||||||||||||||||||||||||||| |||||
Sbjct: 82  tccgcacat-caagtggtgtc-ggtgccgcagcactcagcgcagcgtgcgccgt-caaaa 26


Query: 857 gcactccaaaccgtccagagaacat 881
           |||||||||||||||||||||||||
Sbjct: 25  gcactccaaaccgtccagagaacat 1
```

Figure A.41: Clone B14

```
 Score = 1689 bits (852), Expect = 0.0
 Identities = 860/863 (99%)
 Strand = Plus / Minus

Query: 17  taccacaagtgagccaaaacgtccaccgttgcttcgcctgcactccccgccgtcgaattg 76
           |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct: 863 taccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattg 804

Query: 77  attccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatc 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 803 attccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatc 744

Query: 137 cagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatg 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 743 cagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatg 684

Query: 197 tcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcc 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 683 tcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcc 624

Query: 257 agcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtca 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 623 agcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtca 564

Query: 317 tttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaag 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 563 tttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaag 504

Query: 377 tagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtct 436
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 503 tagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtct 444

Query: 437 gcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtca 496
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 443 gcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtca 384

Query: 497 tcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcct 556
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 383 tcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcct 324

Query: 557 cggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcct 616
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 323 cggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcct 264

Query: 617 ccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgat 676
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 263 ccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgat 204

Query: 677 ggacaggcgccggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaa 736
           ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 203 ggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaa 144

Query: 737 taagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagaca 796
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 143 taagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagaca 84

Query: 797 ctccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgngcgccgtcaaaagc 856
           |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct: 83  ctccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagc 24

Query: 857 actccaaaccgtccagagaacat 879
           |||||||||||||||||||||||
Sbjct: 23  actccaaaccgtccagagaacat 1
```

Figure A.42: Clone B15

```
 Score = 1705 bits (860), Expect = 0.0
 Identities = 860/860 (100%)
 Strand = Plus / Minus

Query: 20  cacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgatt 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 860 cacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgatt 801


Query: 80  ccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccag 139
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 800 ccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccag 741


Query: 140 tattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcg 199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 740 tattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcg 681


Query: 200 ttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagc 259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 680 ttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagc 621


Query: 260 gcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcattt 319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 620 gcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcattt 561


Query: 320 cgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtag 379
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 560 cgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtag 501


Query: 380 agggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgca 439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 500 agggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgca 441


Query: 440 gcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcg 499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 440 gcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcg 381


Query: 500 ttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgg 559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 380 ttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgg 321


Query: 560 aaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcca 619
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 320 aaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcca 261


Query: 620 aagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgga 679
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 260 aagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgga 201


Query: 680 caggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataa 739
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 200 caggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataa 141


Query: 740 gctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactc 799
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 140 gctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactc 81


Query: 800 cgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcact 859
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 80  cgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcact 21


Query: 860 ccaaaccgtccagagaacat 879
           ||||||||||||||||||||
Sbjct: 20  ccaaaccgtccagagaacat 1
```

Figure A.43: Clone B17

```
 Score = 1657 bits (836), Expect = 0.0
 Identities = 859/863 (99%), Gaps = 3/863 (0%)
 Strand = Plus / Minus


Query: 22  cacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgatt 81
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 860 cacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgatt 801


Query: 82  ccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccag 141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 800 ccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccag 741


Query: 142 tattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcg 201
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 740 tattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcg 681


Query: 202 ttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagc 261
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 680 ttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagc 621


Query: 262 gcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcattt 321
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 620 gcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcattt 561


Query: 322 cgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtag 381
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 560 cgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtag 501


Query: 382 agggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgca 441
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 500 agggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgca 441


Query: 442 gcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcg 501
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 440 gcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcg 381


Query: 502 ttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgg 561
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 380 ttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgg 321


Query: 562 aaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcca 621
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 320 aaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcca 261


Query: 622 aagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgga 681
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 260 aagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgga 201


Query: 682 caggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataa 741
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 200 caggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataa 141


Query: 742 gctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactc 801
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 140 gctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactc 81


Query: 802 cgcacatcaagtggtgtcgntgccgcagcactcagcgcagcgtgcgcccgtcaaaagcac 861
           |||||||||||||||||| |||||||||||||||||||||||| ||||||||||||||
Sbjct: 80  cgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcg-ccgtcaaaagcac 22


Query: 862 tccaaaaccgtcccagagaacat 884
           ||| ||||||| ||||||||||
Sbjct: 21  tcc-aaaccgt-ccagagaacat 1
```

Figure A.44: Clone C2

```
 Score = 1701 bits (858), Expect = 0.0
 Identities = 858/858 (100%)
 Strand = Plus / Minus

Query: 23  caagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 82
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 858 caagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 799

Query: 83  ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 798 ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 739

Query: 143 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 738 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 679

Query: 203 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 678 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 619

Query: 263 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 618 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 559

Query: 323 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 382
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 558 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 499

Query: 383 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 442
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 498 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 439

Query: 443 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 502
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 438 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 379

Query: 503 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 562
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 378 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 319

Query: 563 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 622
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 318 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 259

Query: 623 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 682
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 258 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 199

Query: 683 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 742
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 198 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 139

Query: 743 tgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccg 802
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 138 tgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccg 79

Query: 803 cacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcactcc 862
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 78  cacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcactcc 19

Query: 863 aaaccgtccagagaacat 880
           ||||||||||||||||||
Sbjct: 18  aaaccgtccagagaacat 1
```

Figure A.45: Clone C3

```
 Score = 1705 bits (860), Expect = 0.0
 Identities = 860/860 (100%)
 Strand = Plus / Minus

Query: 16  cacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgatt 75
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 860 cacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgatt 801


Query: 76  ccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccag 135
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 800 ccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccag 741


Query: 136 tattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcg 195
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 740 tattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcg 681


Query: 196 ttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagc 255
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 680 ttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagc 621


Query: 256 gcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcattt 315
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 620 gcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcattt 561


Query: 316 cgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtag 375
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 560 cgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtag 501


Query: 376 agggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgca 435
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 500 agggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgca 441


Query: 436 gcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcg 495
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 440 gcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcg 381


Query: 496 ttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgg 555
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 380 ttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgg 321


Query: 556 aaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcca 615
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 320 aaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcca 261


Query: 616 aagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgga 675
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 260 aagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgga 201


Query: 676 caggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataa 735
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 200 caggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataa 141


Query: 736 gctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactc 795
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 140 gctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactc 81


Query: 796 cgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcact 855
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 80  cgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcact 21


Query: 856 ccaaaccgtccagagaacat 875
           ||||||||||||||||||||
Sbjct: 20  ccaaaccgtccagagaacat 1
```

Figure A.46: Clone C5

```
 Score = 1673 bits (844), Expect = 0.0
 Identities = 859/863 (99%), Gaps = 1/863 (0%)
 Strand = Plus / Minus


Query: 17  accacaagtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattga 76
           |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 862 accacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattga 803


Query: 77  ttccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatcc 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 802 ttccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatcc 743


Query: 137 agtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgt 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 742 agtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgt 683


Query: 197 cgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcca 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 682 cgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcca 623


Query: 257 gcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcat 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 622 gcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcat 563


Query: 317 ttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagt 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 562 ttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagt 503


Query: 377 agagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctg 436
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 502 agagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctg 443


Query: 437 cagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcat 496
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 442 cagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcat 383


Query: 497 cgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctc 556
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 382 cgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctc 323


Query: 557 ggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaatcggctgtgcctc 616
           |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct: 322 ggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctc 263


Query: 617 caaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatg 676
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 262 caaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatg 203


Query: 677 gacaggcgtcggccgtgcatgccacgtttagagtcgtccgagtcgatattgttcgagcaa 736
           |||||||||||||||||||| |||| ||||||||||||||||||||||||||||||||
Sbjct: 202 gacaggcgtcggccgtgcatgtcacg-ttagagtcgtccgagtcgatattgttcgagcaa 144


Query: 737 taagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagaca 796
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 143 taagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagaca 84


Query: 797 ctccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagc 856
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 83  ctccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagc 24


Query: 857 actccaaaccgtccagagaacat 879
           |||||||||||||||||||||||
Sbjct: 23  actccaaaccgtccagagaacat 1
```

Figure A.47: Clone C6

```
 Score = 1687 bits (851), Expect = 0.0
 Identities = 858/859 (99%), Gaps = 1/859 (0%)
 Strand = Plus / Minus

Query: 23  caagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 82
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 858 caagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 799

Query: 83  ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 798 ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 739

Query: 143 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 738 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 679

Query: 203 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 678 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 619

Query: 263 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 618 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 559

Query: 323 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 382
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 558 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 499

Query: 383 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 442
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 498 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 439

Query: 443 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 502
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 438 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 379


Query: 503 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 562
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 378 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 319

Query: 563 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 622
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 318 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 259

Query: 623 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 682
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 258 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 199

Query: 683 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 742
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 198 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 139

Query: 743 tgcggcagaccattgcgagaacaattgcagctcatccaacgtgggaagtcgagacactcc 802
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct: 138 tgcggcagaccattgcgagaacaattgcagctcatccaacgt-ggaagtcgagacactcc 80

Query: 803 gcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcactc 862
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 79  gcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcactc 20

Query: 863 caaaccgtccagagaacat 881
           ||||||||||||||||||
Sbjct: 19  caaaccgtccagagaacat 1
```

Figure A.48: Clone C7

```
 Score = 1703 bits (859), Expect = 0.0
 Identities = 862/863 (99%)
 Strand = Plus / Minus

Query: 16  taccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattg 75
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 863 taccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattg 804

Query: 76  attccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatc 135
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 803 attccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatc 744

Query: 136 cagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatg 195
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 743 cagtattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatg 684

Query: 196 gcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcc 255
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 683 tcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggcc 624

Query: 256 agcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtca 315
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 623 agcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtca 564

Query: 316 tttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaag 375
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 563 tttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaag 504

Query: 376 tagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtct 435
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 503 tagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtct 444

Query: 436 gcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtca 495
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 443 gcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtca 384

Query: 496 tcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcct 555
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 383 tcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcct 324

Query: 556 cggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcct 615
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 323 cggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcct 264

Query: 616 ccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgat 675
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 263 ccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgat 204

Query: 676 ggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaa 735
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 203 ggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaa 144

Query: 736 taagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagaca 795
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 143 taagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagaca 84

Query: 796 ctccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagc 855
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 83  ctccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagc 24

Query: 856 actccaaaccgtccagagaacat 878
           ||||||||||||||||||||||
Sbjct: 23  actccaaaccgtccagagaacat 1
```

Figure A.49: Clone C8

```
 Score = 1655 bits (835), Expect = 0.0
 Identities = 853/859 (99%), Gaps = 1/859 (0%)
 Strand = Plus / Minus


Query: 22  caagtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 81
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 858 caagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 799


Query: 82  ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 798 ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 739


Query: 142 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 201
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 738 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 679


Query: 202 caagtgtgtaacgcggaagtccgctccagatccctggctggtgatgtgctcggccagcgc 261
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct: 678 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 619


Query: 262 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 321
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 618 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 559


Query: 322 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 381
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 558 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 499


Query: 382 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 441
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 498 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 439


Query: 442 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 501
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 438 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 379


Query: 502 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 561
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 378 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 319


Query: 562 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 621
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 318 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 259


Query: 622 gttatttgtcaggtcaaactccagcagcatcttgntgctcgcctcctcgactgatggaca 681
           |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct: 258 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 199


Query: 682 ggcgtcggccgtgcatgtcacgttagagtcgtccgagncgatattgttcgagcaataagc 741
           |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct: 198 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 139


Query: 742 tgcggcagancattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccg 801
           ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 138 tgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccg 79


Query: 802 cacatcaagtggtgtcggtgccgcagcactcagcgcaggcgtgcgccgtcaaaagcactc 861
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct: 78  cacatcaagtggtgtcggtgccgcagcactcagcgca-gcgtgcgccgtcaaaagcactc 20


Query: 862 caaaccgtccagagaacat 880
           ||||||||||||||||||
Sbjct: 19  caaaccgtccagagaacat 1
```

Figure A.50: Clone C9

```
 Score = 1616 bits (815), Expect = 0.0
 Identities = 855/862 (99%), Gaps = 5/862 (0%)
 Strand = Plus / Minus


Query: 21  aagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattccc 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 857 aagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattccc 798


Query: 81  tcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagtat 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 797 tcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagtat 738


Query: 141 tctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgttc 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 737 tctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgttc 678


Query: 201 aagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgca 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 677 aagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgca 618


Query: 261 tagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcgc 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 617 tagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcgc 558


Query: 321 aagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagagg 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 557 aagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagagg 498


Query: 381 gtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagcg 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 497 gtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagcg 438


Query: 441 gcttcccatgccttccagaatccagtgcgaaccttgcagccagtacagaggtcatcgtta 500
           |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct: 437 gcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtta 378


Query: 501 tcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaag 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 377 tcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaag 318


Query: 561 gcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaag 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 317 gcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaag 258


Query: 621 ttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggacag 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 257 ttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggacag 198


Query: 681 gcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagct 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 197 gcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagct 138


Query: 741 gcggcagaccattgcgagaacaatttgcagctcatccaacgtggaagtcgagacactccg 800
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct: 137 gcggcagaccattgcgagaacaa-ttgcagctcatccaacgtggaagtcgagacactccg 79


Query: 801 cacatcaagtggtgtcggtgcccgcagcactcagcgcagcgtgcgccgttcaaaangcac 860
           |||||||||||||||||||| |||||||||||||||||||||||| |||||| ||||
Sbjct: 78  cacatcaagtggtgtcggtg-ccgcagcactcagcgcagcgtgcgccg-tcaaaa-gcac 22


Query: 861 tccaaaccgnnccagagaacat 882
           |||||||||  ||||||||||
Sbjct: 21  tccaaaccg-tccagagaacat 1
```

Figure A.51: Clone C12

```
 Score = 1586 bits (800), Expect = 0.0
 Identities = 851/863 (98%), Gaps = 5/863 (0%)
 Strand = Plus / Minus


Query: 22  caagtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 81
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 858 caagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattcc 799


Query: 82  ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 798 ctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagta 739


Query: 142 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 201
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 738 ttctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgtt 679


Query: 202 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 261
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 678 caagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgc 619


Query: 262 atagtttccgactcgaggacatccataggtgtacagttcaccgcnnncnccgtcatttcg 321
           |||||||||||||||||||||||||||||||||||| |||     ||||||||||
Sbjct: 618 atagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcg 559


Query: 322 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 381
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 558 caagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagag 499


Query: 382 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 441
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 498 ggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagc 439


Query: 442 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 501
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 438 ggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtt 379


Query: 502 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 561
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 378 atcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaa 319


Query: 562 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 621
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 318 ggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaa 259


Query: 622 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 681
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 258 gttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggaca 199


Query: 682 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 741
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 198 ggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagc 139


Query: 742 tgcggcagaccattgcgagaacaattgcagctcatccaacgtgggaagtcgagacactcc 801
           |||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct: 138 tgcggcagaccattgcgagaacaattgcagctcatccaacgt-ggaagtcgagacactcc 80


Query: 802 gcaccatcaagtgggtgtcggtgccgcagcactcagcgcaggcgtgcgcccgtcaaaagc 861
           ||| |||||||| |||||||||||||||||||||||||| ||||||| ||||||||||
Sbjct: 79  gca-catcaagt-ggtgtcggtgccgcagcactcagcgca-gcgtgcg-ccgtcaaaagc 24


Query: 862 actccaaaccgtccagagaacat 884
           |||||||||||||||||||||||
Sbjct: 23  actccaaaccgtccagagaacat 1
```

Figure A.52: Clone C13

```
 Score = 1616 bits (815), Expect = 0.0
 Identities = 850/857 (99%), Gaps = 4/857 (0%)
 Strand = Plus / Minus

Query: 26  gtgngccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattccctc 85
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 855 gtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattccctc 796

Query: 86  gatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagtattc 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 795 gatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagtattc 736

Query: 146 tggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgttcaa 205
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 735 tggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgttcaa 676

Query: 206 gtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgcata 265
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 675 gtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgcata 616

Query: 266 gtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcgcaa 325
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 615 gtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcgcaa 556

Query: 326 gaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagagggt 385
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 555 gaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagagggt 496

Query: 386 atagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagcggc 445
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 495 atagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagcggc 436

Query: 446 ttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgttatc 505
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 435 ttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgttatc 376

Query: 506 ttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaaggc 565
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 375 ttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaaggc 316

Query: 566 gaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaagtc 625
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 315 gaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaagtt 256

Query: 626 atttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggacaggc 685
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 255 atttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggacaggc 196

Query: 686 gtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagctgc 745
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 195 gtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagctgc 136

Query: 746 gggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccgca 805
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 135 -ggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccgca 77

Query: 806 catcaagtggntgtcggtgcccgcagcactcagcgcagcgtgcgccgtcaaaagcactcc 865
           |||||||||| |||||||| |||||||||||||||||||||||||||||||||||| |
Sbjct: 76  catcaagtgg-tgtcggtg-ccgcagcactcagcgcagcgtgcgccgtcaaaagcact-c 20

Query: 866 caaancgtccagagaac 882
           |||| ||||||||||||
Sbjct: 19  caaaccgtccagagaac 3
```

Figure A.53: Clone C14

```
 Score = 1681 bits (848), Expect = 0.0
 Identities = 860/864 (99%)
 Strand = Plus / Minus

Query: 14  gtaccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaatt 73
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 864 gtaccacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaatt 805

Query: 74  gattccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgat 133
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 804 gattccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgat 745

Query: 134 ccagtattctggacttggctggctgaatccaaagtccatgggtggcaaccggggacgat 193
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 744 ccagtattctggacttggctggctgaatccaaagtccatgggtggcaaccggggacgat 685

Query: 194 gtcgttcaagtgtgtagcgcggaagttcgctccagatccctggctggtgatgtgctcggc 253
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct: 684 gtcgttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggc 625

Query: 254 cagcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtc 313
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 624 cagcgcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtc 565

Query: 314 atttcgcaagaccgttgctcccagtgtagccaatgcgctgcccaagctgtgcccggtgaa 373
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct: 564 atttcgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaa 505

Query: 374 gtagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcggattgtc 433
           |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct: 504 gtagagggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtc 445

Query: 434 tgcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtc 493
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 444 tgcagcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtc 385

Query: 494 atcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcc 553
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 384 atcgttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcc 325

Query: 554 tcggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcc 613
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 324 tcggaaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcc 265

Query: 614 tccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactga 673
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 264 tccaaagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactga 205

Query: 674 tggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagca 733
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 204 tggacaggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagca 145

Query: 734 ataagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagccgagac 793
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct: 144 ataagctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagac 85

Query: 794 actccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaag 853
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 84  actccgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaag 25

Query: 854 cactccaaaccgtccagagaacat 877
           |||||||||||||||||||||||
Sbjct: 24  cactccaaaccgtccagagaacat 1
```

Figure A.54: Clone C15

```
 Score = 1699 bits (857), Expect = 0.0
 Identities = 859/860 (99%)
 Strand = Plus / Minus

Query: 17  cacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgatt 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 860 cacaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgatt 801


Query: 77  ccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccag 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 800 ccctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccag 741


Query: 137 tattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcg 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 740 tattctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcg 681


Query: 197 ttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagc 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 680 ttcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagc 621


Query: 257 gcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcattt 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 620 gcatagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcattt 561


Query: 317 cgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtag 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 560 cgcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtag 501


Query: 377 agggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgca 436
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 500 agggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgca 441


Query: 437 gcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcg 496
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 440 gcggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcg 381


Query: 497 ttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgg 556
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 380 ttatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgg 321


Query: 557 aaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcca 616
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 320 aaggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctcca 261


Query: 617 aagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgga 676
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 260 aagttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatgga 201


Query: 677 caggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataa 736
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 200 caggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataa 141


Query: 737 gctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactc 796
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 140 gctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactc 81


Query: 797 cgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagnact 856
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct: 80  cgcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcact 21


Query: 857 ccaaaccgtccagagaacat 876
           ||||||||||||||||||||
Sbjct: 20  ccaaaccgtccagagaacat 1
```

Figure A.55: Clone C16

```
 Score = 1689 bits (852), Expect = 0.0
 Identities = 857/859 (99%)
 Strand = Plus / Minus

Query: 20  acaagtgngccaaaacatccaccgttgcttcgcctgcattccccgccgtcgaattgattc 79
           ||||||| |||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct: 859 acaagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattc 800

Query: 80  cctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagt 139
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 799 cctcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagt 740

Query: 140 attctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgt 199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 739 attctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgt 680

Query: 200 tcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcg 259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 679 tcaagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcg 620

Query: 260 catagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttc 319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 619 catagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttc 560

Query: 320 gcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtaga 379
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 559 gcaagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtaga 500

Query: 380 gggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcag 439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 499 gggtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcag 440

Query: 440 cggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgt 499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 439 cggcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgt 380

Query: 500 tatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgga 559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 379 tatcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcgga 320

Query: 560 aggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaa 619
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 319 aggcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaa 260

Query: 620 agttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggac 679
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 259 agttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggac 200

Query: 680 aggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataag 739
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 199 aggcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataag 140

Query: 740 ctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactcc 799
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 139 ctgcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactcc 80

Query: 800 gcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcactc 859
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 79  gcacatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaagcactc 20

Query: 860 caaaccgtccagagaacat 878
           ||||||||||||||||||
Sbjct: 19  caaaccgtccagagaacat 1
```

Figure A.56: Clone C18

```
 Score = 1624 bits (819), Expect = 0.0
 Identities = 849/859 (98%), Gaps = 2/859 (0%)
 Strand = Plus / Minus

Query: 23  aagtgagccaaaacgtccaccgntgnttcgcctgcattccccgccgtcgaattgattccc 82
           |||||||||||||||||||||| || ||||||||||||||||||||||||||||||||||
Sbjct: 857 aagtgagccaaaacgtccaccgttgcttcgcctgcattccccgccgtcgaattgattccc 798

Query: 83  tcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagtat 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 797 tcgatgagttcaatatccgacgccgtgacactggctccggtgccactggtgatccagtat 738

Query: 143 tctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgttc 202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 737 tctggacttggctggctgaatccaaagtccatgggtggcaaccgggggacgatgtcgttc 678

Query: 203 aagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgca 262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 677 aagtgtgtaacgcggaagttcgctccagatccctggctggtgatgtgctcggccagcgca 618

Query: 263 tagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcgc 322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 617 tagtttccgactcgaggacatccataggtgtacagttcaacgctataaccgtcatttcgc 558

Query: 323 aagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagagg 382
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 557 aagaccgttgctcccagtgtagccaatgcgccgcccaagctgtgcccggtgaagtagagg 498

Query: 383 gtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagcg 442
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 497 gtatagcccgaatacgtgctcatcgcggacttgatcttgctcgtcagattgtctgcagcg 438

Query: 443 gcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtta 502
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 437 gcttcccatgccttccagaatccagtgtgaaccttgcagccagtacagaggtcatcgtta 378

Query: 503 tcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaag 562
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 377 tcttgcaggatgaagtcgagatcagcaatccagttcttgatggtgctactgcctcggaag 318

Query: 563 gcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaag 622
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 317 gcgaccacgagccgcttgttggtgttgtccgcggccaggaaaccggctgtgcctccaaag 258

Query: 623 ttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggacag 682
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 257 ttatttgtcaggtcaaactccagcagcatcttggtgctcgcctcctcgactgatggacag 198

Query: 683 gcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagct 742
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 197 gcgtcggccgtgcatgtcacgttagagtcgtccgagtcgatattgttcgagcaataagct 138

Query: 743 gcggcagaccattgcgagaacaattgcagctcatccaacgtgnaagtcgagacactccgc 802
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct: 137 gcggcagaccattgcgagaacaattgcagctcatccaacgtggaagtcgagacactccgc 78

Query: 803 acatcaantnnngtcggtgccgcagcactcagcgcagcgtgcgccgtcaaaaagcactcc 862
           ||||||| |   ||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct: 77  acatcaagtggtgtcggtgccgcagcactcagcgcagcgtgcgccgtc-aaaagcactcc 19

Query: 863 aaaancgtccagagaacat 881
            ||| ||||||||||||||
Sbjct: 18  -aaaccgtccagagaacat 1
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Figure A.57: Clone C20