

A Genetic Comparison of Baker's and Brewer's Yeast

**By
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April, 2023**



**Allegheny College
Department of Biology**

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**A Senior Comprehensive Project in Partial Fulfillment of the Requirements
for a Bachelor of Science Degree from Allegheny College**

*I hereby recognize and pledge to fulfill my responsibilities as defined in the Honor Code
and to maintain the integrity of both myself and the College community as a whole.*



Trenton Kramer

This work is mine unless otherwise cited

Approval by the Senior Thesis Committee:

Dr. 1st Reader

Dr. 2nd Reader

Abstract

Brewer's yeast and baker's yeast are two strains of *Saccharomyces cerevisiae* with a long history of domestication by humans to perform best in the production of beer and bread, respectively. Despite being the same species, brewer's yeast and baker's yeast have significant differences in gene expression for at least 20 genes (Davydenko et al., 2020). However, it is not known whether the amino acid sequence of these 20 genes differs between brewer's and baker's yeast, and whether there is any evidence that positive natural selection acting on the different strains may have been responsible for any differences in amino acid sequence. To answer this question I performed a dN/dS comparison of the 20 genes for baker's, brewer's, and wild yeast. dN/dS is the ratio of the rate of nonsynonymous changes over the rate of synonymous changes in the DNA sequence. A dN/dS ratio greater than 1 provides strong evidence that the difference in the DNA sequence was caused by positive Darwinian selection acting on variation in the amino acid sequence of the resulting protein. A ratio less than 1 is more consistent with the hypothesis that changes in amino acid sequence were likely caused by genetic drift acting on selectively neutral mutations rather than natural selection. Overall, I found no evidence of positive selection acting on any of the 20 genes, as dN/dS ratios were all <1 and generally low. However, comparisons for 3 genes —IPP1, YCP4, and ZRT1 — produced intriguing results suggesting a possible role for positive selection and should be investigated further.

Introduction

Brewer's yeast and baker's yeast are two strains of *Saccharomyces cerevisiae* with a long history of domestication by humans to perform best in the production of beer and bread, respectively. Bakers want the bread to rise fast and produce little ethanol, so Baker's yeast has been domesticated to release less ethanol and more carbon dioxide. Brewers want the yeast to produce ethanol and flocculate after they die. The main difference between the two strains is alcohol tolerance, ideal temperature range, and flocculation. Ethanol is a by-product of cellular fermentation in yeast, but it is also toxic in high concentrations. Brewer's yeast has been domesticated to survive in higher concentrations of ethanol than baker's yeast (Distillique, 2023). The ideal temperature range of the two strains is different too. Many baker's yeast strains thrive in temperature ranges of 32 C to 54 C while brewer's yeast strains tend to thrive in 12C to 28 C (Fleischmann's®,2023)(Scherz, 2021). While Baker's yeast can live at room temperature too, it does not do as well and goes dormant at higher temperatures than brewer's. This is due to the length of time each strain is needed to ferment. Bread requires a fast fermentation to raise the dough faster than ethanol is produced, while brewer's yeast will be left at room temperature for weeks to months to ferment. Lastly, the flocculation of yeast is different between the two strains. Brewer's yeast has been selected over time to fall out of suspension after fermentation is completed, while that is not needed in bread due to the yeast being baked in, so baker's yeast does not flocculate as well as brewer's.

Brewer's yeast and baker's yeast, despite being the same species, have significant differences in gene expression. There are a total of 20 genes that have different amounts of protein expression (Davydenko et al., 2020). Although there are differences in expression, it is unknown if there are differences in amino acid sequence, and whether artificial selection by humans has caused an evolutionary change in the amino acid sequence of yeast proteins. The changes in protein expression could be caused by changes in gene expression or changes in the amino acid sequence could be caused by genetic drift.

dN/dS is the ratio of nonsynonymous changes over synonymous changes in the DNA sequence. An example of a synonymous change would be the original DNA sequence AGT (UCA in RNA) which codes for serine. The synonymous change could be AGT changing to AGA, now coding UCU instead of UCA but still producing serine. An example of a nonsynonymous change would be going from AGT to AAT, with the RNA now being

transcribed as UUA instead of AGT and producing a leucine instead of a serine. Each position of the codon is also weighted, so a change in the 1st base pair spot of a codon is weighted heavier than a change in the 3rd base pair spot because a change in the first base pair spot is more likely to cause an amino acid change. The possible amino acid which the codon codes for is also weighted for synonymous changes. For example, if the codon is GAG and the 3rd is changed to GAA, coding for glutamic acid, it is considered a twofold synonymous substitution because there are only 2 base pairs in the 3rd position, G and A, which code for the glutamic acid. The other possible synonymous substitution is a fourfold substitution. A fourfold substitution is a substitution in which the change in base pair always leads to the same amino acid. For example, in the codon GCG, a change in the 3rd amino acid always results in alanine. The twofold synonymous changes will be weighted higher than the fourfold changes due to them being more likely to result in a change in the amino acid. If there are more nonsynonymous changes than synonymous changes, then the dN/dS ratio is greater than one, and positive Darwinistic selection is implied. However, if the ratio is less than one, then positive selection is not implied and the changes most likely come from genetic drift. Using dN/dS, one can compare 2 or more DNA sequences (Herron, & Freeman, 2014).

dN/dS can show selection and change it may cause to an organism. DFR genes were shown to have different selection based on how many copies the organism had in Des Marais & Rausher, 2008. In organisms with only one copy of DFR, the dN/dS ratio was low, especially for DFR-B. While organisms with multiple copies of DFRs have shown high dN/dS ratios implying positive selection may be the cause, specifically for DFR-A/C. The substrate production of the organisms was done with each organism and each DFR gene. Overall, DFR-B produced the most substrate while DFR-A/C produced the least (Des Marais & Rausher, 2008).

To learn what specifically causes the difference in gene expression between different yeast strains of *saccharomyces cerevisiae*, a dN/dS comparison of 20 genes of baker's, brewer's, and wild yeast was performed to test if there is a change in the nucleotide sequence in the genes which have a significant difference in gene expression.

Methods

DNA sequences for all yeast strains were accessed through <https://www.yeastgenome.org/> under the tabs sequence, strains and species, align strain, and sequences. Baker's yeast strains used were Redstar baking yeast and CLIB324, a Vietnamese baker's strain. The Brewer's yeast used were LalvinQA23, K11, and Kyokai. LalvinQA23 is used for making wine and beer. K11 and Kyokai are both used to make sake. YPS128, YPS163, and T7 were the wild strains used. YPS128 and YPS163 both are wild Pennsylvania strains and T7 is a wild Missouri strain (Table 1). Redstar, Lalvin, and YPS128 were the base yeast strains for most comparisons but the other sequences were used when sequences for the base strains were not available (Table 1). Twenty genes were examined based on expression differences found in Davydenko et al. (2020) (Table 2).

Table 1: Yeast strain used for each gene.

Gene	Baker's yeast	Brewer's yeast	Wild yeast
IPP1	Redstar	LalvinQA23	YPS128
GDH2	Redstar	LalvinQA23	YPS128
MDH3	N/A	LalvinQA23	YPS128
ADH4	Redstar	K11	YPS128
ZRT1	Redstar	K11	YPS128
COF1	Redstar	LalvinQA23	YPS163
PHO11	N/A	K11	YPS128
RPS14A	N/A	LalvinQA23	T7
RPS19A	N/A	LalvinQA23	T7
RPS26B	Redstar	LalvinQA23	YPS128

HHF1	N/A	Kyokai	T7
RPL8A	CLIB324	Kyokai	T7
HOM2	Redstar	LalvinQA23	YPS128
ADE13	Redstar	K11	YPS128
GRE1	Redstar	LalvinQA23	YPS128
YCP4	Redstar	LalvinQA23	YPS128
ERG9	Redstar	LalvinQA23	YPS128
SEC23	Redstar	K11	YPS128
RG11	N/A	N/A	N/A
RVB1	Redstar	K11	YPS128

Table 2: Yeast gene and function of gene analyzed in the study.

Gene	Function	Gene	Function
IPP1	Inorganic pyrophosphatase	HHF1	Histone H4
GDH2	NAD-specific glutamate dehydrogenase	RPL8A	60S ribosomal protein
MDH3	Malate dehydrogenase, peroxisomal	HOM2	Aspartic beta-semialdehyde dehydrogenase
ADH4	Alcohol dehydrogenase 4	ADE13	Aspartic beta-aldehyde dehydrogenase
ZRT1	Zinc-regulated transporter 1	GRE1	GRE1p protein
COF1	Cofilin protein	YCP4	Flavoprotein-like protein YCP4P
PHO11	Acid phosphatase PHO11	ERG9	Squalene synthase
RPS14A	40S ribosomal protein	SEC23	Transport protein SEC23p
RPS19A	40S ribosomal protein	RG11	Induced Respiratory Growth
RPS26B	40S ribosomal protein	RVB1	Ru VB-like protein 1

The sequences were then converted into Fasta format using <http://avermitilis.lis.kitasato-u.ac.jp/readseq.cgi>. The Fasta formatted sequences were aligned and saved in ClustalW format using <https://www.genome.jp/tools-bin/clustalw>. The aligned sequences were then imported into Rstudio and a dN/dS calculation was run using the ape package (Paradis et al. 2004). This provides a dN/dS ratio for each pairwise sequence comparison. A dN/dS ratio greater than 1 provides strong evidence that the difference in the DNA sequence was caused by positive Darwinian selection acting on variation in the amino acid sequence of the resulting protein. A ratio less than 1 is more consistent with the hypothesis that changes in amino acid sequence were likely caused by genetic drift rather than natural selection. In these cases, the changes in gene expression reported by Davydenko et al. (2020) are more likely attributable to evolutionary changes in gene regulation and gene expression and not to significant changes in the amino acid sequence of the resulting protein.

Results

Of the 20 genes examined, RG11 did not have a DNA sequence available, and 4 genes (COF1, HHH1, RPS14A, and RPS26B) had identical DNA sequences for baker's, brewer's, and wild and were therefore excluded from further study. Of the 15 remaining genes, 2 (RPS19A and PHO11) lacked sequence data for a baker's strain, so only the brewer's-wild comparison was possible for them. Sequences for 3 other genes (MDH3, HOM2, and GRE1) were identical for baker's and brewer's strains, so pairwise baker's-brewer's dN/dS comparisons were not possible for them. As a result, the total number of target genes available for dN/dS pairwise comparisons was 11 for baker's-brewer's comparisons, 12 for baker's-wild comparisons, and 15 for brewer's-wild comparisons.

dN/dS ratios ranged from 0 to 0.685, with the highest values noted for the genes ZRT1 in all three comparisons and YCP4 for the baker's-wild comparison (Figure 1). For one gene, IPP1, the baker's and brewer's strains differed by a single non-synonymous nucleotide substitution, yielding an infinite dN/dS ratio. Ratios averaged slightly higher in the baker's-brewer's and baker's-wild comparisons than in the brewer's-wild comparisons (Figure 1), but the differences were not statistically significant (Wilcoxon test Chi-square = 1.29, df = 2, $P = 0.53$).

IPP1 only had one semi-conservative protein change from proline in the brewer's and wild strain to a serine in the baker's strain. IPP1 makes inorganic pyrophosphatase and can be found in bacteria to humans. YCP4 had one semi-conservative protein change from a proline in the brewer's and wild strain to a serine in the baker's strain. YCP4 is only found in yeast and is thought to be a flavoprotein-like protein (Cherry et al., 2012). ZRT1 is a gene responsible for producing zinc pump proteins and is active when zinc is low in the cell. This protein is found in bacteria in humans. ZRT1 has 23 conservative changes, 9 semi-conservative changes, and 3 non-conservative changes. All 3 non-conservative changes were baker's yeast having a different amino acid than brewer's and wild.

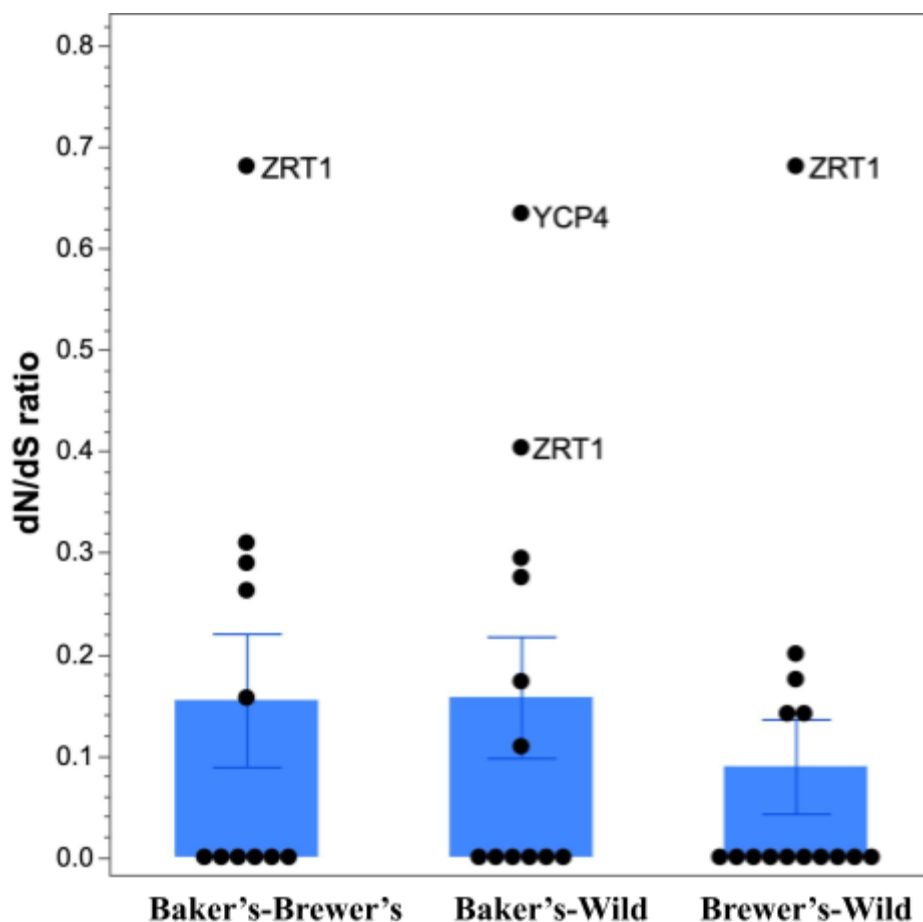


Figure 1. Distribution of dN/dS ratios for the genes of interest and the three pairwise comparisons among baker's, brewer's, and wild yeast strains. Blue bars and error bars indicate the mean and standard error. The baker's-brewers comparison included one gene (IPP1) with an infinite dN/dS ratio that could not be plotted. Four outliers with unusually high dN/dS ratios are noted.

Discussion

There was generally no evidence of adaptive evolution in the amino acid sequence of the 20 genes of interest; most of the comparisons revealed either no non-synonymous differences between the strains, or a low dN/dS <0.35. Thus, adaptive evolution of bread and brewer's strains seems to primarily involve evolutionary changes in gene expression rather than evolutionary changes in the amino acid sequence of proteins.

Nonetheless, my analysis did reveal some intriguing possible examples of adaptive amino acid change that are worth investigating further. While no dN/dS ratio was over 1, there were 3 genes that had interesting results. YCP4 had the highest dN/dS ratio of baker's strain to the wild

strain at 0.635. ZRT1 had the highest dN/dS ratio for both brewer's to wild and brewer's to baker's at 0.635 and 0.681 respectively. IPP1 had a dN/dS ratio of infinite for baker's to Brewer's, meaning that there was one nonsynonymous substitution but no synonymous substitutions.

There are some problems with dN/dS though. The first problem is that all sequences must be the same length or a comparison is not possible. So deletion, insertions, and early stop codons are not able to be analyzed with dN/dS. The other main problem with dN/dS is DNA sequence quality. If the DNA is not sequenced well, then non-base pair DNA symbols may appear in the sequence. The solution used to fix this problem was to look at the non-base pair symbol and compare it to the other known sequences. For example, if brewer's strain had a K and in the same spot, both the wild and baker's strain had a G, then it was assumed that the brewer's K was a G for the dN/dS sequencing (Table 3). This was used due to not always having perfectly sequenced DNA available. Population genetics, the genetic sequencing of a whole population, could avoid some of the problems with dN/dS, but ultimately is too expensive and time-consuming to be done at the undergraduate level.

Table 3: List of all non-base pair DNA symbols and meanings.

Non-base Pair DNA symbol	Meaning
W	Weak A or T
S	Strong C or G
M	Amino A or C
K	Ketone G or T
R	Purine A or G
Y	Pyrimidine C or T
B	Not A
D	Not C
H	Not G
V	Not T
N	Any

YCP4 is a gene responsible for making flavoproteins of unknown function. The protein is mostly found in highly purified mitochondria (Cherry et al., 2012). Flavoproteins are proteins that contain flavins and are involved in oxidative reactions in the cell. This gene is only found in yeast, so it may have the potential to vary more from strain to strain than a gene that is found in most living organisms. (Massy, 1995) YCP4 only had one nonsynonymous change which was a semiconservative change from proline in brewer's and wild strain to serine in the baker's strain.

While this change is from a nonpolar amino acid to a polar amino acid, it does not change the protein structure enough to be considered a nonconservative substitution. The high dN/dS ratio of 0.635 in baker's to wild compared to the dN/dS of 0.263 in baker's to brewer's may be caused by the difference in weights of the base pair changes. There were two synonymous base pair changes in YCP4. The first was at base pair 126 which was a C in both baker's and brewer's and the 3rd base pair of its codon to a T in the wild strain. This change is a transitional change as it is from a C to a T. The 2nd synonymous change is at base pair 480. The change is located on the 3rd base pair of the codon and it is a change from T in baker's and wild to an A in brewer's. This change is a transversional change as it is from a T to an A. The transversional synonymous change was weighted higher as transversional changes are less frequent than transitional changes so this resulted in the dS of the baker's to brewer's comparison being lower than the dS of the baker's to wild comparison, resulting in a higher dN/dS ratio for baker's to wild (Lyons & Lauring, 2017).

The IPP1 gene is responsible for cytoplasmic inorganic pyrophosphate, PPase protein. This gene is very important for the viability of an organism and versions of it can be found in bacteria to humans (Cherry et al., 2012). Due to the need of this gene for survival, high variability would not be expected between strains. There were only 3 total changes between strains and only one nonsynonymous change. The first synonymous change is at base pair 63 and was a twofold transitional change in the 3rd codon position from G in baker's and brewer's to A in wild. The 2nd synonymous change came from base pair 546 and was a fourfold change from A in baker's and brewer's to G in wild. The nonsynonymous change came at base pair 814, and was a change of the 1st base pair of the codon, from a C in brewer's and wild to a T in baker's. This is a semiconservative change to the amino acid from a proline in brewer's and wild to a serine in baker's. The dN/dS is Infinite because there were no synonymous changes between baker's and brewer's but is not conclusive evidence of positive selection because it was only one amino acid and the change resulted in only a semiconservative amino acid substitution.

ZRT1 is responsible for producing a high-affinity zinc transporter protein. It is most active when zinc is low in the cell (Cherry et al., 2012). It was shown before to be expressed more in brewer's yeast than in baker's yeast (Davydenko et al., 2020). ZRT1 is 376 amino acids long and has 14 active sites. (Wang et al., 2020) The 3D structure of ZRT1 has been proposed with high confidence, except for the binding area from amino acids 156 through 205 (Figure 2).

Table 4: Amino acid position of active sites (Wang et al.,2020)

Active site	Amino Acid	Active site	Amino Acid
1	8-10	8	165-175
2	26-33	9	206-242
3	47-73	10	247-270
4	81-111	11	276-278
5	116-119	12	281-303
6	121-125	13	312-343
7	128-155	14	352-372

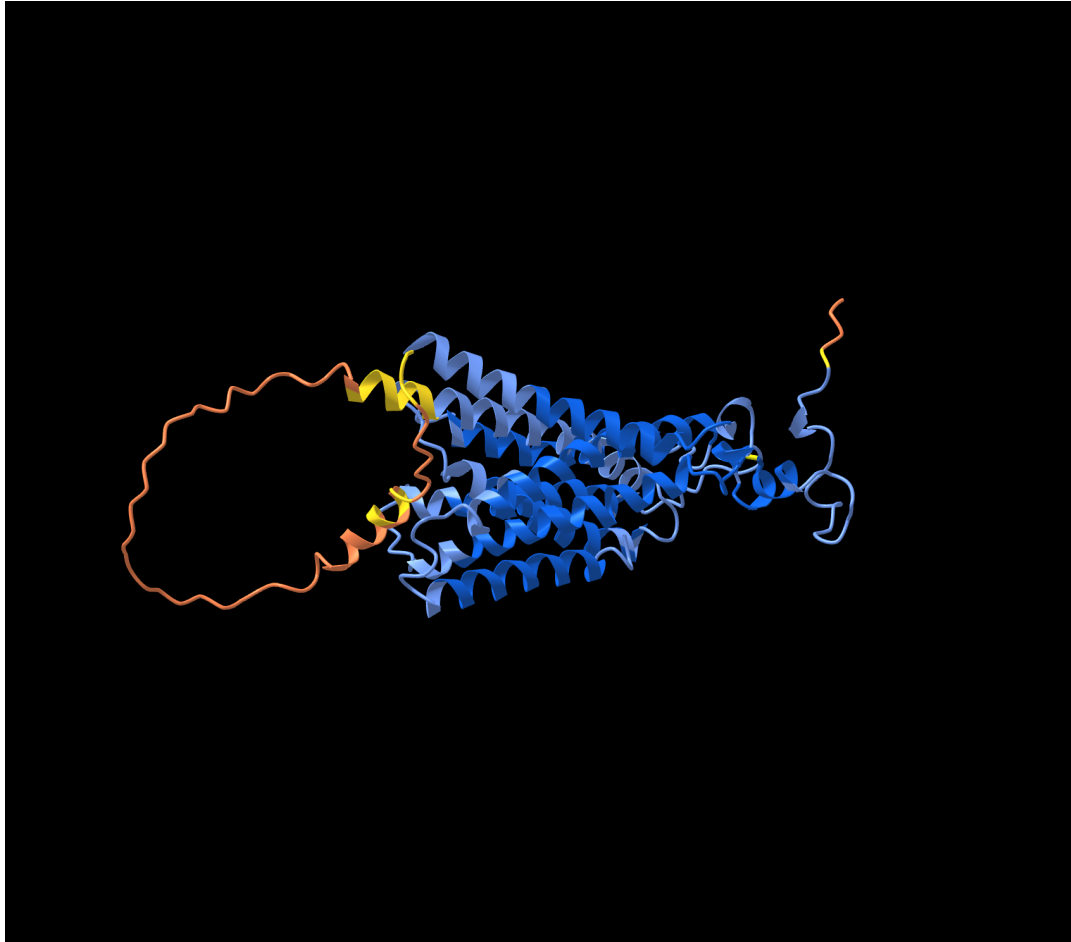


Figure 2: 3D structure of ZRT1. Blue indicates areas where there is high confidence in the 3D structure; light blue is confidence, yellow is low confidence, and orange is very low confidence. (Wang et al.,2020)

The dN/dS ratio for ZRT1 was the highest baker's to brewer's and brewer's to wild with a dN/dS of 0.681 and 0.685 respectively. It was also the 2nd highest in baker's to wild with a dN/dS of 0.404. While all of the dN/dS ratios are less than one, the ratios are still high enough to make positive selection possible. In the baker's to brewer's comparison, there are a total of 41 base pair changes. Nineteen of the changes were nonsynonymous changes, while the other 22 were synonymous. Of the synonymous changes, 13 were twofold and 9 were fourfold substitutions. In the wild to brewer's comparison, there are a total of 50 base pair changes; 24 of the changes were nonsynonymous changes, while the other 26 were synonymous. Of the synonymous changes, 19 were twofold and 7 were fourfold substitutions. In the baker's to wild

comparison, there are a total of 45 base pair changes; 18 of the changes were nonsynonymous changes, while the other 27 were synonymous. Of the synonymous changes, 14 were twofold and 13 were fourfold substitutions. Baker's yeast overall had a total of 14 amino acid substitutions, with 8 being conservative, 3 being semiconservative and 3 being nonconservative. Positive evolution also can not be ruled out for ZRT1 due to the number of amino acid substitutions, and how close they are to each other. There are 35 total amino acid changes between the 3 strains and only 8 of them are not within 5 amino acids of another change. Wild yeast had 7 amino acid substitutions with 5 being conservative and 2 being semi-conservative. Brewer's yeast overall had 16 total amino acid substitutions with 10 being conservative and 6 being semiconservative total. Amino acid 245 was the only substitution in which no strain shared an amino acid. The change was only semi-conservative though and amino acid 245 was not in any of the active sites of ZRT1 (Table 4). Due to the number of substitutions that brewer's has in both the active sites and in the uncertain region active site, it may have experienced positive selection pressure. There are 11 amino acid changes within the active site. Baker's yeast has 3 conservative, wild has 5 conservative, brewer's has 3 conservative and 3 semi conservative. There is also one active site, site 8, within the low confidence area. This active site has 3 amino acid substitutions with 165 as E for baker's and brewer's and D for wild being a conservative change, 172 with N for baker's and wild and R for brewer's being a semiconservative change, and 174 with A for baker's and wild and T for brewer's being a conservative change.

ZRT1 varied more than any other analyzed gene. It had more nucleotide and amino acid changes overall along with the highest average dN/dS ratio of 0.590, with the next closest, YCP4 only being 0.299. A dN/dS ratio was analyzed afterward to compare Missouri wild strain, T7 to Pennsylvania wild strain YPS128 and the ratio was 0.830. The large dN/dS between the two wild strains implies that the gene is highly variable and prone to rapid evolution.

My hypothesis for a possible reason for ZRT1 being different between brewer's, baking, and wild may be the amount of zinc present in their respective environments. Zinc is found inside of the grain being used. Because baking uses ground flour, baker's yeast should have easier access to zinc than brewer's yeast, where the grain is not ground to flour so more zinc is locked inside the grain. It could also be due to the water volume. The hydration of bread is measured as a percent of the weight of flour, so a 1 kg dough with 50% hydration would have 0.5

kg of water, whereas beer and wine are mostly water with fruit or grain added. This can be seen with bread having 1.47 mg and beer having 0.01 mg of zinc per 100 g (USDA. 2023).

Further study of the structure and function of the ZRT1 protein may show how amino acid changes affect the ability of the cell to collect zinc. Possible outcomes for this study could be Changes in the amino acid sequence lead to either more or less efficient pumping of zinc into the cell. A study of the structure of IPP1 with the serine instead of proline may provide interesting results as positive selection may be possible with an infinite dN/dS. Further study on gene regulation may show more insight into the differences between baker's and brewer's yeast.

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Appendix

ADE13

CLUSTAL 2.1 multiple sequence alignment

- Nucleotide Change

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K11      ATGCCTGACTACGACAATTACACTACGCCATTGTCTTCTAGATATGCCTCCAAGGAAATG
128      ATGCCTGACTACGACAATTACACTACGCCATTGTCTTCTAGATATGCCTCCAAGGAAATG
RED      ATGCCTGACTACGACAATTACACTACGCCATTGTCTTCTAGATATGCCTCCAAGGAAATG
          *****

K11      TCAGCAACGTTTTCTTTGAGAAACAGATTTCCACATGGAGAAAACATATGGTTAAATTTG
128      TCAGCAACGTTTTCTTTGAGAAACAGATTTCCACATGGAGAAAACATATGGTTAAATTTG
RED      TCAGCAACGTTTTCTTTGAGAAACAGATTTCCACATGGAGAAAACATATGGTTAAATTTG
          *****

K11      GCTATTGCTGAGAAGGAATTGGGCTTAAGTGTGTTACAGATGAAGCAATTGAGCAAATG
128      GCTATTGCTGAGAAGGAATTGGGCTTAAGTGTGTTACAGATGAAGCAATTGAGCAAATG
RED      GCTATTGCTGAGAAGGAATTGGGCTTAAGTGTGTTACAGATGAAGCAATTGAGCAAATG
          *****

K11      CGCAAACACGTCGAAATCACTGATGATGAAATCGCAAAAGCTTCTGCTCAAGAAGCCATT
128      CGCAAACACGTCGAAATCACTGATGATGAAATCGCAAAAGCTTCTGCTCAAGAAGCCATT
RED      CGCAAACACGTCGAAATCACTGATGATGAAATCGCAAAAGCTTCTGCTCAAGAAGCCATT
          *****

K11      GTAAGACATGATGTTATGGCACATGTTTCATACATTTGGTGAAACTTGTCGGGCTGCTGCG
128      GTAAGACATGATGTTATGGCACATGTTTCATACATTTGGTGAAACTTGTCGGGCTGCTGCG
RED      GTAAGACATGATGTTATGGCACATGTTTCATACATTTGGTGAAACTTGTCGGGCTGCTGCG
          *****

K11      GGTATCATTCACTTAGGTGCTACTTCCTGTTTCGTTACAGACAATGCTGATCTAATCTTT
128      GGTATCATTCACTTAGGTGCTACTTCCTGTTTCGTTACAGACAATGCTGATCTAATCTTC
RED      GGTATCATTCACTTAGGTGCTACTTCCTGTTTCGTTACAGACAATGCTGATCTAATCTTC
          *****

K11      ATTAGGGACGCCTACGATATTATTATTCAAAACCTTGTTAACGTCATCAACAGATTGGCT
128      ATTAGGGACGCCTACGATATTATTATTCAAAACCTTGTTAACGTCATCAACAGATTGGCT
RED      ATTAGGGACGCCTACGATATTATTATTCAAAACCTTGTTAACGTCATCAACAGATTGGCT
          *****

K11      AAGTTTGCTATGGAATACAAGGATTTGCCTGTATTGGGTTGGACTCACTTTCAACCAGCA
128      AAGTTTGCTATGGAATACAAGGATTTGCCTGTATTGGGTTGGACTCACTTTCAACCAGCA
RED      AAGTTTGCTATGGAATACAAGGATTTGCCTGTATTGGGTTGGACTCACTTTCAACCAGCA
          *****

K11      CAATTAACGACCTTGGGTAAGAGAGCTACTTTATGGATACAAGAGCTATTGTGGGATTTG
128      CAATTAACGACCTTGGGTAAGAGAGCTACTTTATGGATACAAGAGCTATTGTGGGATTTG
RED      CAATTAACGACCTTGGGTAAGAGAGCTACTTTATGGATACAAGAGCTATTGTGGGATTTG
          *****

K11      AGAAACTTTGAAAGAGCTAGAAACGATATCGGTCTACGTGGTGTAAAGGTTACTACTGGT
128      AGAAACTTTGAAAGAGCTAGAAACGATATCGGTCTACGTGGTGTAAAGGTTACTACTGGT
RED      AGAAACTTTGAAAGAGCTAGAAACGATATCGGTCTACGTGGTGTAAAGGTTACTACTGGT
          *****

K11      ACTCAGGCATCATTCCTTGGCCTTATTCCATGGTAATCATGATAAAGTTGAAGCCCTTGAC

```

128 ACTCAGGCATCATTCTTGGCCTTATTCCATGGTAATCATGATAAAGTTGAAGCCCTTGAC
RED ACTCAGGCATCATTCTTGGCCTTATTCCATGGTAATCATGATAAAGTTGAAGCCCTTGAC

K11 GAAAGAGTAACTGAATTATTAGGTTTCGATAAGGTATATCCAGTCACTGGTCAAACCTAC
128 GAAAGAGTAACTGAATTATTAGGTTTCGATAAGGTATATCCAGTCACTGGTCAAACCTAC
RED GAAAGAGTAACTGAATTATTAGGTTTCGATAAGGTATATCCAGTCACTGGTCAAACCTAC

K11 TCAAGAAAAATTGACATTGACGTGTTGGCTCCTTTGTCTTCTTTTGCTGCTACTGCACAC
128 TCAAGAAAAATTGACATTGACGTGTTGGCTCCTTTGTCTTCTTTTGCTGCTACTGCACAC
RED TCAAGAAAAATTGACATTGACGTGTTGGCTCCTTTGTCTTCTTTTGCTGCTACTGCACAC

K11 AAAATGGCTACTGACATAAGATTATTAGCCAACCTGAAGGAAGTTGAGGAACCTTTTGAG
128 AAAATGGCTACTGACATAAGATTATTAGCCAACCTGAAGGAAGTTGAGGAACCTTTTGAG
RED AAAATGGCTACTGACATAAGATTATTAGCCAACCTGAAGGAAGTTGAGGAACCTTTTGAG

K11 AAATCACAAATCGGATCCTCTGCTATGGCTTACAAGAGAAACCCAATGCGTTGTGAGAGA
128 AAATCACAAATCGGATCCTCTGCTATGGCTTACAAGAGAAACCCAATGCGTTGTGAGAGA
RED AAATCACAAATCGGATCCTCTGCTATGGCTTACAAGAGAAACCCAATGCGTTGTGAGAGA

K11 GTGTGCTCCTTGGCTAGACACTTAGGTTCCCTTGTTTAGTGACGCCGTTCAAACCTGCATCC
128 GTGTGCTCCTTGGCTAGACACTTAGGTTCCCTTGTTTAGTGACGCCGTTCAAACCTGCATCC
RED GTGTGCTCCTTGGCTAGACACTTAGGTTCCCTTGTTTAGTGACGCTGTTCAAACCTGCATCC

K11 GTTCAATGGTTCGAAAGAACTCTGGATGATTCTGCTATTAGAAGAATTTCTTTACCAAGT
128 GTTCAATGGTTCGAAAGAACTCTGGATGATTCTGCTATTAGAAGAATTTCTTTACCAAGT
RED GTTCAATGGTTCGAAAGAACTCTGGATGATTCTGCTATTAGAAGAATTTCTTTACCAAGT

K11 GCATTTTTTAACCGCAGATATTCTATTATCTACTTTGTTGAACATCTCATCCGGTTTAGTT
128 GCATTTTTTAACCGCAGATATTCTATTATCTACTTTGTTGAACATCTCATCCGGTTTAGTT
RED GCATTTTTTAACCGCAGATATTCTATTATCTACTTTGTTGAACATCTCATCCGGTTTAGTT

K11 GTGTATCCAAAGGTTATCGAAAGGAGAATTAAGGGTGAACCTTTTATGGCTACTGAA
128 GTGTATCCAAAGGTTATCGAAAGGAGAATTAAGGGTGAACCTTTTATGGCTACTGAA
RED GTGTATCCAAAGGTTATCGAAAGGAGAATTAAGGGTGAACCTTTTATGGCTACTGAA

K11 AATATCATCATGGCTATGGTAGAAAAGAATGCCTCCAGACAAGAAGTACATGAGCGTATT
128 AATATCATCATGGCCATGGTAGAAAAGAATGCCTCCAGACAAGAAGTACATGAGCGTATT
RED AATATCATCATGGCCATGGTAGAAAAGAATGCCTCCAGACAAGAAGTACATGAGCGTATT

K11 AGAGTGCTCTCTCATCAAGCCGAGCAGTAGTCAAGGAAGAAGGTGGGGAAAATGATTTA
128 AGAGTGCTCTCTCATCAAGCCGAGCAGTAGTCAAGGAAGAAGGTGGGGAAAATGATTTA
RED AGAGTGCTCTCTCATCAAGCCGAGCAGTAGTCAAGGAAGAAGGTGGGGAAAATGATTTA

K11 ATTGAACGAGTAAAGAGGGATGAATTTTCAAGCCTATCTGGGAAGAATTAGATTCTTTA

```

128      ATTGAACGAGTAAAGAGGGATGAATTTTCAAGCCTATCTGGGAAGAATTAGATTCTTTA
RED      ATTGAACGAGTAAAGAGGGATGAATTTTCAAGCCTATCTGGGAAGAATTAGATTCTTTA
          *****

K11      CTGGAACCATCCACTTTTGTGGTAGAGCTCCACAACAAGTTGAGAAATTTGTTCAAAAA
128      CTGGAACCATCCACTTTTGTGGTAGAGCTCCACAACAAGTTGAGAAATTTGTTCAAAAA
RED      CTGGAACCATCCACTTTTGTGGTAGAGCTCCACAACAAGTTGAGAAATTTGTTCAAAAA
          *****

K11      GACGTTAACAATGCTTTTACAACCTTTCCAAAAGTACCTAAACGATGAACAAGTCAAGTTA
128      GACGTTAACAATGCTTTTACAACCTTTCCAAAAGTACCTAAACGATGAACAAGTCAAGTTA
RED      GACGTTAACAATGCTTTTACAACCTTTCCAAAAGTACCTAAACGATGAACAAGTCAAGTTA
          *****

K11      AATGTTTAG
128      AATGTTTAG
RED      AATGTTTAG
          *****

```

dN/dS

Comparing sequences 1 and 2:

	Nondegenerate	Twofold	Fourfold
Transitions	0	1	1
Transversions	0	0	0

Comparing sequences 1 and 3:

	Nondegenerate	Twofold	Fourfold
Transitions	0	1	3
Transversions	0	0	0

Comparing sequences 2 and 3:

	Nondegenerate	Twofold	Fourfold
Transitions	0	0	2
Transversions	0	0	0

> output1

```

      K11 128
128    0
RED    0  0

```

ADH4

CLUSTAL 2.1 multiple sequence alignment

- Nucleotide Change

```

seq_K11      ATGTCTTCCGTTACTGGGTTTACATTCCACCAATCTCTTCTTTGGTGAAGGTGCTTTA
seq_128      ATGTCTTCCGTTACTGGGTTTACATTCCACCAATCTCTTCTTTGGTGAAGGTGCTTTA
seq_RED      ATGTCTTCCGTTACTGGGTTTACATTCCACCAATCTCTTCTTTGGTGAAGGTGCTTTA
*****

seq_K11      GAAGAAACCGCTGATTACATCAAAAACAAGGATTACAAAAGGCTTTGATCGTTACTGAT
seq_128      GAAGAAACCGCTGATTACATCAAAAACAAGGATTACAAAAGGCTTTGATCGTTACTGAT
seq_RED      GAAGAAACCGCTGATTACATCAAAAACAAGGATTACAAAAGGCTTTGATCGTTACTGAT
*****

seq_K11      CCTGGTATTGCAGCTATTGGTCTCTCCGGTAGAGTCCAAAAGATGTTGGAAGAACGTGGC
seq_128      CCTGGTATTGCAGCTATTGGTCTCTCCGGTAGAGTCCAAAAGATGTTGGAAGAACGTGGC
seq_RED      CCTGGTATTGCAGCTATTGGTCTCTCCGGTAGAGTCCAAAAGATGTTGGAAGAACGTGGC
*****

seq_K11      TTAAACGTTGCTATCTATGACAAAACCTCAACCAACCCAAATATTGCCAATGTCACAGCT
seq_128      TTAAACGTTGCTATCTATGACAAAACCTCAACCAACCCAAATATTGCCAATGTCACAGCT
seq_RED      TTAAACGTTGCTATCTATGACAAAACCTCAACCAACCCAAATATTGCCAATGTCACAGCT
*****

seq_K11      GGTTTGAAGGTTTGAAGGAACAAACTCTGAAATTGTTGTTCCATTGGTGGTGGTTCT
seq_128      GGTTTGAAGGTTTGAAGGAACAAACTCTGAAATTGTTGTTCCATTGGTGGTGGTTCT
seq_RED      GGTTTGAAGGTTTGAAGGAAGAAACTCTGAAATTGTCGTTTCCATTGGTGGTGGTTCT
*****

seq_K11      GCTCACGACAACGCTAAGGCCATTGCTTTATTGGCTACTAACGGTGGGGAAATCGGAGAT
seq_128      GCTCACGACAATGCTAAGGCCATTGCTTTATTGGCTACTAACGGTGGGGAAATCGGAGAC
seq_RED      GCTCACGACAATGCTAAGGCCATTGCTTTATTGGCTACTAACGGTGGGGAAATGGAGAT
*****

seq_K11      TATGAAGGTGTCAATCAATCTAAGAAGGCTGCTTTACCACTATTTGCCATCAACACTACT
seq_128      TATGAAGGTGTCAATCAATCTAAGAAGGCTGCTTTACCACTATTTGCCATCAACACTACT
seq_RED      TATGAAGGTGTCAACCAATCTAAGAAGGCTGCTTTACCGCTATTTGCCATCAACACTACT
*****

seq_K11      GCTGGTACTGCTTCCGAATGACCAGATTCACTATTATCTCTAATGAAGAAAAGAAAATC
seq_128      GCTGGTACTGCTTCCGAATGACCAGATTCACTATTATCTCTAATGAAGAAAAGAAAATC
seq_RED      GCTGGTACTGCTTCCGAGATGACCAGATTCACTATTATCTCTAATGAAGAAAAGAAAATC
*****

seq_K11      AAGATGGCTATCATTGACAACAACGTCACTCCAGCTGTTGCTGTCAACGATCCATCTACC
seq_128      AAGATGGCTATCATTGACAACAACGTCACTCCAGCTGTTGCTGTCAACGATCCATCTACC
seq_RED      AAGATGGCCATCATTGACAACAACGTCACTCCAGCTGTTGCTGTCAACGACCCATCTACC
*****

seq_K11      ATGTTTGGTTTGCCACCTGCTTTGACTGCTGCTACTGGTCTAGATGCTTTGACTCACTGT
seq_128      ATGTTTGGTTTGCCACCTGCTTTGACTGCTGCTACTGGTCTAGATGCTTTGACTCACTGT
seq_RED      ATGTTTGGTTTGCCACCTGCTTTGACTGCTGCTACTGGTCTAGATGCTTTGACTCACTGT
*****

seq_K11      ATCGAAGCTTATGTTTCCACCGCCTCTAACCCAATCACCGATGCCGTGTGCTTTGAAGGGT

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seq_128      ATCGAAGCTTATGTTTCCACCGCCTCTAACCCAATCACCGATGCTGTGCTTTGAAGGGT
seq_RED      ATCGAAGCTTACGTTTCCACCGCCTCTAACCCAATCACCGATGCTTGTGCTTTGAAGGGT
*****

seq_K11      ATTGATTTGATCAATGAAAGCTTAGTCGCGCATACAAAGACGGTAAAGACAAGAAGGCC
seq_128      ATTGATTTGATCAATGAAAGCTTAGTCGCTGCATACAAAGACGGTAAAGACAAGAAGGCC
seq_RED      ATTGATTTGATCAATGAAAGCTTAGTCGCGCATACAAAGACGGTAAAGACAAGAAGGCC
*****

seq_K11      AGAACTGACATGTGTTACGCTGAATACTTGGCAGGTATGGCTTTCAACAATGCTTCTCTA
seq_128      AGAACTGACATGTGTTACGCTGAATACTTGGCAGGTATGGCTTTCAACAATGCTTCTCTA
seq_RED      AGAACTGATATGTGTTACGCAGAATACTTGGCAGGTATGGCTTTCAACAATGCTTCTCTA
*****

seq_K11      GGTATGTTTCATGCCCTTGCTCATCAACTTGGTGGTTTCTACCACTTGCCCTCATGGTGTT
seq_128      GGTATGTTTCATGCCCTTGCTCATCAACTTGGTGGTTTCTACCACTTGCCCTCATGGTGTT
seq_RED      GGTATGTTTCATGCCCTTGCTCATCAACTTGGTGGTTTCTACCACTTGCCCTCATGGTGTT
*****

seq_K11      TGTAACGCTGTCTTGTTGCCTCATGTTCAAGAGGCCAACATGCAATGTCCAAAGGCCAAG
seq_128      TGTAACGCTGTCTTGTTGCCTCATGTTCAAGAGGCCAACATGCAATGTCCAAAGGCCAAG
seq_RED      TGTAACGCTGTCTTGTTGCCTCATGTTCAAGAGGCCAACATGCAATGTCCAAAGGCCAAG
*****

seq_K11      AAGAGATTAGATGAAATTGCTTTGCATTTCGGTGCTTCTCAAGAAGATCCAGAAGAAACC
seq_128      AAGAGATTAGGTGAAATTGCTTTGCATTTCGGTGCTTCTCAAGAAGATCCAGAAGAAACC
seq_RED      AAGAGATTAGGTGAAATTGCTTTGCATTTCGGTGCTTCTCAAGAAGATCCAGAAGAAACC
*****

seq_K11      ATCAAGGCTTTGCACGTTTTAAACAGAACCATGAACATTCCAAGAACTTGAAAGAAATTA
seq_128      ATCAAGGCTTTGCACGTTTTAAACAGAACCATGAACATTCCAAGAACTTGAAAGAAATTA
seq_RED      ATCAAGGCTTTGCACGTTTTAAACAGAACCATGAACATTCCAAGAACTTGAAAGACTTA
*****

seq_K11      GGTGTAAAACCGAAGATTTTGAAATTTTGGCTGAACACGCCATGCATGATGCCTGCCAT
seq_128      GGTGTAAAACCGAAGATTTTGAAATTTTGGCTGAACACGCCATGCATGATGCCTGCCAT
seq_RED      GGTGTAAAACCGAAGATTTTGACATTTTGGCTGAACACGCCATGCATGATGCCTGCCAT
*****

seq_K11      TTGACTAACCAGTTCAATTCACCAAAGAACAAGTGGTTGCCATTATCAAGAAAGCCTAT
seq_128      TTGACTAACCAGTTCAATTCACCAAAGAACAAGTGGTTGCCATTATCAAGAAAGCCTAT
seq_RED      TTGACTAACCAGTTCAATTCACCAAAGAACAAGTGGTTGCCATTATCAAGAAAGCCTAT
*****

seq_K11      GAATATTAA
seq_128      GAATATTAA
seq_RED      GAATATTAA
*****

```

dN/dS

Comparing sequences 1 and 2:

	Nondegenerate	Twofold	Fourfold
Transitions	1	2	1
Transversions	0	0	0

Comparing sequences 1 and 3:

	Nondegenerate	Twofold	Fourfold
Transitions	1	7	5
Transversions	2	2	1

Comparing sequences 2 and 3:

	Nondegenerate	Twofold	Fourfold
Transitions	0	7	6
Transversions	2	2	1

> output1

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      seq_K11    seq_128
seq_128 0.2004519
seq_RED 0.1570541 0.1090512

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CLUSTAL 2.1 multiple sequence alignment

All sequences are the same

```

seq_Red      ATGTGGGGGAAAAAATTCATAAGAAGCCAGGAAAATGTGAAGTTTCTGTGTAGTGTGCT
seq_Wild-163 ATGTGGGGGAAAAAATTCATAAGAAGCCAGGAAAATGTGAAGTTTCTGTGTAGTGTGCT
seq_Sake     ATGTGGGGGAAAAAATTCATAAGAAGCCAGGAAAATGTGAAGTTTCTGTGTAGTGTGCT
*****

seq_Red      GTTGCTGATGAATCCCTTACCGCTTTCAATGACTTGAAATTGGGTAAAAAATACAAATTT
seq_Wild-163 GTTGCTGATGAATCCCTTACCGCTTTCAATGACTTGAAATTGGGTAAAAAATACAAATTT
seq_Sake     GTTGCTGATGAATCCCTTACCGCTTTCAATGACTTGAAATTGGGTAAAAAATACAAATTT
*****

seq_Red      ATTTTATTCGGATTGAACGATGCTAAAACCGAAATTGTTGTCAAGGAAACCTCTACTGAC
seq_Wild-163 ATTTTATTCGGATTGAACGATGCTAAAACCGAAATTGTTGTCAAGGAAACCTCTACTGAC
seq_Sake     ATTTTATTCGGATTGAACGATGCTAAAACCGAAATTGTTGTCAAGGAAACCTCTACTGAC
*****

seq_Red      CCATCTTACGATGCCTTCTTAGAGAAATTGCCAGAAAACGACTGTCTTTACGCCATTAC
seq_Wild-163 CCATCTTACGATGCCTTCTTAGAGAAATTGCCAGAAAACGACTGTCTTTACGCCATTAC
seq_Sake     CCATCTTACGATGCCTTCTTAGAGAAATTGCCAGAAAACGACTGTCTTTACGCCATTAC
*****

seq_Red      GATTTTGAATACGAAATTAATGGTAATGAAGGTAAGAGATCCAAGATTGTTTTCTTCACT
seq_Wild-163 GATTTTGAATACGAAATTAATGGTAATGAAGGTAAGAGATCCAAGATTGTTTTCTTCACT
seq_Sake     GATTTTGAATACGAAATTAATGGTAATGAAGGTAAGAGATCCAAGATTGTTTTCTTCACT
*****

seq_Red      TGGTCTCCAGACACTGCTCCAGTCAGATCTAAGATGGTCTATGCATCCTCCAAGGATGCC
seq_Wild-163 TGGTCTCCAGACACTGCTCCAGTCAGATCTAAGATGGTCTATGCATCCTCCAAGGATGCC
seq_Sake     TGGTCTCCAGACACTGCTCCAGTCAGATCTAAGATGGTCTATGCATCCTCCAAGGATGCC
*****

seq_Red      TTAAGAAGAGCCTTAAACGGTGTCTCTACCGATGTTCAAGGTACTGATTTTCCGAAGTT
seq_Wild-163 TTAAGAAGAGCCTTAAACGGTGTCTCTACCGATGTTCAAGGTACTGATTTTCCGAAGTT
seq_Sake     TTAAGAAGAGCCTTAAACGGTGTCTCTACCGATGTTCAAGGTACTGATTTTCCGAAGTT
*****

seq_Red      TCTTACGATTCTGTTTTGGAAAGAGTCAGCAGAGGCGCTGGTTCTCATTA
seq_Wild-163 TCTTACGATTCTGTTTTGGAAAGAGTCAGCAGAGGCGCTGGTTCTCATTA
seq_Sake     TCTTACGATTCTGTTTTGGAAAGAGTCAGCAGAGGCGCTGGTTCTCATTA
*****

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ERG9

CLUSTAL 2.1 multiple sequence alignment

 - Nucleotide Change

RED	ATGGGAAAGCTATTACAATTGGCATTGCATCCGGTCGAGATGAAGGCAGCTTTGAAGCTG
128	ATGGGAAAGCTATTACAATTGGCATTGCATCCGGTCGAGATGAAGGCAGCTTTGAAGCTG
LALVIN	ATGGGAAAGCTATTACAATTGGCATTGCATCCGGTCGAGATGAAGGCAGCTTTGAAGCTG *****
RED	AAGTTTTGCAGAACACCGCTATTCTCCATCTATGATCAGTCCACGTCTCCATATCTCTTG
128	AAGTTTTGCAGAACACCGCTATTCTCCATCTATGATCAGTCCACGTCTCCATATCTCTTG
LALVIN	AAGTTTTGCAGAACACCGCTATTCTCCATCTATGATCAGTCCACGTCTCCATATCTCTTG *****
RED	CACTGTTTCGAACTGTTGAACTTGACCTCCAGATCGTTTGCTGCTGTGATCAGAGAGCTG
128	CACTGTTTCGAACTGTTGAACTTGACCTCCAGATCGTTTGCTGCTGTGATCAGAGAGCTG
LALVIN	CACTGTTTCGAACTGTTGAACTTGACCTCCAGATCGTTTGCTGCTGTGATCAGAGAGCTG *****
RED	CATCCAGAATTGAGAACTGTGTTACTCTCTTTTATTTGATTTTAAGGGCTTTGGATACC
128	CATCCAGAATTGAGAACTGTGTTACTCTCTTTTATTTGATTTTAAGGGCTTTGGATACC
LALVIN	CATCCAGAATTGAGAACTGTGTTACTCTCTTTTATTTGATTTTAAGGGCTTTGGATACC *****
RED	ATCGAAGACGATATGTCCATCGAACACGATTTGAAAATTGACTTGTTGCGTCACCTCCAC
128	ATCGAAGACGATATGTCCATCGAACACGATTTGAAAATTGACTTGTTGCGTCACCTCCAC
LALVIN	ATCGAAGACGATATGTCCATCGAACACGATTTGAAAATTGACTTGTTGCGTCACCTCCAC *****
RED	GAGAAATTGTTGTTAACTAAATGGAGTTTCGACGGAATGCCCGATGTGAAGGACAGA
128	GAGAAATTGTTGTTAACTAAATGGAGTTTCGACGGAATGCCCGATGTGAAGGACAGA
LALVIN	GAGAAATTGTTGTTAACTAAATGGAGTTTCGACGGAATGCCCGATGTGAAGGACAGA *****
RED	GCCGTTTTGACAGATTTGGAATCGATTCTTATTGAATCCACAAATTGAAACCAGAATAT
128	GCCGTTTTGACAGATTTGGAATCGATTCTTATTGAATCCACAAATTGAAACCAGAATAT
LALVIN	GCCGTTTTGACAGATTTGGAATCGATTCTTATTGAATCCACAAATTGAAACCAGAATAT *****
RED	CAAGAAGTCATCAAGGAGATCACCGAGAAAATGGGTAATGGTATGGCCGACTACATCTTG
128	CAAGAAGTCATCAAGGAGATCACCGAGAAAATGGGTAATGGTATGGCCGACTACATCTTA
LALVIN	CAAGAAGTCATCAAGGAGATCACCGAGAAAATGGGTAATGGTATGGCCGACTACATCTTA *****
RED	GATGAAAATTACAACCTGAATGGGTTGCAAACCGTCCACGACTACGACGTGTACTGTCAC
128	GATGAAAATTACAACCTGAATGGGTTGCAAACCGTCCACGACTACGACGTGTACTGTCAC
LALVIN	GATGAAAATTACAACCTGAATGGGTTGCAAACCGTCCACGACTACGACGTGTACTGTCAC *****
RED	TACGTAGCTGGTTTGGTTCGGTGATGGTTTGACCCGTTTGATTGTCATTGCCAAGTTTGCC
128	TACGTAGCTGGTTTGGTTCGGTGATGGTTTGACCCGTTTGATTGTCATTGCCAAGTTTGCC
LALVIN	TACGTAGCTGGTTTGGTTCGGTGATGGTTTGACCCGTTTGATTGTCATTGCCAAGTTTGCC *****
RED	AACGAATCTTTGTATTCTAATGAGCAATTGTATGAAAGCATGGGTCTTTTCCTACAAAA

128 AACGAATCTTTGTATTCTAATGAGCAATTGTATGAAAGCATGGGTCTTTTCCTACAAAAA
 LALVIN AACGAATCTTTGTATTCTAATGAGCAATTGTATGAAAGCATGGGTCTTTTCCTACAAAAA

RED ACCAACATCATCAGAGACTACAATGAAGATTTGGTCGATGGTAGATCCTTCTGCCCCAAG
 128 ACCAACATCATCAGAGACTACAATGAAGATTTGGTCGATGGTAGATCCTTCTGCCCCAAG
 LALVIN ACCAACATCATCAGAGATTACAATGAAGATTTGGTCGATGGTAGATCCTTCTGCCCCAAG

RED GAAATCTGGTCACAATACGCTCCTCAGTTGAAGGACTTCATGAAACCTGAAAACGAACAA
 128 GAAATCTGGTCACAATACGCTCCTCAGTTGAAGGACTTCATGAAACCTGAAAACGAACAA
 LALVIN GAAATCTGGTCACAATACGCTCCTCAGTTGAAGGACTTCATGAAACCTGAAAACGAACAA

RED CTGGGGTTGGACTGTATAAACCACCTCGTCTTAAACGCATTGAGTCATGTTATCGATGTG
 128 CTGGGGTTGGACTGTATAAACCACCTCGTCTTAAACGCATTGAGTCATGTTATCGATGTG
 LALVIN CTGGGGTTGGACTGTATAAACCACCTCGTCTTAAACGCATTGAGTCATGTTATCGATGTG

RED TTGACTTATTTGGCCAGTATCCACGAGCAATCCACTTTCCAATTTTGTGCCATTCCCCAA
 128 TTGACTTATTTGGCCAGTATCCACGAGCAATCCACTTTCCAATTTTGTGCCATTCCCCAA
 LALVIN TTGACTTATTTGGCCAGTATCCACGAGCAATCCACTTTCCAATTTTGTGCCATTCCCCAA

RED GTTATGGCCATTGCAACCTTGGCTTTGGTATTCAACAACCGTGAAGTGCTACATGGCAAT
 128 GTTATGGCCATTGCAACCTTGGCTTTGGTATTCAACAACCGTGAAGTGCTACATGGCAAT
 LALVIN GTTATGGCCATTGCAACCTTGGCTTTGGTATTCAACAACCGTGAAGTGCTACATGGCAAT

RED GTAAAGATTTCGTAAGGGTACTACCTGCTATTTAATTTTGAATCAAGGACTTTGCGTGCC
 128 GTAAAGATTTCGTAAGGGTACTACCTGCTATTTAATTTTGAATCAAGGACTTTGCGTGCC
 LALVIN GTAAAGATTTCGTAAGGGTACTACCTGCTATTTAATTTTGAATCAAGGACTTTGCGTGCC

RED TGTGTCGAGATTTTGTACTATTACTTACGTGATATCAAATCTAAATTGGCTGTGCAAGAT
 128 TGTGTCGAGATTTTGTACTATTACTTACGTGATATCAAATCTAAATTGGCTGTGCAAGAT
 LALVIN TGTGTCGAGATTTTGTACTATTACTTACGTGATATCAAATCTAAATTGGCTGTGCAAGAT

RED CCAAATTTCTTAAATTTGAACATTCAAATCTCCAAGATCGAACAATTCATGGAAGAAATG
 128 CCAAATTTCTTAAATTTGAACATTCAAATCTCCAAGATCGAACAATTCATGGAAGAAATG
 LALVIN CCAAATTTCTTAAATTTGAACATTCAAATCTCCAAGATCGAACAATTCATGGAAGAAATG

RED TACCAGGATAAATTACCTCCTAACGTGAAGCCAAATGAACTCCAATTTTCTTGAAAGTT
 128 TACCAGGATAAATTACCTCCTAACGTGAAGCCAAATGAACTCCAATTTTCTTGAAAGTT
 LALVIN TACCAGGATAAATTACCTCCTAACGTGAAGCCAAATGAACTCCAATTTTCTTGAAAGTT

RED AAAGAAAGATCCAGATACGATGATGAATTGGTTCCAACCCAACAAGAAGAAGAGTACAAG
 128 AAAGAAAGATCCAGATACGATGATGAATTGGTTCCAACCCAACAAGAAGAAGAGTACAAG
 LALVIN AAAGAAAGATCCAGATACGATGATGAATTGGTTCCAACCCAACAAGAAGAAGAGTACAAG

RED TTCAATATGGTTTTATCTATCATCTTGTCGGTTCTTCTTGGGTTTTATTATATATACACT

```

128          TTCAATATGGTTTTATCTATCATCTTGTCGGTTCTTCTGGGTTTTATTATATATACT
LALVIN       TTCAATATGGTTTTATCTATCATCTTGTCGGTTCTTCTGGGTTTTATTATATATACT
              *****

RED          TTACACAGAGCGTGA
128          TTACACAGAGCGTGA
LALVIN       TTACACAGAGCGTGA
              *****

```

dN/dS

Comparing sequences 1 and 2:

	Nondegenerate	Twofold	Fourfold
Transitions	0	1	2
Transversions	0	0	0

Comparing sequences 1 and 3:

	Nondegenerate	Twofold	Fourfold
Transitions	0	4	0
Transversions	0	0	0

Comparing sequences 2 and 3:

	Nondegenerate	Twofold	Fourfold
Transitions	0	3	2
Transversions	0	0	0

> output1

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          RED 128
128        0
LALVIN    0  0

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GDH2

CLUSTAL 2.1 multiple sequence alignment

 - Nucleotide Change
 Wild is YPS128

seq_Redstar	ATGCTTTTGGATAACAAAAATCGCGGTGCTTTAACTCACTGAACACACCAGATATTGCT
seq_Wild	ATGCTTTTGGATAACAAAAATCGCGGTGCTTTAACTCACTGAACACACCAGATATTGCT
seq_Lalvin	ATGCTTTTGGATAACAAAAATCGCGGTGCTTTAACTCACTGAACACACCAGATATTGCT *****
seq_Redstar	TCTTTATCAATATCATCCATGTGCGACTATCACGTGTTTGATTTTCCCGGTAAGGACCTG
seq_Wild	TCTTTATCAATATCATCCATGTGCGACTATCACGTGTTTGATTTTCCCGGTAAGGACCTG
seq_Lalvin	TCTTTATCAATATCATCCATGTGCGACTATCACGTGTTTGATTTTCCCGGTAAGGACCTG *****
seq_Redstar	CAGAGAGAGGAAGTGATAGATTGCTAGATCAGCAAGGATTTATTCCCGACGATTTGATC
seq_Wild	CAGAGAGAGGAAGTGATAGATTGCTAGATCAGCAAGGATTTATTCCCGACGATTTGATC
seq_Lalvin	CAGAGAGAGGAAGTGATAGATTGCTAGATCAGCAAGGATTTATTCCCGACGATTTGATC *****
seq_Redstar	GAACAAGAAGTAGATTGGTTTTATAACTCATTGGGTATTGACGATTGTCTTCTCGAGA
seq_Wild	GAACAAGAAGTAGATTGGTTTTATAACTCATTGGGTATTGACGATTGTCTTCTCGAGA
seq_Lalvin	GAACAAGAAGTAGATTGGTTTTATAACTCATTGGGTATTGACGATTGTCTTCTCGAGA *****
seq_Redstar	GAATCTCCCCAATTAATCTCGAATATCATACATTCTTTGTATGCTTCAAAGCTAGATTTC
seq_Wild	GAATCTCCCCAATTAATCTCGAATATCATACATTCTTTGTATGCTTCAAAGCTAGATTTC
seq_Lalvin	GAATCTCCCCAATTAATCTCGAATATCATACATTCTTTGTATGCTTCAAAGCTAGATTTC *****
seq_Redstar	TTTGCGAAGTCCAAATTCAACGGAATTCAGCCAAGGCTATTTCAGCATTAAAAACAAAATT
seq_Wild	TTTGCGAAGTCCAAATTCAACGGAATTCAGCCAAGGCTATTTCAGCATTAAAAACAAAATT
seq_Lalvin	TTTGCGAAGTCCAAATTCAACGGAATTCAGCCAAGGCTATTTCAGCATTAAAAACAAAATT *****
seq_Redstar	ATAACTAATGATAATCATGCCATCTTTATGGAATCTAATACTGGTGTGAGCATAAGCGAT
seq_Wild	ATAACTAATGATAATCATGCCATCTTTATGGAATCTAATACTGGTGTGAGCATAAGCGAT
seq_Lalvin	ATAACTAATGATAATCATGCCATCTTTATGGAATCTAATACTGGTGTGAGCATAAGCGAT *****
seq_Redstar	TCTCAGCAAAAAAACTTTAAATTTGCTAGTGAAGCCGTCGGAACGATACTTTGGAGCAT
seq_Wild	TCTCAGCAAAAAAACTTTAAATTTGCTAATGACGCCGTCGGAACGATACTTTGGAGCAT
seq_Lalvin	TCTCAGCAAAAAAACTTTAAATTTGCTAGTGAAGCCGTCGGAACGATACTTTGGAGCAT *****
seq_Redstar	GGTAAGGATACCATCAAAAAAATAGGATTGAAATGGATGATTCTTGTCCACCTTATGAA
seq_Wild	GGTAAGGATACCATCAAAAAAATAGGATTGAAATGGATGATTCTTGTCCACCTTATGAA
seq_Lalvin	GGTAAGGATACCATCAAAAAAATAGGATTGAAATGGATGATTCTTGTCCACCTTATGAA *****
seq_Redstar	TTAGATTCGAAATTGATGACCTTTTCCTGGATAACAAGTCTCAAAAAAACTGCAGATTA
seq_Wild	TTAGATTCGAAATTGATGACCTTTTCCTGGATAACAAGTCTCAAAAAAACTGCAGATTA
seq_Lalvin	TTAGATTCGAAATTGATGACCTTTTCCTGGATAACAAGTCTCAAAAAAACTGCAGATTA *****
seq_Redstar	GTTTCTTTTGGGCTCCAGAAAGCGAATTAAAGCTAACTTTTGTATTGAGAGTGTTTAC
seq_Wild	GTTTCTTTTGGGCTCCAGAAAGCGAATTAAAGCTAACTTTTGTATTGAGAGTGTTTAC

```

seq_Lalvin      GTTTCCTTTTGGGCTCCAGAAAGCGAATTAAAGCTAACTTTTGTTTATGAGAGTGTTTAC
*****

seq_Redstar     CCTAATGATGATCCAGCCGGCGTAGATATTTCTCTCAGGATTTGCTGAAAGGTGATATT
seq_Wild        CCTAATGATGATCCAGCCGGCGTAGATATTTCTCTCAGGATTTGCTGAAAGGTGATATT
seq_Lalvin      CCTAATGATGATCCAGCCGGCGTAGATATTTCTCTCAGGATTTGCTGAAAGGTGATATT
*****

seq_Redstar     GAATCTATTAGTGATAAGACCATGTACAAAGTTTCGTCGAACGAAAATAAAAACTATAC
seq_Wild        GAATCTATTAGTGATAAGACCATGTACAAAGTTTCGTCGAACGAAAATAAAAACTATAC
seq_Lalvin      GAATCTATTAGTGATAAGACCATGTACAAAGTTTCGTCGAACGAAAATAAAAACTATAC
*****

seq_Redstar     GGTCTCTTACTTAAGTTGGTTAAAGAAAGAGAAGGTCCTGTCATTAAGACTACTCGCTCC
seq_Wild        GGTCTCTTACTTAAGTTGGTTAAAGAAAGAGAAGGTCCTGTCATTAAGACTACTCGCTCC
seq_Lalvin      GGTCTCTTACTTAAGTTGGTTAAAGAAAGAGAAGGTCCTGTCATTAAGACTACTCGCTCC
*****

seq_Redstar     GTAGAAAATAAGGATGAAATTAGGTTATTAGTCGCTTACAAGCGATTCACTACTAAGCGT
seq_Wild        GTAGAAAATAAGGATGAAATTAGGTTATTAGTCGCTTACAAGCGATTCACTACTAAGCGT
seq_Lalvin      GTAGAAAATAAGGATGAAATTAGGTTATTAGTCGCTTACAAGCGATTCACTACTAAGCGT
*****

seq_Redstar     TATTACTCTGCTTTGAACTCTTTGTTCCACTATTACAAGTTGAAACCTTCTAAGTTCTAT
seq_Wild        TATTACTCTGCTTTGAACTCTTTGTTCCACTATTACAAGTTGAAACCTTCTAAGTTCTAT
seq_Lalvin      TATTACTCTGCTTTGAACTCTTTGTTCCACTATTACAAGTTGAAACCTTCTAAGTTCTAT
*****

seq_Redstar     TTGGAGTCGTTTAAATGTTAAGGATGATGACATCATTATCTTTTCCGTTTATTTGAACGAG
seq_Wild        TTGGAGTCGTTTAAATGTTAAGGATGATGACATCATTATCTTTTCCGTTTATTTGAACGAG
seq_Lalvin      TTGGAGTCGTTTAAATGTTAAGGATGATGACATCATTATCTTTTCCGTTTATTTGAACGAG
** *****

seq_Redstar     AACCAGCAATTGGAAGATGTTCTACTCCATGATGTGGAGGCAGCATTGAAACAGGTTGAA
seq_Wild        AACCAGCAATTGGAAGATGTTCTACTCCATGATGTGGAGGCAGCATTGAAACAGGTTGAA
seq_Lalvin      AACCAGCAATTGGAAGATGTTCTACTCCATGATGTGGAGGCAGCATTGAAACAGGTTGAA
***** ** *****

seq_Redstar     AGAGAAGCTTCATTGCTATACGCTATCCCAAACAATTCTTTCCATGAGGTTTACCAGAGA
seq_Wild        AGAGAAGCTTCATTGCTATACGCTATCCCAAACAATTCTTTCCATGAGGTTTACCAGAGA
seq_Lalvin      AGAGAAGCTTCATTGCTATACGCTATCCCAAACAATTCTTTCCATGAGGTTTACCAGAGA
*****

seq_Redstar     CGTCAATTCTCGCCCAAAGAAGCTATATATGCTCATATTGGTGCTATATTCATTAACCAT
seq_Wild        CGTCAATTCTCGCCCAAAGAAGCTATATATGCTCATATTGGTGCTATATTCATTAACCAT
seq_Lalvin      CGTCAATTCTCGCCCAAAGAAGCTATATATGCTCATATTGGTGCTATATTCATTAACCAT
*****

seq_Redstar     TTTGTTAATCGTTTAGGCTCTGATTATCAAAACCTTTTATCTCAAATCACCATTAAGCGT
seq_Wild        TTTGTTAATCGTTTAGGCTCTGATTATCAAAACCTTTTATCTCAAATCACCATTAAGCGT
seq_Lalvin      TTTGTTAATCGTTTAGGCTCTGATTATCAAAACCTTTTATCTCAAATCACCATTAAGCGT
*****

seq_Redstar     AATGATACTACTCTTTTGGAGATTGTAGAAAACCTAAAAAGAAAGTTAAGAAATGAAACC

```

```

seq_Wild      AATGATACTACTCTTTTGGAGATTGTAGAAAACCTAAAAAGAAAGTTAAGAAATGAAACC
seq_Lalvin    AATGATACTACTCTTTTGGAGATTGTAGAAAACCTAAAAAGAAAGTTAAGAAATGAAACC
*****

seq_Redstar   TTAACCTCAGCAAACCTATTATCAACATCATGTCTGAAGCATTACACTATAATTTCCAAGTTG
seq_Wild      TTAACCTCAGCAAACCTATTATCAACATCATGTCTGAAGCATTACACTATAATTTCCAAGTTG
seq_Lalvin    TTAACCTCAGCAAACCTATTATCAACATCATGTCTGAAGCATTACACTATAATTTCCAAGTTG
*****

seq_Redstar   TATAAAAATTTTGCTCAAATTCACCTATTATCATAATAGTACTAAAGATATGGAAAGACA
seq_Wild      TATAAAAATTTTGCTCAAATTCACCTATTATCATAATAGTACTAAAGATATGGAAAGACA
seq_Lalvin    TATAAAAATTTTGCTCAAATTCACCTATTATCATAATAGTACTAAAGATATGGAGAAGACA
*****

seq_Redstar   TTATCTTTTCAAAGACTGGAAAAAGTGGAGCCTTTTAAAGATGACCAAGAGTTCGAAGCT
seq_Wild      TTATCTTTTCAAAGACTGGAAAAAGTGGAGCCTTTTAAAGATGACCAAGAGTTCGAAGCT
seq_Lalvin    TTATCTTTTCAAAGACTGGAAAAAGTGGAGCCTTTTAAAGATGACCAAGAGTTCGAAGCT
*****

seq_Redstar   TACTTGAATAAAATTCATTCCAAATGATTACCTGATTGTGTGATCTTGAAAACACTGAAC
seq_Wild      TACTTGAATAAAATTCATTCCAAATGATTACCTGATTGTGTGATCTTGAAAACACTGAAC
seq_Lalvin    TACTTGAATAAAATTCATTCCAAATGATTACCTGATTGTGTGATCTTGAAAACACTGAAC
*****

seq_Redstar   ATCTTCAACAAGTCTATTTTAAAGACAAATTTCTTTATTACAAGAAAAGTAGCAATATCA
seq_Wild      ATCTTCAACAAGTCTATTTTAAAGACAAATTTCTTTATTACAAGAAAAGTAGCAATATCA
seq_Lalvin    ATCTTCAACAAGTCTATTTTAAAGACAAATTTCTTTATTACAAGAAAAGTAGCAATATCA
*****

seq_Redstar   TTCAGATTGGATCCTTCCCTGGTGATGACAAAATTCGAATATCCAGAGACACCCTATGGT
seq_Wild      TTCAGATTGGATCCTTCCCTGGTGATGACAAAATTCGAATATCCAGAGACACCCTATGGT
seq_Lalvin    TTCAGATTGGATCCTTCCCTGGTGATGACAAAATTCGAATATCCAGAGACACCCTATGGT
*****

seq_Redstar   ATATTTTTTGTCTGTTGGTAATACTTTCAAAGGGTTCCATATCAGGTTCCAGAGATATCGCA
seq_Wild      ATATTTTTTGTCTGTTGGTAATACTTTCAAAGGGTTCCATATCAGGTTCCAGAGATATCGCA
seq_Lalvin    ATATTTTTTGTCTGTTGGTAATACTTTCAAAGGGTTCCATATCAGGTTCCAGAGATATCGCA
*****

seq_Redstar   AGGGGCGGTATTTCGTATAGTCTGTTCCAGGAATCAGGATATTTATGATTGAATTCCAAG
seq_Wild      AGGGGCGGTATTTCGTATAGTCTGTTCCAGGAATCAGGATATTTATGATTGAATTCCAAG
seq_Lalvin    AGGGGCGGTATTTCGTATAGTCTGTTCCAGGAATCAGGATATTTATGATTGAATTCCAAG
*****

seq_Redstar   AACGTTATTGATGAGAACTATCAATTGGCCTCTACTCAGCAACGTAAAAATAAGGATATT
seq_Wild      AACGTTATTGATGAGAACTATCAATTGGCCTCTACTCAGCAACGTAAAAATAAGGATATT
seq_Lalvin    AACGTTATTGATGAGAACTATCAATTGGCCTCTACTCAGCAACGTAAAAATAAGGATATT
*****

seq_Redstar   CCAGAGGGTGGCTCTAAAGGTGTCATCTTATTGAACCCAGGATTGGTAGAACATGACCAG
seq_Wild      CCAGAGGGTGGCTCTAAAGGTGTCATCTTATTGAACCCAGGATTGGTAGAACATGACCAG
seq_Lalvin    CCAGAGGGTGGCTCTAAAGGTGTCATCTTATTGAACCCAGGATTGGTAGAACATGACCAG
*****

seq_Redstar   ACATTTGTCGCCTTTTCCCAATATGTGGATGCAATGTTGACATTCTAATCAACGATCCA

```

```

seq_Wild      ACATTTGTCGCCTTTTCCCAATATGTGGATGCAATGATTGACATTCTAATCAACGATCCA
seq_Lalvin    ACATTTGTCGCCTTTTCCCAATATGTGGATGCAATGATTGACATTCTAATCAACGATCCA
*****

seq_Redstar   TTAAAGGAAAACCTATGTCAACCTTTTACCAAAGGAGGAAATATTATTTTTTGGCCCAGAT
seq_Wild      TTAAAGGAAAACCTATGTCAACCTTTTACCAAAGGAGGAAATATTATTTTTTGGCCCAGAT
seq_Lalvin    TTAAAGGAAAACCTATGTCAACCTTTTACCAAAGGAGGAAATATTATTTTTTGGCCCAGAT
*****

seq_Redstar   GAAGGAACTGCTGGTTTCGTGGATTGGGCAACTAACCATGCTCGTGTGAGGAACTGCCCCA
seq_Wild      GAAGGAACTGCTGGTTTCGTGGATTGGGCAACTAACCATGCTCGTGTGAGGAACTGCCCCA
seq_Lalvin    GAAGGAACTGCTGGTTTCGTGGATTGGGCAACTAACCATGCTCGTGTGAGGAACTGCCCCA
*****

seq_Redstar   TGGTGGAAATCATTTTTGACTGGAAAATCCCCATCTTTGGGTGGTATTCCCCATGACGAA
seq_Wild      TGGTGGAAATCATTTTTGACTGGAAAATCCCCATCTTTGGGTGGTATTCCCCATGACGAA
seq_Lalvin    TGGTGGAAATCATTTTTGACTGGAAAATCCCCATCTTTGGGTGGTATTCCCCATGACGAA
*****

seq_Redstar   TATGGTATGACTTCTCTGGGTGTTTCGTGCTTATGTTAATAAAATTTACGAACTTTAAAC
seq_Wild      TATGGTATGACTTCTCTGGGTGTTTCGTGCTTATGTTAATAAAATTTACGAACTTTAAAC
seq_Lalvin    TATGGTATGACTTCTCTGGGTGTTTCGTGCTTATGTTAATAAAATTTACGAACTTTAAAC
*****

seq_Redstar   TTGACAAATTCTACTGTTTACAAATTCCAAACTGGTGGTCCGGATGGTGATTTAGGATCC
seq_Wild      TTGACAAATTCTACTGTTTACAAATTCCAAACTGGTGGTCCGGATGGTGATTTAGGATCC
seq_Lalvin    TTGACAAATTCTACTGTTTACAAATTCCAAACTGGTGGTCCGGATGGTGATTTAGGATCC
*****

seq_Redstar   AATGAAATTCTTTTATCTTCGCCAAACGAATGTTATTTGGCAATTCTGGACGGTTCAGGT
seq_Wild      AATGAAATTCTTTTATCTTCGCCAAACGAATGTTATTTGGCAATTCTGGACGGTTCAGGT
seq_Lalvin    AATGAAATTCTTTTATCTTCGCCAAACGAATGTTATTTGGCAATTCTGGACGGTTCAGGT
*****

seq_Redstar   GTCCTGTGTGATCCTAAAGGTTTAGATAAAAGATGAATTATGCCGCTTGGCACATGCAAGG
seq_Wild      GTCCTGTGTGATCCTAAAGGTTTAGATAAAAGATGAATTATGCCGCTTGGCACATGCAAGG
seq_Lalvin    GTCCTGTGTGATCCTAAAGGTTTAGATAAAAGATGAATTATGCCGCTTGGCACATGCAAGG
*****

seq_Redstar   AAAATGATTTCGATTTTCGACACTTCCAAATTATCAAACAACGGATTTTTTGTTCCTGTG
seq_Wild      AAAATGATTTCGATTTTCGACACTTCCAAATTATCAAACAACGGATTTTTTGTTCCTGTG
seq_Lalvin    AAAATGATTTCGATTTTCGACACTTCCAAATTATCAAACAACGGATTTTTTGTTCCTGTG
*****

seq_Redstar   GATGCAATGGATATCATGCTACCAAATGGTACAATTGTAGCTAACGGCACAACCTTCAGA
seq_Wild      GATGCAATGGATATCATGCTACCAAATGGTACAATTGTAGCTAACGGCACAACCTTCAGA
seq_Lalvin    GATGCAATGGATATCATGCTACCAAATGGTACAATTGTAGCTAACGGCACAACCTTCAGA
*****

seq_Redstar   AACACCTTTCATACTCAAATTTTCAAATTTGTGGATCATGTCGACATTTTTGTTCCATGC
seq_Wild      AACACCTTTCATACTCAAATTTTCAAATTTGTGGATCATGTCGACATTTTTGTTCCATGC
seq_Lalvin    AACACCTTTCATACTCAAATTTTCAAATTTGTGGATCATGTCGACATTTTTGTTCCATGC
*****

seq_Redstar   GGTGGTAGACCAAACCTCAATTACTCTAAATAATCTACATTATTTTGTGACGAAAAGACT

```

```

seq_Wild      GGTGGTAGACCAAACCTCAATTACTCTAAATAATCTACATTATTTTGGTTGACGAAAAGACT
seq_Lalvin    GGTGGTAGACCAAACCTCAATTACTCTAAATAATCTACATTATTTTGGTTGACGAAAAGACT
*****

seq_Redstar   GGGAAATGTAAAAATCCCATATATTGTGGAGGGTGCCAATCTATTTATAACGCAACCTGCT
seq_Wild      GGGAAATGTAAAAATCCCATATATTGTGGAGGGTGCCAATCTATTTATAACGCAACCTGCT
seq_Lalvin    GGGAAATGTAAAAATCCCATATATTGTGGAGGGTGCCAATCTATTTATAACGCAACCTGCT
*****

seq_Redstar   AAAAATGCTTTAGAGGAACATGGCTGTATTCTGTTCAAAGATGCTTCTGCCAACAAAGGT
seq_Wild      AAAAATGCTTTAGAGGAACATGGCTGTATTCTGTTCAAAGATGCTTCTGCCAACAAAGGT
seq_Lalvin    AAAAATGCTTTAGAGGAACATGGCTGTATTCTGTTCAAAGATGCTTCTGCCAACAAAGGT
*****

seq_Redstar   GGTGTCACATCTTCATCAATGGAAGTGTGGCCTCACTAGCGCTTAACGATAACGACTTC
seq_Wild      GGTGTCACATCTTCATCAATGGAAGTGTGGCCTCACTAGCGCTTAACGATAACGACTTC
seq_Lalvin    GGTGTCACATCTTCATCAATGGAAGTGTGGCCTCACTAGCGCTTAACGATAACGACTTC
*****

seq_Redstar   GTGCACAAATTTATTGGAGATGTTAGTGGTGAGAGGTCTGCGTTGTACAAGTCGTACGTT
seq_Wild      GTGCACAAATTTATTGGAGATGTTAGTGGTGAGAGGTCTGCGTTGTACAAGTCGTACGTT
seq_Lalvin    GTGCACAAATTTATTGGAGATGTTAGTGGTGAGAGGTCTGCGTTGTACAAGTCGTACGTT
*****

seq_Redstar   GTAGAAGTGCAGTCAAGAATTCAGAAAAATGCTGAATTAGAGTTTGGTCAGTTATGGAAT
seq_Wild      GTAGAAGTGCAGTCAAGAATTCAGAAAAATGCTGAATTAGAGTTTGGTCAGTTATGGAAT
seq_Lalvin    GTAGAAGTGCAGTCAAGAATTCAGAAAAATGCTGAATTAGAGTTTGGTCAGTTATGGAAT
*****

seq_Redstar   TTGAATCAACTAAATGGAACCCACATTTAGAAATTTCAAACCAATTGTCCTTCACTATA
seq_Wild      TTGAATCAACTAAATGGAACCCACATTTAGAAATTTCAAACCAATTGTCCTTCACTATA
seq_Lalvin    TTGAATCAACTAAATGGAACCCACATTTAGAAATTTCAAACCAATTGTCCTTCACTATA
*****

seq_Redstar   AACAAATTGAACGACGATTTAGTTGCTTCTCAAGAGTTGTGGCTCAATGATCTAAAATTA
seq_Wild      AACAAATTGAACGACGATTTAGTTGCTTCTCAAGAGTTGTGGCTCAATGATCTAAAATTA
seq_Lalvin    AACAAATTGAACGACGATTTAGTTGCTTCTCAAGAGTTGTGGCTCAATGATCTAAAATTA
*****

seq_Redstar   AGAAACTACCTATTGTTGGATAAAATAATTCCAAAAATCTGATTGATGTTGCTGGGCCT
seq_Wild      AGAAACTACCTATTGTTGGATAAAATAATTCCAAAAATCTGATTGATGTTGCTGGGCCT
seq_Lalvin    AGAAACTACCTATTGTTGGATAAAATAATTCCAAAAATCTGATTGATGTTGCTGGGCCT
*****

seq_Redstar   CAGTCCGTATTGGAACACATTCCAGAGAGCTATTTGAAAGTTCTTCTGTCGAGTTACTTA
seq_Wild      CAGTCCGTATTGGAACACATTCCAGAGAGCTATTTGAAAGTTCTTCTGTCGAGTTACTTA
seq_Lalvin    CAGTCCGTATTGGAACACATTCCAGAGAGCTATTTGAAAGTTCTTCTGTCGAGTTACTTA
*****

seq_Redstar   TCAAGCACTTTTGTGTTACCAAAACGGTATCGATGTTAACATTGGAAAAATCTTGGAATTT
seq_Wild      TCAAGCACTTTTGTGTTACCAAAACGGTATCGATGTTAACATTGGAAAAATCTTGGAATTT
seq_Lalvin    TCAAGCACTTTTGTGTTACCAAAACGGTATCGATGTTAACATTGGAAAAATCTTGGAATTT
*****

seq_Redstar   ATTGGTGGGTAAAAAGAGAAGCGGAGGCAAGTGCTTGA

```

```
seq_Wild      ATTGGTGGGTAAAAAGAGAAGCGGAGGCAAGTGCTTGA
seq_Lalvin    ATTGGTGGGTAAAAAGAGAAGCGGAGGCAAGTGCTTGA
*****
```

dN/dS

```
> library(ape)
> setwd("~/")
> setwd("C:/Users/krame/OneDrive/Pictures/Documents/GDH2")
> rfilename <- read.dna("GDH2.aln", format = "clustal")
> output1 <- dnds(rfilename, code = 1, codonstart = 1, quiet = FALSE, details
= TRUE)
```

Comparing sequences 1 and 2:

	Nondegenerate	Twofold	Fourfold
Transitions	2	2	1
Transversions	0	1	1

Comparing sequences 1 and 3:

	Nondegenerate	Twofold	Fourfold
Transitions	1	4	1
Transversions	1	1	0

Comparing sequences 2 and 3:

	Nondegenerate	Twofold	Fourfold
Transitions	1	6	2
Transversions	1	2	1

```
> output1
      seq_Redstar  seq_Wild
seq_Wild      0.2759127
seq_Lalvin    0.3098746 0.1752724
```

GRE1

CLUSTAL 2.1 multiple sequence alignment

- Nucleotide Change

Lalvin and Redstar are same sequence

```

LALVIN      ATGTCCAATCTATTAAACAAGTTTGCTGATAAGTTGCACGGCAACGATCATGATGAACGT
128          ATGTCCAATCTATTAAACAAGTTTGCTGATAAGTTGCACGGCAACGATCATGATGAACGT
          *****

LALVIN      TACGAAGACGACAATGACGACCAGACTAGACAACAGCGTCATGAAAAACATCAACAGAGG
128          TACGAAGACGATAATGACGACCAGACTAGACAACAGCGTCATGAAAAACATCAACAGAGG
          *****

LALVIN      GAATTCAGGAATCAAGGATCCAAGGCCGATCCCTACGGCGAAGAAAACCAAGGGAATTTC
128          GAATTCAGGAATCAAGGATCCAAGGCCGATCCCTACGGCGAAGAAAACCAAGGAAATTTC
          *****

LALVIN      CCTCAACGCCAGCAGCCACAGTCTAATCTAGGCGGTAACACGCAGTTTGGCGGTAACGAC
128          CCTCAACGCCAGCAGCCACAGTCTAATCTAGGCGGTAACACGCAGTTTGGCGGTAACGAC
          *****

LALVIN      TTCCAGCAACAACTACTGACTACACTGCCGGCACTGGTGGTGGCACTTATACCCAACT
128          TTCCAGCAACAACTACTGACTACACTGCCGGCACTGGTGGTGGCACTTATACCCAACT
          *****

LALVIN      TACCGCGAACTAACACTCAAGGTCAGTTGGACGACGATGAAGACGATGACTTCTTGACT
128          TACCGCGAACTAACACTCAAGGTCAGTTGGACGACGATGAAGACGATGACTTCTTGACT
          *****

LALVIN      TCGGGCCAACAGCAAAAACAAGGTCGTACAAGAGGTGCTCAAAATAACCGCTACCAATCC
128          TCGGGCCAACAGCAAAAACAAGGTCGTACAAGAGGTGCTCAAAATAACCGCTACCAATCC
          *****

LALVIN      TCTAATATTGGCAGCGGTAGACGCGACTGTGTCTGGGTCAGGAAACGATGAATATGATGAT
128          TCTAATATTGGCAGCGGTAGACGCGACTGTGTCTGGGTCAGGAAACGATGAATATGATGAT
          *****

LALVIN      GATAGTGGGAACCAAGGCGTCTGGTAG
128          GATAGTGGGAACCAAGGCGTCTGGTAG
          *****

```

dN/dS

Comparing sequences 1 and 2:

	Nondegenerate	Twofold	Fourfold
Transitions	1	3	1
Transversions	0	0	0

> output1

LALVIN
128 0.144549

HHF1

CLUSTAL 2.1 multiple sequence alignment

All sequences are the same

```

KYOKAI      ATGTCCGGTAGAGGTAAAGGTGGTAAAGGTCTAGGTAAAGGTGGTGCCAAGCGTCACAGA
T7          ATGTCCGGTAGAGGTAAAGGTGGTAAAGGTCTAGGTAAAGGTGGTGCCAAGCGTCACAGA
          *****

KYOKAI      AAGATTCTAAGAGATAACATCCAAGGTATTACTAAGCCAGCTATCAGAAGATTAGCTAGA
T7          AAGATTCTAAGAGATAACATCCAAGGTATTACTAAGCCAGCTATCAGAAGATTAGCTAGA
          *****

KYOKAI      AGAGGTGGTGTCAAGCGTATTTCTGGTTTGATCTACGAAGAAGTCAGAGCTGTCTTGAAA
T7          AGAGGTGGTGTCAAGCGTATTTCTGGTTTGATCTACGAAGAAGTCAGAGCTGTCTTGAAA
          *****

KYOKAI      TCCTTCTTGGAATCCGTCATCAGAGACTCTGTTACTTACACCGAACACGCCAAGAGAAAG
T7          TCCTTCTTGGAATCCGTCATCAGAGACTCTGTTACTTACACCGAACACGCCAAGAGAAAG
          *****

KYOKAI      ACTGTTACTTCTTTGGATGTTGTTTATGCTTTGAAGAGACAAGGTAGAACCTTATACGGT
T7          ACTGTTACTTCTTTGGATGTTGTTTATGCTTTGAAGAGACAAGGTAGAACCTTATACGGT
          *****

KYOKAI      TTCGGTGGTTAA
T7          TTCGGTGGTTAA
          *****

```

HOM2

CLUSTAL 2.1 multiple sequence alignment

■ -Nucleotide Change

■ -Unknown Nucleotide Fixed

Lalvin and Redstar are same sequence

```
RED      ATGGCTGGAAAGAAAATTGCTGGTGTTTTGGGTGCTACTGGTTCCGTTGGTCAACGTTTC
LALVIN   ATGGCTGGAAAGAAAATTGCTGGTGTTTTGGGTGCTACTGGTTCCGTTGGTCAACGTTTC
128      ATGGCTGGAAAGAAAATTGCTGGTGTTTTGGGTGCTACTGGTTCCGTTGGTCAACGTTTC
          *****
```

```
RED      ATTCTGTTGTTGGCAAATCACCCCTCATTTGAACTGAAAGTTCTTGGTGCCTCTTCTAGA
LALVIN   ATTCTGTTGTTGGCAAATCACCCCTCATTTGAACTGAAAGTTCTTGGTGCCTCTTCTAGA
128      ATTCTGTTGTTGGCAAATCACCCCTCATTTGAACTGAAAGTTCTTGGTGCCTCTTCTAGA
          *****
```

```
RED      TCAGCTGGCAAGAAATACGTTGACGCTGTGAACTGGAAGCAAACCGATTGCTACCGGAA
LALVIN   TCAGCTGGCAAGAAATACGTTGACGCTGTGAACTGGAAGCAAACCGATTGCTACCGGAA
128      TCAGCTGGCAAGAAATACGTTGACGCTGTGAACTGGAAGCAAACCGATTGCTACCGGAA
          *****
```

```
RED      TCTGCTACCGATATTATTGTTTCCGAATGTAAATCTGAATCTTTAAAGAGTGTGACATC
LALVIN   TCTGCTACCGATATTATTGTTTCCGAATGTAAATCTGAATCTTTAAAGAGTGTGACATC
128      TCTGCTACCGATATTATTGTTTCCGAATGTAAATCTGAATCTTTAAAGAGTGTGACATC
          *****
```

```
RED      GTCTTTTCCGATTGGATGCTGACTATGCTGGCGCTATCGAAAAGGAATTCATGGAAGCT
LALVIN   GTCTTTTCCGATTGGATGCTGACTATGCTGGCGCTATCGAAAAGGAATTCATGGAAGCT
128      GTCTTTTCCGATTGGATGCTGACTATGCTGGCGCTATCGAAAAGGAATTCATGGAAGCT
          *****
```

```
RED      GGTATCGCCATTGTTTCCAATGCCAAGAATTATAGAAGAGAACAAGATGTGCCATTGATT
LALVIN   GGTATCGCCATTGTTTCCAATGCCAAGAATTATAGAAGAGAACAAGATGTGCCATTGATT
128      GGTATCGCCATTGTTTCCAATGCCAAGAATTATAGAAGAGAACAAGATGTGCCATTGATT
          *****
```

```
RED      GTTCCTGTTGTCAATCCTGAGCATTGATATTGTAGCTCAAAAGCTTGACACCGCCAAG
LALVIN   GTTCCTGTTGTCAATCCTGAGCATTGATATTGTAGCTCAAAAGCTTGACACCGCCAAG
128      GTTCCTGTTGTCAATCCTGAGCATTGATATTGTAGCTCAAAAGCTTGACACCGCCAAG
          *****
```

```
RED      GCTCAAGGTAAGCCAAGACCAGGGTTCATTATCTGTATTTCGAATTGTTCCACTGCAGGT
LALVIN   GCTCAAGGTAAGCCAAGACCAGGGTTCATTATCTGTATTTCGAATTGTTCCACTGCAGGT
128      GCTCAAGGTAAGCCAAGACCAGGGTTCATTATCTGTATTTCGAATTGTTCCACTGCAGGT
          *****
```

```
RED      TTGGTTGCACCATTTGAAGCCTTTGATTGAAAAATTCGGTCCTATTGATGCTTTGACCACT
LALVIN   TTGGTTGCACCATTTGAAGCCTTTGATTGAAAAATTCGGTCCTATTGATGCTTTGACCACT
128      TTGGTTGCACCATTTGAAGCCTTTGATTGAAAAATTCGGTCCTATTGATGCTTTGACCACT
          *****
```

```
RED      ACTACTTTGCAAGCAATCTCAGGTGCTGGTTTCTCCCCAGGTGTACCAGGTATTGATATT
LALVIN   ACTACTTTGCAAGCAATCTCAGGTGCTGGTTTCTCCCCAGGTGTACCAGGTATTGATATT
128      ACTACTTTGCAAGCAATCTCAGGTGCTGGTTTCTCCCCAGGTGTACCAGGTATTGATATT
          *****
```

```
RED      CTAGACAATATTATTCCATACATTGGTGGTGAAGAAGACAAGATGGAATGGGAGACCAAG
LALVIN   CTAGACAATATTATTCCATACATTGGTGGTGAAGAAGACAAGATGGAATGGGAGACCAAG
```

```

128      CTAGACAATATTATTCCATACATTGGTGGTGAAGAAGACAAGATGGAATGGGAGACCAAG
*****

RED      AAAATCTTGGCTCCATTAGCAGAAGACAAGACACACGTCAAACCTATTGACTCCAGAAGAA
LALVIN   AAAATCTTGGCTCCATTAGCAGAAGACAAGACACACGTCAAACCTATTGACTCCAGAAGAA
128      AAAATCTTGGCTCCATTAGCAGAAGACAAGACACACGTCAAACCTATTGACTCCAGAAGAA
*****

RED      ATCAAAGTCTCTGCTCAATGTAACAGAGTCGCTGTTTCCGATGGGCACACCGAATGTATC
LALVIN   ATCAAAGTCTCTGCTCAATGTAACAGAGTCGCTGTTTCCGATGGGCACACCGAATGTATC
128      ATCAAAGTCTCTGCTCAATGTAACAGAGTCGCTGTTTCCGATGGGCACACCGAATGTATC
*****

RED      TCTTTGAGGTTCAAGAACAGACCTGCTCCATCCGTCGAGCAAGTCAAGACATGCCTAAAA
LALVIN   TCTTTGAGGTTCAAGAACAGACCTGCTCCATCCGTCGAGCAAGTCAAGACATGCCTAAAA
128      TCTTTGAGGTTCAAGAACAGACCTGCTCCATCCGTCGAGCAAGTCAAGACATGCCTAAAA
*****

RED      GAATACGTCTGCGATTGCCTACAAATTAGGCTGTCATTCTGCTCCAAAGCAAACCTATTCAT
LALVIN   GAATACGTCTGCGATTGCCTACAAATTAGGCTGTCATTCTGCTCCAAAGCAAACCTATTCAT
128      GAATACGTCTGCGATGCCTACAAATTAGGCTGTCATTCTGCTCCAAAGCAAACCTATTCAT
*****

RED      GTTTTGGAACAACCAGACAGACCTCAACCAAGGTTGGACAGGAACAGAGACAGCGGTTAC
LALVIN   GTTTTGGAACAACCAGACAGACCTCAACCAAGGTTGGACAGGAACAGAGACAGCGGTTAC
128      GTTTTGGAACAACCAGACAGACCTCAACCAAGGTTGGACAGGAACAGAGACAGCGGTTAC
*****

RED      GGTGTTTCCGTTGGTAGAATCAGAGAAGACCCATTGTTAGATTTCAAATGGTTGTCCTT
LALVIN   GGTGTTTCCGTTGGTAGAATCAGAGAAGACCCATTGTTAGATTTCAAATGGTTGTCCTT
128      GGTGTTTCCGTTGGTAGAATCAGAGAAGACCCATTGTTAGATTTCAAATGGTTGTCCTT
*****

RED      TCCCACAACACCATTATTGGTGCCGCTGGTTCTGGTGTCTTGATTGCCGAAATCTTACTA
LALVIN   TCCCACAACACCATTATTGGTGCCGCTGGTTCTGGTGTCTTGATTGCCGAAATCTTACTA
128      TCCCACAACACCATTATTGGTGCCGCTGGTTCTGGTGTCTTGATTGCCGAAATCTTACTA
*****

RED      GCAAGAAACTTGATTTAA
LALVIN   GCAAGAAACTTGATTTAA
128      GCAAGAAACTTGATTTAA
*****

```

dN/dS

Comparing sequences 1 and 2:

	Nondegenerate	Twofold	Fourfold
Transitions	0	3	0
Transversions	0	0	0

> output1

128 LALVIN 0

> |

IPP1

CLUSTAL 2.1 multiple sequence alignment

-Nucleotide Change

```

seq_Red      ATGACCTACACTACCAGACAAATTGGTGCCAAGAACACCTTGAATACAAAGTTTATATC
seq_Lalvin   ATGACCTACACTACCAGACAAATTGGTGCCAAGAACACCTTGAATACAAAGTTTATATC
seq_Wild     ATGACCTACACTACCAGACAAATTGGTGCCAAGAACACCTTGAATACAAAGTTTATATC
*****

seq_Red      GAGAAGGATGGTAAGCCAGTTTCTGCCTTCCACGACATTCCCTTGACGCTGACAAGGAA
seq_Lalvin   GAGAAGGATGGTAAGCCAGTTTCTGCCTTCCACGACATTCCCTTGACGCTGACAAGGAA
seq_Wild     GAAAGGATGGTAAGCCAGTTTCTGCCTTCCACGACATTCCCTTGACGCTGACAAGGAA
** *****

seq_Red      AACAACATTTTCAACATGGTTGTTGAAATTCACGTTGGACCAACGCCAAGTTAGAAATC
seq_Lalvin   AACAACATTTTCAACATGGTTGTTGAAATTCACGTTGGACCAACGCCAAGTTAGAAATC
seq_Wild     AACAACATTTTCAACATGGTTGTTGAAATTCACGTTGGACCAACGCCAAGTTAGAAATC
*****

seq_Red      ACCAAGGAAGAAACTTTGAACCCAATCATCCAAGACACCAAGAAGGGCAAGTTGAGATTT
seq_Lalvin   ACCAAGGAAGAAACTTTGAACCCAATCATCCAAGACACCAAGAAGGGCAAGTTGAGATTT
seq_Wild     ACCAAGGAAGAAACTTTGAACCCAATCATCCAAGACACCAAGAAGGGCAAGTTGAGATTT
*****

seq_Red      GTTAGAAACTGTTTCCCTCACCATGGTTACATTCACTATGGTGCTTTCCACAAAAC
seq_Lalvin   GTTAGAAACTGTTTCCCTCACCATGGTTACATTCACTATGGTGCTTTCCACAAAAC
seq_Wild     GTTAGAAACTGTTTCCCTCACCATGGTTACATTCACTATGGTGCTTTCCACAAAAC
*****

seq_Red      TGGGAAGACCCAAACGTAAGCCACCCAGAACTAAGGCAGTTGGTGACAACGATCCAATT
seq_Lalvin   TGGGAAGACCCAAACGTAAGCCACCCAGAACTAAGGCAGTTGGTGACAACGATCCAATT
seq_Wild     TGGGAAGACCCAAACGTAAGCCACCCAGAACTAAGGCAGTTGGTGACAACGATCCAATT
*****

seq_Red      GATGTGTTGAAATTGGTGAAACTATTGCTTACACTGGTCAAGTCAAGCAAGTTAAGGCT
seq_Lalvin   GATGTGTTGAAATTGGTGAAACTATTGCTTACACTGGTCAAGTCAAGCAAGTTAAGGCT
seq_Wild     GATGTGTTGAAATTGGTGAAACTATTGCTTACACTGGTCAAGTCAAGCAAGTTAAGGCT
*****

seq_Red      CTAGGTATCATGGCTTTATTTGGATGAAGGTGAGACCGATTGGAAAGTTATTGCCATTGAT
seq_Lalvin   CTAGGTATCATGGCTTTATTTGGATGAAGGTGAGACCGATTGGAAAGTTATTGCCATTGAT
seq_Wild     CTAGGTATCATGGCTTTATTTGGATGAAGGTGAGACCGATTGGAAAGTTATTGCCATTGAT
*****

seq_Red      ATTAACGATCCATTAGCCCCAAAATTGAACGACATTGAGGATGTTGAGAAATACTTCCCA
seq_Lalvin   ATTAACGATCCATTAGCCCCAAAATTGAACGACATTGAGGATGTTGAGAAATACTTCCCA
seq_Wild     ATTAACGATCCATTAGCCCCAAAATTGAACGACATTGAGGATGTTGAGAAATACTTCCCA
*****

seq_Red      GGTCTATTGAGGGCTACTAACGAATGGTTCAGAATTTACAAAATCCCAGATGGTAAGCCA
seq_Lalvin   GGTCTATTGAGGGCTACTAACGAATGGTTCAGAATTTACAAAATCCCAGATGGTAAGCCA
seq_Wild     GGTCTGTTGAGGGCTACTAACGAATGGTTCAGAATTTACAAAATCCCAGATGGTAAGCCA
*****

```

```

seq_Red      GAAAACCAATTTGCCTTCTCCGGTGAAGCTAAGAACAAGAAGTACGCTTTGGATATCATC
seq_Lalvin   GAAAACCAATTTGCCTTCTCCGGTGAAGCTAAGAACAAGAAGTACGCTTTGGATATCATC
seq_Wild     GAAAACCAATTTGCCTTCTCCGGTGAAGCTAAGAACAAGAAGTACGCTTTGGATATCATC
*****

seq_Red      AAGGAAACACATGACTCCTGGAAACAATTAATTGCTGGTAAGTCTTCTGACAGCAAGGGT
seq_Lalvin   AAGGAAACACATGACTCCTGGAAACAATTAATTGCTGGTAAGTCTTCTGACAGCAAGGGT
seq_Wild     AAGGAAACACATGACTCCTGGAAACAATTAATTGCTGGTAAGTCTTCTGACAGCAAGGGT
*****

seq_Red      ATTGATTTGACCAATGTTACTTTGCCTGACACCCCAACCTACTCCAAGGCTGCCTCTGAT
seq_Lalvin   ATTGATTTGACCAATGTTACTTTGCCTGACACCCCAACCTACTCCAAGGCTGCCTCTGAT
seq_Wild     ATTGATTTGACCAATGTTACTTTGCCTGACACCCCAACCTACTCCAAGGCTGCCTCTGAT
*****

seq_Red      GCCATCCCACCAGCTTCTCCAAAGGCAGATGCTTCAATTGACAAGTCTATTGACAAGTGG
seq_Lalvin   GCCATCCCACCAGCTTCTCCAAAGGCAGATGCTCCAATTGACAAGTCTATTGACAAGTGG
seq_Wild     GCCATCCCACCAGCTTCTCCAAAGGCAGATGCTCCAATTGACAAGTCTATTGACAAGTGG
*****

seq_Red      TTCTTCATCTCCGGTTCTGTTTAA
seq_Lalvin   TTCTTCATCTCCGGTTCTGTTTAA
seq_Wild     TTCTTCATCTCCGGTTCTGTTTAA
*****

```

CLUSTAL 2.1 multiple sequence alignment Protein

-Amino Acid Change

```

Lalvin      MTYTTTRQIGAKNTLEYKVYIEKDGKPVSAFHDIPLYADKENNIFNMVVEIPRWTNAKLEI
128         MTYTTTRQIGAKNTLEYKVYIEKDGKPVSAFHDIPLYADKENNIFNMVVEIPRWTNAKLEI
Red         MTYTTTRQIGAKNTLEYKVYIEKDGKPVSAFHDIPLYADKENNIFNMVVEIPRWTNAKLEI
*****

Lalvin      TKEETLNPIIQDTKKGKLRFVRNCFPHHGYIHNYGAFPQTWEDPNVSHPETKAVGDNDPI
128         TKEETLNPIIQDTKKGKLRFVRNCFPHHGYIHNYGAFPQTWEDPNVSHPETKAVGDNDPI
Red         TKEETLNPIIQDTKKGKLRFVRNCFPHHGYIHNYGAFPQTWEDPNVSHPETKAVGDNDPI
*****

Lalvin      DVLEIGETIAYTGQVKQVKALGIMALLDEGETDWKVIAIDINDPLAPKLNIEDVEKYFP
128         DVLEIGETIAYTGQVKQVKALGIMALLDEGETDWKVIAIDINDPLAPKLNIEDVEKYFP
Red         DVLEIGETIAYTGQVKQVKALGIMALLDEGETDWKVIAIDINDPLAPKLNIEDVEKYFP
*****

Lalvin      GLLRATNEWFRYKIPDGKPENQFAFSGEAKNKKYALDIKETHDSWKQLIAGKSSDSKG
128         GLLRATNEWFRYKIPDGKPENQFAFSGEAKNKKYALDIKETHDSWKQLIAGKSSDSKG
Red         GLLRATNEWFRYKIPDGKPENQFAFSGEAKNKKYALDIKETHDSWKQLIAGKSSDSKG
*****

Lalvin      IDLNTVTLPTPTYSKAASDAIPPASPKADAPIDKSIDKWFFISGSV

```

```

128          IDLTNVTLPDTPITYSKAASDAIPPASPKADAPIDKSIDKWFFISGSV
Red         IDLTNVTLPDTPITYSKAASDAIPPASPKADASIDKSIDKWFFISGSV
          *****.*****

```

dN/dS

```

> setwd("C:/Users/krame/OneDrive/Pictures/Documents/IPP1")
> rfilename <- read.dna("ipp1.aln", format = "clustal")
Error in read.dna("ipp1.aln", format = "clustal") :
  could not find function "read.dna"
> rfilename <- read.dna("filename.aln", format = "clustal")
Error in read.dna("filename.aln", format = "clustal") :
  could not find function "read.dna"
> library(ape)
> rfilename <- read.dna("ipp1.aln", format = "clustal")
> output1 <- dnds(rfilename, code = 1, codonstart = 1, quiet = FALSE, detai
ls = TRUE)

```

Comparing sequences 1 and 2:

	Nondegenerate	Twofold	Fourfold
Transitions	1	0	0
Transversions	0	0	0

Comparing sequences 1 and 3:

	Nondegenerate	Twofold	Fourfold
Transitions	1	1	1
Transversions	0	0	0

Comparing sequences 2 and 3:

	Nondegenerate	Twofold	Fourfold
Transitions	0	1	1
Transversions	0	0	0

>

> output1

	seq_Red	seq_Lalvin
seq_Lalvin	Inf	
seq_wild	0.2940228	0.0000000

MDH3

CLUSTAL 2.1 multiple sequence alignment

-Nucleotide Change

Lalvin and Redstar are same sequence

```

seq_red      ATGGTCAAAGTCGCAATTCTTGGCGCTTCTGGTGGCGTGGGACAACCGCTATCATTACTG
seq_lalvin   ATGGTCAAAGTCGCAATTCTTGGCGCTTCTGGTGGCGTGGGACAACCGCTATCATTACTG
seq_128      ATGGTCAAAGTCGCAATTCTTGGCGCTTCTGGTGGCGTGGGACAACCGCTATCATTACTG
*****

seq_red      CTAAAATTAAGCCCTTACGTTTCCGAGCTGGCGTTGTACGATATCCGAGCTGCGGAAGGC
seq_lalvin   CTAAAATTAAGCCCTTACGTTTCCGAGCTGGCGTTGTACGATATCCGAGCTGCGGAAGGC
seq_128      CTAAAATTAAGCCCTTACGTTTCCGAGCTGGCGTTGTACGATATCCGAGCTGCGGAAGGC
*****

seq_red      ATTGGTAAGGATTTATCTCACATCAACACCAACTCAAGTTGTGTCGGTTATGATAAGGAT
seq_lalvin   ATTGGTAAGGATTTATCTCACATCAACACCAACTCAAGTTGTGTCGGTTATGATAAGGAT
seq_128      ATTGGTAAGGATTTATCTCACATCAACACCAACTCAAGTTGTGTCGGTTATGATAAGGAT
*****

seq_red      AGTATTGAGAACACCTTGTCAAATGCTCAGGTGGTGCTAATACCGGCTGGTGTTCACAGA
seq_lalvin   AGTATTGAGAACACCTTGTCAAATGCTCAGGTGGTGCTAATACCGGCTGGTGTTCACAGA
seq_128      AGTATTGAGAACACCTTGTCAAATGCTCAGGTGGTGCTAATACCGGCTGGTGTTCACAGA
*****

seq_red      AAGCCCGGTTTAACTAGAGATGATTTGTTCAAGATGAACGCCGGTATTGTCAAAGCCTG
seq_lalvin   AAGCCCGGTTTAACTAGAGATGATTTGTTCAAGATGAACGCCGGTATTGTCAAAGCCTG
seq_128      AAGCCCGGTTTAACTAGAGATGATTTGTTCAAGATGAACGCCGGTATTGTCAAAGCCTG
*****

seq_red      GTAACCGCTGTTGGAAAGTTCGCACCAAAATGCGAGGATTTAGTCATTTCAAACCTGTA
seq_lalvin   GTAACCGCTGTTGGAAAGTTCGCACCAAAATGCGAGGATTTAGTCATTTCAAACCTGTA
seq_128      GTAACCGCTGTTGGAAAGTTCGCACCAAAATGCGAGGATTTAGTCATTTCAAACCTGTA
*****

seq_red      AACAGTTTGGTCCCTATTGCTGTGGAACCTTTGAAGAAAATGGGTAAGTTCAAACCTGGA
seq_lalvin   AACAGTTTGGTCCCTATTGCTGTGGAACCTTTGAAGAAAATGGGTAAGTTCAAACCTGGA
seq_128      AACAGTTTGGTCCCTATTGCTGTGGAACCTTTGAAGAAAATGGGTAAGTTCAAACCTGGA
*****

seq_red      AACGTTATGGGTGTGACGAACCTTGACCTGGTACGTGCAGAAACCTTTTGGTAGATTAT
seq_lalvin   AACGTTATGGGTGTGACGAACCTTGACCTGGTACGTGCAGAAACCTTTTGGTAGATTAT
seq_128      AACGTTATGGGTGTGACGAACCTTGACCTGGTACGTGCAGAAACCTTTTGGTAGATTAT
*****

seq_red      TTGATGCTAAAAAACCCCAAAATTGGACAAGAACAAGACAAAACCTACAATGCACAGAAAG
seq_lalvin   TTGATGCTAAAAAACCCCAAAATTGGACAAGAACAAGACAAAACCTACAATGCACAGAAAG
seq_128      TTGATGCTAAAAAACCCCAAAATTGGACAAGAACAAGACAAAACCTACAATGCACAGAAAG
*****

seq_red      GTCAGTGTATTGGGGGTCAATTCAGGGGAAACCATATCCCAATAATCACCGACAAATCG
seq_lalvin   GTCAGTGTATTGGGGGTCAATTCAGGGGAAACCATATCCCAATAATCACCGACAAATCG
seq_128      GTCAGTGTATTGGGGGTCAATTCAGGGGAAACCATATCCCAATAATCACCGACAAATCG
*****

```

```

seq_red      CTGGTATTTCAACTTGATAAGCAGTACGAGCACTTCATTCATAGGGTCCAGTTCGGAGGT
seq_lalvin   CTGGTATTTCAACTTGATAAGCAGTACGAGCACTTCATTCATAGGGTCCAGTTCGGAGGT
seq_128      CTGGTATTTCAACTTGATAAGCAGTACGAGCACTTCATTCATAGGGTCCAGTTCGGAGGT
*****

seq_red      GATGAAATTGTCAAAGCTAAACAGGGCGCCGGTTCCGCCACGTTGTCCATGGCGTTTCGCG
seq_lalvin   GATGAAATTGTCAAAGCTAAACAGGGCGCCGGTTCCGCCACGTTGTCCATGGCGTTTCGCG
seq_128      GATGAAATTGTCAAAGCTAAACAGGGCGCCGGTTCCGCCACGTTGTCCATGGCGTTTCGCG
*****

seq_red      GGGGCCAAGTTTGCTGAAGAAGTTTTGAGGAGCTTCCATAATGAGAAACCAGAAACGGAG
seq_lalvin   GGGGCCAAGTTTGCTGAAGAAGTTTTGAGGAGCTTCCATAATGAGAAACCAGAAACGGAG
seq_128      GGGGCCAAGTTTGCTGAAGAAGTTTTGAGGAGCTTCCATAACGAGAAACCAGAAACGGAG
*****

seq_red      TCACTTTCCGCATTTCGTTTATTTACCAGGCTTAAAAACGGTAAGAAAGCGCAGCAATTA
seq_lalvin   TCACTTTCCGCATTTCGTTTATTTACCAGGCTTAAAAACGGTAAGAAAGCGCAGCAATTA
seq_128      TCACTTTCCGCATTTCGTTTATTTACCAGGCTTAAAAACGGTAAGAAAGCGCAGCAATTA
*****

seq_red      GTTGGCGACAACCTCTATTGAGTATTTTCCTTGCCAATTGTTTTGAGAAATGGTAGCGTA
seq_lalvin   GTTGGCGACAACCTCTATTGAGTATTTTCCTTGCCAATTGTTTTGAGAAATGGTAGCGTA
seq_128      GTTGGCGACAACCTCTATTGAGTATTTTCCTTGCCAATTGTTTTGAGAAATGGTAGCGTA
*****

seq_red      GTATCCATCGATACCAAGTGTCTTGAAAACTGTCTCCGAGAGAGGAACAACCTCGTTAAT
seq_lalvin   GTATCCATCGATACCAAGTGTCTTGAAAACTGTCTCCGAGAGAGGAACAACCTCGTTAAT
seq_128      GTATCCATCGATACCAAGTGTCTTGAAAACTGTCTCCGAGAGAGGAACAACCTCGTTAAT
*****

seq_red      ACTGCGGTCAAAGAGCTACGCAAGAATATTGAAAAAGGCAAGAGTTTCATCCTAGACTCT
seq_lalvin   ACTGCGGTCAAAGAGCTACGCAAGAATATTGAAAAAGGCAAGAGTTTCATCCTAGACTCT
seq_128      ACTGCGGTCAAAGAGCTACGCAAGAATATTGAAAAAGGCAAGAGTTTCATCCTAGACTCT
*****

seq_red      TCCAAGCTATGA
seq_lalvin   TCCAAGCTATGA
seq_128      TCCAAGCTATGA
*****

```

dN/dS

Comparing sequences 1 and 2:

	Nondegenerate	Twofold	Fourfold
Transitions	0	2	0
Transversions	0	0	1

> output1

```

seq_lalvin
seq_128      0

```

PHO11

CLUSTAL 2.1 multiple sequence alignment

-Nucleotide Change

```

seq_K11      ATGTTCAAGTCAGCCGTTTATTCAATTTTAGCCGCTTCTTTGGTTAATGCAGGTACCATA
seq_128      ATGTTGAAGTCAGCCGTTTATTCAATTTTAGCCGCTTCTTTGGTTAATGCAGGTACCATA
*****

seq_K11      CCCCTCGGAAAGTTGTCTGACATTGACAAAATCGGAAC TCAAACGGAAATTTTCCCATT T
seq_128      CCCCTCGGAAAGTTGTCTGACATTGACAAAATCGGAAC TCAAACGGAAATTTTCCCATT T
*****

seq_K11      TTGGGTGGTTCTGGGCCATACTACTCTTTCCCTGGTGACTACGGTATTTCTCTTGACTTG
seq_128      TTGGGTGGTTCTGGGCCATACTACTCATTCCCTGGTGATTATGGTATTTCTCTGTGATTG
*****

seq_K11      CCGGAAGGTTGTGAAATGAAGCAAGTGCAAATGGTTGGTAGACACGGTGAAAGATAACCC
seq_128      CCGGAAAGTTGTGAAATGAAGCAAGTGCAAATGGTTGGTAGACACGGTGAGAGATAACCC
*****

seq_K11      ACTGTCAGCAAGGCCAAAAGTATCATGGCAACATGGTATAAGTTGGGTAAC TATACTGGT
seq_128      ACTGTCAGCAAGGCCAAAAGTATCATGCAACATGGTACAAATTGAGTAAC TATAACCGGT
*****

seq_K11      CAATTTAACGGATCATTGTCTTCTTGAACGATGACTACGAATTTTTCATTCTGACACT
seq_128      GAATTTCAGCGGAGCATTGTCTTCTTGAACGATGACTACGAATTTTTCATTCTGACACC
*****

seq_K11      AATAACTTGGAAATGGAACCACGCTTGCAAATTCGGTGGATGTTTTGAACCCATATACT
seq_128      AAAAACCTAGAAATGGAACCACACTTGCCAATTCGGTCAATGTTTTGAACCCATATACC
*****

seq_K11      GGTGAGATGAATGCTAAGAGACACGCTCGTGATTCTTGGCGCAATATGGCTACATGGTC
seq_128      GGTGAGATGAATGCTAAGAGACACGCTCGTGATTCTTGGCGCAATATGGCTACATGGTC
*****

seq_K11      GAAAATCAAACAGTTTTGCTGTTTTTACGTCTAGCTCGCAAAGATGTCATGATACTGCC
seq_128      GAAAACCAAACAGTTTTGCGGTTTTTACGTCTAACTCGAACAGATGTCATGATACTGCC
*****

seq_K11      CAATTTTTCATTGACGGTTTGGGTGACCAATTCAACATTCCTTACAAACCATCAGTGAA
seq_128      CAGTATTTTCATTGACGGTTTGGGTGATAAATTCAACATTCCTTGCAAACCATCAGTGAA
*****

seq_K11      GCTGAGTCCGCTGGTGCCAATACTTTAAGTGCTCATCATTCGTGTCCTGCTTGGGACGAT
seq_128      GCCGAGTCTGCTGGTGCCAATACTCTGAGTGCCCATCATTCGTGTCCTGCTTGGGACGAT
*****

seq_K11      GATGTCAACGACGACATTTTAAAGAAATACAATACTAAATATTTGAGTGGTATTGCCAAG
seq_128      GATGTCAACGATGACATTTTGAAAAAATATGATACCAATATTTGAGTGGTATTGCCAAG
*****

seq_K11      AGATTAAACAAGGAAAACAAGGGTTTGAATCTGACTTCAAGCGATGCAACCACCTTTTTT
seq_128      AGATTAAACAAGGAAAACAAGGGTTTGAATCTGACTTCAAGTATGCAAAACACTTTTTTT
*****

```

```

seq_K11      GCATGGTGTGCATATGAAATTGAATGCTAGAGGTTACAGTGACATCTGTAAACATTTTTTACC
seq_128      GCATGGTGTGCATATGAAATAAACGCTAGAGGTTACAGTGACATCTGTAAACATCTTCACC
*****
seq_K11      AAAGATGAATTAGTCCGTTTCTCCTACAGCCAAGACTTGGAAACTTATTATCAGACAGGA
seq_128      AAAGATGAATTGGTCCGTTTCTCCTACAGCCAAGACTTGGAAACTTATTATCAAACGGGA
*****
seq_K11      CCAGGTTATGACGTTGTTAGATCCGTCGGTGCCAACCTTGTTCAACGCTTCAGTGAAACTA
seq_128      CCAGGCTATGACGTCGTCAGATCCGTCGGTGCCAACCTTGTTCAACGCTTCAGTAAACTA
*****
seq_K11      CTAAAGGAAAGTGAGGTCCAGGACCAAAAGGTTTGGTTGAGTTTCACCCACGATACAGAT
seq_128      CTAAAGGAAAGTGAGGTCCAGGACCAAAAGGTTTGGTTGAGTTTCACCCACGATACCGAT
*****
seq_K11      ATCTTGAAC TATTTGACTACTATTGGTATAATTGATGACAAGAATAACTTGACCGCCGAA
seq_128      ATTTTGAATTATTTGACTACTATCGGCATTATCGATGACAAAATAACTTGACCGCCGAA
*****
seq_K11      TATGTTCCATTTCATGGGCAACACTTTCCACAGATCCTGGTACGTTCC TCAAGGTGCTCGT
seq_128      CATGTTCCATTTCATGGAAAACACTTTCCACAGATCCTGGTACGTTCCACAAGGTGCTCGT
*****
seq_K11      GTTTACACCGAAAAGTTCAGTGTTCCAACGACACTTATGTTAGATACGTCATCAACGAT
seq_128      GTTTACACTGAAAAGTTCAGTGTTCCAATGACACCTATGTTAGATACGTCATCAACGAT
*****
seq_K11      GCTGTCGTTCCAATTGAAACCTGTTCCACTGGTCCAGGGTTCTCTCTGTGAAATAAACGAC
seq_128      GCTGTCGTTCCAATTGAAACCTGTTCTACTGGTCCAGGGTTCTCTTGTGAAATAAATGAC
*****
seq_K11      TTCTACGACTATGCTGAAAAGAGAGTAGCCGGCACC GACTTCCTAAAGGTCTGTAACGTC
seq_128      TTCTACGACTATGCTGAAAAGAGAGTAGCCGGTACTGACTTCCTAAAGGTCTGTAACGTC
*****
seq_K11      AGCAGCGTCAGTAATTCTACTGAATTGACCTTTTTCTGGGACTGGAATACCAAACTACTAC
seq_128      AGCAGCGTCAGTAAC TCTACTGAATTGACCTTTTTCTGGGACTGGAATACCAAGCACTAC
*****
seq_K11      AACGACACTTTATTAAAACAGTAA
seq_128      AACGACACTTTATTAAAACAGTAA
*****

```

dN/dS

Comparing sequences 1 and 2:

	Nondegenerate	Twofold	Fourfold
Transitions	11	35	25
Transversions	7	5	6

> output1

```

      seq_K11
seq_128 0.1385265

```

RPL8A

CLUSTAL 2.1 multiple sequence alignment

-Nucleotide Change

```

KYOKAI      ATGGCCCCAGGTAAGAAAGTCGCTCCAGCTCCATTTCGGTGCTAAGTCAACCAAGTCTAAC
T7          ATGGCCCCAGGTAAGAAAGTCGCTCCAGCTCCATTTCGGTGCTAAGTCAACCAAGTCTAAC
CLIB324     ATGGCCCCAGGTAAGAAAGTCGCTCCAGCTCCATTTCGGTGCTAAGTCAACTAAGTCTAAC
*****

KYOKAI      AAGACTAGAAACCCATTGACTCACTCTACTCCAAAGAACTTCGGTATTGGTCAAGCTGTC
T7          AAGACTAGAAACCCATTGACTCACTCTACTCCAAAGAACTTCGGTATTGGTCAAGCTGTC
CLIB324     AAGACTAGAAACCCATTGACTCACTCTACTCCAAAGAACTTCGGTATTGGTCAAGCTGTC
*****

KYOKAI      CAACCAAAGAGAAACTTGTCCAGATACGTCAAATGGCCAGAATACGTCAGATTGCAAAGA
T7          CAACCAAAGAGAAACTTGTCCAGATACGTCAAATGGCCAGAATACGTCAGATTGCAAAGA
CLIB324     CAACCAAAGAGAAACTTGTCCAGATACGTCAAATGGCCAGAATACGTCAGAGTGCAAAGA
*****

KYOKAI      CAAAAGAAGATCTTGTCCATCAGATTGAAGGTTCTCTCAACCATTGCTCAATTCCAATAC
T7          CAAAAGAAGATCTTGTCCATCAGATTGAAGGTTCTCTCAACCATTGCTCAATTCCAATAC
CLIB324     CAAAAGAAGATCTTGTCCATCAGATTGAAGGTTCTCTCAACCATTGCTCAATTCCAATAC
*****

KYOKAI      ACTTTGGACAGAAACACCGCTGCTGAAACCTTCAAGTTGTTCAACAAGTACAGACCAGAA
T7          ACTTTGGACAGAAACACCGCTGCTGAAACCTTCAAGTTGTTCAACAAGTACAGACCAGAA
CLIB324     ACTTTGGACAGAAACACCGCTGCTGAAACCTTCAAGTTGTTCAACAAGTACAGACCAGAA
*****

KYOKAI      ACTGCTGCTGAAAAGAAGGAAAGATTGACCAAAGAAGCTGCCGCTGTTGCTGAAGGTAAG
T7          ACTGCTGCTGAAAAGAAGGAAAGATTGACCAAAGAAGCTGCCGCTGTTGCTGAAGGTAAG
CLIB324     ACTGCTGCTGAAAAGAAGGAAAGATTGACCAAAGAAGCTGCCGCTGTTGCTGAAGGTAAG
*****

KYOKAI      TCCAAGCAAGATGCTTCTCCAAAGCCATACGCTGTCAAGTACGGTTTGAACCACGTTGTT
T7          TCCAAGCAAGATGCTTCTCCAAAGCCATACGCTGTCAAGTACGGTTTGAACCACGTTGTT
CLIB324     TCCAAGCAAGATGCTTCTCCAAAGCCATACGCTGTCAAGTACGGTTTGAACCACGTTGTT
*****

KYOKAI      GCCTTGATCGAAAACAAGAAGGCTAAGTTGGTTTTGATTGCTAACGATGTCGACCCAATT
T7          GCCTTGATCGAAAACAAGAAGGCTAAGTTGGTTTTGATTGCTAACGATGTCGACCCAATT
CLIB324     GCCTTGATCGAAAACAAGAAGGCTAAGTTGGTTTTGATTGCTAACGATGTCGACCCAATT
*****

KYOKAI      GAATTGGTTGTCTTTTTGCCAGCTTTGTGTAAGAAGATGGGTGTTCCATACGCCATTGTC
T7          GAATTGGTTGTCTTTTTGCCAGCTTTGTGTAAGAAGATGGGTGTTCCATACGCCATTGTC
CLIB324     GAATTGGTTGTCTTTTTGCCAGCTTTGTGTAAGAAGATGGGTGTTCCATACGCCATTGTC
*****

KYOKAI      AAGGGTAAGGCTAGATTGGGTACCTTGGTTAACCAAAAGACCTCTGCCGTTGCCGCTTTG
T7          AAGGGTAAGGCTAGATTGGGTACCTTGGTTAACCAAAAGACCTCTGCCGTTGCCGCTTTG
CLIB324     AAGGGTAAGGCTAGATTGGGTACCTTGGTTAACCAAAAGACCTCTGCCGTTGCCGCTTTG
*****

```

```

KYOKAI      ACTGAAGTCAGAGCCGAAGACGAAGCTGCTTTGGCTAAGTTGGTTTCACCATTGACGCT
T7          ACTGAAGTCAGAGCCGAAGACGAAGCTGCTTTGGCTAAGTTGGTTTCACCATTGACGCT
CLIB324     ACTGAAGTCAGAGCCGAAGACGAAGCTGCTTTGGCTAAGTTGGTTTCACCATTGACGCT
*****

```

```

KYOKAI      AACTTCGCTGACAAATACGATGAAGTCAAGAAGCACTGGGGTGGTGGTATCCTTGGTAAC
T7          AACTTCGCTGACAAATACGATGAAGTCAAGAAGCACTGGGGTGGTGGTATCCTTGGTAAC
CLIB324     AACTTCGCTGACAAATACGATGAAGTCAAGAAGCACTGGGGTGGTGGTATCCTTGGTAAC
*****

```

```

KYOKAI      AAGGCTCAAGCCAAGATGGACAAGAGAGCTAAGACCTCCGACTCCGCTTAA
T7          AAGGCTCAAGCCAAGATGGACAAGAGAGCTAAGACCTCCGACTCCGCTTAA
CLIB324     AAGGCTCAAGCCAAGATGGACAAGAGAGCTAAGAACTCCGACTCCGCTTAA
*****

```

dN/dS

Comparing sequences 1 and 2:

	Nondegenerate	Twofold	Fourfold
Transitions	0	1	1
Transversions	0	0	0

Comparing sequences 1 and 3:

	Nondegenerate	Twofold	Fourfold
Transitions	0	0	3
Transversions	1	1	0

Comparing sequences 2 and 3:

	Nondegenerate	Twofold	Fourfold
Transitions	0	1	4
Transversions	1	1	0

> output1

```

          KYOKAI      T7
T7      0.0000000
CLIB324 0.2899925 0.1732122

```

RPS14A

CLUSTAL 2.1 multiple sequence alignment

All sequences are the same

```

LALVIN      ATGTCTAACGTTGTTCAAGCTCGTGACAATTCCCAAGTTTTTGGTGTTGCTAGAATTTAC
T7          ATGTCTAACGTTGTTCAAGCTCGTGACAATTCCCAAGTTTTTGGTGTTGCTAGAATTTAC
          *****

LALVIN      GCTTCTTTCAACGATACTTTCGTTTCATGTTACCGATTTATCTGGTAAGGAAACCATCGCC
T7          GCTTCTTTCAACGATACTTTCGTTTCATGTTACCGATTTATCTGGTAAGGAAACCATCGCC
          *****

LALVIN      AGAGTTACTGGTGGTATGAAGGTTAAGGCTGACAGAGATGAATCTTCTCCATACGCTGCT
T7          AGAGTTACTGGTGGTATGAAGGTTAAGGCTGACAGAGATGAATCTTCTCCATACGCTGCT
          *****

LALVIN      ATGTTGGCTGCCCCAAGATGTTGCCGCTAAGTGTAAGGAAGTCGGTATCACTGCCGTTTAC
T7          ATGTTGGCTGCCCCAAGATGTTGCCGCTAAGTGTAAGGAAGTCGGTATCACTGCCGTTTAC
          *****

LALVIN      GTTAAGATCAGAGCTACCGGTGGTACTAGAACCAAGACTCCAGGTCCAGGTGGTCAAGCT
T7          GTTAAGATCAGAGCTACCGGTGGTACTAGAACCAAGACTCCAGGTCCAGGTGGTCAAGCT
          *****

LALVIN      GCTTTGAGAGCTTTGGCCAGATCTGGTTTGAGAATTGGCCGTATCGAAGATGTTACCCCA
T7          GCTTTGAGAGCTTTGGCCAGATCTGGTTTGAGAATTGGCCGTATCGAAGATGTTACCCCA
          *****

LALVIN      GTTCCATCTGACTCCACCAGAAAGAAGGGTGGTAGAAGAGGTAGAAGATTATGA
T7          GTTCCATCTGACTCCACCAGAAAGAAGGGTGGTAGAAGAGGTAGAAGATTATGA
          *****

```

RPS19A

CLUSTAL 2.1 multiple sequence alignment

-Nucleotide Change

```

LALVIN      ATGCCAGGTGTTTCCGTTAGAGACGTTGCTGCTCAAGATTTCATTAATGCTTACGCTTCT
T7          ATGCCAGGTGTTTCCGTTAGAGACGTTGCTGCTCAAGATTTCATTAATGCTTACGCTTCT
          *****

LALVIN      TTCTTGCAAAGACAAGGTAAGCTAGAAGTTCCAGGTTACGTTGACATTGTCAAGACCTCT
T7          TTCTTGCAAAGACAAGGTAAGCTAGAAGTTCCAGGTTACGTTGACATTGTCAAGACCTCT
          *****

LALVIN      TCTGGTAACGAAATGCCACCACAAGATGCCGAAGGTTGGTTCTACAAGCGTGCTGCCTCT
T7          TCTGGTAACGAAATGCCACCACAAGATGCCGAAGGTTGGTTCTACAAGCGTGCTGCCTCT
          *****

LALVIN      GTTGCCAGACACATTTACATGAGAAAACAAGTTGGTGTGGTAAATTGAACAAATTATAC
T7          GTTGCCAGACACATTTACATGAGAAAACAAGTTGGTGTGGTAAATTGAACAAATTATAC
          *****

LALVIN      GGTGGTGCCAAGAGCAGAGGTGTTAGACCATACAAACACATTGACGCTTCCGGTTCTATC
T7          GGTGGTGCCAAGAGCAGAGGTGTTAGACCATACAAGCACATTGACGCTTCCGGTTCTATC
          *****

LALVIN      AACAGAAAGGTTTTGCAAGCTTTGGAAAAGATTGGTATCGTCGAAATCTCTCCAAAGGGT
T7          AACAGAAAGGTTTTGCAAGCTTTGGAAAAGATTGGTATCGTCGAAATCTCTCCAAAGGGT
          *****

LALVIN      GGTAGAAGAATCTCTGAAAACGGTCAAAGAGATTGGATCGTATTGCCGCTCAAACTTTG
T7          GGTAGAAGAATCTCTGAAAACGGTCAAAGAGATTGGATCGTATTGCCGCTCAAACTTTG
          *****

LALVIN      GAAGAAGACGAATAA
T7          GAAGAAGACGAATAA
          *****

```

dN/dS

Comparing sequences 1 and 2:

	Nondegenerate	Twofold	Fourfold
Transitions	0	1	0
Transversions	0	0	0

> output1

```

      LALVIN
T7      0

```

RPS26B

CLUSTAL 2.1 multiple sequence alignment

All sequences are the same

```

RED          ATGCCAAAAAAGAGAGCTTCCAACGGTAGAAACAAGAAGGGTAGAGGTCACGTCAAGCCA
128          ATGCCAAAAAAGAGAGCTTCCAACGGTAGAAACAAGAAGGGTAGAGGTCACGTCAAGCCA
LALVIN       ATGCCAAAAAAGAGAGCTTCCAACGGTAGAAACAAGAAGGGTAGAGGTCACGTCAAGCCA
              *****

RED          GTGAGATGTGTTAACTGTTCCAAGTCCATTCCAAAGGATAAGGCTATCAAGAGAATGGCT
128          GTGAGATGTGTTAACTGTTCCAAGTCCATTCCAAAGGATAAGGCTATCAAGAGAATGGCT
LALVIN       GTGAGATGTGTTAACTGTTCCAAGTCCATTCCAAAGGATAAGGCTATCAAGAGAATGGCT
              *****

RED          ATTAGAAACATTGTTGAAGCTGCTGCCGTCAGAGATTTGTCCGAAGCTTCTGTCTACCCA
128          ATTAGAAACATTGTTGAAGCTGCTGCCGTCAGAGATTTGTCCGAAGCTTCTGTCTACCCA
LALVIN       ATTAGAAACATTGTTGAAGCTGCTGCCGTCAGAGATTTGTCCGAAGCTTCTGTCTACCCA
              *****

RED          GAATACGCCTTGCCAAAGACTTACAACAAGTTGCACTACTGTGTCTCCTGTGCTATTTCAC
128          GAATACGCCTTGCCAAAGACTTACAACAAGTTGCACTACTGTGTCTCCTGTGCTATTTCAC
LALVIN       GAATACGCCTTGCCAAAGACTTACAACAAGTTGCACTACTGTGTCTCCTGTGCTATTTCAC
              *****

RED          GCCAGAATTGTTAGAGTTAGATCCAGAGAAGACAGAAAGAACAGAGCTCCTCCACAAAGA
128          GCCAGAATTGTTAGAGTTAGATCCAGAGAAGACAGAAAGAACAGAGCTCCTCCACAAAGA
LALVIN       GCCAGAATTGTTAGAGTTAGATCCAGAGAAGACAGAAAGAACAGAGCTCCTCCACAAAGA
              *****

RED          CCAAGATTTAACAGGGATAACAAAGTTTCTCCAGCAGCTGCCGCAAAGAAAGCTTTGTAA
128          CCAAGATTTAACAGGGATAACAAAGTTTCTCCAGCAGCTGCCGCAAAGAAAGCTTTGTAA
LALVIN       CCAAGATTTAACAGGGATAACAAAGTTTCTCCAGCAGCTGCCGCAAAGAAAGCTTTGTAA
              *****

```

RVB1

CLUSTAL 2.1 multiple sequence alignment

-Nucleotide Change

```

seq_RED      ATGGTCGCTATCAGTGAAGTCAAAGAAAATCCTGGCGTAAACAGCAGTAATTCTGGTGCA
seq_K11      ATGGTCGCTATCAGTGAAGTCAAAGAAAATCCTGGCGTAAACAGCAGTAATTCTGGTGCA
seq_128      ATGGTCGCTATCAGTGAAGTCAAAGAAAATCCTGGCGTAAACAGCAGTAATTCTGGTGCA
*****

seq_RED      GTTACGAGAACTGCGGCACATACACATATTAAAGGTTTAGGTCTGGATGAAAGTGGTGTG
seq_K11      GTTACGAGAACTGCGGCACATACACATATTAAAGGTTTAGGTCTGGATGAAAGTGGTGTG
seq_128      GTTACGAGAACTGCGGCACATACACATATTAAAGGTTTAGGTCTGGATGAAAGTGGTGTG
*****

seq_RED      GCCAAGAGGGTTGAAGGAGGGTTTGTGGACAAATAGAAGCTCGTGAAGCGTGCGGTGTA
seq_K11      GCCAAGAGGGTTGAAGGAGGGTTTGTGGACAAATAGAAGCTCGTGAAGCGTGCGGTGTA
seq_128      GCCAAGAGGGTTGAAGGAGGGTTTGTGGACAAATAGAAGCTCGTGAAGCGTGCGGTGTA
*****

seq_RED      ATTGTAGATTTAATCAAGGCTAAAAAATGTCAGGTAGAGCTATCCTATTAGCTGGTGGC
seq_K11      ATTGTAGATTTAATCAAGGCTAAAAAATGTCAGGTAGAGCTATCCTATTAGCTGGTGGC
seq_128      ATTGTAGATTTAATCAAGGCTAAAAAATGTCAGGTAGAGCTATCCTATTAGCTGGTGGT
*****

seq_RED      CCTTCTACAGGTAAGACGGCATTGGCTCTCGCCATTTACAAGAGTTAGGCCCAAAGTT
seq_K11      CCTTCTACAGGTAAGACGGCATTGGCTCTCGCCATTTACAAGAGTTAGGCCCAAAGTT
seq_128      CCTTCTACAGGTAAGACGGCATTGGCTCTCGCCATTTACAAGAGTTAGGCCCAAAGTT
*****

seq_RED      CCATTCTGTCCTCTTGTGGTAGCGAATTATATTCCGTGGAGGTCAAGAAAAACAGAAACC
seq_K11      CCATTCTGTCCTCTTGTGGTAGCGAATTATATTCCGTGGAGGTCAAGAAAAACAGAAACC
seq_128      CCATTCTGTCCTCTTGTGGTAGCGAATTATATTCCGTGGAGGTCAAGAAAAACAGAAACC
*****

seq_RED      CTAATGGAATTTTAGAAGAGCAATTGGGTTAAGAATCAAAGAACTAAGGAAGTTTAT
seq_K11      CTAATGGAATTTTAGAAGAGCAATTGGGTTAAGAATCAAAGAACTAAGGAAGTTTAT
seq_128      CTAATGGAATTTTAGAAGAGCAATTGGGTTAAGAATCAAAGAACTAAGGAAGTTTAT
*****

seq_RED      GAGGGTGAAGTGACAGAACTAACCCCTGAAGACGCAGAGAATCCGTTGGGCGGATATGGT
seq_K11      GAGGGTGAAGTGACAGAACTAACCCCTGAAGACGCAGAGAATCCGTTGGGCGGATATGGT
seq_128      GAGGGTGAAGTGACAGAACTAACCCCTGAAGACGCAGAGAATCCGTTGGGCGGATATGGT
*****

seq_RED      AAAACTATCTCACATGTAATTGTGCGGGCTCAAGTCTGCCAAGGGTACCAAGACACTAAGA
seq_K11      AAAACTATCTCACATGTAATTGTGCGGGCTCAAGTCTGCCAAGGGTACCAAGACACTAAGA
seq_128      AAAACTATCTCACATGTAATTGTGCGGGCTCAAGTCTGCCAAGGGTACCAAGACACTAAGA
*****

seq_RED      TTAGACCCAACGATATATGAAAGTATTCAAAGAGAAAAGGTTAGTATTGGTGATGTCATT
seq_K11      TTAGACCCAACGATATATGAAAGTATTCAAAGAGAAAAGGTTAGTATTGGTGATGTCATT
seq_128      TTAGACCCAACGATATATGAAAGTATTCAAAGAGAAAAGGTTAGTATTGGTGATGTCATT
*****

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seq_RED      TATATAGAGGCCAACACCGGTGCAGTTAAGCGAGTTGGCAGATCTGATGCATACGCTACT
seq_K11      TATATAGAGGCCAACACCGGTGCAGTTAAGCGAGTTGGCAGATCTGATGCATACGCTACT
seq_128      TATATAGAGGCCAACACCGGTGCAGTTAAGCGAGTTGGCAGATCTGATGCATACGCTACT
*****

seq_RED      GAATTTGATTTGGAAACTGAGGAATACGTACCATTGCCAAAAGGCGAAGTGCATAAGAAA
seq_K11      GAATTTGATTTGGAAACTGAGGAATACGTACCATTGCCAAAAGGCGAAGTGCATAAGAA
seq_128      GAATTTGATTTGGAAACTGAGGAATACGTACCATTGCCAAAAGGCGAAGTGCATAAGAAA
*****

seq_RED      AAGGAAATTGTACAAGATGTTACCTTGCACGATTTGGATGTTGCAAACGCAAGACCACAA
seq_K11      AAGGAAATTGTACAAGATGTTACCTTGCACGATTTGGATGTTGCAAACGCAAGACCACAA
seq_128      AAGGAAATTGTACAAGATGTTACCTTGCACGATTTGGATGTTGCAAACGCAAGACCACAA
*****

seq_RED      GGTGGTCAAGATGTCATATCAATGATGGGCCAGTTGCTCAAACCTAAGAAGACTGAAATA
seq_K11      GGTGGTCAAGATGTCATATCAATGATGGGCCAGTTGCTCAAACCTAAGAAGACTGAAATA
seq_128      GGTGGTCAAGATGTCATATCAATGATGGGCCAGTTGCTCAAACCTAAGAAGACTGAAATA
*****

seq_RED      ACCGAGAAATTAAGACAAGAGGTGAATAAAGTTGTTGCTAAATATATTGATCAAGGTGTC
seq_K11      ACCGAGAAATTAAGACAAGAGGTGAATAAAGTTGTTGCTAAATATATTGATCAAGGTGTC
seq_128      ACCGAGAAATTAAGACAAGAGGTGAATAAAGTTGTTGCTAAATATATTGATCAAGGTGTC
*****

seq_RED      GCAGAACTTATTCCAGGTGTTTTGTTTCATTGATGAAGTTAATATGCTAGACATTGAAATA
seq_K11      GCAGAACTTATTCCAGGTGTTTTGTTTCATTGATGAAGTTAATATGCTAGACATTGAAATA
seq_128      GCAGAACTTATTCCAGGTGTTTTGTTTCATTGATGAAGTTAATATGCTAGACATTGAAATA
*****

seq_RED      TTCACGTATTTGAACAAAGCGCTTGAGTCTAATATTGCCCCCGTTGTTGTATTGGCTTCT
seq_K11      TTCACGTATTTGAACAAAGCGCTTGAGTCTAATATTGCCCCCGTTGTTGTATTGGCTTCT
seq_128      TTCACGTATTTGAACAAAGCGCTTGAACTAATATCGCCCGGTTGTTGTATTGGCTTCT
*****

seq_RED      AATAGGGGCATGACTACAGTCCGTGGCACTGAGGATGTGATATCACCACATGGTGTGCCA
seq_K11      AATAGGGGCATGACTACAGTCCGTGGCACTGAGGATGTGATATCACCACATGGTGTGCCA
seq_128      AATAGGGGCATGACTACAGTCCGTGGCACTGAGGATGTGATATCACCACATGGTGTGCCA
*****

seq_RED      CCTGATTTGATCGATAGATTGTTAATTGTTTCGTACATTACCATATGACAAGGACGAGATC
seq_K11      CCTGATTTGATCGATAGATTGTTAATTGTTTCGTACATTACCATATGACAAGGACGAGATC
seq_128      CCTGATTTGATCGATAGATTGTTAATTGTTTCGTACATTACCATATGACAAGGACGAGATC
*****

seq_RED      CGTACCATTATAGAGAGAAGAGCTACCGTTGAAAGATTGCAAGTAGAAAGTAGCGCATTG
seq_K11      CGTACCATTATAGAGAGAAGAGCTACCGTTGAAAGATTGCAAGTAGAAAGTAGCGCATTG
seq_128      CGTACCATTATAGAGAGAAGAGCTACCGTTGAAAGATTGCAAGTAGAAAGTAGCGCATTG
*****

seq_RED      GACCTTTTAGCCACGATGGGTACAGAACTTCGTTACGTTACGCTTTACAATTATTGGCA
seq_K11      GACCTTTTAGCCACGATGGGTACAGAACTTCGTTACGTTACGCTTTACAATTATTGGCA
seq_128      GACCTTTTAGCCACGATGGGTACAGAACTTCGTTACGTTACGCTTTACAATTATTGGCA
*****
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```

seq_RED      CCATGTGGTATCCTAGCACAAACAAGCAATCGTAAGGAGATTGTTGTTAATGACGTTAAT
seq_K11      CCATGTGGTATCCTAGCACAAACAAGCAATCGTAAGGAGATTGTTGTTAATGACGTTAAT
seq_128      CCATGTGGTATCCTAGCACAAACAAGCAATCGTAAGGAGATTGTTGTTAATGACGTTAAT
              *****

seq_RED      GAAGCCAAATTGCTGTTTTTGGATGCCAAAAGGTCAACAAAGATTTTAGAACTTCCGCA
seq_K11      GAAGCCAAATTGCTGTTTTTGGATGCCAAAAGGTCAACAAAGATTTTAGAACTTCCGCA
seq_128      GAAGCCAAATTGCTGTTTTTGGATGCCAAAAGGTCAACAAAGATTTTAGAACTTCCGCA
              *****

seq_RED      AATTATTTGTAA
seq_K11      AATTATTTGTAA
seq_128      AATTATTTGTAA
              *****

```

dN/dS

Comparing sequences 1 and 2:

	Nondegenerate	Twofold	Fourfold
Transitions	0	2	0
Transversions	0	0	0

Comparing sequences 1 and 3:

	Nondegenerate	Twofold	Fourfold
Transitions	0	3	2
Transversions	0	0	0

Comparing sequences 2 and 3:

	Nondegenerate	Twofold	Fourfold
Transitions	0	3	2
Transversions	0	0	0

> output1

	seq_RED	seq_K11
seq_K11	0	
seq_128	0	0

SEC23

CLUSTAL 2.1 multiple sequence alignment

-Nucleotide Change

```

K11      ATGGACTTCGAGACTAATGAAGACATCAACGGGGTCCGTTTCACCTGGAACGTGTTTCCC
128      ATGGACTTCGAGACTAATGAAGACATCAACGGGGTCCGTTTCACCTGGAACGTGTTTCCC
RED      ATGGACTTCGAGACTAATGAAGACATCAACGGGGTCCGTTTCACCTGGAACGTGTTTCCC
          *****

K11      TCTACCAGAAGCGACGCTAACAGCAACGTCGTCCTGTGGGCTGTTGTACACACCTTTG
128      TCTACCAGAAGCGACGCCAACAGCAACGTCGTCCTGTGGGCTGTTGTACACACCTTTG
RED      TCTACTAGAAGCGACGCTAACAGCAACGTCGTCCTGTGGGCTGTTGTACACACCTTTG
          *****

K11      AAGGAGTATGACGAATTGAACGTTGCCCCATACAATCCAGTTGTGTGTTCCGGTCCACAC
128      AAGGAGTATGACGAATTGAACGTTGCCCCATACAATCCAGTTGTGTGTTCCGGTCCACAC
RED      AAGGAGTATGACGAATTGAACGTTGCCCCATACAATCCAGTTGTGTGTTCCGGTCCACAC
          *****

K11      TGTAAGTCGATTCTAAATCCTTACTGTGTGATTGATCCGCGCAATTCGTCTTGAGATTGT
128      TGTAAGTCGATTCTAAATCCTTACTGTGTGATTGATCCGCGCAATTCGTCTTGAGATTGT
RED      TGTAAGTCGATTCTAAATCCTTACTGTGTGATTGATCCGCGCAATTCGTCTTGAGATTGT
          *****

K11      CCCATCTGTAACTCCAGGAACCATTTACCTCCACAGTACACCAACTTGTCACAGGAGAAT
128      CCCATCTGTAACTCCAGGAACCATTTACCTCCACAGTACACCAACTTGTCACAGGAGAAT
RED      CCCATCTGTAACTCCAGGAACCATTTACCTCCACAGTACACCAACTTGTCACAGGAGAAT
          *****

K11      ATGCCGCTAGAGTTACAGTCCACCACCATTGAGTACATCACCAATAAGCCCGTTACCGTT
128      ATGCCGCTAGAGTTACAGTCCACCACCATTGAGTACATCACCAATAAGCCCGTTACCGTT
RED      ATGCCGCTAGAGTTACAGTCCACCACCATTGAGTACATCACCAATAAGCCCGTTACCGTT
          *****

K11      CCTCCCATTTCTTCTTTGTGTGGATTGACTTCGGAACCGAGAACCTCGATTGCTA
128      CCTCCCATTTCTTCTTTGTGTGGATTGACTTCGGAACCGAGAACCTCGATTGCTA
RED      CCTCCCATTTCTTCTTTGTGTGGATTGACTTCGGAACCGAGAACCTCGATTGCTA
          *****

K11      AAGGAGTCTATCATCACTTCTTTGTCTCTATTACCTCCCAACGCGCTGATTGGGTTGATC
128      AAGGAGTCTATCATCACTTCTTTGTCTCTATTACCTCCCAACGCGCTGATTGGGTTGATC
RED      AAGGAGTCTATCATCACTTCTTTGTCTCTATTACCTCCCAACGCGCTGATTGGGTTGATC
          *****

K11      ACTTACGGAAACGTTGTTCAATTGCACGATCTGTCCAGCGAAACTATTGACAGGTGCAAC
128      ACTTACGGAAACGTTGTTCAATTGCACGATCTGTCCAGCGAAACTATTGACAGGTGCAAC
RED      ACTTACGGAAACGTTGTTCAATTGCACGATCTGTCCAGCGAAACTATTGACAGGTGCAAC
          *****

K11      GTGTTTCAGAGGAGACAGGGAGTACCAGCTCGAAGCGTTGACGGAAATGTTGACCGGCCAA
128      GTGTTTCAGAGGAGACAGGGAGTACCAGCTCGAAGCGTTGACGGAAATGTTGACCGGCCAA
RED      GTGTTTCAGAGGAGACAGGGAGTACCAGCTCGAAGCGTTGACGGAAATGTTGACCGGCCAA
          *****

```

K11 AAGCCTACCGCCCCGGCGGTGCTGCATCTCATCTACCGAACGCCATGAACAAAGTTACG
 128 AAGCCTACCGCCCCGGTGGTGCTGCATCTCATCTACCGAACGCCATGAACAAAGTTACG
 RED AAGCCTACCGCCCCGGCGGTGCTGCATCTCATCTACCGAACGCCATGAACAAAGTTACG

 K11 CCCTTCTCTTTGAATAGGTTCTTCTGCCCCTTGAACAGGTCGAGTTCAAACCTGAATCAA
 128 CCCTTCTCTTTGAATAGGTTCTTCTGCCCCTTGAACAGGTCGAGTTCAAACCTGAATCAA
 RED CCCTTCTCTTTGAATAGGTTCTTCTGCCCCTTGAACAGGTCGAGTTCAAACCTGAATCAA

 K11 TTACTGGAAAATCTGTCTCCAGACCAATGGTCTGTTCCAGCGGGTCATAGACCATTAAGG
 128 TTACTGGAAAATCTGTCTCCAGACCAATGGTCTGTTCCAGCGGGTCATAGACCATTAAGG
 RED TTACTGGAAAATCTGTCTCCAGACCAATGGTCTGTTCCAGCGGGTCATAGGCCATTAAGG

 K11 GCCACAGGTTCCGCTTTGAACATTGCATCTTTGCTTTTACAGGGCTGCTATAAGAACATC
 128 GCCACAGGTTCCGCTTTGAACATTGCATCTTTGCTTTTACAGGGCTGCTATAAGAACATC
 RED GCCACAGGTTCCGCTTTGAACATTGCATCTTTGCTTTTACAGGGCTGCTATAAGAACATC

 K11 CCAGCAAGAATCATTCTTTTCGCCTCCGGTCCAGGCACCGTGGCCCCAGGTTTGATTGTT
 128 CCAGCAAGAATCATTCTTTTCGCCTCCGGTCCAGGCACCGTGGCCCCAGGTTTGATTGTT
 RED CCAGCAAGAATCATTCTTTTCGCCTCCGGTCCAGGCACCGTGGCCCCAGGTTTGATTGTT

 K11 AACTCAGAGTTAAAAGATCCCTTAAGATCCCACCACGACATCGATTCTGATCACGCGCAA
 128 AACTCAGAGTTAAAAGATCCCTTAAGATCCCACCACGACATCGATTCTGATCACGCGCAA
 RED AACTCAGAGTTAAAAGATCCCTTAAGATCCCACCACGACATCGATTCTGATCACGCGCAA

 K11 CATTACAAGAAGGCCTGTAAGTTTTACAACCAGATTGCACAAAGAGTTGCCGCCAATGGA
 128 CATTACAAGAAGGCCTGTAAGTTTTACAACCAGATTGCACAAAGAGTTGCCGCCAATGGA
 RED CATTACAAGAAGGCCTGTAAGTTTTACAACCAGATTGCACAAAGAGTTGCCGCCAATGGA

 K11 CACACTGTTGATATTTTTGCCGGTTGTTACGATCAAATCGGTATGTCTGAAATGAAACAG
 128 CACACTGTTGACATTTTTGCCGGTTGTTACGATCAAATCGGTATGTCTGAAATGAAACAG
 RED CACACTGTTGATATTTTTGCCGGTTGTTACGATCAAATCGGTATGTCTGAAATGAAACAG

 K11 TTGACCGACTCTACGGGAGGTGTGTTGTTGCTAACCGATGCCTTCTCTACCGCGATTTTT
 128 TTGACCGACTCTACTGGAGGTGTGTTGTTGCTAACCGATGCCTTCTCTACCGCGATTTTT
 RED TTGACCGACTCTACTGGAGGTGTGTTGTTGCTAACCGATGCCTTCTCTACCGCGATTTTT

 K11 AAGCAATCATACTTGAGATTGTTTGCCAAGGATGAAGAAGGGTATTTGAAGATGGCTTTC
 128 AAGCAATCATACTTGAGATTGTTTGCCAAGGATGAAGAAGGGTATTTGAAGATGGCTTTC
 RED AAGCAATCATACTTGAGATTGTTTGCCAAGGATGAAGAAGGGTATTTGAAGATGGCTTTC

 K11 AATGGTAATATGGCAGTCAAGACAAGTAAAGACTTGAAGGTACAAGGTTTGATTGGACAT
 128 AATGGTAATATGGCAGTCAAGACAAGTAAAGACTTGAAGGTACAAGGTTTGATTGGACAT
 RED AATGGTAATATGGCAGTCAAGACAAGTAAAGACTTGAAGGTACAAGGTTTGATTGGGCAT

```

K11      GCTTCTGCTGTAAAGAAGACAGACGCTAACAAACATCAGTGAATCTGAAATCGGTATAGGT
128      GCTTCTGCTGTAAAGAAGACAGACGCTAACAAACATCAGTGAATCTGAAATCGGTATAGGT
RED      GCTTCTGCTGTAAAGAAGACAGACGCTAACAAACATCAGTGAATCTGAAATCGGTATAGGT
          *****

K11      GCAACGTCCACCTGGAAGATGGCTTCCTTATCGCCTTATCACTCGTATGCGATTTTCTTT
128      GCAACGTCCACCTGGAAGATGGCTTCCTTATCGCCTTATCACTCGTATGCGATTTTCTTT
RED      GCAACGTCCACCTGGAAGATGGCTTCCTTATCGCCTTATCACTCGTATGCGATTTTCTTT
          *****

K11      GAAATTGCAAACTGCGGCTAATTCTAACCCAATGATGTCTGCCCCTGGTTCAGCAGAT
128      GAAATTGCAAACTGCGGCTAATTCTAACCCAATGATGTCTGCCCCTGGTTCAGCAGAT
RED      GAAATTGCAAACTGCGGCTAATTCTAACCCAATGATGTCTGCCCCTGGTTCAGCAGAT
          *****

K11      AGACCTCATCTAGCATATACTCAATTCATCACTACTTATCAAACTCCTCTGGTACCAAC
128      AGACCTCATCTAGCATATACTCAATTCATCACTACTTATCAAACTCCTCTGGTACCAAC
RED      AGACCTCATCTAGCATATACTCAATTCATCACTACTTATCAAACTCCTCTGGTACCAAC
          *****

K11      CGTATCAGAGTCACCACCGTCGCAAACCAGCTTTTGCCCTTCGGCACTCCTGCCATTGCA
128      CGTATCAGAGTCACCACCGTCGCAAACCAGCTTTTGCCCTTCGGCACTCCTGCCATTGCA
RED      CGTATCAGAGTCACCACCGTCGCAAACCAGCTTTTGCCCTTCGGTACTCCTGCCATTGCA
          *****

K11      GCTTCTTTTCGATCAAGAAGCTGCTGCCGTTTGTGATGGCTCGTATTGCTGTGCACAAGGCT
128      GCTTCTTTTCGATCAAGAAGCTGCTGCCGTTTGTGATGGCTCGTATTGCTGTGCACAAGGCT
RED      GCTTCTTTTCGATCAAGAAGCTGCTGCCGTTTGTGATGGCTCGTATTGCTGTGCACAAGGCT
          *****

K11      GAAACCGATGATGGTGCAGATGTTATCAGATGGTTAGACAGAAGCTTTGATTAAGCTATGT
128      GAAACCGATGATGGTGCAGATGTTATCAGATGGTTAGACAGAAGCTTTGATTAAGCTATGT
RED      GAAACCGATGATGGTGCAGATGTTATCAGATGGTTAGACAGAAGCTTTGATTAAGCTATGT
          *****

K11      CAAAAGTACGCCGACTATAATAAAGATGATCCTCAATCTTTCAGGTTGGCTCCAAATTTTC
128      CAAAAGTACGCCGACTATAATAAAGATGATCCTCAATCTTTCAGGTTGGCTCCAAATTTTC
RED      CAAAAGTACGCCGACTATAATAAAGATGATCCTCAATCTTTCAGGTTGGCTCCAAATTTTC
          *****

K11      TCACTGTATCCTCAATTTACCTATTATTTAAGAAGATCCCAATTCTTAAGTGTCTTTAAC
128      TCACTGTATCCTCAATTTACCTATTATTTAAGAAGATCCCAATTCTTAAGTGTCTTTAAC
RED      TCACTGTATCCTCAATTTACCTATTATTTAAGAAGATCCCAATTCTTAAGTGTCTTTAAC
          *****

K11      AATTCTCCGATGAACTGCATTTTATAGACATATTTTCACAAGAGAGGATACGACTAAT
128      AATTCTCCGATGAACTGCATTTTATAGACATATTTTCACAAGAGAGGATACGACTAAT
RED      AATTCTCCGATGAACTGCATTTTATAGACATATTTTCACAAGAGAGGATACGACTAAT
          *****

K11      TCTTTAATCATGATTCAACCAACTCTAACTTCTTTCTCAATGGAGGACGATCCACAACCG
128      TCTTTAATCATGATTCAACCAACTCTAACTTCTTTCTCAATGGAGGACGATCCACAACCG
RED      TCTTTAATCATGATTCAACCAACTCTAACTTCTTTCTCAATGGAGGACGATCCACAACCG
          *****

```

K11 GTATTGTTAGACTCTATCTCCGTCAAACCCAATACCATTCTATTATTAGATACATTTTTC
128 GTATTGTTAGACTCTATCTCCGTCAAACCCAATACCATTCTATTATTAGATACATTTTTC
RED GTATTATTAGACTCTATCTCCGTCAAACCCAATACCATTCTATTATTAGATACATTTTTC

K11 TTCATCTTAATATACCACGGTGAGCAAATCGCTCAATGGAGAAAAGCCGGTTACCAAGAC
128 TTCATCTTAATATACCACGGTGAGCAAATCGCTCAATGGAGAAAAGCCGGTTACCAAGAC
RED TTCATCTTAATATACCACGGTGAGCAAATCGCTCAATGGAGAAAAGCCGGTTACCAAGAC

K11 GATCCACAGTACGCAGATTTCAAAGCTCTTCTTGAAGAGCCAAAATTAGAAGCCGCAGAA
128 GATCCACAGTACGCAGATTTCAAAGCTCTTCTTGAAGAGCCAAAATTAGAAGCCGCAGAA
RED GATCCACAGTACGCAGATTTCAAAGCTCTTCTTGAAGAGCCAAAATTAGAAGCCGCAGAA

K11 TTGTTAGTAGATAGGTTCCCGCTACCAAGGTTCAATTGATACTGAAGCCGGTGGTTCTCAA
128 TTGTTAGTAGATAGGTTCCCGCTACCAAGGTTCAATTGATACTGAAGCCGGTGGTTCTCAA
RED TTGTTAGTAGATAGGTTCCCGCTACCAAGGTTCAATTGATACTGAAGCCGGTGGTTCTCAA

K11 GCCAGATTCTTGTTATCTAAATTGAATCCTTCCGATAACTATCAAGACATGGCGCGCGGA
128 GCCAGATTCTTGTTATCTAAATTGAATCCTTCCGATAACTATCAAGACATGGCGCGCGGA
RED GCCAGATTCTTGTTATCTAAATTGAATCCTTCCGATAACTATCAAGACATGGCGCGCGGA

K11 GGATCTACAATTGTCTTAACAGATGATGTTTCCTTACAAAATTTTCATGACTCACTTACAA
128 GGATCTACAATTGTCTTAACAGATGATGTTTCCTTACAAAATTTTCATGACTCACTTACAA
RED GGATCTACAATTGTCTTAACAGATGATGTTTCCTTACAAAATTTTCATGACTCACTTACAA

K11 CAAGTAGCCGTCTCTGGTCAGGCATAG
128 CAAGTAGCCGTCTCTGGTCAGGCATAG
RED CAAGTAGCCGTCTCTGGTCAGGCATAG

dN/dS

Comparing sequences 1 and 2:

	Nondegenerate	Twofold	Fourfold
Transitions	0	2	2
Transversions	0	0	1

Comparing sequences 1 and 3:

	Nondegenerate	Twofold	Fourfold
Transitions	0	3	3
Transversions	0	0	4

Comparing sequences 2 and 3:

	Nondegenerate	Twofold	Fourfold
Transitions	0	5	5
Transversions	0	0	3

> output1

```

      K11 128
128    0
RED    0   0

```

YCP4

CLUSTAL 2.1 multiple sequence alignment

 -Nucleotide Change -Unknown Nucleotide Fixed

```

RED          ATGGTAAAGATTGCGATAATTACTTACTCTACCTACGGGCACATAGACGTTTtagcccaa
128          ATGGTAAAGATTGCGATAATTACTTACTCTACCTACGGGCACATAGACGTTTtagcccaa
LALVIN       ATGGTAAAGATTGCGATAATTACTTACTCTACTACGGGCACATAGACGTTTtagcccaa
*****

RED          GCTGTTAAGAAAGGTGTGGAGGCAGCTGGTGGTAAAGCTGATATATACAGGGTCGAGGAA
128          GCTGTTAAGAAAGGTGTGGAGGCAGCTGGTGGTAAAGCTGATATATACAGGGTCGAGGAA
LALVIN       GCTGTTAAGAAAGGTGTGGAGGCAGCTGGTGGTAAAGCTGATATATACAGGGTCGAGGAA
*****

RED          ACTTTACCTGATGAAGTCCTCACCAAGATGAACGCTCCTCAGAAACCTGAAGATATTCCT
128          ACTTTACCTGATGAAGTCCTCACCAAGATGAACGCTCCTCAGAAACCTGAAGATATTCCT
LALVIN       ACTTTACCTGATGAAGTCCTCACCAAGATGAACGCTCCTCAGAAACCTGAAGATATTCCT
*****

RED          GTTGCCACTGAGAAAACGTTGCTCGAATATGACGCCTTTTGTTCGGTGTTCCAACTAGG
128          GTTGCTACTGAGAAAACGTTGCTCGAATATGACGCCTTTTGTTCGGTGTTCCAACTAGG
LALVIN       GTTGCCACTGAGAAAACGTTGCTCGAATATGACGCCTTTTGTTCGGTGTTCCAACTAGG
*****

RED          TTTGGTAATTTGCCGGCTCAATGGTCCGCCTTTTGGGATAAAACCGGTGGATTATGGGCC
128          TTTGGTAATTTGCCGGCTCAATGGTCCGCCTTTTGGGATAAAACCGGTGGATTATGGGCC
LALVIN       TTTGGTAATTTGCCGGCTCAATGGTCCGCCTTTTGGGATAAAACCGGTGGATTATGGGCC
*****

RED          AAGGGCTCTTTGAACGGCAAAGCTGCGGGGATATTCGTTAGTACTTCCAGTTACGGAGGT
128          AAGGGCTCTTTGAACGGCAAAGCTGCGGGGATATTCGTTAGTACTTCCAGTTACGGAGGT
LALVIN       AAGGGCTCTTTGAACGGCAAAGCTGCGGGGATATTCGTTAGTACTTCCAGTTACGGAGGT
*****

RED          GGTCAAGAAAGTACCGTTAAAGCCTGTTTGTCTTATTAGCTCATCACGGAATTATCTTT
128          GGTCAAGAAAGTACCGTTAAAGCCTGTTTGTCTTATTAGCTCATCACGGAATTATCTTT
LALVIN       GGTCAAGAAAGTACCGTTAAAGCCTGTTTGTCTTATTAGCTCATCACGGAATTATCTTT
*****

RED          TTACCACTGGGTTATAAGAATTCATTTGCTGAGTTAGCCAGTATAGAAGAGGTACACGGT
128          TTACCACTGGGTTATAAGAATTCATTTGCTGAGTTAGCCAGTATAGAAGAGGTACACGGT
LALVIN       TTACCACTGGGTTATAAGAATTCATTTGCTGAGTTAGCCAGTATAGAAGAGGTACACGGT
*****

RED          GGCTCTCCATGGGGTGCTGGTACCCTTGCAGGACTGACGGCTCAAGAAGTGCCTCTCCT
128          GGCTCTCCATGGGGTGCTGGTACCCTTGCAGGACTGACGGCTCAAGAAGTGCCTCTCCT
LALVIN       GGCTCTCCATGGGGTGCTGGTACCCTTGCAGGACTGACGGCTCAAGAAGTGCCTCTCCA
*****

RED          CTTGAATTGAGAATTGCTGAAATTCAGGTAAAACATTCTACGAAACCGCCAAAAAACTT
128          CTTGAATTGAGAATTGCTGAAATTCAGGTAAAACATTCTACGAAACCGCCAAAAAACTT
LALVIN       CTTGAATTGAGAATTGCTGAAATTCAGGTAAAACATTCTACGAAACCGCCAAAAAACTT
*****

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RED      TTCCTGCAAAAGAAGCCAAGCCCTCCACTGAAAAGAAGACCACTACTTCTGATGCGGCT
128      TTCCTGCAAAAGAAGCCAAGCCCTCCACTGAAAAGAAGACCACTACTTCTGATGCGGCT
LALVIN   TTCCTGCAAAAGAAGCCAAGCCCTCCACTGAAAAGAAGACCACTACTTCTGATGCGGCT
*****

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RED      AAGAGACAACTAAACCTGCAGCAGCTACAACCTGCAGAAAAGAAGGAGGACAAAGGATTA
128      AAGAGACAACTAAACCTGCAGCAGCTACAACCTGCAGAAAAGAAGGAGGACAAAGGATTA
LALVIN   AAGAGACAACTAAACCTGCAGCAGCTACAACCTGCAGAAAAGAAGGAGGACAAAGGATTA
*****

```

```

RED      TTATCCTGCTGCACTGTCATGTAA
128      TTATCCTGCTGCACTGTCATGTAA
LALVIN   TTATCCTGCTGCACTGTCATGTAA
*****

```

CLUSTAL 2.1 multiple sequence alignment

- Amino Acid Change

```

lalvin   MVKIAIITYSTYGHIDVLAQAVKKGVEAAGGKADIYRVEETLPDEVLTGMNAPQKPEDIP
128      MVKIAIITYSTYGHIDVLAQAVKKGVEAAGGKADIYRVEETLPDEVLTGMNAPQKPEDIP
Red      MVKIAIITYSTYGHIDVLAQAVKKGVEAAGGKADIYRVEETLPDEVLTGMNAPQKPEDIP
*****

```

```

lalvin   VATEKTLLEYDAFLFGVPTRFGNLPQWSAFWDKTGGLWAKGSLNGKAAGIFVSTSSYGG
128      VATEKTLLEYDAFLFGVPTRFGNLPQWSAFWDKTGGLWAKGSLNGKAAGIFVSTSSYGG
Red      VATEKTLLEYDAFLFGVPTRFGNLPQWSAFWDKTGGLWAKGSLNGKAAGIFVSTSSYGG
*****

```

```

lalvin   GQESTVKACLSYLAHHGIIIFLPLGYKNSFAELASIEEVHGGSPWGAGTLAGEPDGSRTASP
128      GQESTVKACLSYLAHHGIIIFLPLGYKNSFAELASIEEVHGGSPWGAGTLAGEPDGSRTASP
Red      GQESTVKACLSYLAHHGIIIFLPLGYKNSFAELASIEEVHGGSPWGAGTLAGEPDGSRTASP
*****

```

```

lalvin   LELRIAIEIQGKTFYETAKKLFPAKEAKPSTEKKTTTSDAAKRQTKPAAATTAEEKKEDKGL
128      LELRIAIEIQGKTFYETAKKLFPAKEAKPSTEKKTTTSDAAKRQTKPAAATTAEEKKEDKGL
Red      LELRIAIEIQGKTFYETAKKLFPAKEAKPSTEKKTTTSDAAKRQTKPAAATTAEEKKEDKGL
*****

```

```

lalvin   LSCCTVM
128      LSCCTVM
Red      LSCCTVM
*****

```

dN/dS

Comparing sequences 1 and 2:

	Nondegenerate	Twofold	Fourfold
Transitions	1	0	1
Transversions	0	0	0

Comparing sequences 1 and 3:

	Nondegenerate	Twofold	Fourfold
Transitions	1	0	0
Transversions	0	0	1

Comparing sequences 2 and 3:

	Nondegenerate	Twofold	Fourfold
Transitions	0	0	1
Transversions	0	0	1

> output1

```

          RED      128
128      0.6348279
LALVIN 0.2629160 0.0000000
```

ZRT1

CLUSTAL 2.1 multiple sequence alignment

-Nucleotide Change

```

seq_K11      ATGAGCAACGTTACTACGCCGTGGTGGAAACAATGGGACCCTTCTGAAGTTACACTTGCC
seq_YSP128   ATGAGCAACGTTACTACGCCGTGGTGGAAACAATGGGACCCTTCTGAAGTTACACTTACC
seq_Red      ATGAGCAACGTTACTACGCCGTGGTGGAAACAATGGGACCCTGATACCGTTACACTTACC
***** * ***** **

seq_K11      GATAAAACCCCTGATGATGTGTGGAAGACCTGTGTTTTGCAAGGTGTTTACTTTGGTGGA
seq_YSP128   GATGAAACCCCTGATGATGTGTGGAAGACCTGTGTTTTGCAAGGTGTTTACTTTGGTGGA
seq_Red      GCTGAAACCCCTGATGATGTGTGGAAGACCTGTGTTTTGCAAGGTGTTTATTTTGGTGAA
* * ***** ***** *

seq_K11      AACGAGTACAATGGTAACCTAGGTGCCAGAATATCTTCCGTCCTTTGTTATTCTTTTCGTG
seq_YSP128   AACGAGTACAATGGTAACCTAGGTGCCAGAATATCTTCCGTCCTTTGTTATTCTTTTCGTG
seq_Red      AACGAGTACAATGGTAACCTAGGTGCCAGAATATCTTCCGTCCTTTGTTATTCTTTTCGTG
*****

seq_K11      AGTACTTTTTTCACCATGTTCCTATTAATCTCAACAAAAGTGAAAAGATTGAGAATTCCT
seq_YSP128   AGTACTTTTTCTCACTATGTTCCTATTAATCTCAACAAAAGTGAAAAGATTGAGAATTCCT
seq_Red      AGTACTTTTTTAACATATGTTCCTATTAATCTCAACAAAAGTGAAAAGATTGAGAATTCCT
***** * ** *****

seq_K11      CTATATGTTTACCTTTTTCGCAAAAGTATTTTGGTTCCGGTGTTATTGTTGCAACCGCATTT
seq_YSP128   TTATATGCTTACCTTTTTCGCAAAATATTTTGGTTCTGGTGTTATTGTTGCAACCGCATTT
seq_Red      TTATATGCTTACCTTTTTCGCAAAATATTTTGGTTCCGGTGTTATTGTTGCAACTGCATTT
***** ***** ***** *****

seq_K11      ATCCACTTAATGGACCCTGCTTATGGTGCATTGGTGGTACCACTTGTGTAGGACAAACC
seq_YSP128   ATCCACTTAATGGACCCTGCTTATGGTGCATTGGTGGTACCACTTGTGTGGGACAAACC
seq_Red      ATCCACTTAATGGACCCTGCTTATGGTGCATTGGTGGTAACTTGTGTAGGACAAACC
***** ***** *****

seq_K11      GGTAAGTGGGGTCTTTATTCATGGTGTCTCTGCCATTATGCTAACGAGTTTGACCTTCACT
seq_YSP128   GGTAAGTGGGGCATCTATTCATGGTGTCTCTGCCATTATGCTAACGAGTTTGACCTTCACT
seq_Red      GGTAAGTGGGGTCTTTATTCATGGTGTCTCTGCCATTATGCTAACGAGTTTGACCTTCACT
***** * *****

seq_K11      TTCCTTACTGATCTATTTCAGTAGCGTCTGGGTTGAAAGAAAGTATGGTCTTTCCCATGAC
seq_YSP128   TTCCTTACTGACTTATTTCAGTAGCGTCTGGGTTGAAAGAAAGTATGGTCTTTCCCATGAC
seq_Red      TTCCTTACTGACCTGTTTCAGTAGCGTCTGGGTTGAAAGAAAGTATGGGCTTTCCCATGAC
***** * *****

seq_K11      CATACCCACGATGAAATTAAGACACTGTTGTGAGAAACACTGCAGCTGTTTCAAGTGAG
seq_YSP128   CATACCCACGATGACATTAAGACACTGTTGTGAATAACGCTGCAGTTGTTTCAACTGAG
seq_Red      CATACCAACGATGAAATTAAGACACTGTTGTGAATAACGCTGCAGTTGTTTCAACTGAG
***** ***** ***** *****

seq_K11      AATGACAATGAGAATGGTACTGCAAATGGATCTCATGACACCAAGAACGGAGTAGAGTAT
seq_YSP128   AATGAGAATGAGAATGCTACTGCAAATGGATCTCATGACACCAAGAACGGAATAGAGTAT
seq_Red      AATGAGAATGAGAATGGTACCGCAAATGGATCTCATGACACCAAGAATGGAATAGAAATAT
***** ***** ***** *****

```

```
seq_K11      TATGAAGATTTCAGACGCTACATCCATGGATGTTGTTCAATCATTTCAAGCACAATTTTAT
seq_YP128    TATGAAGATTTCAGACGCTACATCCATGGATGTTGTTCAATCATTTCAAGCACAATTTTAT
seq_Red      TTtGAAGAATcAGAcGCTAcATccGTGGATGTTGTTCAATCATTTCAAACACAATTTTAT
*   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
```

```
seq_K11      GCCTTTTAAATTTAGAATTGGGTGTGATTTCCACTCGTTATGATCGGTCTAAACCTG
seq_YP128    GCCTTTTAAATTTAGAATTGGGTGTGATTTCCACTCGTTATGATCGGTCTAAATCTG
seq_Red      GCCTTTTAAATTTAGAATTGGGTGTGATTTCCACTCGTTATGATCGGTCTAAATCTG
*****
```

```
seq_K11      GGAAGTGTGGTGATGAGTTCTCCTCCCTATACCCTGTCTTAATGTTCCATCAATCATTT
seq_YP128    GGAAGTACTGGTAAAGAGTTGCGCACCTATACCCTGTCTTAGTGTTCATCAATCATTT
seq_Red      GGAAGTACTGGTGAAGAGTTGCGCACCTATACCCTGTCTTAGTGTTCATCAATCATTT
*****      ***** * ***** ** *****
```

```
seq_K11      GAAGGTTTAGGTATTGGTGCAGATTGTCAGCCATTGAATTCCTAGATCAAAGAGATGG
seq_YP128    GAAGGTTTAGGTATTGGTGCAGATTGTCAGCCATTGAATTCCTAGATCAAAGAGATGG
seq_Red      GAAGGTTTAGGTATTGGTGCAGATTGTCAGCCATTGAATTCCTAGATCAAAGAGATGG
*****
```

```
seq_K11      TGGCCATGGGCCCTATGTGTTGCGTATGGGTTAACCACACCAATCTGTGTGGCCATCGGT
seq_YP128    TGGCCATGGGCCCTATGTGTTGCGTATGGGTTAACCACACCAATCTGTGTAGCCATCGGT
seq_Red      TGGCCATGGGCCCTATGTGTTGCGTATGGGTTAACCACACCAATCTGTGTGGCCATCGGT
*****
```

```
seq_K11      TTGGGTGTTTCGTACAGATACGTAGCGGTTCTTAACTGCGCTTGTTATCTCTGGTGTT
seq_YP128    TTGGGTGTTTCGTACACAATACGTAGCGGTTCTTAACTGCGCTTGTTGTTCTCTGGTGTT
seq_Red      TTGGGTGTTTCGTACAGATACGTAGCGGTTCTTAACTGCGCTTGTTATCTCTGGTGTT
*****      *****
```

```
seq_K11      TTGGATGCCATTTCTGCTGGTATCTTATTGTACACTGGTTTGGTTGAACTACTAGCAAGA
seq_YP128    TTGGATGCCATTTCTGCTGGTATCTTATTGTACACTGGTTTGGTTGAACTACTAGCAAGA
seq_Red      TTGGATGCCATTTCTGCTGGTATCTTATTGTACACTGGTTTGGTTGAACTACTAGCAAGA
*****
```

```
seq_K11      GACTTTATATTCAATCCTCAAAGAACAAAGGATCTAAGAGAATTGTCCTTCAACGTTATA
seq_YP128    GACTTTATATTCAATCCTCAAAGAACAAAGGATCTAAGACAACGTGTCCTTCAACGTTATA
seq_Red      GACTTTATATTCAATCCTCATAGAACAAAGAATTTAAAGAGTTGTCCTTCAACGTTATA
*****
```

```
seq_K11      TGCACCTCTTTTCGGTGCTGGTATCATGGCTTTGATCGGTAAGTGGGTTTAA
seq_YP128    TGCACCTCTTTTCGGTGCTGGTATCATGGCTTTGATCGGTAAGTGGGCTTAA
seq_Red      TGCACCTCTTTTCGGTGCTGGTATCATGGCTTTGATCGGTAAGTGGGCTTAA
*****
```

CLUSTAL 2.1 multiple sequence alignment

- Amino Acid Change

Red MSNVTPPWKQWDPDTVTLTAE TPDDVWKTCVLQGVYFGENEYNGNLGARISSVFILFV
128 MSNVTPPWKQWDPSEVTLTDE TPDDVWKTCVLQGVYFGENEYNGNLGARISSVFILFV
K11 MSNVTPPWKQWDPSEVTLADK TPDDVWKTCVLQGVYFGENEYNGNLGARISSVFILFV
***** .*****

```

Red      STFLTMFPLISTKVKRLRIPLYAYLFAKYFGSGVIVATAFIHLMDPAYGAIGGNTCVGQT
128      STFLTMFPLISTKVKRLRIPLYAYLFAKYFGSGVIVATAFIHLMDPAYGAIGGTTCVGQT
K11      STFFTMTFPLISTKVKRLRIPLYVYLFAKYFGSGVIVATAFIHLMDPAYGAIGGTTCVGQT
          ***:*****.*****.*****

Red      GNWGLYSWCPAIMLTSLTFTFLTDLFSSVWVERKYGLSHDHTNDEIKDTVVNNAAVVSTE
128      GNWGIYSWCPAIMLTSLTFTFLTDLFSSVWVERKYGLSHDHTHDDIKDTVVNNAAVVSTE
K11      GNWGLYSWCPAIMLTSLTFTFLTDLFSSVWVERKYGLSHDHTHDEIKDTVVRNTAAVSSE
          ***:*****:*****.***.*

Red      NENENG TANGSHDTKNGIEYFEESDATSV DVVQSFQTQFYAFLILEFGVIFHSVMIGLNL
128      NENENATANGSHDTKNGIEYYEDSDATSM DVVQSFQAQFYAFLILEFGVIFHSVMIGLNL
K11      NDNENG TANGSHDTKNGVEYYEDSDATSM DVVQSFQAQFYAFLILEFGVIFHSVMIGLNL
          *:***.*****:***:*****:*****:*****

Red      GSTGEEFATLYPVLVFHQSFEGLGIGARLSAIEFPRSKRWWPWALCVAYGLTTPICVAIG
128      GSTGKEFATLYPVLVFHQSFEGLGIGARLSAIEFPRSKRWWPWALCVAYGLTTPICVAIG
K11      GSVGDEFSSLYPVLMFHQSFEGLGIGARLSAIEFPRSKRWWPWALCVAYGLTTPICVAIG
          **.*.***.*****:*****

Red      LGVRTRYVSGSYTALVISGVLD AISAGILLYTGLVELLARDFIFNPHRTKNLKELSFNVI
128      LGVRTQYVSGSYTALVVISGVLD AISAGILLYTGLVELLARDFIFNPQRTKDLRQLSFNVI
K11      LGVRTRYVSGSYTALVISGVLD AISAGILLYTGLVELLARDFIFNPQRTKDLRELSFNVI
          *****:*****:*****:*****:*****

Red      CTLFGAGIMALIGKWA
128      CTLFGAGIMALIGKWA
K11      CTLFGAGIMALIGKWV
          *****

```

dN/dS

Comparing sequences 1 and 2:

	Nondegenerate	Twofold	Fourfold
Transitions	13	8	7
Transversions	6	5	2

Comparing sequences 1 and 3:

	Nondegenerate	Twofold	Fourfold
Transitions	14	13	4
Transversions	10	6	3

Comparing sequences 2 and 3:

	Nondegenerate	Twofold	Fourfold
Transitions	8	10	9
Transversions	10	4	4

> output1

```

          seq_K11 seq_YSP128
seq_YSP128 0.6851964
seq_Red    0.6813422 0.4037520

```