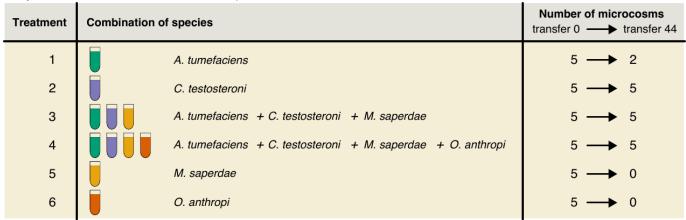
Sequencing analysis Evomicrocomm

Introduction

We analyze genomic sequencing data derived from Philippe Piccardis evolution experiment. In this experiment Agrobacterium tumefaciens, Comamonas testosteroni, Microbacterium saperdae and Ochrobactrum anthropi were evolved over 44 weeks ether in mono- or in co-culture. The experiment consisted of batch cultures for which Piccardi transferred cultures at week 11, 22, 33 and 44

Whether a strain is grown in mono- or co-culture depends on the strain composition of an experiment. We refer to those strain compositions as treatments.

Below you can see an overview of the different treatments and repetitions.



During the transfers at week 11, 22, 33 and 44 Piccardi took samples and isolated the DNA of the samples which was then sequenced with Illumina sequencing.

At timepoint 44 Piccardi additionally plated the samples. From those plates, colonies were picked and amplified. Afterwards, the DNA was extracted and sequenced with PacBio.

Results

PacBio

The PacBio data is derived from picked colonies. The long and accurate reads resulting from PacBio sequencing allow us to assemble the genomes of the cultured strains. Additionally we can use the PacBio data to get a better understanding of genome rearrangement caused by evolution.

To follow genome rearrangement we look at the length of the assemblies from the evolved strains compared to the wild-type. We also try to identify sequences in the genomes of the evolved strains that were lost or inserted.

We can indeed observe that some strains integrate DNA and the assembled genomes get longer. Other strains shrink their genomes.

The following data is presented from a treatment specific perspective.

This allows us to study whether we see an impact on evolution depending on strain composition.

Methods:

The PacBio data was assembled using canu. For finding out how many base pairs were deleted I aligned the corrected reads of the evolved strains to the wild-type genome. Then I summed all deleted bases from regions with no coverage or reads with deletions marked in their CIGAR string.

The code is available as a PyPI python package $\underline{\text{deletion_detection}}.$

For finding out how many base pairs were inserted, I aligned the assembly of the wild-type to the assembly of the evolved strains.

This may sounds confusing but works pretty well. I then again summed the bases with no coverage, only this time those are regions which are not present in the wild-type genome. Therefore, those sequences were likely inserted into the genome of the evolved strain.

Because I made this little trick I could use again the same tool <u>deletion_detection</u>

Because it's possible to submit a genbank file, deletion_detection annotates also the identified deletions and insertions.

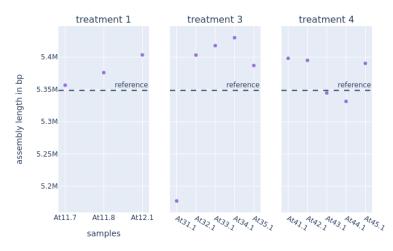
Lastly we look at how many contigs were generated by assembling the PacBio data. Even though this is very interesting, we need to be careful with interpretations for this data. While the assemblies are very accurate, thanks to the accurate and long PacBio reads, assemblers sometimes struggle to close contigs. Additionally assemblers are often trained with commonly used strains and work worse with less know strains like we study.

The complete sample processing is implemented as Snakemake workflow and can be found here pacbio workflow.

Agrobacterium tumefaciens

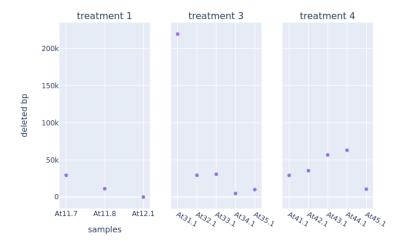
The plotted genome lengths below show that the genome size increased for most samples when compared to the assembly of the reference (dashed line).

Assembly length in Agrobacterium tumefaciens



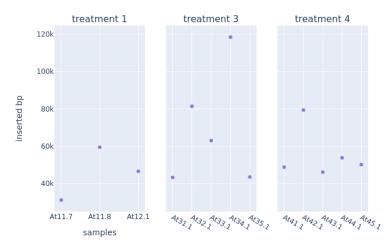
If we look at the sum of deleted bases we can see that the large deletion in At31.1 reflects in the assembled genome length.

Deleted bases in Agrobacterium tumefaciens



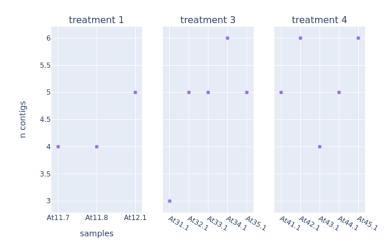
Looking at inserted bases we see that many samples have medium to large insertions. We can see for example that the large insertion in At34.1 again reflects in the assembled genome length.

Inserted bases in Agrobacterium tumefaciens



The wild-type assembly of Agrobacterium tumefaciens has four contigs. We can see below that most assemblies have more than four contigs which could be caused by the insertions. Sample At31.1 with the large deletion lost a plasmid.

N contigs in Agrobacterium tumefaciens



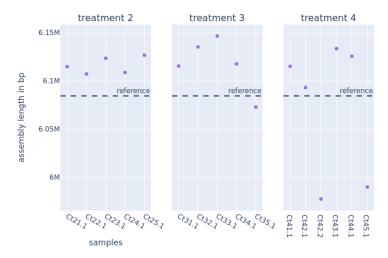
Since there is clearly rearrangement visible in the evolved genomes of Agrobacterium tumefaciens it might be interesting to look what products were affected deletions and insertions. This is unfortunately a pretty long list, because sometimes entire plasmids were deleted or taken up.

The list can be found in the <u>Appendix > Deleted and inserted products > Agrobacterium tumefaciens</u>.

Comamonas testosteroni

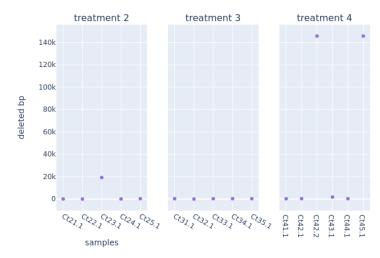
Except for three strains we can see again an increase in the genome size. Just as we observed for *Agrobacterium tumefaciens*, the variation in genome length can be explained by looking at the sum of deleted and inserted baes.

Assembly length in Comamonas testosteroni



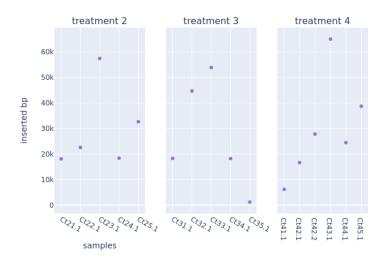
Only the samples Ct42.2 and Ct45.1 have large deletions.

Deleted bases in Comamonas testosteroni



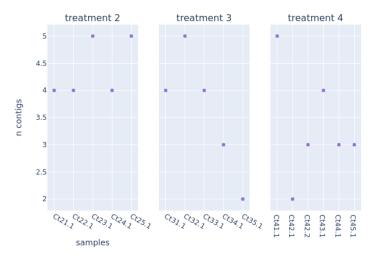
For almost all samples we observe inserted bases.

Inserted bases in Comamonas testosteroni



The assembly of the wild-type of Comamonas testosteroni has two contigs. Most of the samples assembled into more than two contigs which could be due to the insertions. Interestingly Sample Ct35.1 which has no deletions or insertions did in fact assemble into two contigs.

N contigs in Comamonas testosteroni

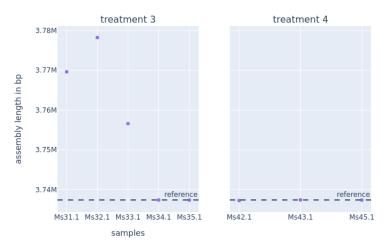


A list of deleted and inserted products can be found in the Appendix > Deleted and inserted products > Comamonas testosteroni]

Microbacterium saperdae

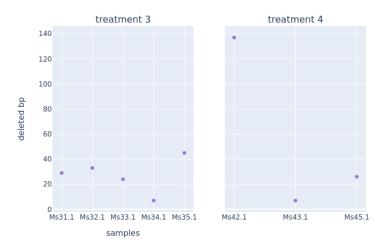
Microbacterium saperdae can not be grown in mono-culture which is why we only have treatment three and four. For once, the genome size of the majority of the assemblies remains similar compared to the wild-type assembly.

Assembly length in Microbacterium saperdae



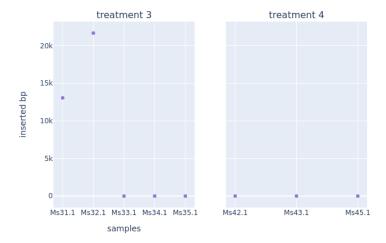
Also almost no deleted bases are visible for Microbacterium saperdae .

Deleted bases in Microbacterium saperdae



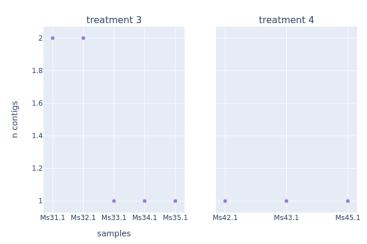
We can see how the insertions of Ms31.1 and Ms32.1 are causing the difference in the genome length.

Inserted bases in Microbacterium saperdae



The wild-type assembly of Microbacterium saperdae has one contig, which is also what we observe in the majority of the samples. Only the samples with the insertions assembled into two contigs, which could mean that those samples have taken up a plasmid.

N contigs in Microbacterium saperdae

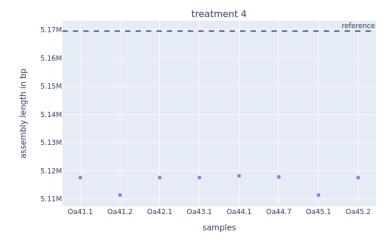


For *Microbacterium saperdae* no products were deleted. Inserted products:

product	treatment 3	treatment 4
NAD kinase	1	
DNA repair protein RecN	1	
Histidinol dehydrogenase	1	
NADP-specific glutamate dehydrogenase	1	
HTH-type transcriptional regulator KmtR	1	
Tyrosine recombinase XerC	1	
Capsule biosynthesis protein CapD proenzyme	1	
Tyrosine recombinase XerD	1	
Putrescine importer PuuP	1	

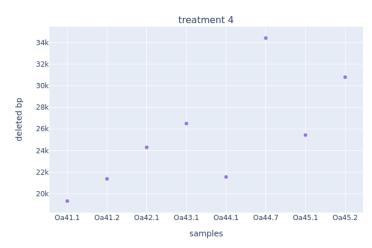
Ochrobactrum anthropi

Assembly length in Ochrobactrum anthropi



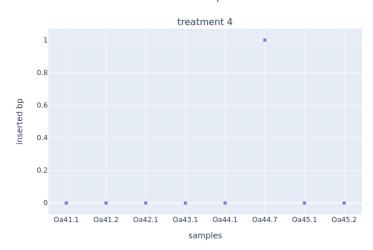
This is again very nicely in line with the observed sum of deleted basepairs.

Deleted bases in Ochrobactrum anthropi



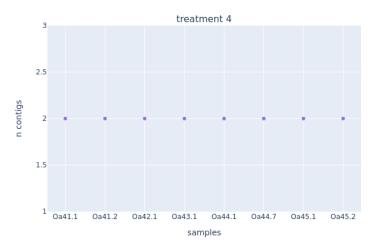
For once we can't observe any inserted bases.

Inserted bases in Ochrobactrum anthropi



The wild-type genome assembles into two contigs. Interestingly this is exactly the amount of contigs we observe for all samples in Ochrobactrum anthropi. This could be, because we don't

N contigs in Ochrobactrum anthropi



Deleted products observed in n microcosms:

product	treatment 4
30S ribosomal protein S20	8
DNA replication and repair protein RecF	8
Glucose-1-phosphate thymidylyltransferase	8
Trehalose-6-phosphate phosphatase	8
Inner membrane ABC transporter permease protein YejB	8
DNA polymerase III subunit beta	8
Trehalose-6-phosphate synthase	8
putative adenylyltransferase/sulfurtransferase MoeZ	8
dTDP-glucose 4,6-dehydratase 2	8
Chromosomal replication initiator protein DnaA	8
Glyoxylate/hydroxypyruvate reductase A	8
Inner membrane ABC transporter permease protein YejE	8
dTDP-4-dehydrorhamnose reductase	8
Glutathione import ATP-binding protein GsiA	8
dTDP-4-dehydrorhamnose 3,5-epimerase	8
Transcriptional activator FeaR	6
NAD/NADP-dependent betaine aldehyde dehydrogenase	5
Oligopeptide-binding protein AppA	6
Oxygen-dependent choline dehydrogenase	2
HTH-type transcriptional regulator Betl	2
3-deoxy-manno-octulosonate cytidylyltransferase	1
Cytochrome c-552	1
P-protein	1
Penicillin-binding protein 1F	1
Histidine protein kinase DivJ	1
Cysteine desulfuration protein SufE	1

Illumina

The isolated DNA from the samples of transfers 11, 22, 33, and 44 was sequenced with Illumina sequencing. Because the DNA was extracted and sequenced from samples sometimes consisting of multiple strains, we see uneven proportions of read mapping for samples derived form such co-cultures. This is caused by extraction "favoring" strains but also by sequencing itself. Illumina sequencing is based on PCR which amplifies fragments biased by their sequence. This caused issues for *Microbacterium saperdae* and *Comamonas testosteroni*. The majority of reads from samples of co-cultures mapped to *Agrobacterium tumefaciens*. In fact, at least 90 % of all reads mapped to *Agrobacterium tumefaciens* in every sample of treatment three and four.

Mapping proportion for all microcosms of timepoint 33 and 44 in treatment 4:

	T33.4.1	T33.4.2	T33.4.3.rep	T33.4.4	T33.4.5
ct	5.87%	4.21%	3.82%	5.33%	3.92%
at	90.14%	92.44%	94.93%	89.21%	94.98%
ms	0.08%	1.53%	0.73%	0.08%	0.60%
oa	5.68%	3.53%	2.18%	7.14%	2.15%

	T44.4.1	T44.4.2	T44.4.3	T44.4.4	T44.4.5.rep
ct	4.81%	2.40%	2.77%	3.79%	4.47%
at	93.74%	96.79%	96.09%	95.45%	94.04%
ms	0.09%	0.23%	0.36%	0.08%	0.56%

	T44.4.1	T44.4.1 T44.4.2 T44.4.3		T44.4.4	T44.4.5.rep
oa	2.92%	2.24%	2.63%	2.39%	2.66%

As you can see from those two examples, we only get a small fraction of reads not mapping to Agrobacterium tumefaciens. This causes some coverage issues for some strains sampled from co-culture. To get a better overview of the quality of the sequencing data when aligned to the individual strains I developed gc_bias. Using the report feature on the report branch, I created a PDF report for every alignment of every sample. You can find all reports here. Every report consists of mapping stats, a coverage histogram and a sequence bias visualization. We see that for Microbacterium saperdae, Comamonas testosteroni and Ochrobactrum anthropi we often have small regions with no coverage caused by unproportional strain composition of the extracted DNA and sequence bias. Luckily the samples were sequenced very deeply and despite the uneven mapping proportions we can still use the Illumina sequencing data for most samples. Based on the reports we will need to exclude some samples due to low coverage.

Methods:

The Illumina reads were trimmed and then aligned to the wild-type reference genomes of the strains present in the treatment. Afterwards, the alignment files were used to identify SNPs using snippy.

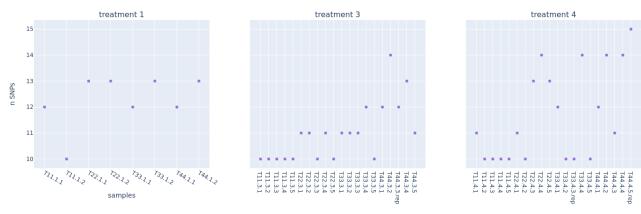
The complete sample processing is implemented as Snakemake workflow and can be found here.

We use the Illumina data to identify SNPs and study the affect of the mutations on the products. Looking at the different treatments we can try to make estimates on the impact of mono- vs. co-culture on evolution.

Agrobacterium tumefaciens

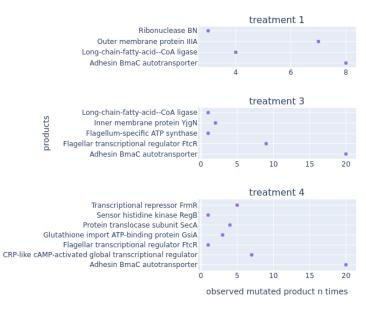
Below we compare the amount of SNPs over all time points and microcosms. The amount of SNPs seems to be independent of the treatment in Agrobacterium tumefaciens.

N SNPs in Agrobacterium tumefaciens



Below we see how many times a product was affected by mutations over all time points and microcosms. Different products were affected by mutations depending on the treatment.

Products affected by mutations in Agrobacterium tumefaciens



<u>bmaC</u> is mutated in almost every microcosm and time point. Apparently the translated protein is involved in adhesion to host cells.

For treatment three we can find products affected by mutations which are involved in flagella expression.

Treatment four shows one very interesting product affected by mutations. The protein is called cAMP-activated global transcriptional regulator CRP (uniprot). As the name tells, it's a global transcription regulator which complexes with cyclic AMP which activates DNA binding. For *E. coli* it's estimated that about 300 genes and about 200 operons are directly regulated by CRP. About half of the genome is regulated by CRP indirectly. CRP is nucleotide bindings and mutations could have a big impact on the ability to bind to specific nucleotide sequences. We can have a closer look at the mutations in *crp*:

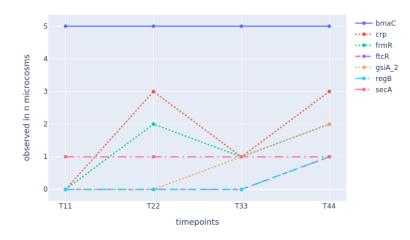
sample	CHROM	POS	TYPE	EFFECT	GENE
T22.4.3	AGTU001.0001.c01	2351459	del	frameshift_variant	crp
T22.4.4	AGTU001.0001.c01	2351324	del	frameshift_variant	crp
T22.4.5	AGTU001.0001.c01	2351347	snp	stop_gained	crp
T33.4.4	AGTU001.0001.c01	2351324	del	frameshift_variant	crp
T44.4.3	AGTU001.0001.c01	2351459	del	frameshift_variant	crp
T44.4.4	AGTU001.0001.c01	2351324	del	frameshift_variant	crp
T44.4.5.rep	AGTU001.0001.c01	2351347	snp	stop_gained	crp

We see that mutations evolved independently in three different microcosms. The mutations were ether deletions or point mutations. Deletions caused a frame shift in the amino acid sequence. Therefore, the protein is completely different and it's unlikely that it's able to recognize nucleotide sequences correctly. The point mutations caused the introduction of a stop codon in the amino acid sequence. The stop codon is introduced at amino acid position 22 of 151 which means that the translation is stopped pretty early. It's likely that the drastically shortened protein is not able to recognize nucleotides properly. We can conclude that the genome expression of *Agrobacterium tumefaciens* is likely heavily impacted by mutations in CRP but without transcriptional data it's difficult to tell which genes are up or down regulated. Checking the literature reveals that mutations in *crp* often lead to decreased transcription. I found this interesting paper about CRP here.

fmR codes for a regulatory protein which regulates the frmRAB operon which apparently is involved in formaldehyde degradation.

Below I plotted in how many microcosms a mutation came up during every time point for treatment four. The complete output of snippy can be found in the Appendix > SNPs > Agrobacterium tumefaciens

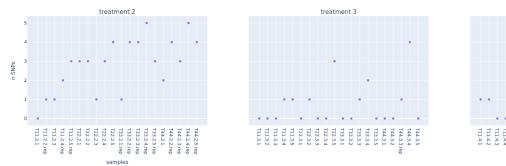
Mutated genes in Agrobacterium tumefaciens in treatment 4

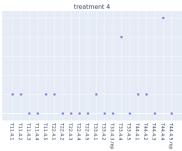


Comamonas testosteroni

Again we see a similar distributions of SNPs over all treatments.

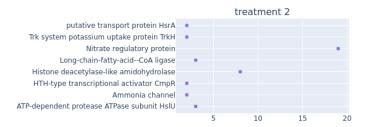
N SNPs in Comamonas testosteroni

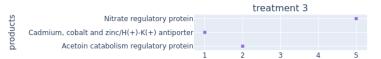


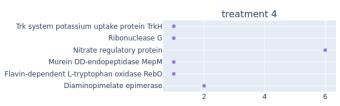


Looking at products affected by mutations we see that Comamonas testosteroni likely has adapted it's nitrate related pathways. For treatment three and four, most mutations only arouse in one sample.

Products affected by mutations in Comamonas testosteroni





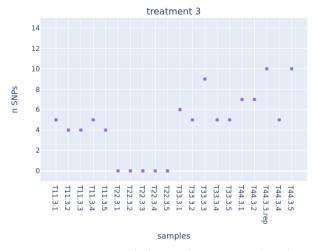


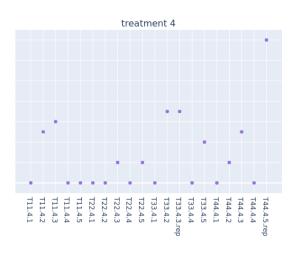
observed mutated product n times

The complete output of snippy can be found in the Appendix > SNPs > Comamonas testosteroni

Microbacterium saperdae

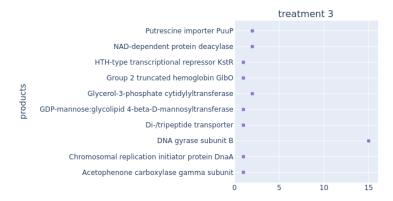
N SNPs in Microbacterium saperdae

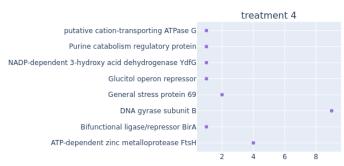




We can see that the DNA gyrase subunit B is mutated in many samples. This protein negatively supercoils DNA. Negative supercoiling favors strand separation and therfore DNA replication, transcription, recombination and repair. All mutations that we observe in the gene gyrB_2 coding for this protein are deletions causing a frame shift. The deleted nucleotide is at position 59 of 1236 which means that the protein is completely different and likely not able anymore to negatively supercoil DNA. A deffect DNA gyrase subunit B could cause that the transcription and

Products affected by mutations in Microbacterium saperdae



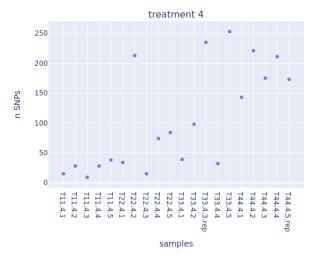


observed mutated product n times

Ochrobactrum anthropi

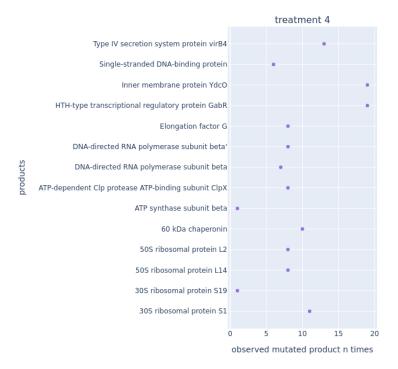
For Ochrobactrum anthropi we observe many mutations. It's unsure if Ochrobactrum anthropi accumulated more mutations than the other strains or if it has something to do with the low coverage that we observe for some samples.

N SNPs in Ochrobactrum anthropi



We see many changed ribosomal proteins. I checked the mutatios in the genes and they are all causing a synonymous variant and should not have an impact on the phenotype. The protein Single-stranded DNA-binding protein plays an important role in DNA replication. The mutations causing a missense variant could impact the growth rate. We see that a modified transcriptional regulatory protein GabR shows up in almost all samples. The underlying mutation was a deletion in all cases causing a frame shift. GabR is a transcriptional activator that regulates transcription for genes which are involved in biosynthesis of glutamate from GABA. It's again DNA binding meaning that the frame shift could have a big impact on it's functionality.

Products affected by mutations in Ochrobactrum anthropi



The complete output of snippy can be found in the Appendix > SNPs > Ochrobactrum anthropi

Appendix

Deleted and inserted products

Agrobacterium tumefaciens

Deleted products observed in n microcosms:

product	treatment 1	treatment 3	treatment 4
Sporulation initiation inhibitor protein Soj	1		
Modification methylase DpnIIB	2		
Conjugal transfer protein TraG	2		
Biofilm dispersion protein BdIA	2		
DNA-invertase hin	1		
putative metal-dependent hydrolase YjjV		1	
Putative undecaprenyl-diphosphatase YbjG		1	
60 kDa chaperonin		1	
Divalent metal cation transporter MntH		1	
Bicarbonate transporter BicA		1	
Disulfide bond formation protein D		1	
Cytochrome bo(3) ubiquinol oxidase subunit 3		1	
Protease HtpX		1	
Chromosome-partitioning protein Spo0J		1	
HTH-type transcriptional regulator ZntR		1	
D-alanyl-D-alanine carboxypeptidase DacF		1	
Transcriptional activator protein TraR		1	
Ribonuclease BN		1	
Serine/threonine-protein kinase HipA		1	
Thioredoxin 2		1	
Na(+)/H(+) antiporter NhaA		1	
Swarming motility regulation protein RssB		1	
Mobilization protein A		1	
Lipoprotein signal peptidase		1	
DNA replication and repair protein RecF		1	
putative helicase HelY		1	
Multicopper oxidase MmcO		1	
RNA polymerase-binding transcription factor DksA		1	
Quaternary ammonium compound-resistance protein SugE		1	
Cytochrome bo(3) ubiquinol oxidase subunit 1		1	
HTH-type transcriptional regulator DdrOP3		1	

product	treatment 1	treatment 3	treatment 4
Cytochrome bo(3) ubiquinol oxidase subunit 4		1	
Cyclopropane-fatty-acyl-phospholipid synthase		1	
Polyamine aminopropyltransferase		1	
Tyrosine recombinase XerD		1	
Diacylglycerol kinase		1	
DNA primase TraC		1	
Type IV secretion system protein virB9		1	
Cadmium, cobalt and zinc/H(+)-K(+) antiporter		1	
Type IV secretion system protein virB4		1	
Cytochrome bo(3) ubiquinol oxidase subunit 2		1	
Chromosome-partitioning protein ParB		1	
putative L,D-transpeptidase ErfK/SrfK		1	
putative oxidoreductase CzcO		1	
Sensor protein RstB		1	
ATP-dependent Clp protease ATP-binding subunit ClpC		1	
Acyl-homoserine-lactone synthase		1	
Lead, cadmium, zinc and mercury-transporting ATPase		1	
HTH-type transcriptional regulator HmrR		1	
Multiple antibiotic resistance protein MarR		1	
Endonuclease YncB		1	
ATP-dependent zinc metalloprotease FtsH 4		1	
Transcriptional repressor TraM		1	
Putative L-lactate dehydrogenase operon regulatory protein		1	
Glutathione-regulated potassium-efflux system protein KefC		1	
Spore protein SP21		1	
Disulfide bond formation protein C		1	
RecBCD enzyme subunit RecB		1	
Phosphoethanolamine transferase EptA		1	
2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase		1	
Tyrosine recombinase XerC		1	
Rhomboid protease GluP		1	
SC01 protein		1	
Putative serine protease HtrA		1	
putative L,D-transpeptidase YbiS		1	
7-cyano-7-deazaguanine synthase		1	
L-cystine import ATP-binding protein TcyN		1	
Thiamine-monophosphate kinase		1	
Allantoate amidohydrolase			2
Atrazine chlorohydrolase			2
Nickel-binding periplasmic protein			2
Oligopeptide transport system permease protein OppC			2
Acetophenone carboxylase delta subunit			2
Glutathione transport system permease protein GsiC			2
Glutathione import ATP-binding protein GsiA			2
Acetophenone carboxylase gamma subunit			2
Na(+)/H(+) antiporter subunit C1			1
Chemotaxis protein CheY			1
Chemotaxis protein CheA			1
Na(+)/H(+) antiporter subunit F			1
Chemotaxis protein methyltransferase			1
Na(+)/H(+) antiporter subunit A			1
Na(+)/H(+) antiporter subunit E1			1
Aerotaxis receptor			1
Na(+)/H(+) antiporter subunit G			1
Chemotaxis response regulator protein-glutamate methylesterase			1
Na(+)/H(+) antiporter subunit D			1
Chemoreceptor glutamine deamidase CheD			1
Flagellar M-ring protein			1
Type-1 restriction enzyme R protein			1
<u> </u>	i	1	

Inserted products observed in n microcosms:

product	treatment 1	treatment 3	treatment 4
putative cyclic di-GMP phosphodiesterase PdeC	1		

modicat	treatment 1	treatment 3	treatment 4
product putative cyclic di-GMP phosphodiesterase PdeB	3	treatments	treatment 4
Cold shock protein CspA	3		
	1		
Aerobic respiration control sensor protein ArcB	1		
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial			
Pertactin autotransporter	1		
Cystathionine beta-lyase MetC	2		
DNA-binding transcriptional activator DecR	1		
Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	1		
putative chromate transport protein	1		
Superoxide dismutase [Fe]	1		
O-succinylhomoserine sulfhydrylase	2		
Putrescinepyruvate aminotransferase	2		
Leucine-responsive regulatory protein	2		
Succinate-semialdehyde dehydrogenase [NADP(+)] GabD	2		
ATM1-type heavy metal exporter	1		
Purine ribonucleoside efflux pump Nepl	2		
Ubiquinone biosynthesis O-methyltransferase, mitochondrial	1		
Ectoine hydrolase	1		
Alanine dehydrogenase	1		
Taurinepyruvate aminotransferase	1		
L-threonine dehydratase catabolic TdcB	1		
L-methionine gamma-lyase		4	
High-affinity branched-chain amino acid transport system permease protein LivH		1	
Nucleoid occlusion protein		2	
D-3-phosphoglycerate dehydrogenase		1	
Histidinol-phosphate aminotransferase		1	
L-threonine ammonia-lyase		1	
DNA primase TraC		1	
Type IV secretion system protein virB4		2	
1,2-phenylacetyl-CoA epoxidase, subunit E		1	
Acyl-coenzyme A thioesterase Paal		1	
High-affinity branched-chain amino acid transport ATP-binding protein LivF		1	
Lipopolysaccharide export system ATP-binding protein LptB		1	
N-alpha-acetyl-L-2,4-diaminobutyric acid deacetylase		1	
Bifunctional protein PaaZ		1	
1,2-epoxyphenylacetyl-CoA isomerase		1	
Phenylacetate-coenzyme A ligase		1	
Phenylserine dehydratase		1	
Voltage-gated CIC-type chloride channel ClcB		1	
NAD/NADP-dependent betaine aldehyde dehydrogenase		1	
2-aminoadipate transaminase		1	
Divalent metal cation transporter MntH		1	
Cadmium-transporting ATPase		1	
Transcriptional activator protein TraR		1	
Zinc/cadmium/lead-transporting P-type ATPase		1	
Foldase protein PrsA		1	
putative phosphatidylethanolamine transferase Mcr-1		1	
ATP-dependent RecD-like DNA helicase		1	
Cadmium, cobalt and zinc/H(+)-K(+) antiporter		1	
Acyl-homoserine-lactone synthase		1	
Transcriptional repressor TraM		1	
N-ethylmaleimide reductase		1	
Phosphoethanolamine transferase EptA		1	
Tyrosine recombinase XerC		1	
putative L,D-transpeptidase YbiS		1	
Multidrug resistance ABC transporter ATP-binding/permease protein BmrA		1	
Glutarate-semialdehyde dehydrogenase		1	
Glutarate-Sernialderryde derrydrogenase			1
HTH-type transcriptional regulator NorG			
			1
HTH-type transcriptional regulator NorG			1
HTH-type transcriptional regulator NorG Adhesin BmaC autotransporter			
HTH-type transcriptional regulator NorG Adhesin BmaC autotransporter disulfide formation protein			1

product	treatment 1	treatment 3	treatment 4
DNA-invertase hin			1
L-alanine/L-glutamate racemase			1
putative multidrug resistance ABC transporter ATP-binding/permease protein YheH			1

Comamonas testosteroni

Deleted products observed in n microcosms:

Deleted products observed in n microcosms:			
product	treatment 2	treatment 3	treatment 4
Gentisate transporter	1		
Acyl-CoA dehydrogenase	1		
1,2-epoxyphenylacetyl-CoA isomerase	1		
2,3-dehydroadipyl-CoA hydratase	1		
Acetyl-CoA:oxalate CoA-transferase	1		
Hydroxyacylglutathione hydrolase	1		
4-hydroxybenzoate transporter PcaK	1		
Electron transfer flavoprotein subunit alpha	1		
Electron transfer flavoprotein subunit beta	1		
3-ketoacyl-CoA thiolase	1		
3-methylmercaptopropionyl-CoA dehydrogenase	1		
Molybdenum-pterin-binding protein MopA			2
putative manganese efflux pump MntP			2
Copper resistance protein C			2
Sensor kinase CusS			2
Copper resistance protein A			2
NADPH-dependent FMN reductase ArsH			2
Toxin coregulated pilus biosynthesis protein T			2
Arsenate reductase			2
Cation efflux system protein CusB			2
Lipoprotein signal peptidase			2
DNA replication and repair protein RecF			2
Glutaredoxin arsenate reductase			2
Copper resistance protein D			2
Transcriptional activator protein CopR			2
putative cadmium-transporting ATPase			2
Cobalt-zinc-cadmium resistance protein CzcC			2
Tyrosine recombinase XerD			2
Cobalt-zinc-cadmium resistance protein CzcB			2
putative amino-acid racemase			2
Outer membrane lipoprotein BfpB			2
Nickel and cobalt resistance protein CnrB			2
RNA polymerase-associated protein RapA			2
Ferrous iron permease EfeU			2
Sensor protein CzcS			2
Cation efflux system protein CusA			2
putative oxidoreductase CzcO			2
Undecaprenyl-diphosphatase			2
GMP synthase [glutamine-hydrolyzing]			2
Soluble lytic murein transglycosylase			2
Phosphoethanolamine transferase EptC			2
Arsenical pump membrane protein			2
Copper resistance protein B			2
Modification methylase BspRI			2
Mercuric resistance operon regulatory protein			2
Chromosome partitioning protein ParA			2
putative thiol:disulfide interchange protein DsbC			2
Phosphoethanolamine transferase EptA			2
			2
Transcriptional activator protein CzcR			
Cobalt-zinc-cadmium resistance protein CzcA			2
Silver exporting P-type ATPase			2

Inserted products observed in n microcosms:

product	treatment 2	treatment 3	treatment 4
2-hydroxymuconate tautomerase	5		
Putative glutamine amidotransferase YafJ	5		

product	treatment 2	treatment 3	treatment 4
HTH-type transcriptional activator CmpR	1		
Cadmium-transporting ATPase	1		
Potassium-transporting ATPase ATP-binding subunit	1		
Transcriptional activator protein CzcR	1		
Undecaprenyl-diphosphatase	1		
Cobalt-zinc-cadmium resistance protein CzcA	1		
Cobalt-zinc-cadmium resistance protein CzcC	1		
putative phosphatidylethanolamine transferase Mcr-1	1		
Protein UmuC	1		
Putative transposase InsK for insertion sequence element IS150	1		
LexA repressor	1		
Ribosomal small subunit pseudouridine synthase A	1		
PhenylalaninetRNA ligase beta subunit		1	
Type I secretion system membrane fusion protein PrsE		1	
Isocitrate dehydrogenase kinase/phosphatase		1	
Alpha-hemolysin translocation ATP-binding protein HlyB		1	
Carbonic anhydrase 2		1	
50S ribosomal protein L20		1	
Aspartokinase		1	
tRNA(IIe)-lysidine synthase		1	
Acetyl-CoA acetyltransferase		1	
PhenylalaninetRNA ligase alpha subunit		1	
Hydroxyacylglutathione hydrolase		1	
CysteinetRNA ligase		1	
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha		1	
Acyl-CoA dehydrogenase		1	
2-succinylbenzoateCoA ligase		1	
HTH-type transcriptional regulator CueR		1	
Integration host factor subunit alpha		1	
UDP-2,3-diacylglucosamine hydrolase		1	
ArgininetRNA ligase		1	
HTH-type transcriptional regulator DmIR		1	
Lipopolysaccharide export system protein LptA		1	
Sensory transduction protein regX3		1	
Adaptive-response sensory-kinase SasA		1	
Cell division protein FtsN		1	
Malate synthase G		1	
1,4-dihydroxy-2-naphthoyl-CoA synthase			1
Putative acyltransferase			1
Bicarbonate transporter BicA			1
Protein-glutamate methylesterase/protein-glutamine glutaminase			1
RNA polymerase-binding transcription factor DksA			1
(2S)-methylsuccinyl-CoA dehydrogenase			1
Acyl-CoA dehydrogenase, short-chain specific			2
Putative aminoacrylate hydrolase RutD			1
3-ketoacyl-CoA thiolase			1
Glutathione synthetase			1
Low affinity potassium transport system protein kup			1
Acryloyl-CoA reductase (NADH)			1
Inner membrane protein YdcO			1
	1	1	1

SNPs

Agrobacterium tumefaciens

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T11.1.1	c01	703340	snp	66/348	stop_gained c.196C>T p.Gln66*	ropA_2	Outer membrane protein IIIA
T11.1.1	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T11.1.2	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T11.3.1	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T11.3.2	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T11.3.3	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T11.3.4	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T11.3.5	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter

T11.4.1 c02 555455 snp 506/905 missense_variant c.15176>T p.Gly506Val secA Protein translocase su T11.4.1 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T11.4.2 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T11.4.3 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T11.4.4 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T11.4.5 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.1.1 c01 83654 snp 275/569 missense_variant c.824G>A p.Cys275Tyr fadD Long-chain-fatty-acid T22.1.1 c01 703240 snp 275/569 missense_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.1.2 c01	ransporter ransporter ransporter ransporter ransporter ransporter ransporter dCoA ligase tein IIIA ransporter dCoA ligase tein IIIA ransporter dCoA ligase tein IIIA
T11.4.2 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotre T11.4.3 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotre T11.4.4 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotre T11.4.5 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotre T22.1.1 c01 83654 snp 275/569 missense_variant c.824G>A p.Cys275Tyr fadD Long-chain-fatty-acid T22.1.1 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotre T22.1.2 c01 83654 snp 275/569 missense_variant c.824G>A p.Cys275Tyr fadD Long-chain-fatty-acid T22.1.2 c01 703263 ins 4/825 frameshift_variant c.12dupC p.Asp41fs ropA_2 Outer membrane prote T22.1.2 c01	ransporter ransporter ransporter ransporter ransporter ransporter dCoA ligase tein IIIA ransporter dCoA ligase tein IIIA ransporter
T11.4.3 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T11.4.4 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T11.4.5 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.1.1 c01 703340 snp 66/348 stop_gained c.196C>T p.Gln66* ropA_2 Outer membrane prote T22.1.1 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.1.2 c01 1936877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.1.2 c01 703263 ins 41/348 frameshift_variant c.120dupC p.Asp41fs ropA_2 Outer membrane prote T22.1.2 c01 2352216 ins 38/226 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.1 c01	ransporter ransporter dCoA ligase tein IIIA ransporter dCoA ligase tein IIIIA ransporter ransporter ransporter ransporter ransporter ranal regulator FtcR
T11.4.4 C02	ransporter dCoA ligase tein IIIA ransporter dCoA ligase tein IIIA ransporter dCoA ligase tein IIIA ransporter tein IIIA ransporter nal regulator FtcR
T11.4.5 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.1.1 c01 83654 snp 275/569 missense_variant c.824G>A p.Cys275Tyr fadD Long-chain-fatty-acid T22.1.1 c01 703340 snp 66/348 stop_gained c.196C>T p.Gln66* ropA_2 Outer membrane prote T22.1.1 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.1.2 c01 83654 snp 275/569 missense_variant c.824G>A p.Cys275Tyr fadD Long-chain-fatty-acid T22.1.2 c01 703263 ins 41/348 frameshift_variant c.120dupC p.Asp41fs ropA_2 Outer membrane prote T22.1.2 c01 2352216 ins 38/266 frameshift_variant c.112dupT p.Tyr38fs rbn_3 Ribonuclease BN T22.1.2 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.1 c02	ransporter dCoA ligase tein IIIA ransporter dCoA ligase tein IIIA ransporter dCoA ligase tein IIIA ransporter ransporter nal regulator FtcR
T22.1.1 c01 83654 snp 275/569 missense_variant c.824G>A p.Cys275Tyr fadD Long-chain-fatty-acid T22.1.1 c01 703340 snp 66/348 stop_gained c.196C>T p.Gln66* ropA_2 Outer membrane prote T22.1.1 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.1.2 c01 83654 snp 275/569 missense_variant c.824G>A p.Cys275Tyr fadD Long-chain-fatty-acid T22.1.2 c01 703263 ins 41/348 frameshift_variant c.120dupC p.Asp41fs ropA_2 Outer membrane prote T22.1.2 c01 2352216 ins 38/226 frameshift_variant c.12dupT p.Tyr38fs rbn_3 Ribonuclease BN T22.1.2 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.1 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT ftcR Flagellar transcription T22.3.2	dCoA ligase tein IIIA ransporter dCoA ligase tein IIIA ransporter nal regulator FtcR ransporter nal regulator FtcR
T22.1.1 c01 703340 snp 66/348 stop_gained c.196C>T p.Gln66* ropA_2 Outer membrane prote T22.1.1 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.1.2 c01 83654 snp 275/569 missense_variant c.824G>A p.Cys275Tyr fadD Long-chain-fatty-acid T22.1.2 c01 703263 ins 41/348 frameshift_variant c.12dupC p.Asp41fs ropA_2 Outer membrane prote T22.1.2 c01 2352216 ins 38/226 frameshift_variant c.112dupT p.Tyr38fs rbn_3 Ribonuclease BN T22.1.2 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.1 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT ftcR Flagellar transcription T22.3.2 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT ftcR Flagellar transcription	tein IIIA ransporter dCoA ligase tein IIIA ransporter nal regulator FtcR ransporter nal regulator FtcR
T22.1.1 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.1.2 c01 83654 snp 275/569 missense_variant c.824G>A p.Cys275Tyr fadD Long-chain-fatty-acid T22.1.2 c01 703263 ins 41/348 frameshift_variant c.12dupC p.Asp41fs ropA_2 Outer membrane prote T22.1.2 c01 2352216 ins 38/226 frameshift_variant c.112dupT p.Tyr38fs rbn_3 Ribonuclease BN T22.1.2 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.1 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT ftcR Flagellar transcriptions T22.3.2 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT ftcR Flagellar transcriptions T22.3.2 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra	ransporter dCoA ligase tein IIIA ransporter nal regulator FtcR ransporter nal regulator FtcR
T22.1.2 c01 83654 snp 275/569 missense_variant c.824G>A p.Cys275Tyr fadD Long-chain-fatty-acid T22.1.2 c01 703263 ins 41/348 frameshift_variant c.120dupC p.Asp41fs ropA_2 Outer membrane prote T22.1.2 c01 2352216 ins 38/226 frameshift_variant c.112dupT p.Tyr38fs rbn_3 Ribonuclease BN T22.1.2 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.1 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del ftcR Flagellar transcriptions T22.3.2 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del ftcR Flagellar transcriptions T22.3.2 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.3 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin Bma	dCoA ligase tein IIIA ransporter nal regulator FtcR ransporter nal regulator FtcR
T22.1.2 c01 703263 ins 41/348 frameshift_variant c.120dupC p.Asp41fs ropA_2 Outer membrane prote T22.1.2 c01 2352216 ins 38/226 frameshift_variant c.112dupT p.Tyr38fs rbn_3 Ribonuclease BN T22.1.2 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.1 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del ftcR Flagellar transcriptions T22.3.2 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del ftcR Flagellar transcriptions T22.3.2 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.3 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.4 c01 238024 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC a	ransporter ransporter ransporter ransporter ransporter ransporter nal regulator FtcR
T22.1.2 c01 2352216 ins 38/226 frameshift_variant c.112dupT p.Tyr38fs rbn_3 Ribonuclease BN T22.1.2 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.1 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del ftcR Flagellar transcriptions T22.3.2 c01 238024 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.2 c01 238024 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.3 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.3 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.4 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del ftcR Flagellar transcription	ransporter nal regulator FtcR ransporter nal regulator FtcR
T22.1.2 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.1 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del ftcR Flagellar transcriptions T22.3.1 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.2 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del ftcR Flagellar transcriptions T22.3.2 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.3 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.4 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del ftcR Flagellar transcriptions	ransporter nal regulator FtcR
T22.3.1 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del ftcR Flagellar transcription. Flagellar transcripti	ransporter nal regulator FtcR
T22.3.1	ransporter nal regulator FtcR
T22.3.2 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del ftcR Flagellar transcription. T22.3.2 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.3 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.4 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del ftcR Flagellar transcriptions	nal regulator FtcR
T22.3.2 c01 238024 del 201/223 p.Arg202_Leu205del ftck Flagellar transcription. T22.3.2 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.3 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.4 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del ftcR Flagellar transcriptions	
T22.3.3 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra T22.3.4 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT ftcR Flagellar transcriptions	ansporter
T22.3.4 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del ftcR Flagellar transcriptions	
122.3.4 C01 238024 del 201/223 p.Arg202_Leu205del ftcR Flagellar transcription	ransporter
	nal regulator FtcR
T22.3.4 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra	ansporter
T22.3.5 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra	ransporter
T22.4.1 c02 555455 snp 506/905 missense_variant c.1517G>T p.Gly506Val secA Protein translocase su	ubunit SecA
T22.4.1 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra	ansporter
T22.4.2 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra	ransporter
T22.4.3 c01 2351459 del 60/151 frameshift_variant c.178delG p.Val60fs crp CRP-like cAMP-activa transcriptional regulat	-
T22.4.3 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra	ansporter
T22.4.4 c01 2351324 del 17/151 frameshift_variant c.49delT p.Ser17fs crp CRP-like cAMP-activa transcriptional regulat	-
T22.4.4 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra	ansporter
T22.4.4 p02 181352 snp 71/93 stop_gained c.211C>T p.Gln71* frmR Transcriptional repres	ssor FrmR
T22.4.5 c01 2351347 snp 22/151 stop_gained c.65C>A p.Ser22* crp CRP-like cAMP-activa transcriptional regulat	-
T22.4.5 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra	ansporter
T22.4.5 p02 181297 snp 89/93 missense_variant c.266G>C p.Arg89Pro frmR Transcriptional repres	ssor FrmR
T33.1.1 c01 703340 snp 66/348 stop_gained c.196C>T p.Gln66* ropA_2 Outer membrane prote	tein IIIA
T33.1.1 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra	ransporter
T33.1.2 c01 83654 snp 275/569 missense_variant c.824G>A p.Cys275Tyr fadD Long-chain-fatty-acid	dCoA ligase
T33.1.2 c01 703263 ins 41/348 frameshift_variant c.120dupC p.Asp41fs ropA_2 Outer membrane prote	tein IIIA
T33.1.2 c01 2352216 ins 38/226 frameshift_variant c.112dupT p.Tyr38fs rbn_3 Ribonuclease BN	
T33.1.2 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra	ansporter
T33.3.1 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT ftcR Flagellar transcription: p.Arg202_Leu205del	
T33.3.1 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra	ansporter
T33.3.2 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT ftcR Flagellar transcription: p.Arg202_Leu205del	nal regulator FtcR
T33.3.2 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra	ransporter
T33.3.3 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra	ransporter
T33.3.4 c01 238024 del 201/223 disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT ftcR Flagellar transcription: p.Arg202_Leu205del	nal regulator FtcR
T33.3.4 c01 2863371 snp 326/356 synonymous_variant c.978C>A p.Gly326Gly yjgN Inner membrane prote	
T33.3.4 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra	
T33.3.5 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra	-
	TP-binding protein GsiA
T33.4.1 c02 555455 snp 506/905 missense_variant c.1517G>T p.Gly506Val secA Protein translocase su	
T33.4.1 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra	
T33.4.2 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra	
T33.4.3.rep c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra	
T33.4.4 c01 2351324 del 17/151 frameshift_variant c.49delT p.Ser17fs crp CRP-like cAMP-activa transcriptional regulat	itor
T33.4.4 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra	
T33.4.4 p02 181352 snp 71/93 stop_gained c.211C>T p.Gln71* frmR Transcriptional repres	
T33.4.5 c02 1946877 del 4/825 frameshift_variant c.10delG p.Val4fs bmaC Adhesin BmaC autotra	ransporter

sample	СНКОМ	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T44.1.1	c01	703340	snp	66/348	stop_gained c.196C>T p.Gln66*	ropA_2	Outer membrane protein IIIA
T44.1.1	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T44.1.2	c01	83654	snp	275/569	missense_variant c.824G>A p.Cys275Tyr	fadD	Long-chain-fatty-acidCoA ligase
T44.1.2	c01	703263	ins	41/348	frameshift_variant c.120dupC p.Asp41fs	ropA_2	Outer membrane protein IIIA
T44.1.2	c01	2352216	ins	38/226	frameshift_variant c.112dupT p.Tyr38fs	rbn_3	Ribonuclease BN
T44.1.2	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T44.3.1	c01	238024	del	201/223	disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del	ftcR	Flagellar transcriptional regulator FtcR
T44.3.1	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T44.3.2	c01	238024	del	201/223	disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del	ftcR	Flagellar transcriptional regulator FtcR
T44.3.2	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T44.3.3.rep	c01	222268	snp	348/468	missense_variant c.1043G>A p.Gly348Asp	flil	Flagellum-specific ATP synthase
T44.3.3.rep	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T44.3.4	c01	238024	del	201/223	disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del	ftcR	Flagellar transcriptional regulator FtcR
T44.3.4	c01	2863371	snp	326/356	synonymous_variant c.978C>A p.Gly326Gly	yjgN	Inner membrane protein YjgN
T44.3.4	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T44.3.5	c01	83654	snp	275/569	missense_variant c.824G>A p.Cys275Tyr	fadD	Long-chain-fatty-acidCoA ligase
T44.3.5	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T44.4.1	c01	2361041	snp	440/630	stop_gained c.1320T>G p.Tyr440*	gsiA_2	Glutathione import ATP-binding protein GsiA
T44.4.1	c02	555455	snp	506/905	missense_variant c.1517G>T p.Gly506Val	secA	Protein translocase subunit SecA
T44.4.1	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T44.4.2	c01	238024	del	201/223	disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del	ftcR	Flagellar transcriptional regulator FtcR
T44.4.2	c01	2359915	del	68/630	conservative_inframe_deletion c.202_213delAACGGCCGCGTG p.Asn68_Val71del	gsiA_2	Glutathione import ATP-binding protein GsiA
T44.4.2	c01	2695602	snp	240/443	missense_variant c.719T>G p.Val240Gly	regB	Sensor histidine kinase RegB
T44.4.2	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T44.4.3	c01	2351459	del	60/151	frameshift_variant c.178delG p.Val60fs	crp	CRP-like cAMP-activated global transcriptional regulator
T44.4.3	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T44.4.4	c01	2351324	del	17/151	frameshift_variant c.49delT p.Ser17fs	crp	CRP-like cAMP-activated global transcriptional regulator
T44.4.4	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T44.4.4	p02	181352	snp	71/93	stop_gained c.211C>T p.Gln71*	frmR	Transcriptional repressor FrmR
T44.4.5.rep	c01	2351347	snp	22/151	stop_gained c.65C>A p.Ser22*	crp	CRP-like cAMP-activated global transcriptional regulator
T44.4.5.rep	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T44.4.5.rep	p02	181297	snp	89/93	missense_variant c.266G>C p.Arg89Pro	frmR	Transcriptional repressor FrmR

Comamonas testosteroni

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T11.2.2.rep	c01	5466897	snp	29/424	missense_variant c.86T>G p.Val29Gly	nasR	Nitrate regulatory protein
T11.2.3	c01	5466897	snp	29/424	missense_variant c.86T>G p.Val29Gly	nasR	Nitrate regulatory protein
T11.2.4.rep	c01	5466897	snp	29/424	missense_variant c.86T>G p.Val29Gly	nasR	Nitrate regulatory protein
T11.2.5.rep	c01	5466537	snp	149/424	missense_variant c.446A>C p.Asp149Ala	nasR	Nitrate regulatory protein
T11.3.5	c01	1863692	snp	258/389	synonymous_variant c.772C>T p.Leu258Leu	acoR_2	Acetoin catabolism regulatory protein
T11.4.1	c01	5466493	mnp	163/424	missense_variant c.489_490delGCinsAA p.MetGln163lleLys	nasR	Nitrate regulatory protein
T22.2.1	c01	1957165	snp	241/319	missense_variant c.722T>C p.Leu241Pro	hdaH	Histone deacetylase-like amidohydrolase
T22.2.1	c01	5466897	snp	29/424	missense_variant c.86T>G p.Val29Gly	nasR	Nitrate regulatory protein
T22.2.2	c01	1048937	snp	129/439	synonymous_variant c.387G>A p.Glu129Glu	hslU	ATP-dependent protease ATPase subunit HsIU
T22.2.2	c01	1956772	ins	112/319	frameshift_variant c.334dupG p.Ala112fs	hdaH	Histone deacetylase-like amidohydrolase
T22.2.2	c01	5466897	snp	29/424	missense_variant c.86T>G p.Val29Gly	nasR	Nitrate regulatory protein
T22.2.3	c01	5466897	snp	29/424	missense_variant c.86T>G p.Val29Gly	nasR	Nitrate regulatory protein
T22.2.4	c01	1957165	snp	241/319	missense_variant c.722T>C p.Leu241Pro	hdaH	Histone deacetylase-like amidohydrolase
T22.2.4	c01	5466897	snp	29/424	missense_variant c.86T>G p.Val29Gly	nasR	Nitrate regulatory protein
T22.2.5	c01	5466537	snp	149/424	missense_variant c.446A>C p.Asp149Ala	nasR	Nitrate regulatory protein
T22.2.5	c01	5690520	snp	459/558	missense_variant c.1376G>A p.Arg459His	fadD_4	Long-chain-fatty-acidCoA ligase
T22.3.5	c01	1220563	snp	63/336	missense_variant c.187G>C p.Gly63Arg	czcD	Cadmium, cobalt and zinc/H(+)-K(+) antiporter
T22.3.5	c01	1863692	snp	258/389	synonymous_variant c.772C>T p.Leu258Leu	acoR_2	Acetoin catabolism regulatory protein
T22.3.5	c01	5466534	snp	150/424	missense_variant c.449C>G p.Pro150Arg	nasR	Nitrate regulatory protein
T22.4.1	c01	5466493	mnp	163/424	missense_variant c.489_490delGCinsAA p.MetGln163lleLys	nasR	Nitrate regulatory protein
T33.2.1.rep	c01	5466695	snp	96/424	missense_variant c.288T>G p.Asn96Lys	nasR	Nitrate regulatory protein
T33.2.2.rep	c01	1048937	snp	129/439	synonymous_variant c.387G>A p.Glu129Glu	hslU	ATP-dependent protease ATPase subunit HsIU

sample	СНКОМ	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T33.2.2.rep	c01	5466897	snp	29/424	missense_variant c.86T>G p.Val29Gly	nasR	Nitrate regulatory protein
T33.2.2.rep	c01	5538482	snp	13/474	missense_variant c.37C>A p.His13Asn	hsrA_2	putative transport protein HsrA
T33.2.3.rep	c01	1957328	snp	295/319	missense_variant c.885C>A p.Ser295Arg	hdaH	Histone deacetylase-like amidohydrolase
T33.2.3.rep	c01	5466897	snp	29/424	missense_variant c.86T>G p.Val29Gly	nasR	Nitrate regulatory protein
T33.2.3.rep	c01	5643748	snp	378/488	missense_variant c.1132C>G p.His378Asp	trkH	Trk system potassium uptake protein TrkH
T33.2.4.rep	c01	215827	snp	316/450	missense_variant c.946A>C p.Thr316Pro	amtB_2	Ammonia channel
T33.2.4.rep	c01	1957165	snp	241/319	missense_variant c.722T>C p.Leu241Pro	hdaH	Histone deacetylase-like amidohydrolase
T33.2.4.rep	c01	1982399	snp	294/311	missense_variant c.881T>A p.Val294Asp	cmpR_4	HTH-type transcriptional activator CmpR
T33.2.4.rep	c01	5466897	snp	29/424	missense_variant c.86T>G p.Val29Gly	nasR	Nitrate regulatory protein
T33.2.5.rep	c01	5466537	snp	149/424	missense_variant c.446A>C p.Asp149Ala	nasR	Nitrate regulatory protein
T33.2.5.rep	c01	5690520	snp	459/558	missense_variant c.1376G>A p.Arg459His	fadD_4	Long-chain-fatty-acidCoA ligase
T33.3.3	c01	5466905	snp	26/424	missense_variant c.78C>A p.Ser26Arg	nasR	Nitrate regulatory protein
T33.3.4	c01	5466552	snp	144/424	missense_variant c.431C>T p.Ala144Val	nasR	Nitrate regulatory protein
T33.4.1	c01	5466493	mnp	163/424	missense_variant c.489_490delGCinsAA p.MetGln163lleLys	nasR	Nitrate regulatory protein
T33.4.4	c01	1041598	snp	198/296	missense_variant c.593A>C p.Asn198Thr	dapF	Diaminopimelate epimerase
T33.4.4	c01	2625799	snp	3/495	missense_variant c.9A>C p.Gln3His	rng	Ribonuclease G
T33.4.4	c01	5466897	snp	29/424	missense_variant c.86T>G p.Val29Gly	nasR	Nitrate regulatory protein
T44.2.1	c01	5466695	snp	96/424	missense_variant c.288T>G p.Asn96Lys	nasR	Nitrate regulatory protein
T44.2.2.rep	c01	1048937	snp	129/439	synonymous_variant c.387G>A p.Glu129Glu	hslU	ATP-dependent protease ATPase subunit HsIU
T44.2.2.rep	c01	1956772	ins	112/319	frameshift_variant c.334dupG p.Ala112fs	hdaH	Histone deacetylase-like amidohydrolase
T44.2.2.rep	c01	5466897	snp	29/424	missense_variant c.86T>G p.Val29Gly	nasR	Nitrate regulatory protein
T44.2.2.rep	c01	5538482	snp	13/474	missense_variant c.37C>A p.His13Asn	hsrA_2	putative transport protein HsrA
T44.2.3.rep	c01	1957328	snp	295/319	missense_variant c.885C>A p.Ser295Arg	hdaH	Histone deacetylase-like amidohydrolase
T44.2.3.rep	c01	5466897	snp	29/424	missense_variant c.86T>G p.Val29Gly	nasR	Nitrate regulatory protein
T44.2.3.rep	c01	5643748	snp	378/488	missense_variant c.1132C>G p.His378Asp	trkH	Trk system potassium uptake protein TrkH
T44.2.4.rep	c01	215827	snp	316/450	missense_variant c.946A>C p.Thr316Pro	amtB_2	Ammonia channel
T44.2.4.rep	c01	1957165	snp	241/319	missense_variant c.722T>C p.Leu241Pro	hdaH	Histone deacetylase-like amidohydrolase
T44.2.4.rep	c01	1982399	snp	294/311	missense_variant c.881T>A p.Val294Asp	cmpR_4	HTH-type transcriptional activator CmpR
T44.2.4.rep	c01	5466897	snp	29/424	missense_variant c.86T>G p.Val29Gly	nasR	Nitrate regulatory protein
T44.2.5.rep	c01	5466537	snp	149/424	missense_variant c.446A>C p.Asp149Ala	nasR	Nitrate regulatory protein
T44.2.5.rep	c01	5690520	snp	459/558	missense_variant c.1376G>A p.Arg459His	fadD_4	Long-chain-fatty-acidCoA ligase
T44.3.3.rep	c01	5466905	snp	26/424	missense_variant c.78C>A p.Ser26Arg	nasR	Nitrate regulatory protein
T44.3.4	c01	5466552	snp	144/424	missense_variant c.431C>T p.Ala144Val	nasR	Nitrate regulatory protein
T44.4.1	c01	5466493	mnp	163/424	missense_variant c.489_490delGCinsAA p.MetGln163lleLys	nasR	Nitrate regulatory protein
T44.4.2	c01	785206	snp	272/531	missense_variant c.815A>C p.Glu272Ala	rebO	Flavin-dependent L-tryptophan oxidase RebO
T44.4.4	c01	1041598	snp	198/296	missense_variant c.593A>C p.Asn198Thr	dapF	Diaminopimelate epimerase
T44.4.4	c01	5466897	snp	29/424	missense_variant c.86T>G p.Val29Gly	nasR	Nitrate regulatory protein
T44.4.4	c01	5529374	snp	357/452	missense_variant c.1069A>C p.Thr357Pro	mepM_2	Murein DD-endopeptidase MepM
T44.4.4	c01	5644708	del	57/488	frameshift_variant c.171delG p.Leu58fs	trkH	Trk system potassium uptake protein TrkH

Microbacterium saperdae

sample	СНКОМ	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T11.3.1	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T11.3.1	c01	1739320	del	37/411	frameshift_variant c.110_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T11.3.2	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T11.3.2	c01	1739320	del	37/411	frameshift_variant c.110_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T11.3.3	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T11.3.3	c01	1739320	del	37/411	frameshift_variant c.110_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T11.3.4	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T11.3.4	c01	1739320	del	37/411	frameshift_variant c.110_111deICC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T11.3.5	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T11.3.5	c01	1739320	del	37/411	frameshift_variant c.110_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T11.4.2	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T11.4.2	c01	1739320	del	37/411	frameshift_variant c.110_111deICC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T11.4.3	c01	699272	snp	520/666	missense_variant c.1559C>T p.Thr520lle	ftsH_1	ATP-dependent zinc metalloprotease FtsH
T11.4.3	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T11.4.3	c01	1739320	del	37/411	frameshift_variant c.110_111deICC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T22.4.3	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T22.4.3	c01	1739320	del	37/411	frameshift_variant c.110_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T22.4.5	c01	1739320	del	37/411	frameshift_variant c.110_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T33.3.1	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T33.3.1	c01	1739320	del	37/411	frameshift_variant c.110_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T33.3.1	c01	2588030	del	176/475	frameshift_variant c.526delA p.lle176fs	puuP_3	Putrescine importer PuuP
T33.3.1	c01	2638764	snp	37/200	missense_variant c.109T>C p.Ser37Pro	kstR	HTH-type transcriptional repressor
T33.3.2	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	NA gyrase subunit B
T33.3.2	c01	1739320	del	37/411	frameshift_variant c.110_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
100.0.2	001	1733320	uei	37/411	Trainesini Cyanant C.110_111de100 p.1103713	gyrb_z	Glycerol-3-phosphate
T33.3.3	c01	657367	snp	55/151	missense_variant c.163A>C p.Thr55Pro	tagD	cytidylyltransferase
T33.3.3	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T33.3.3	c01	1739320	del	37/411	frameshift_variant c.110_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T33.3.3	c01	1913025	snp	274/279	missense_variant c.821T>C p.Leu274Pro	cobB	NAD-dependent protein deacylase
T33.3.4	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T33.3.4	c01	1739320	del	37/411	frameshift_variant c.110_111deICC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T33.3.5	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T33.3.5	c01	1739320	del	37/411	frameshift_variant c.110_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T33.4.2	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T33.4.2	c01	1739320	del	37/411	frameshift_variant c.110_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T33.4.2	c01	3615511	snp	145/328	missense_variant c.435A>C p.Glu145Asp	yhdN_3	General stress protein 69
T33.4.3.rep	c01	699272	snp	520/666	missense_variant c.1559C>T p.Thr520lle	ftsH_1	ATP-dependent zinc metalloprotease FtsH
T33.4.3.rep	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T33.4.3.rep	c01	1739320	del	37/411	frameshift_variant c.110_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T33.4.3.rep	c01	3100708	del	30/219	frameshift_variant c.90_91delGC p.Leu31fs	ydfG	NADP-dependent 3-hydroxy acid dehydrogenase YdfG
T33.4.5	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T33.4.5	c01	1739320	del	37/411	frameshift_variant c.110_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T44.3.1	c01	1088	snp	363/463	missense_variant c.1088C>A p.Thr363Lys	dnaA	Chromosomal replication initiator
		.000	оп.р		microsico_tanant chocce. At primicros_jo	ana,	protein DnaA
T44.3.1	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T44.3.1	c01	1739320	del	37/411	frameshift_variant c.110_111deICC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T44.3.2	c01	660917	snp	366/665	missense_variant c.1096T>C p.Ser366Pro	guml	GDP-mannose:glycolipid 4-beta-D- mannosyltransferase
T44.3.2	c01	826998	snp	305/515	missense_variant c.913T>C p.Phe305Leu	apc3_2	Acetophenone carboxylase gamma subunit
T44.3.2	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T44.3.2	c01	1739320	del	37/411	frameshift_variant c.110_111deICC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T44.3.2	c01	3382652	del	88/516	conservative_inframe_deletion c.262_285delCCCGAGGCGGTCGCGGGCGCATC p.Pro88_lle95del	dtpT	Di-/tripeptide transporter
T44.3.3.rep	c01	657367	snp	55/151	missense_variant c.163A>C p.Thr55Pro	tagD	Glycerol-3-phosphate cytidylyltransferase
T44.3.3.rep	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T44.3.3.rep	c01	1739320	del	37/411	frameshift_variant c.110_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T44.3.3.rep	c01	1913025	snp	274/279	missense_variant c.821T>C p.Leu274Pro	cobB	NAD-dependent protein deacylase
T44.3.3.rep	c01	1940379	snp	116/149	missense_variant c.347A>C p.Tyr116Ser	glbO	Group 2 truncated hemoglobin GlbO
T44.3.4	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T44.3.4	c01	1739320	del	37/411	frameshift_variant c.110_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T44.3.5	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T44.3.5	c01	1739320	del	37/411	frameshift_variant c.110_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T44.3.5	c01	2587322	snp	412/475	missense_variant c.1235T>G p.Met412Arg	puuP_3	Putrescine importer PuuP
T44.4.2	c01	3615511	snp	145/328	missense_variant c.435A>C p.Glu145Asp	yhdN_3	General stress protein 69
T44.4.3	c01	699272	snp	520/666	missense_variant c.1559C>T p.Thr520lle	ftsH_1	ATP-dependent zinc metalloprotease
T44.4.3	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	PtsH DNA gyrase subunit B
T44.4.3	c01	1739271	del	37/411	frameshift_variant c.130_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T44.4.5.rep	c01	698447	snp	245/666	missense_variant c.rto_rtruelcc p.Pros7rs	ftsH_1	ATP-dependent zinc metalloprotease
T44.4.5.rep	c01	804045	snp	222/651	synonymous_variant c.666C>T p.Gly222Gly	ctpG_2	PtsH putative cation-transporting ATPase G
T44.4.5.rep	c01	804921	snp	514/651	synonymous_variant c.1542A>C p.Arg514Arg	ctpG_2	putative cation-transporting ATPase G
T44.4.5.rep	c01	804978	snp	533/651	synonymous_variant c.1599A>G p.Gly533Gly	ctpG_2	putative cation-transporting ATPase G
T44.4.5.rep	c01	808055	del	31/324	frameshift_variant c.91_95delCTCGG p.Leu31fs	birA_1	Bifunctional ligase/repressor BirA
T44.4.5.rep	c01	831593	snp	237/504	missense_variant c.709A>G p.Met237Val	pucR_1	Purine catabolism regulatory protein
T44.4.5.rep	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T44.4.5.rep	c01	1739320	del	37/411	frameshift_variant c.110_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T44.4.5.rep	c01	3643534	snp	91/249	missense_variant c.272A>C p.Asp91Ala	srIR	Glucitol operon repressor
олер		00 10004	5.1P	0.,240		1 5.41	2.20.00. 000.011 100100001

Ochrobactrum anthropi

sample	СНКОМ	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT

1.14 1.05 1.06	sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
11141	-			-				
10.10 10.0						· ·	<u> </u>	·
1942 1971 1989	T11.4.1	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs		
1912 1919	T11.4.2	c01	1008848	del	218/239	frameshift variant c.653delG p.Glv218fs	vdcO 1	•
11.14.2				-		· ·		·
11.4.5								HTH-type transcriptional regulatory
19.1 19.5	T11 // 3	c01	1008848	del	218/230	frameshift variant c 653delG n Glv218fc	vdcO 1	•
111.4.1. 101.				-		· ·	_	·
Till								HTH-type transcriptional regulatory
Tili.4.4 Oil 1008861 Oil 100987 Oil 14229 Transecht Levilation C.4600 p. Arg2546 Oil 190024 Oil 1009264 Oil 12429 Transecht Levilation C.4600 p. Arg254 Oil 190024 Oil 190024 Oil 190024 Oil 190024 Oil 190024 Oil 190024 Oil O	T11 4 4	c01	1008848	del	218/239	frameshift variant c 653delG n Glv218fs	vdcO 1	
Page								,
								HTH-type transcriptional regulatory
TH.	T11 4 5	c01	1008848	del	218/239	frameshift variant c 653delG n Glv218fs	vdcO 1	
1111-14.5 111				-		· ·	_	·
11.1.1.5						Trainestin Cyanana 6.0400cio p.///g21415		· ·
11.14.2.4.1	T11.4.5	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	protein GabR
				·				virB4
				-				,
	T22.4.1	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ydcO_1	·
122.4.2	T22.4.1	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	
T22.4.2	T22.4.1	c01	2022111	snp	309/840	synonymous_variant c.927C>A p.Ala309Ala	virB4_2	
1722.4.2	T22.4.2	c01	96441	snp	171/546	synonymous_variant c.513T>C p.Asn171Asn	groL	60 kDa chaperonin
172.4.2	T22.4.2	c01	96450	snp	174/546	synonymous_variant c.522G>C p.Val174Val	groL	60 kDa chaperonin
T22.4.2	T22.4.2	c01	96456	snp	176/546	synonymous_variant c.528G>C p.Thr176Thr	groL	60 kDa chaperonin
T22.4.2	T22.4.2	c01	96534	snp	202/546	synonymous_variant c.606T>C p.Pro202Pro	groL	60 kDa chaperonin
T22.4.2	T22.4.2	c01	96543	snp	205/546	synonymous_variant c.615C>G p.Val205Val	groL	60 kDa chaperonin
T22.4.2	T22.4.2	c01	96549	complex	207/546	synonymous_variant c.621_624delCCCTinsTCCG p.209	groL	60 kDa chaperonin
T22.4.2	T22.4.2	c01	96567	snp	213/546	synonymous_variant c.639T>G p.Ala213Ala	groL	60 kDa chaperonin
T22.4.2 c01 96833 snp 235/546 synonymous_variant c.705G>T p.Pro235Pro grot 60 kDa chaperonin T22.4.2 c01 96839 snp 237/546 synonymous_variant c.71G>C p.Leu237Leu grot 60 kDa chaperonin T22.4.2 c01 96638 mp 244/546 missense_variant c.73G>731deffClinsGG p.Ser244Gly grot 60 kDa chaperonin T22.4.2 c01 96731 snp 286/546 synonymous_variant c.813G>C p.Leu27Leu grot 60 kDa chaperonin T22.4.2 c01 96731 snp 271/546 synonymous_variant c.83G>C p.Leu27Leu grot 60 kDa chaperonin T22.4.2 c01 96753 snp 275/546 synonymous_variant c.83G>C p.Leu27Leu grot 60 kDa chaperonin T22.4.2 c01 96786 snp 288/546 synonymous_variant c.85G>C p.Asp283Asp grot 60 kDa chaperonin T22.4.2 c01 96785 snp 289/546 synonymous_variant c.87G>C p.Asp283Asp grot 60 kDa chaperonin T22.4.2 c01	T22.4.2	c01	96609	snp	227/546	synonymous_variant c.681C>T p.Leu227Leu	groL	60 kDa chaperonin
T22.4.2 C01 96639 snp 237/546 synonymous_variant c.71(0>c p.Leu237Leu grol. 80 kDa chaperonin T22.4.2 C01 96658 mnp 244/546 missense_variant c.730_731delTCinsGG p.Ser244Gly grol. 60 kDa chaperonin T22.4.2 C01 96732 snp 286/546 synonymous_variant c.804C>T p.Arg268Arg grol. 60 kDa chaperonin T22.4.2 C01 96751 snp 271/546 synonymous_variant c.823T>C p.Leu27Leu grol. 60 kDa chaperonin T22.4.2 C01 96753 snp 275/546 synonymous_variant c.825T>C p.Leu275Ha grol. 60 kDa chaperonin T22.4.2 C01 96786 snp 286/546 synonymous_variant c.8576-C p.Leu289Leu grol. 60 kDa chaperonin T22.4.2 C01 96785 snp 286/546 synonymous_variant c.867c-O p.Leu289Leu grol. 60 kDa chaperonin T22.4.2 C01 96795 snp 289/546 synonymous_variant c.876-O-P p.Leu2780Leu grol. 60 kDa chaperonin T22.4.2 <	T22.4.2	c01	96624	complex	232/546	missense_variant c.696_699delTCTTinsCATG p.Leu233Met	groL	60 kDa chaperonin
T22.4.2 c01 96658 mp 244/546 missense_variant c.730_731deffCinsGQ p.Ser/244Gly grol. 60 kDa chaperonin T22.4.2 c01 96732 snp 268/546 synonymous_variant c.804C>T p.Arg268Arg grol. 60 kDa chaperonin T22.4.2 c01 96741 snp 271/546 synonymous_variant c.8136>C p.Leu271Leu grol. 60 kDa chaperonin T22.4.2 c01 96777 snp 275/546 synonymous_variant c.825T>C p.Ala275Ala grol. 60 kDa chaperonin T22.4.2 c01 96777 snp 283/546 synonymous_variant c.858A>G p.Lys288Lys grol. 60 kDa chaperonin T22.4.2 c01 96786 snp 289/546 synonymous_variant c.876C>G p.Leu289Leu grol. 60 kDa chaperonin T22.4.2 c01 96807 snp 283/546 synonymous_variant c.777G>C p.Leu289Leu grol. 60 kDa chaperonin T22.4.2 c01 2021961 snp 259/840 synonymous_variant c.777G>C p.Ser259Ser vir84.2 vir84.2 vir96 l.Vser24	T22.4.2	c01	96633	snp	235/546	synonymous_variant c.705G>T p.Pro235Pro	groL	60 kDa chaperonin
T22.4.2 CO1 96732 snp 268/546 synonymous_variant c.804C>T p.Arg268Arg grol 60 kDa chaperonin T22.4.2 CO1 96741 snp 271/546 synonymous_variant c.813G>C p.Leu271Leu grol 60 kDa chaperonin T22.4.2 CO1 96753 snp 275/546 synonymous_variant c.835T>C p.Aa275Ala grol 60 kDa chaperonin T22.4.2 CO1 96777 snp 283/546 synonymous_variant c.85BAPS p.Lys288Lys grol 60 kDa chaperonin T22.4.2 CO1 96795 snp 289/546 synonymous_variant c.867C>G p.Leu289Leu grol 60 kDa chaperonin T22.4.2 CO1 96807 snp 289/546 synonymous_variant c.879G>C p.Leu289Leu grol 60 kDa chaperonin T22.4.2 CO1 96807 snp 289/546 synonymous_variant c.879G>C p.Leu289Leu grol 60 kDa chaperonin T22.4.2 CO1 2021961 snp 259/840 synonymous_variant c.777G>C p.Ser259Ser vir84.2 Type IV secretion system protein vrir84 T22.4.2	T22.4.2	c01	96639	snp	237/546	synonymous_variant c.711G>C p.Leu237Leu	groL	60 kDa chaperonin
T22.4.2 CO1 96741 snp 271/546 synonymous_variant c.813G>C p.Leu271Leu grol. 60 kDa chaperonin T22.4.2 CO1 96753 snp 275/546 synonymous_variant c.825T>C p.Ala275Ala grol. 60 kDa chaperonin T22.4.2 CO1 96777 snp 283/546 synonymous_variant c.849T>C p.Asp283Asp grol. 60 kDa chaperonin T22.4.2 CO1 96786 snp 286/546 synonymous_variant c.8767>G p.Leu289Leu grol. 60 kDa chaperonin T22.4.2 CO1 96786 snp 289/546 synonymous_variant c.8767>G p.Leu289Leu grol. 60 kDa chaperonin T22.4.2 CO1 968907 snp 293/546 synonymous_variant c.777G>C p.Ser259Ser virB4.2 VirB4.2 Type IV secretion system protein virB4 T22.4.2 CO1 2021973 complex 263/840 missense_variant c.815G>A p.Arg27ZLys virB4.2 Type IV secretion system protein virB4 T22.4.2 CO1 2021999 snp 278/840 synonymous_variant c.815G>A p.Arg27ZLys virB4.2 Type	T22.4.2	c01	96658	mnp	244/546	missense_variant c.730_731delTCinsGG p.Ser244Gly	groL	60 kDa chaperonin
T22.4.2 CO1 96753 snp 275/546 synonymous_variant c.825T>C p.Ala275Ala grol. 60 kDa chaperonin T22.4.2 CO1 96777 snp 283/546 synonymous_variant c.849T>C p.Asp283Asp grol. 60 kDa chaperonin T22.4.2 CO1 96786 snp 286/546 synonymous_variant c.8567C>G p.Leu289Leu grol. 60 kDa chaperonin T22.4.2 CO1 96807 snp 293/546 synonymous_variant c.8769C p.Leu289Leu grol. 60 kDa chaperonin T22.4.2 CO1 96807 snp 293/546 synonymous_variant c.777G>C p.Ser259Ser virB4.2 Type IV secretion system protein virB4 T22.4.2 CO1 2021961 snp 259/840 missense_variant c.7769C p.Ser259Ser virB4.2 Type IV secretion system protein virB4 T22.4.2 CO1 2021973 complex 263/840 missense_variant c.815G>A p.Arg27ZLys virB4.2 Type IV secretion system protein virB4 T22.4.2 CO1 2022198 snp 278/840 synonymous_variant c.815G>A p.Arg27ZLys virB4.2 Type IV s	T22.4.2	c01	96732	snp	268/546	synonymous_variant c.804C>T p.Arg268Arg	groL	60 kDa chaperonin
T22.4.2 C01 96777 snp 283/546 synonymous_variant c.849T>C p.Asp283Asp grol 60 kDa chaperonin T22.4.2 C01 96786 snp 286/546 synonymous_variant c.858A>G p.Lys286Lys grol 60 kDa chaperonin T22.4.2 C01 96795 snp 289/546 synonymous_variant c.876C>G p.Leu289Leu grol 60 kDa chaperonin T22.4.2 C01 96807 snp 293/546 synonymous_variant c.879G>C p.Be293Ala grol 60 kDa chaperonin T22.4.2 C01 2021961 snp 259/840 synonymous_variant c.777G>C p.Ser259Ser virB4_2 Type IV secretion system protein virB4 T22.4.2 C01 2021973 complex 263/840 missense_variant c.789_793delTCTGAinsCCTGC p.Met26SLeu virB4_2 Type IV secretion system protein virB4 T22.4.2 C01 2021993 snp 272/840 missense_variant c.815G>A p.Arg272Lys virB4_2 Type IV secretion system protein virB4 T22.4.2 C01 202218 snp 278/840 synonymous_variant c.834C>T p.Arg278Arg virB4_2	T22.4.2	c01	96741	snp	271/546	synonymous_variant c.813G>C p.Leu271Leu	groL	60 kDa chaperonin
T22.4.2 c01 96786 snp 286/546 synonymous_variant c.858A>G p.Lys286Lys groL 60 kDa chaperonin T22.4.2 c01 96795 snp 289/546 synonymous_variant c.876C>G p.Leu289Leu groL 60 kDa chaperonin T22.4.2 c01 96807 snp 293/546 synonymous_variant c.879C>C p.Ala293Ala groL 60 kDa chaperonin T22.4.2 c01 2021961 snp 259/840 synonymous_variant c.777G>C p.Ser259Ser virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2021993 snp 258/840 missense_variant c.815G>A p.Arg272Lys virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2021999 snp 278/840 synonymous_variant c.834C>T p.Arg278Arg virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022111 snp 309/840 synonymous_variant c.936_938delTGCinsGCT p.Ala313Leu virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022103 snp 317/840 missense_variant c.924_957delGCTAinsCTTG p.320	T22.4.2	c01	96753	snp	275/546	synonymous_variant c.825T>C p.Ala275Ala	groL	60 kDa chaperonin
T22.4.2 c01 96795 snp 289/546 synonymous_variant c.867C>G p.Leu289Leu grot 60 kDa chaperonin T22.4.2 c01 96807 snp 293/546 synonymous_variant c.87G>C p.Ala293Ala grot 60 kDa chaperonin T22.4.2 c01 2021961 snp 259/840 synonymous_variant c.777G>C p.Ser259Ser virB4.2 Type IV secretion system protein virB4 T22.4.2 c01 2021973 complex 263/840 missense_variant c.789_793delTCTGAinsCCTGC p.Met265Leu virB4.2 Type IV secretion system protein virB4 T22.4.2 c01 2021999 snp 272/840 missense_variant c.815G>A p.Arg272Lys virB4.2 Type IV secretion system protein virB4 T22.4.2 c01 202218 snp 278/840 synonymous_variant c.934C>T p.Arg278Arg virB4.2 Type IV secretion system protein virB4 T22.4.2 c01 2022111 snp 309/840 synonymous_variant c.927C>A p.Ala309Ala virB4.2 Type IV secretion system protein virB4 T22.4.2 c01 2022100 mnp 312/840 missense_variant c.936_93	T22.4.2	c01	96777	snp	283/546	synonymous_variant c.849T>C p.Asp283Asp	groL	60 kDa chaperonin
T22.4.2 c01 96807 snp 293/546 synonymous_variant c.879G>C p.Ala293Ala grol. 60 kDa chaperonin T22.4.2 c01 2021961 snp 259/840 synonymous_variant c.777G>C p.Ser259Ser virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2021973 complex 263/840 missense_variant c.777G>C p.Ser259Ser virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2021999 snp 272/840 missense_variant c.815G>A p.Arg272Lys virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022018 snp 278/840 synonymous_variant c.834C>T p.Arg278Arg virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022111 snp 309/840 synonymous_variant c.927C>A p.Ala309Ala virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022120 mnp 312/840 missense_variant c.936_938delTGCinsGCT p.Ala313Leu virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022138 complex 318/840 <t< td=""><td>T22.4.2</td><td>c01</td><td>96786</td><td>snp</td><td>286/546</td><td>synonymous_variant c.858A>G p.Lys286Lys</td><td>groL</td><td>60 kDa chaperonin</td></t<>	T22.4.2	c01	96786	snp	286/546	synonymous_variant c.858A>G p.Lys286Lys	groL	60 kDa chaperonin
T22.4.2 c01 2021961 snp 259/840 synonymous_variant c.777g>C p.Ser259Ser virB4.2 Type IV secretion system protein virB4 T22.4.2 c01 2021973 complex 263/840 missense_variant c.789_793delTCTGAinsCCTGC p.Met265Leu virB4.2 Type IV secretion system protein virB4 T22.4.2 c01 2021999 snp 272/840 missense_variant c.815G>A p.Arg272Lys virB4.2 type IV secretion system protein virB4 T22.4.2 c01 2022018 snp 278/840 synonymous_variant c.834C>T p.Arg278Arg virB4.2 type IV secretion system protein virB4 T22.4.2 c01 2022111 snp 309/840 synonymous_variant c.93C>A p.Ala309Ala virB4.2 type IV secretion system protein virB4 T22.4.2 c01 2022120 mnp 312/840 missense_variant c.936_938delTGCinsGCT p.Ala313Leu virB4.2 type IV secretion system protein virB4 T22.4.2 c01 2022133 snp 317/840 missense_variant c.949C>A p.Leu317Met virB4.2 type IV secretion system protein virB4 T22.4.2 c01 2022138 complex </td <td>T22.4.2</td> <td>c01</td> <td>96795</td> <td>snp</td> <td>289/546</td> <td>synonymous_variant c.867C>G p.Leu289Leu</td> <td>groL</td> <td>60 kDa chaperonin</td>	T22.4.2	c01	96795	snp	289/546	synonymous_variant c.867C>G p.Leu289Leu	groL	60 kDa chaperonin
122.4.2 C01 2021973 Complex 263/840 missense_variant c.789_793delTCTGAinsCCTGC p.Met265Leu VirB4_2 Type IV secretion system protein virB4_3 Type IV secretion system protein virB4_4 Type IV secretion system protein virB4_5 Type IV secretion system protein virB4_6 Type IV secretion system protein virB4_6 Type IV secretion system protein virB4_7 Type IV secretion system protein virB4_	T22.4.2	c01	96807	snp	293/546	synonymous_variant c.879G>C p.Ala293Ala	groL	60 kDa chaperonin
T22.4.2 C01 202199 Snp 272/840 missense_variant c.815G>A p.Arg272Lys VirB4_2 VirB4_2 VirB4_2 VirB4_2 VirB4_3 VirB4_4 VirB4_4 VirB4_4 VirB4_4 VirB4_4 VirB4_4 VirB4_5 VirB4_6 VirB4_7 VirB4_7 VirB4_7 VirB4_8 Vir	T22.4.2	c01	2021961	snp	259/840	synonymous_variant c.777G>C p.Ser259Ser	virB4_2	
T22.4.2 c01 2021999 snp 272/840 missense_variant c.815GSA p.Arg2/2Lys virB4_2 virB4 T22.4.2 c01 2022018 snp 278/840 synonymous_variant c.834C>T p.Arg278Arg virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022111 snp 309/840 synonymous_variant c.927C>A p.Ala309Ala virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022120 mnp 312/840 missense_variant c.936_938delTGCinsGCT p.Ala313Leu virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022133 snp 317/840 missense_variant c.949C>A p.Leu317Met virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022138 complex 318/840 synonymous_variant c.954_957delGCTAinsCTTG p.320 virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022160 complex 326/840 missense_variant c.976_978delATCinsGTG p.lle326Val virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022206 complex 341/84	T22.4.2	c01	2021973	complex	263/840	missense_variant c.789_793delTCTGAinsCCTGC p.Met265Leu	virB4_2	
122.4.2 c01 2022018 snp 278/840 synonymous_variant c.934C>1 p.Arg2/8Arg virB4_2 virB4_2 virB4 T22.4.2 c01 2022111 snp 309/840 synonymous_variant c.927C>A p.Ala309Ala virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022120 mnp 312/840 missense_variant c.936_938delTGCinsGCT p.Ala313Leu virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022133 snp 317/840 missense_variant c.949C>A p.Leu317Met virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022138 complex 318/840 synonymous_variant c.954_957delGCTAinsCTTG p.320 virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022160 complex 326/840 missense_variant c.976_978delATCinsGTG p.lle326Val virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022206 complex 341/840 missense_variant c.1022_1031delCCGATGCCGCinsAGGACGCCCG virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022225 <td>T22.4.2</td> <td>c01</td> <td>2021999</td> <td>snp</td> <td>272/840</td> <td>missense_variant c.815G>A p.Arg272Lys</td> <td>virB4_2</td> <td></td>	T22.4.2	c01	2021999	snp	272/840	missense_variant c.815G>A p.Arg272Lys	virB4_2	
T22.4.2 C01 2022120 mnp 312/840 missense_variant c.936_938delTGCinsGCT p.Ala313Leu virB4_2 virB4 vir	T22.4.2	c01	2022018	snp	278/840	synonymous_variant c.834C>T p.Arg278Arg	virB4_2	
T22.4.2 c01 2022120 mnp 312/840 missense_variant c.936_938delTGCinsGCT p.Ala313Leu virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022133 snp 317/840 missense_variant c.949C>A p.Leu317Met virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022138 complex 318/840 synonymous_variant c.954_957delGCTAinsCTTG p.320 virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022160 complex 326/840 missense_variant c.976_978delATCinsGTG p.lle326Val virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022206 complex 341/840 missense_variant c.1022_1031delCCGATGCCGCinsAGGACGCCCG p.4164_2 virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022225 snp 347/840 missense_variant c.1041A>C p.Glu347Asp virB4_2 Type IV secretion system protein virB4	T22.4.2	c01	2022111	snp	309/840	synonymous_variant c.927C>A p.Ala309Ala	virB4_2	
T22.4.2 c01 2022133 snp 317/840 missense_variant c.949C>A p.Leu317Met virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022138 complex 318/840 synonymous_variant c.954_957delGCTAinsCTTG p.320 virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022160 complex 326/840 missense_variant c.976_978delATCinsGTG p.lle326Val virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022206 complex 341/840 missense_variant c.1022_1031delCCGATGCCGCinsAGGACGCCCG p.404Acg virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022225 snp 347/840 missense_variant c.1041Acg p.Glu347Asp virB4_2 Type IV secretion system protein virB4	T22.4.2	c01	2022120	mnp	312/840	missense_variant c.936_938delTGCinsGCT p.Ala313Leu	virB4_2	Type IV secretion system protein
T22.4.2 c01 2022138 complex 318/840 synonymous_variant c.954_957delGCTAinsCTTG p.320 virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022160 complex 326/840 missense_variant c.976_978delATCinsGTG p.lle326Val virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022206 complex 341/840 missense_variant c.1022_1031delCCGATGCCGCinsAGGACGCCCG p.AlaAspAlaArg virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022225 snp 347/840 missense_variant c.1041A>C p.Glu347Asp virB4_2 Type IV secretion system protein	T22.4.2	c01	2022133	snp	317/840	missense_variant c.949C>A p.Leu317Met	virB4_2	Type IV secretion system protein
T22.4.2 c01 2022160 complex 326/840 missense_variant c.976_978delATCinsGTG p.lle326Val virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022206 complex 341/840 missense_variant c.1022_1031delCCGATGCCGCinsAGGACGCCCG p.AlaAspAlaArg virB4_2 Type IV secretion system protein virB4 T22.4.2 c01 2022225 snp 347/840 missense_variant c.1041A>C p.Glu347Asp virB4_2 Type IV secretion system protein	T22.4.2	c01	2022138	complex	318/840	synonymous_variant c.954_957delGCTAinsCTTG p.320	virB4_2	Type IV secretion system protein
T22.4.2 c01 2022206 complex 341/840 missense_variant c.1022_1031delCCGATGCCGCinsAGGACGCCCG virB4_2 Type IV secretion system protein virB4 virB4 T22.4.2 c01 2022225 snp 347/840 missense_variant c.1041A>C p.Glu347Asp virB4 2 Type IV secretion system protein	T22.4.2	c01	2022160	complex	326/840	missense_variant c.976_978deIATCinsGTG p.Ile326Val	virB4_2	Type IV secretion system protein
T22.4.2 c01 2022225 snp 347/840 missense variant c.1041A>C p.Glu347Asp virB4 2 Type IV secretion system protein	T22.4.2	c01	2022206	complex	341/840		virB4_2	Type IV secretion system protein
	T22.4.2	c01	2022225	snp	347/840		virB4_2	

	c01						
T22.4.2 c		2022253	snp	357/840	missense_variant c.1069A>G p.lle357Val	virB4_2	Type IV secretion system protein virB4
	c01	2022276	snp	364/840	synonymous_variant c.1092G>C p.Val364Val	virB4_2	Type IV secretion system protein virB4
T22.4.2 c	c01	2022318	snp	378/840	synonymous_variant c.1134C>G p.Ser378Ser	virB4_2	Type IV secretion system protein virB4
T22.4.2 C	c01	2022324	snp	380/840	synonymous_variant c.1140G>C p.Pro380Pro	virB4_2	Type IV secretion system protein virB4
T22.4.2 c	c01	2022330	complex	382/840	synonymous_variant c.1146_1149delCGCCinsTGCT p.384	virB4_2	Type IV secretion system protein virB4
T22.4.2 c	c01	2022339	snp	385/840	synonymous_variant c.1155A>C p.Ala385Ala	virB4_2	Type IV secretion system protein virB4
T22.4.2 C	c01	2022358	snp	392/840	missense_variant c.1174G>A p.Val392lle	virB4_2	Type IV secretion system protein virB4
T22.4.2 c	c01	2023410	snp	742/840	synonymous_variant c.2226A>G p.Gln742Gln	virB4_2	Type IV secretion system protein virB4
T22.4.2 C	c01	2023416	complex	744/840	synonymous_variant c.2232_2233delCAinsGC p.746	virB4_2	Type IV secretion system protein virB4
T22.4.2 C	c01	2023443	snp	753/840	synonymous_variant c.2259C>T p.Gly753Gly	virB4_2	Type IV secretion system protein virB4
T22.4.2 c	c01	2023509	snp	775/840	synonymous_variant c.2325T>C p.Asp775Asp	virB4_2	Type IV secretion system protein virB4
T22.4.2 c	c01	2023515	snp	777/840	synonymous_variant c.2331C>A p.Leu777Leu	virB4_2	Type IV secretion system protein virB4
T22.4.2 c	c01	2023521	snp	779/840	synonymous_variant c.2337G>A p.Glu779Glu	virB4_2	Type IV secretion system protein virB4
T22.4.2 c	c02	436029	snp	508/1377	synonymous_variant c.1524T>A p.Ala508Ala	rpoB	DNA-directed RNA polymerase subunit beta
T22.4.2 c	c02	436035	snp	510/1377	synonymous_variant c.1530A>C p.Ala510Ala	rpoB	DNA-directed RNA polymerase subunit beta
T22.4.2 c	c02	436041	snp	512/1377	synonymous_variant c.1536G>T p.Val512Val	rpoB	DNA-directed RNA polymerase subunit beta
T22.4.2 c	c02	436047	snp	514/1377	synonymous_variant c.1542G>A p.Glu514Glu	rpoB	DNA-directed RNA polymerase subunit beta
T22.4.2 c	c02	436083	complex	526/1377	missense_variant c.1578_1584delTCAGACCinsCCAGGTG p.Thr528Val	rpoB	DNA-directed RNA polymerase subunit beta
T22.4.2 C	c02	436125	snp	540/1377	synonymous_variant c.1620C>T p.Leu540Leu	rpoB	DNA-directed RNA polymerase subunit beta
T22.4.2 c	c02	436143	snp	546/1377	synonymous_variant c.1638C>T p.Gly546Gly	rpoB	DNA-directed RNA polymerase subunit beta
T22.4.2 c	c02	439829	snp	329/1400	synonymous_variant c.987G>C p.Leu329Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2 C	c02	439856	snp	338/1400	synonymous_variant c.1014T>C p.Gly338Gly	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2 c	c02	439865	snp	341/1400	synonymous_variant c.1023T>C p.Arg341Arg	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2 c	c02	439874	snp	344/1400	synonymous_variant c.1032G>T p.Leu344Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2 c	c02	439910	snp	356/1400	synonymous_variant c.1068C>T p.Val356Val	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2 c	c02	439931	snp	363/1400	synonymous_variant c.1089C>G p.Leu363Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2 c	c02	439985	snp	381/1400	synonymous_variant c.1143A>G p.Pro381Pro	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2 c	c02	440172	snp	444/1400	missense_variant c.1330A>G p.lle444Val	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2 c	c02	440186	snp	448/1400	synonymous_variant c.1344T>C p.Ala448Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2 c	c02	440198	snp	452/1400	synonymous_variant c.1356T>C p.His452His	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2 C	c02	440207	complex	455/1400	synonymous_variant c.1365_1368delTTGTinsCTGC p.457	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2 c	c02	440216	snp	458/1400	synonymous_variant c.1374G>C p.Ala458Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2 C	c02	440264	snp	474/1400	synonymous_variant c.1422G>C p.Leu474Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2 C	c02	440270	snp	476/1400	synonymous_variant c.1428C>G p.Leu476Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2 c	c02	440282	snp	480/1400	synonymous_variant c.1440T>G p.Leu480Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2 c	c02	440288	snp	482/1400	synonymous_variant c.1446A>G p.Ala482Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2 c	c02	441065	snp	741/1400	synonymous_variant c.2223T>C p.Arg741Arg	rpoC	DNA-directed RNA polymerase subunit beta'

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T22.4.2	c02	441071	snp	743/1400	synonymous_variant c.2229T>G p.Leu743Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	441077	snp	745/1400	synonymous_variant c.2235C>A p.Ala745Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	441101	complex	753/1400	synonymous_variant c.2259_2262delAACCinsGACG p.755	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	441110	snp	756/1400	synonymous_variant c.2268A>C p.lle756lle	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	441195	snp	785/1400	synonymous_variant c.2353T>C p.Leu785Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	441203	complex	787/1400	synonymous_variant c.2361_2364delTGCTinsGGCG p.789	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	445987	snp	360/694	synonymous_variant c.1078T>C p.Leu360Leu	fusA	Elongation factor G
T22.4.2	c02	446031	complex	374/694	synonymous_variant c.1122_1125delTGCAinsCGCC p.376	fusA	Elongation factor G
T22.4.2	c02	446133	complex	408/694	missense_variant c.1224_1227delGGATinsCGAG p.Asp409Glu	fusA	Elongation factor G
T22.4.2	c02	451038	snp	252/277	synonymous_variant c.756T>C p.Pro252Pro	rplB	50S ribosomal protein L2
T22.4.2	c02	451051	complex	257/277	missense_variant c.769_777delAAGACGCGCinsCGCACCCGT p.Lys257Arg	rplB	50S ribosomal protein L2
T22.4.2	c02	453539	snp	13/122	synonymous_variant c.39C>T p.Asn13Asn	rplN	50S ribosomal protein L14
T22.4.2	c02	453590	complex	30/122	missense_variant c.90_96delGCGTTACinsCAAATAT p.Arg31Lys	rplN	50S ribosomal protein L14
T22.4.2	c02	453602	snp	34/122	synonymous_variant c.102C>T p.Ser34Ser	rplN	50S ribosomal protein L14
T22.4.2	c02	453620	complex	40/122	synonymous_variant c.120_126delGGTGTCGinsCGTTTCC p.43	rplN	50S ribosomal protein L14
T22.4.2	c02	453659	snp	53/122	synonymous_variant c.159A>G p.Lys53Lys	rplN	50S ribosomal protein L14
T22.4.2	c02	453665	complex	55/122	synonymous_variant c.165_168delTGATinsCGAC p.57	rplN	50S ribosomal protein L14
T22.4.2	c02	698351	snp	242/424	synonymous_variant c.726G>C p.Thr242Thr	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T22.4.2	c02	698357	snp	240/424	synonymous_variant c.720C>T p.Asp240Asp	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T22.4.2	c02	698399	snp	226/424	synonymous_variant c.678A>G p.Gln226Gln	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T22.4.2	c02	698420	snp	219/424	synonymous_variant c.657C>G p.Thr219Thr	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T22.4.2	c02	698474	snp	201/424	synonymous_variant c.603C>T p.Arg201Arg	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T22.4.2	c02	698492	snp	195/424	synonymous_variant c.585T>C p.Asp195Asp	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T22.4.2	c02	698505	complex	190/424	synonymous_variant c.570_572delCAGinsTTC p.192	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T22.4.2	c02	698546	complex	176/424	synonymous_variant c.528_531delTGCGinsCGCC p.178	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T22.4.2	c02	698555	snp	174/424	synonymous_variant c.522G>C p.Val174Val	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T22.4.2	c02	698618	complex	152/424	synonymous_variant c.456_459delAGGCinsCGGT p.154	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T22.4.2	c02	698627	snp	150/424	synonymous_variant c.450G>C p.Thr150Thr	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T22.4.2	c02	698633	snp	148/424	synonymous_variant c.444A>G p.Thr148Thr	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T22.4.2	c02	698639	snp	146/424	synonymous_variant c.438G>A p.Ala146Ala	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T22.4.2	c02	698645	snp	144/424	synonymous_variant c.432C>G p.Ala144Ala	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T22.4.2	c02	698657	complex	138/424	synonymous_variant c.414_420delTGTGCCAinsCGTTCCC p.141	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T22.4.2	c02	698675	snp	134/424	synonymous_variant c.402A>C p.Ala134Ala	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T22.4.2	c02	698726	complex	116/424	missense_variant c.348_351delTCTTinsCATG p.Leu117Met	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T22.4.2	c02	698752	snp	109/424	missense_variant c.325A>G p.lle109Val	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T22.4.2	c02	1908928	snp	189/566	synonymous_variant c.567G>T p.Ser189Ser	rpsA	30S ribosomal protein S1
T22.4.2	c02	1908937	snp	192/566	synonymous_variant c.576C>T p.Val192Val	rpsA	30S ribosomal protein S1
T22.4.2	c02	1908946	snp	195/566	synonymous_variant c.585T>C p.Leu195Leu	rpsA	30S ribosomal protein S1
T22.4.2	c02	1908955	snp	198/566	synonymous_variant c.594T>C p.Gly198Gly	rpsA	30S ribosomal protein S1
T22.4.2	c02	1908961	snp	200/566	synonymous_variant c.600C>T p.Val200Val	rpsA	30S ribosomal protein S1
T22.4.2	c02	1908967	snp	202/566	missense_variant c.606A>C p.Glu202Asp	rpsA	30S ribosomal protein S1
T22.4.2	c02	1909027	complex	222/566	synonymous_variant c.666_669delTCTCinsCCTG p.224	rpsA	30S ribosomal protein S1
T22.4.2	c02	1909039	snp	226/566	synonymous_variant c.678G>T p.Val226Val	rpsA	30S ribosomal protein S1
T22.4.2	c02	1909072	snp	237/566	synonymous_variant c.711G>T p.Pro237Pro	rpsA	30S ribosomal protein S1
T22.4.2	c02	1909086	complex	242/566	missense_variant c.725_729delCCATCinsACATT p.Thr242Asn	rpsA	30S ribosomal protein S1
T22.4.2	c02	1909097	mnp	246/566	missense_variant c.736_737delACinsCA p.Thr246Gln	rpsA	30S ribosomal protein S1

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T22.4.2	c02	1909108	snp	249/566	synonymous_variant c.747G>T p.Val249Val	rpsA	30S ribosomal protein S1
T22.4.2	c02	2279042	snp	9/134	synonymous_variant c.27T>C p.Gly9Gly	ssb_4	Single-stranded DNA-binding protein
T22.4.2	c02	2279055	complex	14/134	missense_variant c.40_41delGAinsAC p.Asp14Thr	ssb_4	Single-stranded DNA-binding protein
T22.4.3	c01	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ydcO_1	Inner membrane protein YdcO
T22.4.3	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ydcO_1	Inner membrane protein YdcO
T22.4.3	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	HTH-type transcriptional regulatory protein GabR
T22.4.4	c01	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ydcO_1	Inner membrane protein YdcO
T22.4.4	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ydcO_1	Inner membrane protein YdcO
T22.4.4	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	HTH-type transcriptional regulatory protein GabR
T22.4.4	c01	2022018	snp	278/840	synonymous_variant c.834C>T p.Arg278Arg	virB4_2	Type IV secretion system protein virB4
T22.4.4	c01	2022111	snp	309/840	synonymous_variant c.927C>A p.Ala309Ala	virB4_2	Type IV secretion system protein virB4
T22.4.4	c01	2022120	complex	312/840	missense_variant c.936_938delTGCinsGCT p.Ala313Leu	virB4_2	Type IV secretion system protein virB4
T22.4.4	c01	2022133	snp	317/840	missense_variant c.949C>A p.Leu317Met	virB4_2	Type IV secretion system protein virB4
T22.4.4	c01	2022138	complex	318/840	synonymous_variant c.954_957delGCTAinsCTTG p.320	virB4_2	Type IV secretion system protein virB4
T22.4.4	c01	2022160	complex	326/840	missense_variant c.976_978delATCinsGTG p.lle326Val	virB4_2	Type IV secretion system protein virB4
T22.4.4	c01	2022225	snp	347/840	missense_variant c.1041A>C p.Glu347Asp	virB4_2	Type IV secretion system protein virB4
T22.4.4	c01	2022276	snp	364/840	synonymous_variant c.1092G>C p.Val364Val	virB4_2	Type IV secretion system protein virB4
T22.4.4	c02	1908961	snp	200/566	synonymous_variant c.600C>T p.Val200Val	rpsA	30S ribosomal protein S1
T22.4.4	c02	1908967	snp	202/566	missense_variant c.606A>C p.Glu202Asp	rpsA	30S ribosomal protein S1
T22.4.4	c02	1909027	complex	222/566	synonymous_variant c.666_669delTCTCinsCCTG p.224	rpsA	30S ribosomal protein S1
T22.4.4	c02	1909039	snp	226/566	synonymous_variant c.678G>T p.Val226Val	rpsA	30S ribosomal protein S1
T22.4.4	c02	1909072	snp	237/566	synonymous_variant c.711G>T p.Pro237Pro	rpsA	30S ribosomal protein S1
T22.4.4	c02	1909086	complex	242/566	missense_variant c.725_729delCCATCinsACATT p.Thr242Asn	rpsA	30S ribosomal protein S1
T22.4.5	c01	96609	snp	227/546	synonymous_variant c.681C>T p.Leu227Leu	groL	60 kDa chaperonin
T22.4.5	c01	96658	mnp	244/546	missense_variant c.730_731delTCinsGG p.Ser244Gly	groL	60 kDa chaperonin
T22.4.5	c01	96732	snp	268/546	synonymous_variant c.804C>T p.Arg268Arg	groL	60 kDa chaperonin
T22.4.5	c01	96741	snp	271/546	synonymous_variant c.813G>C p.Leu271Leu	groL	60 kDa chaperonin
T22.4.5	c01	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ydcO_1	Inner membrane protein YdcO
T22.4.5	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ydcO_1	Inner membrane protein YdcO
T22.4.5	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	HTH-type transcriptional regulatory protein GabR
T22.4.5	c01	2021999	snp	272/840	missense_variant c.815G>A p.Arg272Lys	virB4_2	Type IV secretion system protein virB4
T22.4.5	c01	2022018	snp	278/840	synonymous_variant c.834C>T p.Arg278Arg	virB4_2	Type IV secretion system protein virB4
T22.4.5	c01	2022111	snp	309/840	synonymous_variant c.927C>A p.Ala309Ala	virB4_2	Type IV secretion system protein virB4
T22.4.5	c01	2022120	mnp	312/840	missense_variant c.936_938delTGCinsGCT p.Ala313Leu	virB4_2	Type IV secretion system protein virB4
T22.4.5	c01	2022133	snp	317/840	missense_variant c.949C>A p.Leu317Met	virB4_2	Type IV secretion system protein virB4
T22.4.5	c01	2022138	complex	318/840	synonymous_variant c.954_957delGCTAinsCTTG p.320	virB4_2	Type IV secretion system protein virB4
T22.4.5	c01	2022160	complex	326/840	missense_variant c.976_978delATCinsGTG p.lle326Val	virB4_2	Type IV secretion system protein virB4
T22.4.5	c01	2022225	snp	347/840	missense_variant c.1041A>C p.Glu347Asp	virB4_2	Type IV secretion system protein virB4
T22.4.5	c01	2022253	snp	357/840	missense_variant c.1069A>G p.lle357Val	virB4_2	Type IV secretion system protein virB4
T22.4.5	c01	2022276	snp	364/840	synonymous_variant c.1092G>C p.Val364Val	virB4_2	Type IV secretion system protein virB4
T22.4.5	c02	1908955	snp	198/566	synonymous_variant c.594T>C p.Gly198Gly	rpsA	30S ribosomal protein S1
T22.4.5	c02	1908961	snp	200/566	synonymous_variant c.600C>T p.Val200Val	rpsA	30S ribosomal protein S1
T22.4.5	c02	1908967	snp	202/566	missense_variant c.606A>C p.Glu202Asp	rpsA	30S ribosomal protein S1
T22.4.5	c02	1909027	complex	222/566	synonymous_variant c.666_669delTCTCinsCCTG p.224	rpsA	30S ribosomal protein S1
T22.4.5	c02	1909039	snp	226/566	synonymous_variant c.678G>T p.Val226Val	rpsA	30S ribosomal protein S1
T22.4.5	c02	1909072	snp	237/566	synonymous_variant c.711G>T p.Pro237Pro	rpsA	30S ribosomal protein S1

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sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T33.4.1	c01	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ydcO_1	Inner membrane protein YdcO
T33.4.1	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ydcO_1	Inner membrane protein YdcO
T33.4.1	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	HTH-type transcriptional regulatory protein GabR
T33.4.2	c01	96534	snp	202/546	synonymous_variant c.606T>C p.Pro202Pro	groL	60 kDa chaperonin
T33.4.2	c01	96543	snp	205/546	synonymous_variant c.615C>G p.Val205Val	groL	60 kDa chaperonin
T33.4.2	c01	96549	complex	207/546	synonymous_variant c.621_624delCCCTinsTCCG p.209	groL	60 kDa chaperonin
T33.4.2	c01	96567	snp	213/546	synonymous_variant c.639T>G p.Ala213Ala	groL	60 kDa chaperonin
T33.4.2	c01	96609				-	60 kDa chaperonin
			snp	227/546	synonymous_variant c.681C>T p.Leu227Leu	groL	·
T33.4.2	c01	96633	snp	235/546	synonymous_variant c.705G>T p.Pro235Pro	groL	60 kDa chaperonin
T33.4.2	c01	96639	snp	237/546	synonymous_variant c.711G>C p.Leu237Leu	groL	60 kDa chaperonin
T33.4.2	c01	96658	mnp	244/546	missense_variant c.730_731delTCinsGG p.Ser244Gly	groL	60 kDa chaperonin
T33.4.2	c01	96732	snp	268/546	synonymous_variant c.804C>T p.Arg268Arg	groL	60 kDa chaperonin
T33.4.2	c01	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ydcO_1	Inner membrane protein YdcO
T33.4.2	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ydcO_1	Inner membrane protein YdcO
T33.4.2	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	HTH-type transcriptional regulatory protein GabR
T33.4.2	c01	2021999	snp	272/840	missense_variant c.815G>A p.Arg272Lys	virB4_2	Type IV secretion system protein virB4
T33.4.2	c01	2022018	snp	278/840	synonymous_variant c.834C>T p.Arg278Arg	virB4_2	Type IV secretion system protein virB4
T33.4.2	c01	2022111	snp	309/840	synonymous_variant c.927C>A p.Ala309Ala	virB4_2	Type IV secretion system protein virB4
T33.4.2	c01	2022120	mnp	312/840	missense_variant c.936_938delTGCinsGCT p.Ala313Leu	virB4_2	Type IV secretion system protein virB4
T33.4.2	c01	2022133	snp	317/840	missense_variant c.949C>A p.Leu317Met	virB4_2	Type IV secretion system protein virB4
T33.4.2	c01	2022138	complex	318/840	synonymous_variant c.954_957delGCTAinsCTTG p.320	virB4_2	Type IV secretion system protein virB4
T33.4.2	c01	2022160	complex	326/840	missense_variant c.976_978delATCinsGTG p.lle326Val	virB4_2	Type IV secretion system protein virB4
T33.4.2	c01	2022225	snp	347/840	missense_variant c.1041A>C p.Glu347Asp	virB4_2	Type IV secretion system protein virB4
T33.4.2	c01	2022253	snp	357/840	missense_variant c.1069A>G p.lle357Val	virB4_2	Type IV secretion system protein virB4
T33.4.2	c01	2022276	snp	364/840	synonymous_variant c.1092G>C p.Val364Val	virB4_2	Type IV secretion system protein
T00.4.0	-00	4000040		405/500			virB4
T33.4.2	c02	1908946	snp	195/566	synonymous_variant c.585T>C p.Leu195Leu	rpsA	30S ribosomal protein S1
T33.4.2	c02	1908955	snp	198/566	synonymous_variant c.594T>C p.Gly198Gly	rpsA	30S ribosomal protein S1
T33.4.2	c02	1908961	snp	200/566	synonymous_variant c.600C>T p.Val200Val	rpsA	30S ribosomal protein S1
T33.4.2	c02	1908967	snp	202/566	missense_variant c.606A>C p.Glu202Asp	rpsA	30S ribosomal protein S1
T33.4.2	c02	1909027	complex	222/566	synonymous_variant c.666_669delTCTCinsCCTG p.224	rpsA	30S ribosomal protein S1
T33.4.2	c02	1909039	snp	226/566	synonymous_variant c.678G>T p.Val226Val	rpsA	30S ribosomal protein S1
T33.4.2	c02	1909072	snp	237/566	synonymous_variant c.711G>T p.Pro237Pro	rpsA	30S ribosomal protein S1
T33.4.2	c02	1909086	complex	242/566	missense_variant c.725_729delCCATCinsACATT p.Thr242Asn	rpsA	30S ribosomal protein S1
T33.4.3.rep	c01	96441	snp	171/546	synonymous_variant c.513T>C p.Asn171Asn	groL	60 kDa chaperonin
T33.4.3.rep	c01	96450	snp	174/546	synonymous_variant c.522G>C p.Val174Val	groL	60 kDa chaperonin
T33.4.3.rep	c01	96456	snp	176/546	synonymous_variant c.528G>C p.Thr176Thr	groL	60 kDa chaperonin
T33.4.3.rep	c01	96534	snp	202/546	synonymous_variant c.606T>C p.Pro202Pro	groL	60 kDa chaperonin
T33.4.3.rep	c01	96543	snp	205/546	synonymous_variant c.615C>G p.Val205Val	groL	60 kDa chaperonin
T33.4.3.rep	c01	96549	complex	207/546	synonymous_variant c.621_624delCCCTinsTCCG p.209	groL	60 kDa chaperonin
T33.4.3.rep	c01	96567	snp	213/546	synonymous_variant c.639T>G p.Ala213Ala	groL	60 kDa chaperonin
T33.4.3.rep	c01	96609	snp	227/546	synonymous_variant c.681C>T p.Leu227Leu	groL	60 kDa chaperonin
T33.4.3.rep	c01	96624	complex	232/546	missense_variant c.696_699delTCTTinsCATG p.Leu233Met	groL	60 kDa chaperonin
T33.4.3.rep	c01	96633	snp	235/546	synonymous_variant c.705G>T p.Pro235Pro	groL	60 kDa chaperonin
T33.4.3.rep	c01	96639	snp	237/546	synonymous_variant c.711G>C p.Leu237Leu	groL	60 kDa chaperonin
T33.4.3.rep	c01	96658	mnp	244/546	missense_variant c.730_731delTCinsGG p.Ser244Gly	groL	60 kDa chaperonin
T33.4.3.rep	c01	96732	snp	268/546	synonymous_variant c.804C>T p.Arg268Arg	groL	60 kDa chaperonin
T33.4.3.rep	c01	96732		271/546		_	•
,			snp		synonymous_variant c.813G>C p.Leu271Leu	groL	60 kDa chaperonin
T33.4.3.rep	c01	96753	snp	275/546	synonymous_variant c.825T>C p.Ala275Ala	groL	60 kDa chaperonin
T33.4.3.rep	c01	96777	snp	283/546	synonymous_variant c.849T>C p.Asp283Asp	groL	60 kDa chaperonin
T33.4.3.rep	c01	96786	snp	286/546	synonymous_variant c.858A>G p.Lys286Lys	groL	60 kDa chaperonin
T33.4.3.rep	c01	96795	snp	289/546	synonymous_variant c.867C>G p.Leu289Leu	groL	60 kDa chaperonin
T33.4.3.rep	c01	96807	snp	293/546	synonymous_variant c.879G>C p.Ala293Ala	groL	60 kDa chaperonin
T00 40	c01	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ydcO_1	Inner membrane protein YdcO
T33.4.3.rep	COT	1000010	40.	,		,	

sample			TVDE		FFFFOT		DDODUOT
T33.4.3.rep	cHROM c01	POS 1010254	TYPE del	2/429	frameshift_variant c.4delG p.Ala2fs	GENE gabR_1	PRODUCT HTH-type transcriptional regulatory
T33.4.3.rep	c01	2007281	snp	55/133	synonymous_variant c.165C>G p.Thr55Thr	ssb_1	protein GabR Single-stranded DNA-binding protein
T33.4.3.rep	c01	2007330	complex	72/133	missense_variant c.214_216delCAAinsGAG p.Gln72Glu	ssb_1	Single-stranded DNA-binding
·	c01				<u> </u>		protein Single-stranded DNA-binding
T33.4.3.rep		2007347	snp	77/133	synonymous_variant c.231T>C p.Gly77Gly	ssb_1	protein Single-stranded DNA-binding
T33.4.3.rep	c01	2007392	snp	92/133	synonymous_variant c.276C>G p.Thr92Thr	ssb_1	protein Type IV secretion system protein
T33.4.3.rep	c01	2021961	snp	259/840	synonymous_variant c.777G>C p.Ser259Ser	virB4_2	virB4 Type IV secretion system protein
T33.4.3.rep	c01	2021973	complex	263/840	missense_variant c.789_793delTCTGAinsCCTGC p.Met265Leu	virB4_2	virB4
T33.4.3.rep	c01	2021999	snp	272/840	missense_variant c.815G>A p.Arg272Lys	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2022018	snp	278/840	synonymous_variant c.834C>T p.Arg278Arg	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2022111	snp	309/840	synonymous_variant c.927C>A p.Ala309Ala	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2022120	mnp	312/840	missense_variant c.936_938delTGCinsGCT p.Ala313Leu	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2022133	snp	317/840	missense_variant c.949C>A p.Leu317Met	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2022138	complex	318/840	synonymous_variant c.954_957delGCTAinsCTTG p.320	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2022160	complex	326/840	missense_variant c.976_978delATCinsGTG p.lle326Val	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2022206	complex	341/840	missense_variant c.1022_1031delCCGATGCCGCinsAGGACGCCCG p.AlaAspAlaAla341GluAspAlaArq	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2022225	snp	347/840	missense_variant c.1041A>C p.Glu347Asp	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2022253	snp	357/840	missense_variant c.1069A>G p.lle357Val	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2022276	snp	364/840	synonymous_variant c.1092G>C p.Val364Val	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2022318	snp	378/840	synonymous_variant c.1134C>G p.Ser378Ser	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2022324	snp	380/840	synonymous_variant c.1140G>C p.Pro380Pro	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2022330	complex	382/840	synonymous_variant c.1146_1149delCGCCinsTGCT p.384	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2022339	snp	385/840	synonymous_variant c.1155A>C p.Ala385Ala	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2022358	snp	392/840	missense_variant c.1174G>A p.Val392lle	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2023443	snp	753/840	synonymous_variant c.2259C>T p.Gly753Gly	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2023509	snp	775/840	synonymous_variant c.2325T>C p.Asp775Asp	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2023515	snp	777/840	synonymous_variant c.2331C>A p.Leu777Leu	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2023521	snp	779/840	synonymous_variant c.2337G>A p.Glu779Glu	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2023532	complex	783/840	missense_variant c.2348_2352delACGGTinsGCGGC p.Asp783Gly	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2023545	complex	787/840	synonymous_variant c.2361_2364delTGCAinsCGCT p.789	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2023554	snp	790/840	synonymous_variant c.2370C>G p.Leu790Leu	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c02	435993	complex	496/1377	synonymous_variant c.1488_1491delGGTCinsCGTG p.498	rpoB	DNA-directed RNA polymerase subunit beta
T33.4.3.rep	c02	436008	snp	501/1377	synonymous_variant c.1503T>C p.Asp501Asp	rpoB	DNA-directed RNA polymerase subunit beta
T33.4.3.rep	c02	436029	snp	508/1377	synonymous_variant c.1524T>A p.Ala508Ala	rpoB	DNA-directed RNA polymerase subunit beta
T33.4.3.rep	c02	436035	snp	510/1377	synonymous_variant c.1530A>C p.Ala510Ala	rpoB	DNA-directed RNA polymerase subunit beta
T33.4.3.rep	c02	436041	snp	512/1377	synonymous_variant c.1536G>T p.Val512Val	гроВ	DNA-directed RNA polymerase subunit beta
T33.4.3.rep	c02	436047	snp	514/1377	synonymous_variant c.1542G>A p.Glu514Glu	rpoB	DNA-directed RNA polymerase subunit beta
	c02	436083	complex	526/1377	missense_variant c.1578_1584delTCAGACCinsCCAGGTG p.Thr528Val	rpoB	DNA-directed RNA polymerase subunit beta

18.4.1.6. 18.2. 18.6.1.6	sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
1846-169 622 440648 470 3504400 570	T33.4.3.rep	c02	436125	snp	540/1377	synonymous_variant c.1620C>T p.Leu540Leu	rpoB	I
19.4.1.0.0 20.7 4.506.5 20.9 3.601.4.0 3.601.4.0 3.601.	T33.4.3.rep	c02	436143	snp	546/1377	synonymous_variant c.1638C>T p.Gly546Gly	rpoB	I
1924-1289 022 429974 279 2441400 279797 279799000000000000000000000000000000000	T33.4.3.rep	c02	439856	snp	338/1400	synonymous_variant c.1014T>C p.Gly338Gly	rpoC	' '
Table Tabl	T33.4.3.rep	c02	439865	snp	341/1400	synonymous_variant c.1023T>C p.Arg341Arg	rpoC	I
133.4.3.pp 02	T33.4.3.rep	c02	439874	snp	344/1400	synonymous_variant c.1032G>T p.Leu344Leu	rpoC	DNA-directed RNA polymerase
T33 A3 Feb 100	T33.4.3.rep	c02	439910	snp	356/1400	synonymous_variant c.1068C>T p.Val356Val	rpoC	DNA-directed RNA polymerase
133.43,00 02	T33.4.3.rep	c02	439931	snp	363/1400	synonymous_variant c.1089C>G p.Leu363Leu	rpoC	DNA-directed RNA polymerase
13.14.1479 202	T33.4.3.rep	c02	439985	snp	381/1400	synonymous_variant c.1143A>G p.Pro381Pro	rpoC	DNA-directed RNA polymerase
133.4.3.4.9 102 4.0156 199 4.991400 9.9907/mone.y.variant.cl33192566CACH964Tp.Thr.442Med 1050 1000-4 microsot.get (4.1)1400 missense_variant.cl333192566CACH964Tp.Thr.442Med 1050 1000-4 microsot.get (4.1)1400 1000-4	T33.4.3.rep	c02	440144	snp	434/1400	synonymous_variant c.1302T>G p.Leu434Leu	rpoC	DNA-directed RNA polymerase
23.4.1.mg	T33.4.3.rep	c02	440156	snp	438/1400	synonymous_variant c.1314C>T p.Ala438Ala	rpoC	DNA-directed RNA polymerase
133.4.3.rs 0.02	T33.4.3.rep	c02	440165	complex	441/1400	missense_variant c.1323_1325delCACinsGAT p.Thr442Met	rpoC	DNA-directed RNA polymerase
13.4.3.rep 10.2 40188 3rp	·					·		DNA-directed RNA polymerase
133.43.rsp 022				·		<u> </u>		
133.4.3.rep CO2								
13.4.3.rep Co. 44020 Compile 459/HoV Synonymous_variant c.13740-C p.Ala-458Ala Fig. C Subunit beta' Synonymous_variant c.13740-C p.Ala-458Ala Fig. C Subunit beta' Fig. C				·	·			
13.4.3.rp CV				·				subunit beta'
133.4.3.rep co 440270 snp 476/1400 synonymous_variant c.1428C>0 p.Leu478Leu p.De. Subunit beta' subunit subunit su	T33.4.3.rep	c02	440216	snp	458/1400	synonymous_variant c.1374G>C p.Ala458Ala	rpoC	subunit beta'
133.4.3.rep CO2	T33.4.3.rep	c02	440264	snp	474/1400	synonymous_variant c.1422G>C p.Leu474Leu	rpoC	subunit beta'
13.34.3.1ep CO2	T33.4.3.rep	c02	440270	snp	476/1400	synonymous_variant c.1428C>G p.Leu476Leu	rpoC	subunit beta'
13.3.4.3.rep CO2	T33.4.3.rep	c02	440282	snp	480/1400	synonymous_variant c.1440T>G p.Leu480Leu	rpoC	subunit beta'
13.3.4.3.rep CO2	T33.4.3.rep	c02	440288	snp	482/1400	synonymous_variant c.1446A>G p.Ala482Ala	rpoC	
13.3.4.3.rep CO2	T33.4.3.rep	c02	441077	snp	745/1400	synonymous_variant c.2235C>A p.Ala745Ala	rpoC	' '
133.4.3.rep C02	T33.4.3.rep	c02	441101	complex	753/1400	synonymous_variant c.2259_2262delAACCinsGACG p.755	rpoC	
133.4.3.rep CO2	T33.4.3.rep	c02	441110	snp	756/1400	synonymous_variant c.2268A>C p.lle756lle	rpoC	I
133.4.3.rep CO2	T33.4.3.rep	c02	441195	snp	785/1400	synonymous_variant c.2353T>C p.Leu785Leu	rpoC	I
T33.4.3.rep c02 445987 snp 360/694 synonymous_variant c.1078T>C p.Leu360Leu fusA Elongation factor G T33.4.3.rep c02 446031 complex 374/694 synonymous_variant c.1122_1125delTGCAinsCGCC p.376 fusA Elongation factor G T33.4.3.rep c02 446133 complex 408/694 missense_variant c.1224_1227delGGATinsCGAG p.Asp409Glu fusA Elongation factor G T33.4.3.rep c02 446142 complex 411/694 missense_variant c.12451>G p.Ala415Ala fusA Elongation factor G T33.4.3.rep c02 446174 snp 415/694 synonymous_variant c.12451>G p.Ala415Ala fusA Elongation factor G T33.4.3.rep c02 446174 snp 422/694 missense_variant c.12451>C p.Ala415Ala fusA Elongation factor G T33.4.3.rep c02 451011 snp 243/277 synonymous_variant c.7291>C p.Arg243Arg rplB 50S ribosomal protein L2 T33.4.3.rep c02 451038 snp 252/277 synonymous_variant c.7561>C p.Pro252Pro rplB	T33.4.3.rep	c02	441203	complex	787/1400	synonymous_variant c.2361_2364delTGCTinsGGCG p.789	rpoC	I
T33.4.3.rep c02 446031 complex 374/694 synonymous_variant c.1122_1125delTGCAinsCGCC p.376 fusA Elongation factor G T33.4.3.rep c02 446133 complex 408/694 missense_variant c.1224_1227delGGATinsCGAG p.Asp409Glu fusA Elongation factor G T33.4.3.rep c02 446142 complex 411/694 missense_variant c.1233_1239delTATCGAAinsCATCCAG p.Glu413Gln fusA Elongation factor G T33.4.3.rep c02 446154 snp 415/694 synonymous_variant c.1265C>G p.Ala415Ala fusA Elongation factor G T33.4.3.rep c02 446174 snp 422/694 missense_variant c.1265C>G p.Ala422Gly fusA Elongation factor G T33.4.3.rep c02 451011 snp 243/277 synonymous_variant c.729T>C p.Arg243Arg rplB 50S ribosomal protein L2 T33.4.3.rep c02 451038 snp 252/277 synonymous_variant c.756T>C p.Pro252Pro rplB 50S ribosomal protein L2 T33.4.3.rep c02 45161 complex 10/92 synonymous_variant c.769_777delAAGCGCGCinsCCGCTT	T33.4.3.rep	c02	445968	snp	353/694	synonymous_variant c.1059T>C p.Arg353Arg	fusA	Elongation factor G
T33.4.3.rep C02 446133 complex 408/694 missense_variant c.1224_1227delGGATinsCGAG p.Asp409Glu fusA Elongation factor G T33.4.3.rep c02 446142 complex 411/694 missense_variant c.1233_1239delTATCGAAinsCATCCAG p.Glu413Gln fusA Elongation factor G T33.4.3.rep c02 446154 snp 415/694 synonymous_variant c.1265C>G p.Ala415Ala fusA Elongation factor G T33.4.3.rep c02 446174 snp 422/694 missense_variant c.1265C>G p.Ala422Gly fusA Elongation factor G T33.4.3.rep c02 451011 snp 243/277 synonymous_variant c.729T>C p.Arg243Arg rplB 50S ribosomal protein L2 T33.4.3.rep c02 451038 snp 252/277 synonymous_variant c.756T>C p.Pro252Pro rplB 50S ribosomal protein L2 T33.4.3.rep c02 451051 complex 257/277 missense_variant c.769_777delAAGACGCGCinsCGCACCCGT rplB 50S ribosomal protein L2 T33.4.3.rep c02 45161 complex 10/92 synonymous_variant c.30_26delCGTTGATinsTGTT	T33.4.3.rep	c02	445987	snp	360/694	synonymous_variant c.1078T>C p.Leu360Leu	fusA	Elongation factor G
T33.4.3.rep C02 446142 complex 411/694 missense_variant c.1233_1239delTATCGAAinsCATCCAG p.Glu413Gln fusA Elongation factor G T33.4.3.rep c02 446154 snp 415/694 synonymous_variant c.1245T>G p.Ala415Ala fusA Elongation factor G T33.4.3.rep c02 446174 snp 422/694 missense_variant c.1265C>G p.Ala422Gly fusA Elongation factor G T33.4.3.rep c02 451011 snp 243/277 synonymous_variant c.729T>C p.Arg243Arg rplB 50S ribosomal protein L2 T33.4.3.rep c02 451017 complex 245/277 synonymous_variant c.756T>C p.Pro252Pro rplB 50S ribosomal protein L2 T33.4.3.rep c02 451051 complex 257/277 missense_variant c.769_777delAAGACGCGCinsCGCACCCGT rplB 50S ribosomal protein L2 T33.4.3.rep c02 451161 complex 257/277 missense_variant c.30_36delCGTCGATinsTGTTGAC p.13 rpsS 30S ribosomal protein L2 T33.4.3.rep c02 453539 snp 13/122 synonymous_variant c.39C-7 p.Asn13Asn <td>T33.4.3.rep</td> <td>c02</td> <td>446031</td> <td>complex</td> <td>374/694</td> <td>synonymous_variant c.1122_1125delTGCAinsCGCC p.376</td> <td>fusA</td> <td>Elongation factor G</td>	T33.4.3.rep	c02	446031	complex	374/694	synonymous_variant c.1122_1125delTGCAinsCGCC p.376	fusA	Elongation factor G
T33.4.3.rep C02 446142 complex 411/694 missense_variant c.1233_1239delTATCGAAinsCATCCAG p.Glu413Gln fusA Elongation factor G T33.4.3.rep c02 446154 snp 415/694 synonymous_variant c.1245T>G p.Ala415Ala fusA Elongation factor G T33.4.3.rep c02 446174 snp 422/694 missense_variant c.1265C>G p.Ala422Gly fusA Elongation factor G T33.4.3.rep c02 451011 snp 243/277 synonymous_variant c.729T>C p.Arg243Arg rplB 50S ribosomal protein L2 T33.4.3.rep c02 451017 complex 245/277 synonymous_variant c.756T>C p.Pro252Pro rplB 50S ribosomal protein L2 T33.4.3.rep c02 451051 complex 257/277 missense_variant c.769_777delAAGACGCGCinsCGCACCCGT rplB 50S ribosomal protein L2 T33.4.3.rep c02 451161 complex 257/277 missense_variant c.30_36delCGTCGATinsTGTTGAC p.13 rpsS 30S ribosomal protein L2 T33.4.3.rep c02 453539 snp 13/122 synonymous_variant c.39C-7 p.Asn13Asn <td>T33.4.3.rep</td> <td>c02</td> <td>446133</td> <td>complex</td> <td>408/694</td> <td>missense variant c.1224 1227delGGATinsCGAG p.Asp409Glu</td> <td>fusA</td> <td>Elongation factor G</td>	T33.4.3.rep	c02	446133	complex	408/694	missense variant c.1224 1227delGGATinsCGAG p.Asp409Glu	fusA	Elongation factor G
T33.4.3.rep C02 446154 snp 415/694 synonymous_variant c.1245T>G p.Ala415Ala fusA Elongation factor G T33.4.3.rep c02 446174 snp 422/694 missense_variant c.1265C>G p.Ala422Gly fusA Elongation factor G T33.4.3.rep c02 451011 snp 243/277 synonymous_variant c.729T>C p.Arg243Arg rplB 50S ribosomal protein L2 T33.4.3.rep c02 451017 complex 245/277 synonymous_variant c.735_738delTGCinsGGTT p.247 rplB 50S ribosomal protein L2 T33.4.3.rep c02 451038 snp 252/277 synonymous_variant c.756T>C p.Pro252Pro rplB 50S ribosomal protein L2 T33.4.3.rep c02 451051 complex 257/277 missense_variant c.769_777delAAGACGCGCinsCGCACCCGT p.13 rplB 50S ribosomal protein L2 T33.4.3.rep c02 451161 complex 10/92 synonymous_variant c.30_36delCGTCGATinsTGTTGAC p.13 rpsS 30S ribosomal protein L14 T33.4.3.rep c02 453539 snp 13/122 synonymous_variant c.90_96delGCGTTACinsCAAATAT								Flongation factor G
T33.4.3.rep CO2 446174 snp 422/694 missense_variant c.1265C>G p.Ala422Gly fusA Elongation factor G T33.4.3.rep cO2 451011 snp 243/277 synonymous_variant c.729T>C p.Arg243Arg rplB 50S ribosomal protein L2 T33.4.3.rep cO2 451017 complex 245/277 synonymous_variant c.735_738delTGCinsGGTT p.247 rplB 50S ribosomal protein L2 T33.4.3.rep cO2 451038 snp 252/277 synonymous_variant c.766T>C p.Pro252Pro rplB 50S ribosomal protein L2 T33.4.3.rep cO2 451051 complex 257/277 missense_variant c.766T>C p.Pro252Pro rplB 50S ribosomal protein L2 T33.4.3.rep cO2 451161 complex 257/277 missense_variant c.30_36delCGTCGATinsTGTTGAC p.13 rpsS 30S ribosomal protein L2 T33.4.3.rep cO2 453539 snp 13/122 synonymous_variant c.39C>T p.Asn13Asn rplN 50S ribosomal protein L14 T33.4.3.rep cO2 453602 snp 34/122 synonymous_variant c.102C>T p.Ser34Ser rplN <td>•</td> <td></td> <td></td> <td>-</td> <td></td> <td></td> <td>-</td> <td>-</td>	•			-			-	-
T33.4.3.rep C02 451011 snp 243/277 synonymous_variant c.729T>C p.Arg243Arg rplB 50S ribosomal protein L2 T33.4.3.rep c02 451017 complex 245/277 synonymous_variant c.735_738delTGTCinsGGTT p.247 rplB 50S ribosomal protein L2 T33.4.3.rep c02 451038 snp 252/277 synonymous_variant c.756T>C p.Pro252Pro rplB 50S ribosomal protein L2 T33.4.3.rep c02 451051 complex 257/277 missense_variant c.769_777delAAGACGCGCinsCGCACCCGT p.Lys257Arg rplB 50S ribosomal protein L2 T33.4.3.rep c02 451161 complex 10/92 synonymous_variant c.30_36delCGTCGATinsTGTTGAC p.13 rpsS 30S ribosomal protein L2 T33.4.3.rep c02 453539 snp 13/122 synonymous_variant c.39c>T p.Asn13Asn rplN 50S ribosomal protein L14 T33.4.3.rep c02 453602 snp 34/122 synonymous_variant c.102c>T p.Ser34Ser rplN 50S ribosomal protein L14 T33.4.3.rep c02 453650 complex 40/122 synonymous_variant c.159A>G p						<u> </u>		-
T33.4.3.rep C02 451017 complex 245/277 synonymous_variant c.735_738delTGTCinsGGTT p.247 rplB 50S ribosomal protein L2 T33.4.3.rep c02 451038 snp 252/277 synonymous_variant c.756T>C p.Pro252Pro rplB 50S ribosomal protein L2 T33.4.3.rep c02 451051 complex 257/277 missense_variant c.769_777delAAGACGCGCinsCGCACCCGT p.Lys257Arg rplB 50S ribosomal protein L2 T33.4.3.rep c02 451161 complex 10/92 synonymous_variant c.30_36delCGTCGATinsTGTTGAC p.13 rpsS 30S ribosomal protein L12 T33.4.3.rep c02 453539 snp 13/122 synonymous_variant c.39C>T p.Asn13Asn rplN 50S ribosomal protein L14 T33.4.3.rep c02 453690 complex 30/122 missense_variant c.102C>T p.Ser34Ser rplN 50S ribosomal protein L14 T33.4.3.rep c02 453602 snp 34/122 synonymous_variant c.102C>T p.Ser34Ser rplN 50S ribosomal protein L14 T33.4.3.rep c02 453659 snp 53/122 synonymous_variant c.159A>G p.L	•					· ·	-	-
T33.4.3.rep c02 451038 snp 252/277 synonymous_variant c.756T>C p.Pro252Pro rplB 50S ribosomal protein L2 T33.4.3.rep c02 451051 complex 257/277 missense_variant c.769_777delAAGACGCGCinsCGCACCCGT p.Lys257Arg rplB 50S ribosomal protein L2 T33.4.3.rep c02 451161 complex 10/92 synonymous_variant c.30_36delCGTCGATinsTGTTGAC p.13 rpsS 30S ribosomal protein S19 T33.4.3.rep c02 453539 snp 13/122 synonymous_variant c.39C>T p.Asn13Asn rplN 50S ribosomal protein L14 T33.4.3.rep c02 453690 complex 30/122 missense_variant c.90_96delGCGTTACinsCAAATAT p.Arg31Lys rplN 50S ribosomal protein L14 T33.4.3.rep c02 453602 snp 34/122 synonymous_variant c.102C>T p.Ser34Ser rplN 50S ribosomal protein L14 T33.4.3.rep c02 453620 complex 40/122 synonymous_variant c.120_126delGGTTCGinsCGTTTCC p.43 rplN 50S ribosomal protein L14 T33.4.3.rep c02 453665 complex 55/122 syno				· ·		· · · · · · · · · · · · · · · · · · ·	<u> </u>	·
T33.4.3.rep c02 451051 complex 257/277 missense_variant c.769_777delAAGACGCGCinsCGCACCCGT p.Lys257Arg rpIB 50S ribosomal protein L2 T33.4.3.rep c02 451161 complex 10/92 synonymous_variant c.30_36delCGTCGATinsTGTTGAC p.13 rpsS 30S ribosomal protein S19 T33.4.3.rep c02 453539 snp 13/122 synonymous_variant c.39C>T p.Asn13Asn rplN 50S ribosomal protein L14 T33.4.3.rep c02 453590 complex 30/122 missense_variant c.90_96delGCGTTACinsCAAATAT p.Arg31Lys rplN 50S ribosomal protein L14 T33.4.3.rep c02 453602 snp 34/122 synonymous_variant c.102C>T p.Ser34Ser rplN 50S ribosomal protein L14 T33.4.3.rep c02 453620 complex 40/122 synonymous_variant c.120_126delGGTGTCGinsCGTTTCC p.43 rplN 50S ribosomal protein L14 T33.4.3.rep c02 453659 snp 53/122 synonymous_variant c.159A>G p.Lys53Lys rplN 50S ribosomal protein L14 T33.4.3.rep c02 453665 complex 55/122 syno	-			complex			<u> </u>	·
133.4.3.rep CO2 451051 complex 257/27/2 p.Lys257Arg rpiB 50S ribosomal protein L2 T33.4.3.rep cO2 451161 complex 10/92 synonymous_variant c.30_36delCGTCGATinsTGTTGAC p.13 rpsS 30S ribosomal protein S19 T33.4.3.rep cO2 453539 snp 13/122 synonymous_variant c.39C>T p.Asn13Asn rplN 50S ribosomal protein L14 T33.4.3.rep cO2 453690 complex 30/122 missense_variant c.102C>T p.Ser34Ser rplN 50S ribosomal protein L14 T33.4.3.rep cO2 453620 complex 40/122 synonymous_variant c.120_126delGGTGTCGinsCGTTTCC p.43 rplN 50S ribosomal protein L14 T33.4.3.rep cO2 453659 snp 53/122 synonymous_variant c.159A>G p.Lys53Lys rplN 50S ribosomal protein L14 T33.4.3.rep cO2 453665 complex 55/122 synonymous_variant c.165_168delTGATinsCGAC p.57 rplN 50S ribosomal protein L14 T33.4.3.rep cO2 688342 snp 245/424 synonymous_variant c.735C>G p.Lei/245I et clpX	T33.4.3.rep	c02	451038	snp	252/277	synonymous_variant c.756T>C p.Pro252Pro	rpIB	50S ribosomal protein L2
T33.4.3.rep c02 453539 snp 13/122 synonymous_variant c.39C>T p.Asn13Asn rplN 50S ribosomal protein L14 T33.4.3.rep c02 453590 complex 30/122 missense_variant c.90_96delGCGTTACinsCAAATAT p.Arg31Lys rplN 50S ribosomal protein L14 T33.4.3.rep c02 453602 snp 34/122 synonymous_variant c.102C>T p.Ser34Ser rplN 50S ribosomal protein L14 T33.4.3.rep c02 453620 complex 40/122 synonymous_variant c.120_126delGGTGTCGinsCGTTTCC p.43 rplN 50S ribosomal protein L14 T33.4.3.rep c02 453659 snp 53/122 synonymous_variant c.159A>G p.Lys53Lys rplN 50S ribosomal protein L14 T33.4.3.rep c02 453665 complex 55/122 synonymous_variant c.165_168delTGATinsCGAC p.57 rplN 50S ribosomal protein L14 T33.4.3.rep c02 688342 snp 245/424 synonymous_variant c.735C>G p.Leu245Leu clpX ATP-dependent Clp protease AT	T33.4.3.rep	c02	451051	complex	257/277		rplB	50S ribosomal protein L2
T33.4.3.rep c02 453590 complex 30/122 missense_variant c.90_96delGCGTTACinsCAAATAT p.Arg31Lys rplN 50S ribosomal protein L14 T33.4.3.rep c02 453602 snp 34/122 synonymous_variant c.102C>T p.Ser34Ser rplN 50S ribosomal protein L14 T33.4.3.rep c02 453620 complex 40/122 synonymous_variant c.120_126delGGTGTCGinsCGTTTCC p.43 rplN 50S ribosomal protein L14 T33.4.3.rep c02 453659 snp 53/122 synonymous_variant c.159A>G p.Lys53Lys rplN 50S ribosomal protein L14 T33.4.3.rep c02 453665 complex 55/122 synonymous_variant c.165_168delTGATinsCGAC p.57 rplN 50S ribosomal protein L14 T33.4.3.rep c02 698342 snp 245/424 synonymous_variant c.735C>G p.Leu245Leu clpX ATP-dependent Clp protease ATP-dependent Clp	T33.4.3.rep	c02	451161	complex	10/92	synonymous_variant c.30_36delCGTCGATinsTGTTGAC p.13	rpsS	30S ribosomal protein S19
T33.4.3.rep c02 453602 snp 34/122 synonymous_variant c.102C>T p.Ser34Ser rplN 50S ribosomal protein L14 T33.4.3.rep c02 453620 complex 40/122 synonymous_variant c.120_126delGGTGTGGinsCGTTTCC p.43 rplN 50S ribosomal protein L14 T33.4.3.rep c02 453659 snp 53/122 synonymous_variant c.159A>G p.Lys53Lys rplN 50S ribosomal protein L14 T33.4.3.rep c02 453665 complex 55/122 synonymous_variant c.165_168delTGATinsCGAC p.57 rplN 50S ribosomal protein L14 T33.4.3.rep c02 698342 snp 245/424 synonymous_variant c.735C>G p.Leu245Leu clpX ATP-dependent Clp protease	T33.4.3.rep	c02	453539	snp	13/122	synonymous_variant c.39C>T p.Asn13Asn	rpIN	50S ribosomal protein L14
T33.4.3.rep c02 453602 snp 34/122 synonymous_variant c.102C>T p.Ser34Ser rplN 50S ribosomal protein L14 T33.4.3.rep c02 453620 complex 40/122 synonymous_variant c.120_126delGGTGTGGinsCGTTTCC p.43 rplN 50S ribosomal protein L14 T33.4.3.rep c02 453659 snp 53/122 synonymous_variant c.159A>G p.Lys53Lys rplN 50S ribosomal protein L14 T33.4.3.rep c02 453665 complex 55/122 synonymous_variant c.165_168delTGATinsCGAC p.57 rplN 50S ribosomal protein L14 T33.4.3.rep c02 698342 snp 245/424 synonymous_variant c.735C>G p.Leu245Leu clpX ATP-dependent Clp protease	T33.4.3.rep	c02	453590	complex	30/122	missense_variant c.90_96delGCGTTACinsCAAATAT p.Arg31Lys	rplN	50S ribosomal protein L14
T33.4.3.rep c02 453620 complex 40/122 synonymous_variant c.120_126delGGTGCGinsCGTTTCC p.43 rplN 50S ribosomal protein L14 T33.4.3.rep c02 453659 snp 53/122 synonymous_variant c.159A>G p.Lys53Lys rplN 50S ribosomal protein L14 T33.4.3.rep c02 453665 complex 55/122 synonymous_variant c.165_168delTGATinsCGAC p.57 rplN 50S ribosomal protein L14 T33.4.3.rep c02 698.342 snp 245/424 synonymous_variant c.735C>G p.Let/245 let/ clpX ATP-dependent Clp protease ATP-dependent							<u> </u>	·
T33.4.3.rep c02 453659 snp 53/122 synonymous_variant c.159A>G p.Lys53Lys rplN 50S ribosomal protein L14 T33.4.3.rep c02 453665 complex 55/122 synonymous_variant c.165_168delTGATinsCGAC p.57 rplN 50S ribosomal protein L14 T33.4.3.rep c02 698.342 snp 245/424 synonymous_variant c.735C>G p.Lei/245Lei clpX ATP-dependent Clp protease ATP-dependent Clp prot	•					<u> </u>	<u> </u>	·
T33.4.3.rep c02 453665 complex 55/122 synonymous_variant c.165_168delTGATinsCGAC p.57 rplN 50S ribosomal protein L14 T33.4.3.rep c02 698342 spp 245/424 synonymous_variant c.735C>G p.Leu245Leu clpX ATP-dependent Clp protease ATP-				-				·
T33.4.3 rep. c02 698342 spp. 245/424 synonymous variant c 735C>G p l eu245l eu	•							·
133.4.3 rep. 1 c02	133.4.3.rep	CUZ	453665	complex	55/122	Synonymous_variant c.ros_fosderrGATINSCGAC p.5/	rpiN	·
	T33.4.3.rep	c02	698342	snp	245/424	synonymous_variant c.735C>G p.Leu245Leu	clpX	1

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T33.4.3.rep	c02	698351	snp	242/424	synonymous_variant c.726G>C p.Thr242Thr	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T33.4.3.rep	c02	698357	snp	240/424	synonymous_variant c.720C>T p.Asp240Asp	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T33.4.3.rep	c02	698399	snp	226/424	synonymous_variant c.678A>G p.Gln226Gln	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T33.4.3.rep	c02	698420	snp	219/424	synonymous_variant c.657C>G p.Thr219Thr	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T33.4.3.rep	c02	698474	snp	201/424	synonymous_variant c.603C>T p.Arg201Arg	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T33.4.3.rep	c02	698492	snp	195/424	synonymous_variant c.585T>C p.Asp195Asp	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T33.4.3.rep	c02	698505	mnp	190/424	synonymous_variant c.570_572delCAGinsTTC p.192	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T33.4.3.rep	c02	698618	complex	152/424	synonymous_variant c.456_459delAGGCinsCGGT p.154	clpX	ATP-dependent Clp protease ATP-
T33.4.3.rep	c02	698627	snp	150/424	synonymous_variant c.450G>C p.Thr150Thr	clpX	ATP-dependent Clp protease ATP-
T33.4.3.rep	c02	698633	snp	148/424	synonymous_variant c.444A>G p.Thr148Thr	clpX	ATP-dependent Clp protease ATP-
T33.4.3.rep	c02	698639	snp	146/424	synonymous_variant c.438G>A p.Ala146Ala	clpX	binding subunit ClpX ATP-dependent Clp protease ATP-
·	c02		·				binding subunit ClpX ATP-dependent Clp protease ATP-
T33.4.3.rep		698645	snp	144/424	synonymous_variant c.432C>G p.Ala144Ala	clpX	binding subunit ClpX ATP-dependent Clp protease ATP-
T33.4.3.rep	c02	698657	complex	138/424	synonymous_variant c.414_420delTGTGCCAinsCGTTCCC p.141	clpX	binding subunit ClpX ATP-dependent Clp protease ATP-
T33.4.3.rep	c02	698675	snp	134/424	synonymous_variant c.402A>C p.Ala134Ala	clpX	binding subunit ClpX ATP-dependent Clp protease ATP-
T33.4.3.rep	c02	698726	complex	116/424	missense_variant c.348_351delTCTTinsCATG p.Leu117Met	clpX	binding subunit ClpX
T33.4.3.rep	c02	698752	snp	109/424	missense_variant c.325A>G p.lle109Val	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T33.4.3.rep	c02	1908916	complex	185/566	synonymous_variant c.555_558delGGAAinsCGAG p.187	rpsA	30S ribosomal protein S1
T33.4.3.rep	c02	1908928	snp	189/566	synonymous_variant c.567G>T p.Ser189Ser	rpsA	30S ribosomal protein S1
T33.4.3.rep	c02	1908937	snp	192/566	synonymous_variant c.576C>T p.Val192Val	rpsA	30S ribosomal protein S1
T33.4.3.rep	c02	1908946	snp	195/566	synonymous_variant c.585T>C p.Leu195Leu	rpsA	30S ribosomal protein S1
T33.4.3.rep	c02	1908955	snp	198/566	synonymous_variant c.594T>C p.Gly198Gly	rpsA	30S ribosomal protein S1
T33.4.3.rep	c02	1908961	snp	200/566	synonymous_variant c.600C>T p.Val200Val	rpsA	30S ribosomal protein S1
T33.4.3.rep	c02	1908967	snp	202/566	missense_variant c.606A>C p.Glu202Asp	rpsA	30S ribosomal protein S1
T33.4.3.rep	c02	1909027	complex	222/566	synonymous_variant c.666_669delTCTCinsCCTG p.224	rpsA	30S ribosomal protein S1
T33.4.3.rep	c02	1909039	snp	226/566	synonymous_variant c.678G>T p.Val226Val	rpsA	30S ribosomal protein S1
T33.4.3.rep	c02	1909072	snp	237/566	synonymous_variant c.711G>T p.Pro237Pro	rpsA	30S ribosomal protein S1
T33.4.3.rep	c02	1909086	complex	242/566	missense_variant c.725_729delCCATCinsACATT p.Thr242Asn	rpsA	30S ribosomal protein S1
T33.4.3.rep					· · · · · · · · · · · · · · · · · · ·		•
	c02	1909097	mnp	246/566	missense_variant c.736_737delACinsCA p.Thr246Gln	rpsA	30S ribosomal protein S1
T33.4.3.rep	c02	1909108	snp	249/566	synonymous_variant c.747G>T p.Val249Val	rpsA	30S ribosomal protein S1
T33.4.4	c01	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ydcO_1	Inner membrane protein YdcO
T33.4.4	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ydcO_1	Inner membrane protein YdcO
T33.4.4	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	HTH-type transcriptional regulatory protein GabR
T33.4.5	c01	96441	snp	171/546	synonymous_variant c.513T>C p.Asn171Asn	groL	60 kDa chaperonin
T33.4.5	c01	96450	snp	174/546	synonymous_variant c.522G>C p.Val174Val	groL	60 kDa chaperonin
T33.4.5	c01	96456	snp	176/546	synonymous_variant c.528G>C p.Thr176Thr	groL	60 kDa chaperonin
T33.4.5	c01	96534	snp	202/546	synonymous_variant c.606T>C p.Pro202Pro	groL	60 kDa chaperonin
T33.4.5	c01	96543	snp	205/546	synonymous_variant c.615C>G p.Val205Val	groL	60 kDa chaperonin
T33.4.5	c01	96549	complex	207/546	synonymous_variant c.621_624delCCCTinsTCCG p.209	groL	60 kDa chaperonin
			· ·				•
T33.4.5	c01	96567	snp	213/546	synonymous_variant c.639T>G p.Ala213Ala	groL	60 kDa chaperonin
T33.4.5	c01	96609	snp	227/546	synonymous_variant c.681C>T p.Leu227Leu	groL	60 kDa chaperonin
T33.4.5	c01	96624	complex	232/546	missense_variant c.696_699delTCTTinsCATG p.Leu233Met	groL	60 kDa chaperonin
T33.4.5	c01	96633	snp	235/546	synonymous_variant c.705G>T p.Pro235Pro	groL	60 kDa chaperonin
T33.4.5	c01	96639	snp	237/546	synonymous_variant c.711G>C p.Leu237Leu	groL	60 kDa chaperonin
T33.4.5	c01	96658	mnp	244/546	missense_variant c.730_731delTCinsGG p.Ser244Gly	groL	60 kDa chaperonin
T33.4.5	c01	96732	snp	268/546	synonymous_variant c.804C>T p.Arg268Arg	groL	60 kDa chaperonin
T33.4.5	c01	96741	snp	271/546	synonymous_variant c.813G>C p.Leu271Leu	groL	60 kDa chaperonin
T33.4.5	c01	96753	snp	275/546	synonymous_variant c.825T>C p.Ala275Ala	groL	60 kDa chaperonin
T33.4.5	c01	96777	snp	283/546	synonymous_variant c.849T>C p.Asp283Asp	groL	60 kDa chaperonin
T33.4.5	c01	96786	snp	286/546	synonymous_variant c.858A>G p.Lys286Lys	groL	60 kDa chaperonin
T33.4.5	c01	96795	snp	289/546	synonymous_variant c.867C>G p.Leu289Leu	groL	60 kDa chaperonin
	1001	20/33	l sub	203/340	Symonymous_variant 6.007 676 p.LeuzosLeu	91UL	OO KDa GliapelUliili
T33.4.5	c01	96807	snp	293/546	synonymous_variant c.879G>C p.Ala293Ala	groL	60 kDa chaperonin

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T33.4.5	cont	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ydcO_1	Inner membrane protein YdcO
T33.4.5	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ydcO_1	Inner membrane protein YdcO
T33.4.5	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	HTH-type transcriptional regulatory protein GabR
T33.4.5	c01	2007281	snp	55/133	synonymous_variant c.165C>G p.Thr55Thr	ssb_1	Single-stranded DNA-binding protein
T33.4.5	c01	2007330	complex	72/133	missense_variant c.214_216delCAAinsGAG p.Gln72Glu	ssb_1	Single-stranded DNA-binding protein
T33.4.5	c01	2007347	snp	77/133	synonymous_variant c.231T>C p.Gly77Gly	ssb_1	Single-stranded DNA-binding protein
T33.4.5	c01	2007392	snp	92/133	synonymous_variant c.276C>G p.Thr92Thr	ssb_1	Single-stranded DNA-binding protein
T33.4.5	c01	2007410	snp	98/133	synonymous_variant c.294T>C p.Asp98Asp	ssb_1	Single-stranded DNA-binding protein
T33.4.5	c01	2021961	snp	259/840	synonymous_variant c.777G>C p.Ser259Ser	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2021973	complex	263/840	missense_variant c.789_793delTCTGAinsCCTGC p.Met265Leu	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2021999	snp	272/840	missense_variant c.815G>A p.Arg272Lys	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2022018	snp	278/840	synonymous_variant c.834C>T p.Arg278Arg	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2022111	snp	309/840	synonymous_variant c.927C>A p.Ala309Ala	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2022120	mnp	312/840	missense_variant c.936_938delTGCinsGCT p.Ala313Leu	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2022133	snp	317/840	missense_variant c.949C>A p.Leu317Met	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2022138	complex	318/840	synonymous_variant c.954_957delGCTAinsCTTG p.320	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2022160	complex	326/840	missense_variant c.976_978delATCinsGTG p.lle326Val	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2022206	complex	341/840	missense_variant c.1022_1031delCCGATGCCGCinsAGGACGCCCG p.AlaAspAlaAla341GluAspAlaArg	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2022225	snp	347/840	missense_variant c.1041A>C p.Glu347Asp	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2022253	snp	357/840	missense_variant c.1069A>G p.lle357Val	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2022276	snp	364/840	synonymous_variant c.1092G>C p.Val364Val	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2022318	snp	378/840	synonymous_variant c.1134C>G p.Ser378Ser	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2022324	snp	380/840	synonymous_variant c.1140G>C p.Pro380Pro	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2022330	complex	382/840	synonymous_variant c.1146_1149delCGCCinsTGCT p.384	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2022339	snp	385/840	synonymous_variant c.1155A>C p.Ala385Ala	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2022358	snp	392/840	missense_variant c.1174G>A p.Val392lle	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2023401	snp	739/840	synonymous_variant c.2217T>C p.Tyr739Tyr	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2023410	snp	742/840	synonymous_variant c.2226A>G p.Gln742Gln	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2023416	complex	744/840	synonymous_variant c.2232_2233delCAinsGC p.746	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2023443	snp	753/840	synonymous_variant c.2259C>T p.Gly753Gly	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2023509	snp	775/840	synonymous_variant c.2325T>C p.Asp775Asp	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2023515	snp	777/840	synonymous_variant c.2331C>A p.Leu777Leu	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2023521	snp	779/840	synonymous_variant c.2337G>A p.Glu779Glu	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2023532	complex	783/840	missense_variant c.2348_2352delACGGTinsGCGGC p.Asp783Gly	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2023545	complex	787/840	synonymous_variant c.2361_2364delTGCAinsCGCT p.789	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2023554	snp	790/840	synonymous_variant c.2370C>G p.Leu790Leu	virB4_2	Type IV secretion system protein virB4
T33.4.5	c02	435993	complex	496/1377	synonymous_variant c.1488_1491delGGTCinsCGTG p.498	rpoB	DNA-directed RNA polymerase subunit beta
		_			synonymous_variant c.1503T>C p.Asp501Asp	rpoB	DNA-directed RNA polymerase

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
			TTPE	_			DNA-directed RNA polymerase
T33.4.5	c02	436029	snp	508/1377	synonymous_variant c.1524T>A p.Ala508Ala	rpoB	subunit beta
T33.4.5	c02	436035	snp	510/1377	synonymous_variant c.1530A>C p.Ala510Ala	rpoB	DNA-directed RNA polymerase subunit beta
T33.4.5	c02	436041	snp	512/1377	synonymous_variant c.1536G>T p.Val512Val	rpoB	DNA-directed RNA polymerase subunit beta
T33.4.5	c02	436047	snp	514/1377	synonymous_variant c.1542G>A p.Glu514Glu	rpoB	DNA-directed RNA polymerase subunit beta
T33.4.5	c02	436083	complex	526/1377	missense_variant c.1578_1584delTCAGACCinsCCAGGTG p.Thr528Val	rpoB	DNA-directed RNA polymerase subunit beta
T33.4.5	c02	436125	snp	540/1377	synonymous_variant c.1620C>T p.Leu540Leu	rpoB	DNA-directed RNA polymerase subunit beta
T33.4.5	c02	439856	snp	338/1400	synonymous_variant c.1014T>C p.Gly338Gly	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	439865	snp	341/1400	synonymous_variant c.1023T>C p.Arg341Arg	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	439874	snp	344/1400	synonymous_variant c.1032G>T p.Leu344Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	439910	snp	356/1400	synonymous_variant c.1068C>T p.Val356Val	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	439931	snp	363/1400	synonymous_variant c.1089C>G p.Leu363Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	439985	snp	381/1400	synonymous_variant c.1143A>G p.Pro381Pro	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	439997	complex	385/1400	synonymous_variant c.1155_1161deIACGTCTTinsCCGCCTC p.388	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	440156	snp	438/1400	synonymous_variant c.1314C>T p.Ala438Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	440165	complex	441/1400	missense_variant c.1323_1325delCACinsGAT p.Thr442Met	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	440172	snp	444/1400	missense_variant c.1330A>G p.lle444Val	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	440186	snp	448/1400	synonymous_variant c.1344T>C p.Ala448Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	440198	snp	452/1400	synonymous_variant c.1356T>C p.His452His	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	440207	complex	455/1400	synonymous_variant c.1365_1368delTTGTinsCTGC p.457	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	440216	snp	458/1400	synonymous_variant c.1374G>C p.Ala458Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	440264	snp	474/1400	synonymous_variant c.1422G>C p.Leu474Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	440270	snp	476/1400	synonymous_variant c.1428C>G p.Leu476Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	440282	snp	480/1400	synonymous_variant c.1440T>G p.Leu480Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	440288	snp	482/1400	synonymous_variant c.1446A>G p.Ala482Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	441065	snp	741/1400	synonymous_variant c.2223T>C p.Arg741Arg	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	441071	snp	743/1400	synonymous_variant c.2229T>G p.Leu743Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	441077	snp	745/1400	synonymous_variant c.2235C>A p.Ala745Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	441101	complex	753/1400	synonymous_variant c.2259_2262delAACCinsGACG p.755	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	441110	snp	756/1400	synonymous_variant c.2268A>C p.lle756lle	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	441195	snp	785/1400	synonymous_variant c.2353T>C p.Leu785Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	441203	complex	787/1400	synonymous_variant c.2361_2364delTGCTinsGGCG p.789	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	441215	snp	791/1400	synonymous_variant c.2373C>T p.Gly791Gly	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	441221	snp	793/1400	synonymous_variant c.2379G>T p.Leu793Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.5	c02	445968	snp	353/694	synonymous_variant c.1059T>C p.Arg353Arg	fusA	Elongation factor G
T33.4.5	c02	445974	complex	355/694	missense_variant c.1065_1066delTAinsCG p.lle356Val	fusA	Elongation factor G
T33.4.5	c02	445987	snp	360/694	synonymous_variant c.1078T>C p.Leu360Leu	fusA	Elongation factor G
T33.4.5	c02	446031	complex	374/694	synonymous_variant c.1122_1125delTGCAinsCGCC p.376	fusA	Elongation factor G
T33.4.5	c02	446133	complex	408/694	missense_variant c.1224_1227delGGATinsCGAG p.Asp409Glu	fusA	Elongation factor G
T33.4.5	c02	446142	complex	411/694	missense_variant c.1233_1239delTATCGAAinsCATCCAG p.Glu413Gln	fusA	Elongation factor G
						Ι	
T33.4.5	c02	446154	snp	415/694	synonymous_variant c.1245T>G p.Ala415Ala	fusA	Elongation factor G

1733.4.5 CO2	sample	СНКОМ	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
173.4.5 227 45001 20070 260777 200707000 2007070 200707000 2007070 200707000 2007070 200707000 2007070 200707000 2007070 200707000 2007070 20070700 2007070 20070700 2007070								
1934.5.1. CC2								· ·
T33.4.5 02						<u> </u>	-	· ·
18.4.5 002 40.000 50.0000 19.00000 19.0000 19.0000 19.0000 19.0000 19.0000 19.0000 19.0000 19.0000 19.0000						· · ·		·
1934.5 CID 405900 Compres SPIT2 Symmyrous variant c. 1906-150 FT (March AMA) p. Angittup Typh SSS income protein. Life Typh	33.4.5	c02	451051	complex	257/277		rpIB	50S ribosomal protein L2
173.4.5 CO2	33.4.5	c02	453539	snp	13/122	synonymous_variant c.39C>T p.Asn13Asn	rplN	50S ribosomal protein L14
1933.45 CG2	33.4.5	c02	453590	complex	30/122	missense_variant c.90_96delGCGTTACinsCAAATAT p.Arg31Lys	rplN	50S ribosomal protein L14
T33.4.5 OZ	33.4.5	c02	453602	snp	34/122	synonymous_variant c.102C>T p.Ser34Ser	rplN	50S ribosomal protein L14
133.4.5 CG2	33.4.5	c02	453620	complex	40/122	synonymous_variant c.120_126delGGTGTCGinsCGTTTCC p.43	rpIN	50S ribosomal protein L14
133.4.5 CO2	33.4.5	c02	453659	snp	53/122	synonymous_variant c.159A>G p.Lys53Lys	rplN	50S ribosomal protein L14
1.8.1.5 Co.2 Control Control	33.4.5	c02	453665	complex	55/122	synonymous_variant c.165_168delTGATinsCGAC p.57	rplN	50S ribosomal protein L14
133.4.5 COZ	33.4.5	c02	698342	snp	245/424	synonymous_variant c.735C>G p.Leu245Leu	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
133.45 CD2 698390 SIND 201/424 SYNCHYMOUS, Verlant C, 270.5-7 CD4724-016 CD4X Shruffing substant Cp4X T33.4.5 CD2 698400 SIND 228/424 SYNCHYMOUS, Verlant C, 676A-0 D, DR 226016 CD4X ATT-Expertation CD part Cp4 CD4 CD4 CD4724 SYNCHYMOUS, Verlant C, 657C-0 D, TTV-19Thr CD4X ATT-Expertation CD472 CD4724 SYNCHYMOUS, Verlant C, 650C-7 D, Acq 201Arg CD4724 CD4724 SYNCHYMOUS, Verlant C, 650C-7 D, Acq 201Arg CD4724 CD4724 SYNCHYMOUS, Verlant C, 650C-7 D, Acq 201Arg CD4724 CD4724 SYNCHYMOUS, Verlant C, 650C-7 D, Acq 201Arg CD4724 CD4724 SYNCHYMOUS, Verlant C, 650C-7 D, Acq 201Arg CD4724 CD4724 SYNCHYMOUS, Verlant C, 650C-7 D, Acq 201Arg CD4724 CD4724 SYNCHYMOUS, Verlant C, 650C-7 D, Acq 201Arg CD4724 CD4724 CD4724 SYNCHYMOUS, Verlant C, 650C-7 D, Acq 201Arg CD4724 CD4	33.4.5	c02	698351	snp	242/424	synonymous_variant c.726G>C p.Thr242Thr	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
133.45 C22 698402 Str. 2191424 Synchymous_variant c.857676 p.Tn219Thr CgX ATP-dispendent Cip protes	33.4.5	c02	698357	snp	240/424	synonymous_variant c.720C>T p.Asp240Asp	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
133.4.5 CO2	33.4.5	c02	698399	snp	226/424	synonymous_variant c.678A>G p.Gln226Gln	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
133.4.5 CD2 698492 snp 195/424 synonymous_variant.c.8981>C p.Asp199Asp cipX ATP-dependent Clip protein S1 133.4.5 CD2 698492 snp 195/424 synonymous_variant.c.8767.572e6CAGinsT C p.192 cipX ATP-dependent Clip protein S1 cipX cipX	33.4.5	c02	698420	snp	219/424	synonymous_variant c.657C>G p.Thr219Thr	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
133.4.5 CO2	33.4.5	c02	698474	snp	201/424	synonymous_variant c.603C>T p.Arg201Arg	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
133.4.5 CO2	33.4.5	c02	698492	snp	195/424	synonymous_variant c.585T>C p.Asp195Asp	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T33.4.5	33.4.5	c02	698505	mnp	190/424	synonymous_variant c.570_572delCAGinsTTC p.192	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T33.4.5	33.4.5	c02	1908908	mnp	183/566	synonymous_variant c.547_548delAGinsTC p.184	rpsA	30S ribosomal protein S1
T33.4.5 CO2 1908937 spp 192/566 synonymous, variant c.576C>*P., Val192Val fpsA 30S ribosomal protein S1 T33.4.5 CO2 1908986 spp 195/568 synonymous, variant c.585T>C_DLeU195Eeu fpsA 30S ribosomal protein S1 T33.4.5 CO2 1908987 spp 198/568 synonymous, variant c.596T>C_DLeU195Eeu fpsA 30S ribosomal protein S1 T33.4.5 CO2 1908987 spp 200/568 synonymous, variant c.696A>C_DGU202Asp rpsA 30S ribosomal protein S1 T33.4.5 CO2 1909027 cmplex 222/566 synonymous_variant c.696A>C_DGU202Asp rpsA 30S ribosomal protein S1 T33.4.5 CO2 1909097 spp 226/566 synonymous_variant c.676A>C_D RU202Asp rpsA 30S ribosomal protein S1 T33.4.5 CO2 1909097 spp 227/566 synonymous_variant c.7110>T_D Pro237Pro rpsA 30S ribosomal protein S1 T33.4.5 CO2 1909098 pp 246/566 missense_variant c.728_729delCCACInseACAT T_D.TTv242Asn rpsA 30S ribosoma	33.4.5	c02	1908916	complex	185/566	synonymous_variant c.555_558delGGAAinsCGAG p.187	rpsA	30S ribosomal protein S1
T33.4.5 c02 1908946 snp 195/566 synonymous_variant c.585T>C_p.Leu195Leu rpsA 30S ribosomal protein S1 T33.4.5 c02 1908955 snp 198/566 synonymous_variant c.594T>C_p.Gip/1986Iy rpsA 30S ribosomal protein S1 T33.4.5 c02 1908967 snp 200/566 synonymous_variant c.600C>T_p.Val200Val rpsA 30S ribosomal protein S1 T33.4.5 c02 1908027 complex 222/566 synonymous_variant c.686.689deffCTClinsCCTG p.224 rpsA 30S ribosomal protein S1 T33.4.5 c02 1908097 snp 228/566 synonymous_variant c.786-T_p.Val226Val rpsA 30S ribosomal protein S1 T33.4.5 c02 1908097 snp 228/566 synonymous_variant c.716-7 p.Pro237Pro rpsA 30S ribosomal protein S1 T33.4.5 c02 1908097 snp 246/566 missense_variant c.726-7 p.Val226Val rpsA 30S ribosomal protein S1 T33.4.5 c02 1909108 snp 249/566 missense_variant c.726-7 p.Gip/36Iy sb.4 psA 3	33.4.5	c02	1908928	snp	189/566	synonymous_variant c.567G>T p.Ser189Ser	rpsA	30S ribosomal protein S1
T33.4.5 c02 1908955 snp 198/566 synonymous_variant c.594T>C p.Giy198Giy rpsA 30S ribosomal protein S1 T33.4.5 c02 1908881 snp 200/568 synonymous_variant c.606A>C p.Giu202Asp rpsA 30S ribosomal protein S1 T33.4.5 c02 1909027 complex 222/566 synonymous_variant c.668_696defTCTCinsCCTQ p.224 rpsA 30S ribosomal protein S1 T33.4.5 c02 1909027 complex 222/566 synonymous_variant c.6786>T p.Val228Val rpsA 30S ribosomal protein S1 T33.4.5 c02 1909022 snp 237/566 synonymous_variant c.716>T p.Val228Val rpsA 30S ribosomal protein S1 T33.4.5 c02 1909096 complex 24/566 sissense_variant c.73E_73felACinsCAP_TTV244Cisn rpsA 30S ribosomal protein S1 T33.4.5 c02 1909096 snp 249/566 sissense_variant c.73E_73felACinsCAP_TTV24Cisn rpsA 30S ribosomal protein S1 T33.4.5 c02 1909108 snp 249/566 synonymous_variant c.73E_73felACinsCAP_TTV24Cisn rpsA <td>33.4.5</td> <td>c02</td> <td>1908937</td> <td>snp</td> <td>192/566</td> <td>synonymous_variant c.576C>T p.Val192Val</td> <td>rpsA</td> <td>30S ribosomal protein S1</td>	33.4.5	c02	1908937	snp	192/566	synonymous_variant c.576C>T p.Val192Val	rpsA	30S ribosomal protein S1
T33.4.5 602 1908961 snp 200/566 synonymous_variant c.800c>T p.Vai200Val rpsA 30S ribosomal protein S1 T33.4.5 c02 1909027 complex 222/566 missense_variant c.606A-C p.Gui202Asp rpsA 30S ribosomal protein S1 T33.4.5 c02 1909027 complex 222/566 synonymous_variant c.686_689delTCTCinsCCT0 p.224 rpsA 30S ribosomal protein S1 T33.4.5 c02 1909027 snp 237/566 synonymous_variant c.7862-Tp.Val226Val rpsA 30S ribosomal protein S1 T33.4.5 c02 1909086 complex 242/566 missense_variant c.736.737delCCinsCARTT p.Thr242Asn rpsA 30S ribosomal protein S1 T33.4.5 c02 1909086 snp 249/566 missense_variant c.736.737delCinsCA p.Thr24GGin rpsA 30S ribosomal protein S1 T33.4.5 c02 1909108 snp 249/566 missense_variant c.736.737delCinsCA p.Thr24GGin rpsA 30S ribosomal protein S1 T33.4.5 c02 2279042 snp 9/134 synonymous_variant c.278.737delCinsCA p.Thr24GGin	33.4.5	c02	1908946	snp	195/566	synonymous_variant c.585T>C p.Leu195Leu	rpsA	30S ribosomal protein S1
T33.4.5 CO2 1908967 snp 202/566 missense_variant c.606A-C p.Glu202Asp rpsA 30S ribosomal protein S1 T33.4.5 CO2 1909027 complex 222/566 synonymous_variant c.666_669delTCTCinsCCTG p.224 rpsA 30S ribosomal protein S1 T33.4.5 CO2 1909027 snp 228/566 synonymous_variant c.71G-Tp.Pro23PPro rpsA 30S ribosomal protein S1 T33.4.5 CO2 1909097 snp 224/566 synonymous_variant c.77E-729delCCATCinsACATT p.Thr242Asn rpsA 30S ribosomal protein S1 T33.4.5 CO2 1909097 mnp 246/566 missense_variant c.72E-729delCCATCinsACATT p.Thr242Can rpsA 30S ribosomal protein S1 T33.4.5 CO2 190907 mnp 246/566 missense_variant c.72E-729delCCATCinsACATT p.Thr242Can rpsA 30S ribosomal protein S1 T33.4.5 CO2 190907 mnp 246/566 missense_variant c.72E-73delCCinsCA p.Thr24GGin rpsA 30S ribosomal protein S1 T33.4.5 CO2 2279042 snp 9/134 synonymous_variant c.62CP-Tp.Qi9Gily	33.4.5	c02	1908955	snp	198/566	synonymous_variant c.594T>C p.Gly198Gly	rpsA	30S ribosomal protein S1
T33.45 COZ 1909027 complex 222/566 synonymous_variant c.668_689delTCTCinsCCTG p.224 rpsA 30S ribosomal protein S1 T33.45 cOZ 1909039 snp 226/566 synonymous_variant c.678G>T p.Val226Val rpsA 30S ribosomal protein S1 T33.45 cOZ 1909086 complex 224/566 mlssense_variant c.726_737delACInsCA_TT p.Thr242Asn rpsA 30S ribosomal protein S1 T33.45 cOZ 19090997 mp 246/566 missense_variant c.73C_737delACInsCA_TT p.Thr242Asn rpsA 30S ribosomal protein S1 T33.45 cOZ 1909108 snp 246/566 missense_variant c.73C_737delACInsCA_D.Thr246Gin rpsA 30S ribosomal protein S1 T33.45 cOZ 1909108 snp 249/566 synonymous_variant c.74C_737delACInsCA_D.Thr246Gin rpsA 30S ribosomal protein S1 T33.45 cOZ 2279042 snp 9/134 synonymous_variant c.74C_75T p.Val249Val rpsA 30S ribosomal protein S1 T33.45 cOZ 2279075 complex 14/134 missense_variant c.24C_41delGAinsAC <td< td=""><td>33.4.5</td><td>c02</td><td>1908961</td><td>snp</td><td>200/566</td><td>synonymous_variant c.600C>T p.Val200Val</td><td>rpsA</td><td>30S ribosomal protein S1</td></td<>	33.4.5	c02	1908961	snp	200/566	synonymous_variant c.600C>T p.Val200Val	rpsA	30S ribosomal protein S1
T33.4.5 CO2 1909039 snp 226/566 synonymous_variant c.678G>T p.Val226Val rpsA 305 ribosomal protein S1 T33.4.5 cO2 1909072 snp 237/566 synonymous_variant c.71G>T p.Pro237Pro rpsA 305 ribosomal protein S1 T33.4.5 cO2 1909097 mnp 246/566 missense_variant c.725_729delCCATCinsACATT p.Thr242Asn rpsA 305 ribosomal protein S1 T33.4.5 cO2 1909097 mnp 246/566 missense_variant c.72G>T p.Val249Val rpsA 305 ribosomal protein S1 T33.4.5 cO2 1909108 snp 249/566 synonymous_variant c.747G>T p.Val249Val rpsA 305 ribosomal protein S1 T33.4.5 cO2 2279042 snp 9/134 synonymous_variant c.27T>C p.Gly9Gly ssb_4 Single-stranded DNA-bind protein T33.4.5 cO2 2279055 complex 20/134 missense_variant c.80_61delCCinsTG p.Gln21Glu ssb_4 sprotein T33.4.5 cO2 2279075 complex 20/134 missense_variant c.89C>T p.Gly23Gly ssb_4 sprotein	33.4.5	c02	1908967	snp	202/566	missense_variant c.606A>C p.Glu202Asp	rpsA	30S ribosomal protein S1
T33.4.5 CO2 1909072 snp 237/566 synonymous_variant c.711G>T p.Pro237Pro rpsA 30S ribosomal protein S1 T33.4.5 cO2 1909086 complex 242/566 missense_variant c.725_729delCCATCinsACATT p.Thr242Aan rpsA 30S ribosomal protein S1 T33.4.5 cO2 1909097 mmp 246/566 missense_variant c.736_73 rdelACinsCA p.Thr24Goln rpsA 30S ribosomal protein S1 T33.4.5 cO2 1909108 snp 249/566 synonymous_variant c.727_C p.Gly9Gly ssb_4 30S ribosomal protein S1 T33.4.5 cO2 2279042 snp 9/134 synonymous_variant c.727_C p.Gly9Gly ssb_4 protein T33.4.5 cO2 2279055 complex 14/134 missense_variant c.60_61delCcinsTG p.Gin21Glu ssb_4 Single-stranded DNA-bind protein T33.4.5 cO2 2279075 complex 20/134 missense_variant c.60_61delCcinsTG p.Gin21Glu ssb_4 Single-stranded DNA-bind protein T33.4.5 cO2 2279084 snp 23/134 synonymous_variant c.69C>T p.Gly23Gly ssb_4	33.4.5	c02	1909027	complex	222/566	synonymous_variant c.666_669delTCTCinsCCTG p.224	rpsA	30S ribosomal protein S1
T33.4.5 c02 1909086 complex 242/566 missense_variant c.725_729delCCATCinsACATT p.Thr/242Asn rpsA 30S ribosomal protein S1 T33.4.5 c02 1909097 mnp 246/568 missense_variant c.736_737delACinsCA p.Thr/246Gin rpsA 30S ribosomal protein S1 T33.4.5 c02 1909108 snp 249/568 synonymous_variant c.747G>T p.Val249Val rpsA 30S ribosomal protein S1 T33.4.5 c02 2279042 snp 9/134 synonymous_variant c.727>C p.Gly9Gly ssb_4 Single-stranded DNA-bind protein T33.4.5 c02 2279075 complex 20/134 missense_variant c.40_41delGAinsAC p.Asp14Thr ssb_4 Single-stranded DNA-bind protein T33.4.5 c02 2279075 complex 20/134 missense_variant c.60_61delCCinsTG p.Gln21Glu ssb_4 Single-stranded DNA-bind protein T33.4.5 c02 2279075 complex 20/134 missense_variant c.60_61delCCinsTG p.Gln21Glu ssb_4 Single-stranded DNA-bind protein T33.4.5 c02 2279084 snp 23/134 synonymous_variant	33.4.5	c02	1909039	snp	226/566	synonymous_variant c.678G>T p.Val226Val	rpsA	30S ribosomal protein S1
T33.4.5 c02 199997 mnp 246/566 missense_variant c.736_737delACinsCA p.Thr/246Gin rpsA 30S ribosomal protein S1 T33.4.5 c02 1909108 snp 249/566 synonymous_variant c.747G>T p.Val249Val rpsA 30S ribosomal protein S1 T33.4.5 c02 2279042 snp 9/134 synonymous_variant c.77C p.Gly9Gly ssb_4 Single-stranded DNA-bind protein T33.4.5 c02 2279075 complex 20/134 missense_variant c.40_41delGAinsAC p.Asp14Thr ssb_4 Single-stranded DNA-bind protein T33.4.5 c02 2279075 complex 20/134 missense_variant c.60_61delCCinsTG p.Gln21Glu ssb_4 Single-stranded DNA-bind protein T33.4.5 c02 2279084 snp 23/134 synonymous_variant c.69C>T p.Gly23Gly ssb_4 Single-stranded DNA-bind protein T33.4.5 c02 2445232 snp 314/521 synonymous_variant c.69C>T p.Gly23Gly ssb_4 ATP synthase subunit beta T33.4.5 c02 2445232 snp 314/521 synonymous_variant c.69C>T p.Gly23Gly <td< td=""><td>33.4.5</td><td>c02</td><td>1909072</td><td>snp</td><td>237/566</td><td>synonymous_variant c.711G>T p.Pro237Pro</td><td>rpsA</td><td>30S ribosomal protein S1</td></td<>	33.4.5	c02	1909072	snp	237/566	synonymous_variant c.711G>T p.Pro237Pro	rpsA	30S ribosomal protein S1
T33.4.5 c02 1909108 snp 249/566 synonymous_variant c.747G>T p.Val249Vel rpsA 30S ribosomal protein S1 T33.4.5 c02 2279042 snp 9/134 synonymous_variant c.27T>C p.Gly9Gly ssb_4 Single-stranded DNA-bind protein T33.4.5 c02 2279055 complex 14/134 missense_variant c.40_41delGAinsAC p.Asp14Thr ssb_4 Single-stranded DNA-bind protein T33.4.5 c02 2279075 complex 20/134 missense_variant c.60_61delCCinsTG p.Gln21Glu ssb_4 Single-stranded DNA-bind protein T33.4.5 c02 2279084 snp 23/134 synonymous_variant c.69C>T p.Gly23Gly ssb_4 Single-stranded DNA-bind protein T33.4.5 c02 2445232 snp 314/521 synonymous_variant c.69C>T p.Gly23Gly ssb_4 ATP synthase subunit beta protein T33.4.5 c02 2445250 complex 320/521 synonymous_variant c.69C>T p.Gly23Gly atpD ATP synthase subunit beta protein T34.4.1 c01 96450 snp 176/546 synonymous_variant c.52CeC p.Val1724Val	33.4.5	c02	1909086	complex	242/566	missense_variant c.725_729delCCATCinsACATT p.Thr242Asn	rpsA	30S ribosomal protein S1
T33.4.5 C02 2279042 snp 9/134 synonymous_variant c.27T>C p.Gly9Gly ssb_4 Single-stranded DNA-bind protein T33.4.5 c02 2279055 complex 14/134 missense_variant c.40_41delGAinsAC p.Asp14Thr ssb_4 Single-stranded DNA-bind protein T33.4.5 c02 2279075 complex 20/134 missense_variant c.60_61delCCinsTG p.Gln21Glu ssb_4 Single-stranded DNA-bind protein T33.4.5 c02 2279084 snp 23/134 synonymous_variant c.60_61delCCinsTG p.Gln21Glu ssb_4 Single-stranded DNA-bind protein T33.4.5 c02 22445232 snp 314/521 synonymous_variant c.960 p.Cleu314Leu atpD ATP synthase subunit beta T33.4.5 c02 2445250 complex 320/521 synonymous_variant c.960 p.Gly323Gly atpD ATP synthase subunit beta T33.4.5 c02 2445250 snp 323/521 synonymous_variant c.960 p.Gly323Gly atpD ATP synthase subunit beta T33.4.5 c02 2445259 snp 323/521	33.4.5	c02	1909097	mnp	246/566	missense_variant c.736_737delACinsCA p.Thr246Gln	rpsA	30S ribosomal protein S1
133.4.5 CO2 2279055 Complex 14/134 missense_variant c.40_41delGAinsAC p.Asp14Thr ssb_4 Single-stranded DNA-bind protein ssb_4 Single-s	33.4.5	c02	1909108	snp	249/566	synonymous_variant c.747G>T p.Val249Val	rpsA	30S ribosomal protein S1
133.4.5 C02 2279075 Complex 14/134 missense_variant c.40_41delGAinsAC p.Asp141nr ssb_4 protein	33.4.5	c02	2279042	snp	9/134	synonymous_variant c.27T>C p.Gly9Gly	ssb_4	Single-stranded DNA-binding protein
133.4.5 C02 22/9075 complex 20/134 missense_variant c.60_61delCclins1G p.Gin21Giu ssb_4 protein T33.4.5 c02 2279084 snp 23/134 synonymous_variant c.69C>T p.Gly23Gly ssb_4 Single-stranded DNA-bind protein T33.4.5 c02 2445232 snp 314/521 synonymous_variant c.96Q-69GleCGCTinsGGCC p.322 atpD ATP synthase subunit beta T33.4.5 c02 2445259 snp 323/521 synonymous_variant c.96Q-69GleCGCTinsGGCC p.322 atpD ATP synthase subunit beta T33.4.5 c02 2445259 snp 323/521 synonymous_variant c.96Q-7T p.Gly323Gly atpD ATP synthase subunit beta T44.4.1 c01 96450 snp 174/546 synonymous_variant c.522G>C p.Val174Val groL 60 kDa chaperonin T44.4.1 c01 96534 snp 202/546 synonymous_variant c.622G>C p.Thr176Thr groL 60 kDa chaperonin T44.4.1 c01 96543 snp 205/546 synonymous_variant c.615C>G p.Val205Val groL 60 kDa chaperonin </td <td>33.4.5</td> <td>c02</td> <td>2279055</td> <td>complex</td> <td>14/134</td> <td>missense_variant c.40_41delGAinsAC p.Asp14Thr</td> <td>ssb_4</td> <td>Single-stranded DNA-binding protein</td>	33.4.5	c02	2279055	complex	14/134	missense_variant c.40_41delGAinsAC p.Asp14Thr	ssb_4	Single-stranded DNA-binding protein
133.4.5 C02 2279084 snp 23/134 synonymous_variant c.osC31 p.Gly23Gly ssp.4 protein T33.4.5 c02 2445232 snp 314/521 synonymous_variant c.960_963delCGCTinsGGCC p.322 atpD ATP synthase subunit beta T33.4.5 c02 2445259 snp 323/521 synonymous_variant c.969C>T p.Gly323Gly atpD ATP synthase subunit beta T44.4.1 c01 96450 snp 174/546 synonymous_variant c.522G>C p.Val174Val groL 60 kDa chaperonin T44.4.1 c01 96456 snp 176/546 synonymous_variant c.528G>C p.Thr176Thr groL 60 kDa chaperonin T44.4.1 c01 96534 snp 202/546 synonymous_variant c.606T>C p.Pro202Pro groL 60 kDa chaperonin T44.4.1 c01 96543 snp 205/546 synonymous_variant c.615C>G p.Val205Val groL 60 kDa chaperonin T44.4.1 c01 96567 snp 213/546 synonymous_variant c.639T>G p.Ala213Ala groL 60 kDa chaperonin T44.4.1	33.4.5	c02	2279075	complex	20/134	missense_variant c.60_61delCCinsTG p.Gln21Glu	ssb_4	Single-stranded DNA-binding protein
T33.4.5 c02 2445250 complex 320/521 synonymous_variant c.960_963delCGCTinsGGCC p.322 atpD ATP synthase subunit beta T33.4.5 c02 2445259 snp 323/521 synonymous_variant c.969C>T p.Gly323Gly atpD ATP synthase subunit beta T44.4.1 c01 96450 snp 174/546 synonymous_variant c.522G>C p.Val174Val groL 60 kDa chaperonin T44.4.1 c01 96456 snp 176/546 synonymous_variant c.528G>C p.Thr176Thr groL 60 kDa chaperonin T44.4.1 c01 96534 snp 202/546 synonymous_variant c.606T>C p.Pro202Pro groL 60 kDa chaperonin T44.4.1 c01 96543 snp 205/546 synonymous_variant c.615C>G p.Val205Val groL 60 kDa chaperonin T44.4.1 c01 96549 complex 207/546 synonymous_variant c.621_624delCCCTinsTCCG p.209 groL 60 kDa chaperonin T44.4.1 c01 96697 snp 213/546 synonymous_variant c.681C>T p.Leu227Leu groL 60 kDa chaperonin	33.4.5	c02	2279084	snp	23/134	synonymous_variant c.69C>T p.Gly23Gly	ssb_4	Single-stranded DNA-binding protein
T33.4.5 c02 2445259 snp 323/521 synonymous_variant c.969C>T p.Gly323Gly atpD ATP synthase subunit beta T44.4.1 c01 96450 snp 174/546 synonymous_variant c.522G>C p.Val174Val groL 60 kDa chaperonin T44.4.1 c01 96456 snp 176/546 synonymous_variant c.528G>C p.Thr176Thr groL 60 kDa chaperonin T44.4.1 c01 96534 snp 202/546 synonymous_variant c.606T>C p.Pro202Pro groL 60 kDa chaperonin T44.4.1 c01 96543 snp 205/546 synonymous_variant c.615C>G p.Val205Val groL 60 kDa chaperonin T44.4.1 c01 96549 complex 207/546 synonymous_variant c.621_624delCCCTinsTCCG p.209 groL 60 kDa chaperonin T44.4.1 c01 96567 snp 213/546 synonymous_variant c.639T>G p.Ala213Ala groL 60 kDa chaperonin T44.4.1 c01 96609 snp 227/546 synonymous_variant c.681C>T p.Leu227Leu groL 60 kDa chaperonin T44.4.1	33.4.5	c02	2445232	snp	314/521	synonymous_variant c.942C>G p.Leu314Leu	atpD	ATP synthase subunit beta
T44.4.1 c01 96450 snp 174/546 synonymous_variant c.522G>C p.Val174Val groL 60 kDa chaperonin T44.4.1 c01 96456 snp 176/546 synonymous_variant c.528G>C p.Thr176Thr groL 60 kDa chaperonin T44.4.1 c01 96534 snp 202/546 synonymous_variant c.606T>C p.Pro202Pro groL 60 kDa chaperonin T44.4.1 c01 96543 snp 205/546 synonymous_variant c.615C>G p.Val205Val groL 60 kDa chaperonin T44.4.1 c01 96549 complex 207/546 synonymous_variant c.621_624delCCCTinsTCCG p.209 groL 60 kDa chaperonin T44.4.1 c01 96567 snp 213/546 synonymous_variant c.639T>G p.Ala213Ala groL 60 kDa chaperonin T44.4.1 c01 96609 snp 227/546 synonymous_variant c.681C>T p.Leu227Leu groL 60 kDa chaperonin T44.4.1 c01 96624 complex 232/546 missense_variant c.696_699delTCTTinsCATG p.Leu233Met groL 60 kDa chaperonin T44.4.1 </td <td>33.4.5</td> <td>c02</td> <td>2445250</td> <td>complex</td> <td>320/521</td> <td>synonymous_variant c.960_963delCGCTinsGGCC p.322</td> <td>atpD</td> <td>ATP synthase subunit beta</td>	33.4.5	c02	2445250	complex	320/521	synonymous_variant c.960_963delCGCTinsGGCC p.322	atpD	ATP synthase subunit beta
T44.4.1 c01 96456 snp 176/546 synonymous_variant c.528G>C p.Thr176Thr groL 60 kDa chaperonin T44.4.1 c01 96534 snp 202/546 synonymous_variant c.606T>C p.Pro202Pro groL 60 kDa chaperonin T44.4.1 c01 96543 snp 205/546 synonymous_variant c.615C>G p.Val205Val groL 60 kDa chaperonin T44.4.1 c01 96549 complex 207/546 synonymous_variant c.621_624delCCCTinsTCCG p.209 groL 60 kDa chaperonin T44.4.1 c01 96567 snp 213/546 synonymous_variant c.639T>G p.Ala213Ala groL 60 kDa chaperonin T44.4.1 c01 96609 snp 227/546 synonymous_variant c.681C>T p.Leu227Leu groL 60 kDa chaperonin T44.4.1 c01 96624 complex 232/546 missense_variant c.696_699delTCTTinsCATG p.Leu233Met groL 60 kDa chaperonin T44.4.1 c01 96633 snp 235/546 synonymous_variant c.705G>T p.Pro235Pro groL 60 kDa chaperonin T44.4.1 </td <td>33.4.5</td> <td>c02</td> <td>2445259</td> <td>snp</td> <td>323/521</td> <td>synonymous_variant c.969C>T p.Gly323Gly</td> <td>atpD</td> <td>ATP synthase subunit beta</td>	33.4.5	c02	2445259	snp	323/521	synonymous_variant c.969C>T p.Gly323Gly	atpD	ATP synthase subunit beta
T44.4.1 c01 96534 snp 202/546 synonymous_variant c.606T>C p.Pro202Pro groL 60 kDa chaperonin T44.4.1 c01 96543 snp 205/546 synonymous_variant c.615C>G p.Val205Val groL 60 kDa chaperonin T44.4.1 c01 96549 complex 207/546 synonymous_variant c.621_624delCCCTinsTCCG p.209 groL 60 kDa chaperonin T44.4.1 c01 96567 snp 213/546 synonymous_variant c.639T>G p.Ala213Ala groL 60 kDa chaperonin T44.4.1 c01 96609 snp 227/546 synonymous_variant c.681C>T p.Leu227Leu groL 60 kDa chaperonin T44.4.1 c01 96624 complex 232/546 missense_variant c.696_699delTCTTinsCATG p.Leu233Met groL 60 kDa chaperonin T44.4.1 c01 96633 snp 235/546 synonymous_variant c.705G>T p.Pro235Pro groL 60 kDa chaperonin T44.4.1 c01 96639 snp 237/546 synonymous_variant c.711G>C p.Leu237Leu groL 60 kDa chaperonin T44.4.1 </td <td>14.4.1</td> <td>c01</td> <td>96450</td> <td>snp</td> <td>174/546</td> <td>synonymous_variant c.522G>C p.Val174Val</td> <td>groL</td> <td>60 kDa chaperonin</td>	14.4.1	c01	96450	snp	174/546	synonymous_variant c.522G>C p.Val174Val	groL	60 kDa chaperonin
T44.4.1 c01 96543 snp 205/546 synonymous_variant c.615C>G p.Val205Val groL 60 kDa chaperonin T44.4.1 c01 96549 complex 207/546 synonymous_variant c.621_624delCCCTinsTCCG p.209 groL 60 kDa chaperonin T44.4.1 c01 96567 snp 213/546 synonymous_variant c.639T>G p.Ala213Ala groL 60 kDa chaperonin T44.4.1 c01 96609 snp 227/546 synonymous_variant c.681C>T p.Leu227Leu groL 60 kDa chaperonin T44.4.1 c01 96624 complex 232/546 missense_variant c.696_699delTCTTinsCATG p.Leu233Met groL 60 kDa chaperonin T44.4.1 c01 96633 snp 235/546 synonymous_variant c.705G>T p.Pro235Pro groL 60 kDa chaperonin T44.4.1 c01 96639 snp 237/546 synonymous_variant c.711G>C p.Leu237Leu groL 60 kDa chaperonin T44.4.1 c01 96658 mnp 244/546 missense_variant c.730_731delTCinsGG p.Ser244Gly groL 60 kDa chaperonin	14.4.1	c01	96456	snp	176/546	synonymous_variant c.528G>C p.Thr176Thr	groL	60 kDa chaperonin
T44.4.1 c01 96549 complex 207/546 synonymous_variant c.621_624delCCCTinsTCCG p.209 groL 60 kDa chaperonin T44.4.1 c01 96567 snp 213/546 synonymous_variant c.639T>G p.Ala213Ala groL 60 kDa chaperonin T44.4.1 c01 96609 snp 227/546 synonymous_variant c.681C>T p.Leu227Leu groL 60 kDa chaperonin T44.4.1 c01 96624 complex 232/546 missense_variant c.696_699delTCTTinsCATG p.Leu233Met groL 60 kDa chaperonin T44.4.1 c01 96633 snp 235/546 synonymous_variant c.705G>T p.Pro235Pro groL 60 kDa chaperonin T44.4.1 c01 96639 snp 237/546 synonymous_variant c.711G>C p.Leu237Leu groL 60 kDa chaperonin T44.4.1 c01 96658 mnp 244/546 missense_variant c.730_731delTCinsGG p.Ser244Gly groL 60 kDa chaperonin T44.4.1 c01 96732 snp 268/546 synonymous_variant c.804C>T p.Arg268Arg groL 60 kDa chaperonin	14.4.1	c01	96534	snp	202/546	synonymous_variant c.606T>C p.Pro202Pro	groL	60 kDa chaperonin
T44.4.1 c01 96567 snp 213/546 synonymous_variant c.639T>G p.Ala213Ala groL 60 kDa chaperonin T44.4.1 c01 96609 snp 227/546 synonymous_variant c.681C>T p.Leu227Leu groL 60 kDa chaperonin T44.4.1 c01 96624 complex 232/546 missense_variant c.696_699delTCTTinsCATG p.Leu233Met groL 60 kDa chaperonin T44.4.1 c01 96633 snp 235/546 synonymous_variant c.705G>T p.Pro235Pro groL 60 kDa chaperonin T44.4.1 c01 96639 snp 237/546 synonymous_variant c.711G>C p.Leu237Leu groL 60 kDa chaperonin T44.4.1 c01 96658 mnp 244/546 missense_variant c.730_731delTCinsGG p.Ser244Gly groL 60 kDa chaperonin T44.4.1 c01 96732 snp 268/546 synonymous_variant c.804C>T p.Arg268Arg groL 60 kDa chaperonin	14.4.1	c01	96543	snp	205/546	synonymous_variant c.615C>G p.Val205Val	groL	60 kDa chaperonin
T44.4.1 c01 96609 snp 227/546 synonymous_variant c.681C>T p.Leu227Leu groL 60 kDa chaperonin T44.4.1 c01 96624 complex 232/546 missense_variant c.696_699delTCTTinsCATG p.Leu233Met groL 60 kDa chaperonin T44.4.1 c01 96633 snp 235/546 synonymous_variant c.705G>T p.Pro235Pro groL 60 kDa chaperonin T44.4.1 c01 96639 snp 237/546 synonymous_variant c.711G>C p.Leu237Leu groL 60 kDa chaperonin T44.4.1 c01 96658 mnp 244/546 missense_variant c.730_731delTCinsGG p.Ser244Gly groL 60 kDa chaperonin T44.4.1 c01 96732 snp 268/546 synonymous_variant c.804C>T p.Arg268Arg groL 60 kDa chaperonin	14.4.1	c01	96549	complex	207/546	synonymous_variant c.621_624delCCCTinsTCCG p.209	groL	60 kDa chaperonin
T44.4.1 c01 96624 complex 232/546 missense_variant c.696_699delTCTTinsCATG p.Leu233Met groL 60 kDa chaperonin T44.4.1 c01 96633 snp 235/546 synonymous_variant c.705G>T p.Pro235Pro groL 60 kDa chaperonin T44.4.1 c01 96639 snp 237/546 synonymous_variant c.711G>C p.Leu237Leu groL 60 kDa chaperonin T44.4.1 c01 96658 mnp 244/546 missense_variant c.730_731delTCinsGG p.Ser244Gly groL 60 kDa chaperonin T44.4.1 c01 96732 snp 268/546 synonymous_variant c.804C>T p.Arg268Arg groL 60 kDa chaperonin	14.4.1	c01	96567	snp	213/546	synonymous_variant c.639T>G p.Ala213Ala	groL	60 kDa chaperonin
T44.4.1 c01 96633 snp 235/546 synonymous_variant c.705G>T p.Pro235Pro groL 60 kDa chaperonin T44.4.1 c01 96639 snp 237/546 synonymous_variant c.711G>C p.Leu237Leu groL 60 kDa chaperonin T44.4.1 c01 96658 mnp 244/546 missense_variant c.730_731delTCinsGG p.Ser244Gly groL 60 kDa chaperonin T44.4.1 c01 96732 snp 268/546 synonymous_variant c.804C>T p.Arg268Arg groL 60 kDa chaperonin	14.4.1	c01	96609	snp	227/546	synonymous_variant c.681C>T p.Leu227Leu	groL	60 kDa chaperonin
T44.4.1 c01 96639 snp 237/546 synonymous_variant c.711G>C p.Leu237Leu groL 60 kDa chaperonin T44.4.1 c01 96658 mnp 244/546 missense_variant c.730_731delTCinsGG p.Ser244Gly groL 60 kDa chaperonin T44.4.1 c01 96732 snp 268/546 synonymous_variant c.804C>T p.Arg268Arg groL 60 kDa chaperonin	14.4.1	c01	96624	complex	232/546	missense_variant c.696_699delTCTTinsCATG p.Leu233Met	groL	60 kDa chaperonin
T44.4.1 c01 96658 mnp 244/546 missense_variant c.730_731delTCinsGG p.Ser244Gly groL 60 kDa chaperonin T44.4.1 c01 96732 snp 268/546 synonymous_variant c.804C>T p.Arg268Arg groL 60 kDa chaperonin	14.4.1	c01	96633	snp	235/546	synonymous_variant c.705G>T p.Pro235Pro	groL	60 kDa chaperonin
T44.4.1 c01 96732 snp 268/546 synonymous_variant c.804C>T p.Arg268Arg groL 60 kDa chaperonin	14.4.1	c01	96639	snp	237/546	synonymous_variant c.711G>C p.Leu237Leu	groL	60 kDa chaperonin
	14.4.1	c01	96658	mnp	244/546	missense_variant c.730_731delTCinsGG p.Ser244Gly	groL	60 kDa chaperonin
T44.4.1 c01 96741 snp 271/546 synonymous_variant c.813G>C p.Leu271Leu groL 60 kDa chaperonin	14.4.1	c01	96732	snp	268/546	synonymous_variant c.804C>T p.Arg268Arg	groL	60 kDa chaperonin
<u> </u>	44.4.1	c01	96741	snp	271/546	synonymous_variant c.813G>C p.Leu271Leu	groL	60 kDa chaperonin
T44.4.1 c01 96753 snp 275/546 synonymous_variant c.825T>C p.Ala275Ala groL 60 kDa chaperonin	14.4.1	c01	96753	snp	275/546	synonymous_variant c.825T>C p.Ala275Ala	groL	60 kDa chaperonin
T44.4.1 c01 96777 snp 283/546 synonymous_variant c.849T>C p.Asp283Asp groL 60 kDa chaperonin	44.4.1	c01	96777	snp	283/546	synonymous_variant c.849T>C p.Asp283Asp	groL	60 kDa chaperonin

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T44.4.1	c01	96786	snp	286/546	synonymous_variant c.858A>G p.Lys286Lys	groL	60 kDa chaperonin
T44.4.1	c01	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ydcO_1	Inner membrane protein YdcO
T44.4.1	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ydcO_1	Inner membrane protein YdcO
T44.4.1	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	HTH-type transcriptional regulatory protein GabR
T44.4.1	c01	2021999	snp	272/840	missense_variant c.815G>A p.Arg272Lys	virB4_2	Type IV secretion system protein virB4
T44.4.1	c01	2022018	snp	278/840	synonymous_variant c.834C>T p.Arg278Arg	virB4_2	Type IV secretion system protein virB4
T44.4.1	c01	2022111	snp	309/840	synonymous_variant c.927C>A p.Ala309Ala	virB4_2	Type IV secretion system protein virB4
T44.4.1	c01	2022120	mnp	312/840	missense_variant c.936_938delTGCinsGCT p.Ala313Leu	virB4_2	Type IV secretion system protein virB4
T44.4.1	c01	2022133	snp	317/840	missense_variant c.949C>A p.Leu317Met	virB4_2	Type IV secretion system protein virB4
T44.4.1	c01	2022138	complex	318/840	synonymous_variant c.954_957delGCTAinsCTTG p.320	virB4_2	Type IV secretion system protein virB4
T44.4.1	c01	2022160	complex	326/840	missense_variant c.976_978delATCinsGTG p.lle326Val	virB4_2	Type IV secretion system protein virB4
T44.4.1	c01	2022206	complex	341/840	missense_variant c.1022_1031delCCGATGCCGCinsAGGACGCCCG	virB4_2	Type IV secretion system protein
T44.4.1	c01	2022225	snp	347/840	p.AlaAspAlaAla341GluAspAlaArg missense_variant c.1041A>C p.Glu347Asp	virB4_2	Type IV secretion system protein
T44.4.1	c01	2022253	snp	357/840	missense_variant c.1069A>G p.lle357Val	virB4_2	Type IV secretion system protein
T44.4.1	c01	2022276	snp	364/840	synonymous_variant c.1092G>C p.Val364Val	virB4_2	Type IV secretion system protein
T44.4.1	c01	2022318	snp	378/840	synonymous_variant c.1134C>G p.Ser378Ser	virB4_2	virB4 Type IV secretion system protein
T44.4.1	c01	2022324	snp	380/840	synonymous_variant c.1140G>C p.Pro380Pro	virB4_2	virB4 Type IV secretion system protein
			·				virB4 DNA-directed RNA polymerase
T44.4.1	c02	436083	complex	526/1377	missense_variant c.1578_1584delTCAGACCinsCCAGGTG p.Thr528Val	rpoB	subunit beta DNA-directed RNA polymerase
T44.4.1	c02	439910	snp	356/1400	synonymous_variant c.1068C>T p.Val356Val	rpoC	subunit beta' DNA-directed RNA polymerase
T44.4.1	c02	439931	snp	363/1400	synonymous_variant c.1089C>G p.Leu363Leu	rpoC	subunit beta' DNA-directed RNA polymerase
T44.4.1	c02	441101	complex	753/1400	synonymous_variant c.2259_2262delAACCinsGACG p.755	rpoC	subunit beta'
T44.4.1	c02	441110	snp	756/1400	synonymous_variant c.2268A>C p.lle756lle	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.1	c02	445987	snp	360/694	synonymous_variant c.1078T>C p.Leu360Leu	fusA	Elongation factor G
T44.4.1	c02	446031	complex	374/694	synonymous_variant c.1122_1125delTGCAinsCGCC p.376	fusA	Elongation factor G
T44.4.1	c02	446133	complex	408/694	missense_variant c.1224_1227delGGATinsCGAG p.Asp409Glu	fusA	Elongation factor G
T44.4.1	c02	446142	complex	411/694	missense_variant c.1233_1239delTATCGAAinsCATCCAG p.Glu413Gln	fusA	Elongation factor G
T44.4.1	c02	446154	snp	415/694	synonymous_variant c.1245T>G p.Ala415Ala	fusA	Elongation factor G
T44.4.1	c02	450996	complex	238/277	synonymous_variant c.714_717delTACCinsCACG p.240	rpIB	50S ribosomal protein L2
T44.4.1	c02	451011	snp	243/277	synonymous_variant c.729T>C p.Arg243Arg	rpIB	50S ribosomal protein L2
T44.4.1	c02	451017	complex	245/277	synonymous_variant c.735_738delTGTCinsGGTT p.247	rplB	50S ribosomal protein L2
T44.4.1	c02	451038	snp	252/277	synonymous_variant c.756T>C p.Pro252Pro	rplB	50S ribosomal protein L2
T44.4.1	c02	451051	complex	257/277	missense_variant c.769_777delAAGACGCGCinsCGCACCCGT p.Lys257Arg	rpIB	50S ribosomal protein L2
T44.4.1	c02	453539	snp	13/122	synonymous_variant c.39C>T p.Asn13Asn	rplN	50S ribosomal protein L14
T44.4.1	c02	453590	complex	30/122	missense_variant c.90_96delGCGTTACinsCAAATAT p.Arg31Lys	rplN	50S ribosomal protein L14
T44.4.1	c02	453602	snp	34/122	synonymous_variant c.102C>T p.Ser34Ser	rplN	50S ribosomal protein L14
T44.4.1	c02	453620	complex	40/122	synonymous_variant c.120_126delGGTGTCGinsCGTTTCC p.43	rplN	50S ribosomal protein L14
T44.4.1	c02	698357	snp	240/424	synonymous_variant c.720C>T p.Asp240Asp	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.1	c02	698399	snp	226/424	synonymous_variant c.678A>G p.Gln226Gln	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.1	c02	698420	snp	219/424	synonymous_variant c.657C>G p.Thr219Thr	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.1	c02	698474	snp	201/424	synonymous_variant c.603C>T p.Arg201Arg	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.1	c02	698492	snp	195/424	synonymous_variant c.585T>C p.Asp195Asp	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.1	c02	1908928	snp	189/566	synonymous_variant c.567G>T p.Ser189Ser	rpsA	30S ribosomal protein S1
T44.4.1	c02	1908937	snp	192/566	synonymous_variant c.576C>T p.Val192Val	rpsA	30S ribosomal protein S1
T44.4.1	c02	1908946	snp	195/566	synonymous_variant c.585T>C p.Leu195Leu	rpsA	30S ribosomal protein S1
T44.4.1	c02	1908955	snp	198/566	synonymous_variant c.594T>C p.Gly198Gly	rpsA	30S ribosomal protein S1
T44.4.1	c02	1908961	snp	200/566	synonymous_variant c.600C>T p.Val200Val	rpsA	30S ribosomal protein S1
177,71	552	1000001] 3.1p	200/000	5,101,5,11040_vallant 0.00007 i p.val200val	I ibay	555 Hibosomai protein 31

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T44.4.1	c02	1908967	snp	202/566	missense_variant c.606A>C p.Glu202Asp	rpsA	30S ribosomal protein S1
T44.4.1	c02	1909027	complex	222/566	synonymous_variant c.666_669delTCTCinsCCTG p.224	rpsA	30S ribosomal protein S1
T44.4.1	c02	1909039	snp	226/566	synonymous_variant c.678G>T p.Val226Val	rpsA	30S ribosomal protein S1
T44.4.1	c02	1909072	snp	237/566	synonymous_variant c.711G>T p.Pro237Pro	rpsA	30S ribosomal protein S1
T44.4.1	c02	1909086	complex	242/566	missense_variant c.725_729delCCATCinsACATT p.Thr242Asn	rpsA	30S ribosomal protein S1
T44.4.1	c02	1909097	mnp	246/566	missense_variant c.736_737delACinsCA p.Thr246Gln	rpsA	30S ribosomal protein S1
T44.4.1	c02	1909108	snp	249/566	synonymous_variant c.747G>T p.Val249Val	rpsA	30S ribosomal protein S1
T44.4.2	c01	96450	snp	174/546	synonymous_variant c.522G>C p.Val174Val	groL	60 kDa chaperonin
T44.4.2	c01	96456 96534	snp	176/546 202/546	synonymous_variant c.528G>C p.Thr176Thr	groL	60 kDa chaperonin
T44.4.2	c01	96543	snp	202/546	synonymous_variant c.606T>C p.Pro202Pro synonymous_variant c.615C>G p.Val205Val	groL groL	60 kDa chaperonin 60 kDa chaperonin
T44.4.2	c01	96549	complex	207/546	synonymous_variant c.631_624delCCCTinsTCCG p.209	groL	60 kDa chaperonin
T44.4.2	c01	96567	snp	213/546	synonymous_variant c.639T>G p.Ala213Ala	groL	60 kDa chaperonin
T44.4.2	c01	96609	snp	227/546	synonymous_variant c.681C>T p.Leu227Leu	groL	60 kDa chaperonin
T44.4.2	c01	96624	complex	232/546	missense_variant c.696_699delTCTTinsCATG p.Leu233Met	groL	60 kDa chaperonin
T44.4.2	c01	96633	snp	235/546	synonymous_variant c.705G>T p.Pro235Pro	groL	60 kDa chaperonin
T44.4.2	c01	96639	snp	237/546	synonymous_variant c.711G>C p.Leu237Leu	groL	60 kDa chaperonin
T44.4.2	c01	96658	mnp	244/546	missense_variant c.730_731delTCinsGG p.Ser244Gly	groL	60 kDa chaperonin
T44.4.2	c01	96732	snp	268/546	synonymous_variant c.804C>T p.Arg268Arg	groL	60 kDa chaperonin
T44.4.2	c01	96741	snp	271/546	synonymous_variant c.813G>C p.Leu271Leu	groL	60 kDa chaperonin
T44.4.2	c01	96753	snp	275/546	synonymous_variant c.825T>C p.Ala275Ala	groL	60 kDa chaperonin
T44.4.2	c01	96777	snp	283/546	synonymous_variant c.849T>C p.Asp283Asp	groL	60 kDa chaperonin
T44.4.2 T44.4.2	c01	96786 96795	snp	286/546 289/546	synonymous_variant c.858A>G p.Lys286Lys	groL	60 kDa chaperonin
T44.4.2	c01	1008848	snp	218/239	synonymous_variant c.867C>G p.Leu289Leu frameshift_variant c.653delG p.Giy218fs	groL ydcO_1	60 kDa chaperonin Inner membrane protein YdcO
T44.4.2	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ydcO_1	Inner membrane protein YdcO
T44.4.2	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	HTH-type transcriptional regulatory protein GabR
T44.4.2	c01	2007281	snp	55/133	synonymous_variant c.165C>G p.Thr55Thr	ssb_1	Single-stranded DNA-binding protein
T44.4.2	c01	2007330	complex	72/133	missense_variant c.214_216delCAAinsGAG p.Gln72Glu	ssb_1	Single-stranded DNA-binding protein
T44.4.2	c01	2007347	snp	77/133	synonymous_variant c.231T>C p.Gly77Gly	ssb_1	Single-stranded DNA-binding protein
T44.4.2	c01	2021961	snp	259/840	synonymous_variant c.777G>C p.Ser259Ser	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2021973	complex	263/840	missense_variant c.789_793delTCTGAinsCCTGC p.Met265Leu	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2021999	snp	272/840	missense_variant c.815G>A p.Arg272Lys	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2022018	snp	278/840	synonymous_variant c.834C>T p.Arg278Arg	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2022111	snp	309/840	synonymous_variant c.927C>A p.Ala309Ala	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2022120	mnp	312/840	missense_variant c.936_938delTGCinsGCT p.Ala313Leu	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2022133	snp	317/840	missense_variant c.949C>A p.Leu317Met	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2022138	complex	318/840	synonymous_variant c.954_957delGCTAinsCTTG p.320	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2022160	complex	326/840	missense_variant c.976_978delATCinsGTG p.lle326Val missense_variant c.1022_1031delCCGATGCCGCinsAGGACGCCCG	virB4_2	Type IV secretion system protein virB4 Type IV secretion system protein
T44.4.2	c01	2022206	complex	341/840	p.AlaAspAlaAla341GluAspAlaArg	virB4_2	virB4 Type IV secretion system protein
T44.4.2	c01	2022225	snp	347/840	missense_variant c.1041A>C p.Glu347Asp	virB4_2	virB4 Type IV secretion system protein
T44.4.2	c01	2022253	snp	357/840	missense_variant c.1069A>G p.lle357Val	virB4_2	virB4 Type IV secretion system protein
T44.4.2	c01	2022276	snp	364/840	synonymous_variant c.1092G>C p.Val364Val	virB4_2	virB4 Type IV secretion system protein
T44.4.2	c01	2022318	snp	378/840	synonymous_variant c.1134C>G p.Ser378Ser	virB4_2	virB4 Type IV secretion system protein
T44.4.2	c01	2022324	snp	380/840	synonymous_variant c.1140G>C p.Pro380Pro	virB4_2	virB4 Type IV secretion system protein
T44.4.2	c01	2022330	complex	382/840 753/840	synonymous_variant c.1146_1149delCGCCinsTGCT p.384	virB4_2	virB4 Type IV secretion system protein
T44.4.2	c01	2023443	snp	753/840	synonymous_variant c.2259C>T p.Gly753Gly	virB4_2	virB4 Type IV secretion system protein
T44.4.2	c01	2023509	snp	775/840	synonymous_variant c.2325T>C p.Asp775Asp	virB4_2	virB4

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T44.4.2	c01	2023515	snp	777/840	synonymous_variant c.2331C>A p.Leu777Leu	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2023521	snp	779/840	synonymous_variant c.2337G>A p.Glu779Glu	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2023532	complex	783/840	missense_variant c.2348_2352delACGGTinsGCGGC p.Asp783Gly	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2023545	complex	787/840	synonymous_variant c.2361_2364delTGCAinsCGCT p.789	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2023554	snp	790/840	synonymous_variant c.2370C>G p.Leu790Leu	virB4_2	Type IV secretion system protein virB4
T44.4.2	c02	436029	snp	508/1377	synonymous_variant c.1524T>A p.Ala508Ala	rpoB	DNA-directed RNA polymerase subunit beta
T44.4.2	c02	436035	snp	510/1377	synonymous_variant c.1530A>C p.Ala510Ala	rpoB	DNA-directed RNA polymerase subunit beta
T44.4.2	c02	436041	snp	512/1377	synonymous_variant c.1536G>T p.Val512Val	rpoB	DNA-directed RNA polymerase subunit beta
T44.4.2	c02	436047	snp	514/1377	synonymous_variant c.1542G>A p.Glu514Glu	гроВ	DNA-directed RNA polymerase subunit beta
T44.4.2	c02	436083	complex	526/1377	missense_variant c.1578_1584delTCAGACCinsCCAGGTG p.Thr528Val	гроВ	DNA-directed RNA polymerase subunit beta
T44.4.2	c02	439856	snp	338/1400	synonymous_variant c.1014T>C p.Gly338Gly	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	439865	snp	341/1400	synonymous_variant c.1023T>C p.Arg341Arg	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	439874	snp	344/1400	synonymous_variant c.1032G>T p.Leu344Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	439910	snp	356/1400	synonymous_variant c.1068C>T p.Val356Val	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	439931	snp	363/1400	synonymous_variant c.1089C>G p.Leu363Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	439985	snp	381/1400	synonymous_variant c.1143A>G p.Pro381Pro	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	440156	snp	438/1400	synonymous_variant c.1314C>T p.Ala438Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	440165	complex	441/1400	missense_variant c.1323_1325delCACinsGAT p.Thr442Met	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	440172	snp	444/1400	missense_variant c.1330A>G p.lle444Val	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	440186	snp	448/1400	synonymous_variant c.1344T>C p.Ala448Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	440198	snp	452/1400	synonymous_variant c.1356T>C p.His452His	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	440207	complex	455/1400	synonymous_variant c.1365_1368delTTGTinsCTGC p.457	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	440216	snp	458/1400	synonymous_variant c.1374G>C p.Ala458Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	440264	snp	474/1400	synonymous_variant c.1422G>C p.Leu474Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	440270	snp	476/1400	synonymous_variant c.1428C>G p.Leu476Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	440282	snp	480/1400	synonymous_variant c.1440T>G p.Leu480Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	440288	snp	482/1400	synonymous_variant c.1446A>G p.Ala482Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	441065	snp	741/1400	synonymous_variant c.2223T>C p.Arg741Arg	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	441071	snp	743/1400	synonymous_variant c.2229T>G p.Leu743Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	441077	snp	745/1400	synonymous_variant c.2235C>A p.Ala745Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	441101	complex	753/1400	synonymous_variant c.2259_2262delAACCinsGACG p.755	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	441110	snp	756/1400	synonymous_variant c.2268A>C p.lle756lle	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	441195	snp	785/1400	synonymous_variant c.2353T>C p.Leu785Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	441203	complex	787/1400	synonymous_variant c.2361_2364delTGCTinsGGCG p.789	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.2	c02	445987	snp	360/694	synonymous_variant c.1078T>C p.Leu360Leu	fusA	Elongation factor G
T44.4.2	c02	446031	complex	374/694	synonymous_variant c.1122_1125delTGCAinsCGCC p.376	fusA	Elongation factor G
T44.4.2	c02	446133	complex	408/694	missense_variant c.1224_1227delGGATinsCGAG p.Asp409Glu	fusA	Elongation factor G
T44.4.2	c02	446142	complex	411/694	missense_variant c.1233_1239delTATCGAAinsCATCCAG p.Glu413Gln	fusA	Elongation factor G
T44.4.2	c02	446154	snp	415/694	synonymous_variant c.1245T>G p.Ala415Ala	fusA	Elongation factor G
	_	446174	snp	422/694	missense_variant c.1265C>G p.Ala422Gly	fusA	Elongation factor G

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T44.4.2	c02	451017	complex	245/277	synonymous_variant c.735_738delTGTCinsGGTT p.247	rplB	50S ribosomal protein L2
T44.4.2	c02	451038	snp	252/277	synonymous_variant c.756T>C p.Pro252Pro	rplB	50S ribosomal protein L2
T44.4.2	c02	451051	complex	257/277	missense_variant c.769_777delAAGACGCGCinsCGCACCCGT p.Lys257Arg	rplB	50S ribosomal protein L2
T44.4.2	c02	453539	snp	13/122	synonymous_variant c.39C>T p.Asn13Asn	rplN	50S ribosomal protein L14
T44.4.2	c02	453590	complex	30/122	missense_variant c.90_96delGCGTTACinsCAAATAT p.Arg31Lys	rplN	50S ribosomal protein L14
T44.4.2	c02	453602	snp	34/122	synonymous_variant c.102C>T p.Ser34Ser	rplN	50S ribosomal protein L14
T44.4.2	c02	453620	complex	40/122	synonymous_variant c.120_126delGGTGTCGinsCGTTTCC p.43	rplN	50S ribosomal protein L14
T44.4.2	c02	698351	snp	242/424	synonymous_variant c.726G>C p.Thr242Thr	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.2	c02	698357	snp	240/424	synonymous_variant c.720C>T p.Asp240Asp	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.2	c02	698399	snp	226/424	synonymous_variant c.678A>G p.Gln226Gln	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.2	c02	698420	snp	219/424	synonymous_variant c.657C>G p.Thr219Thr	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.2	c02	698474	snp	201/424	synonymous_variant c.603C>T p.Arg201Arg	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.2	c02	698492	snp	195/424	synonymous_variant c.585T>C p.Asp195Asp	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.2	c02	698505	complex	190/424	synonymous_variant c.570_572delCAGinsTTC p.192	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.2	c02	698627	snp	150/424	synonymous_variant c.450G>C p.Thr150Thr	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.2	c02	698633	snp	148/424	synonymous_variant c.444A>G p.Thr148Thr	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.2	c02	698726	complex	116/424	missense_variant c.348_351delTCTTinsCATG p.Leu117Met	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.2	c02	1908916	complex	185/566	synonymous_variant c.555_558delGGAAinsCGAG p.187	rpsA	30S ribosomal protein S1
T44.4.2	c02	1908928	snp	189/566	synonymous_variant c.567G>T p.Ser189Ser	rpsA	30S ribosomal protein S1
T44.4.2	c02	1908937	snp	192/566	synonymous_variant c.576C>T p.Val192Val	rpsA	30S ribosomal protein S1
T44.4.2	c02	1908946	snp	195/566	synonymous_variant c.585T>C p.Leu195Leu	rpsA	30S ribosomal protein S1
T44.4.2	c02	1908955	snp	198/566	synonymous_variant c.594T>C p.Gly198Gly	rpsA	30S ribosomal protein S1
T44.4.2	c02	1908961	snp	200/566	synonymous_variant c.600C>T p.Val200Val	rpsA	30S ribosomal protein S1
T44.4.2	c02	1908967	snp	202/566	missense_variant c.606A>C p.Glu202Asp	rpsA	30S ribosomal protein S1
T44.4.2	c02	1909027	complex	222/566	synonymous_variant c.666_669delTCTCinsCCTG p.224	rpsA	30S ribosomal protein S1
T44.4.2	c02	1909039	snp	226/566	synonymous_variant c.678G>T p.Val226Val	rpsA	30S ribosomal protein S1
T44.4.2	c02	1909072	snp	237/566	synonymous_variant c.711G>T p.Pro237Pro	rpsA	30S ribosomal protein S1
T44.4.2	c02	1909086	complex	242/566	missense_variant c.725_729delCCATCinsACATT p.Thr242Asn	rpsA	30S ribosomal protein S1
T44.4.2	c02	1909097	mnp	246/566	missense_variant c.736_737delACinsCA p.Thr246Gln	rpsA	30S ribosomal protein S1
T44.4.2	c02	1909108	snp	249/566	synonymous_variant c.747G>T p.Val249Val	rpsA	30S ribosomal protein S1
T44.4.3	c01	96450	snp	174/546	synonymous_variant c.522G>C p.Val174Val	groL	60 kDa chaperonin
T44.4.3	c01	96456	snp	176/546	synonymous_variant c.528G>C p.Thr176Thr	groL	60 kDa chaperonin
T44.4.3	c01	96534	snp	202/546	synonymous_variant c.606T>C p.Pro202Pro	groL	60 kDa chaperonin
T44.4.3	c01	96543	snp	205/546	synonymous_variant c.615C>G p.Val205Val	groL	60 kDa chaperonin
T44.4.3	c01	96549	complex	207/546	synonymous_variant c.621_624delCCCTinsTCCG p.209	groL	60 kDa chaperonin
T44.4.3	c01	96567	snp	213/546	synonymous_variant c.639T>G p.Ala213Ala	groL	60 kDa chaperonin
T44.4.3	c01	96609	snp	227/546	synonymous_variant c.681C>T p.Leu227Leu	groL	60 kDa chaperonin
T44.4.3	c01	96624	complex	232/546	missense_variant c.696_699delTCTTinsCATG p.Leu233Met	groL	60 kDa chaperonin
T44.4.3	c01	96633	snp	235/546	synonymous_variant c.705G>T p.Pro235Pro	groL	60 kDa chaperonin
T44.4.3	c01	96639	snp	237/546	synonymous_variant c.711G>C p.Leu237Leu	groL	60 kDa chaperonin
T44.4.3	c01	96658	mnp	244/546	missense_variant c.730_731delTCinsGG p.Ser244Gly	groL	60 kDa chaperonin
T44.4.3	c01	96732	snp	268/546	synonymous_variant c.804C>T p.Arg268Arg	groL	60 kDa chaperonin
T44.4.3	c01	96741	snp	271/546	synonymous_variant c.813G>C p.Leu271Leu	groL	60 kDa chaperonin
T44.4.3	c01	96753	snp	275/546	synonymous_variant c.825T>C p.Ala275Ala	groL	60 kDa chaperonin
T44.4.3	c01	96777	snp	283/546	synonymous_variant c.849T>C p.Asp283Asp	groL	60 kDa chaperonin
T44.4.3	c01	96786	snp	286/546	synonymous_variant c.858A>G p.Lys286Lys	groL	60 kDa chaperonin
T44.4.3	c01	96795	snp	289/546	synonymous_variant c.867C>G p.Leu289Leu	groL	60 kDa chaperonin
T44.4.3	c01	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ydcO_1	Inner membrane protein YdcO
T44.4.3	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ydcO_1	Inner membrane protein YdcO
T44.4.3	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	HTH-type transcriptional regulatory protein GabR
T44.4.3	c01	2021961	snp	259/840	synonymous_variant c.777G>C p.Ser259Ser	virB4_2	Type IV secretion system protein virB4
T44.4.3	c01	2021973	complex	263/840	missense_variant c.789_793delTCTGAinsCCTGC p.Met265Leu	virB4_2	Type IV secretion system protein virB4
T44.4.3	c01	2021999	snp	272/840	missense_variant c.815G>A p.Arg272Lys	virB4_2	Type IV secretion system protein virB4

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T44.4.3	c01	2022018	snp	278/840	synonymous_variant c.834C>T p.Arg278Arg	virB4_2	Type IV secretion system protein virB4
T44.4.3	c01	2022111	snp	309/840	synonymous_variant c.927C>A p.Ala309Ala	virB4_2	Type IV secretion system protein virB4
T44.4.3	c01	2022120	mnp	312/840	missense_variant c.936_938delTGCinsGCT p.Ala313Leu	virB4_2	Type IV secretion system protein virB4
T44.4.3	c01	2022133	snp	317/840	missense_variant c.949C>A p.Leu317Met	virB4_2	Type IV secretion system protein virB4
T44.4.3	c01	2022138	complex	318/840	synonymous_variant c.954_957delGCTAinsCTTG p.320	virB4_2	Type IV secretion system protein virB4
T44.4.3	c01	2022160	complex	326/840	missense_variant c.976_978delATCinsGTG p.lle326Val	virB4_2	Type IV secretion system protein virB4
T44.4.3	c01	2022206	complex	341/840	missense_variant c.1022_1031delCCGATGCCGCinsAGGACGCCCG p.AlaAspAlaAla341GluAspAlaArg	virB4_2	Type IV secretion system protein virB4
T44.4.3	c01	2022225	snp	347/840	missense_variant c.1041A>C p.Glu347Asp	virB4_2	Type IV secretion system protein virB4
T44.4.3	c01	2022253	snp	357/840	missense_variant c.1069A>G p.lle357Val	virB4_2	Type IV secretion system protein virB4
T44.4.3	c01	2022276	snp	364/840	synonymous_variant c.1092G>C p.Val364Val	virB4_2	Type IV secretion system protein virB4
T44.4.3	c01	2022318	snp	378/840	synonymous_variant c.1134C>G p.Ser378Ser	virB4_2	Type IV secretion system protein virB4
T44.4.3	c01	2022324	snp	380/840	synonymous_variant c.1140G>C p.Pro380Pro	virB4_2	Type IV secretion system protein virB4
T44.4.3	c01	2023509	snp	775/840	synonymous_variant c.2325T>C p.Asp775Asp	virB4_2	Type IV secretion system protein virB4
T44.4.3	c01	2023515	snp	777/840	synonymous_variant c.2331C>A p.Leu777Leu	virB4_2	Type IV secretion system protein virB4
T44.4.3	c01	2023521	snp	779/840	synonymous_variant c.2337G>A p.Glu779Glu	virB4_2	Type IV secretion system protein virB4
T44.4.3	c02	436035	snp	510/1377	synonymous_variant c.1530A>C p.Ala510Ala	rpoB	DNA-directed RNA polymerase subunit beta
T44.4.3	c02	436041	snp	512/1377	synonymous_variant c.1536G>T p.Val512Val	rpoB	DNA-directed RNA polymerase subunit beta
T44.4.3	c02	436047	snp	514/1377	synonymous_variant c.1542G>A p.Glu514Glu	rpoB	DNA-directed RNA polymerase subunit beta
T44.4.3	c02	436083	complex	526/1377	missense_variant c.1578_1584delTCAGACCinsCCAGGTG p.Thr528Val	rpoB	DNA-directed RNA polymerase subunit beta
T44.4.3	c02	439856	snp	338/1400	synonymous_variant c.1014T>C p.Gly338Gly	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.3	c02	439865	snp	341/1400	synonymous_variant c.1023T>C p.Arg341Arg	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.3	c02	439874	snp	344/1400	synonymous_variant c.1032G>T p.Leu344Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.3	c02	439910	snp	356/1400	synonymous_variant c.1068C>T p.Val356Val	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.3	c02	439931	snp	363/1400	synonymous_variant c.1089C>G p.Leu363Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.3	c02	439985	snp	381/1400	synonymous_variant c.1143A>G p.Pro381Pro	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.3	c02	439997	complex	385/1400	synonymous_variant c.1155_1161delACGTCTTinsCCGCCTC p.388	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.3	c02	440186	snp	448/1400	synonymous_variant c.1344T>C p.Ala448Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.3	c02	440198	snp	452/1400	synonymous_variant c.1356T>C p.His452His	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.3	c02	440207	complex	455/1400	synonymous_variant c.1365_1368delTTGTinsCTGC p.457	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.3	c02	440216	snp	458/1400	synonymous_variant c.1374G>C p.Ala458Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.3	c02	440264	snp	474/1400	synonymous_variant c.1422G>C p.Leu474Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.3	c02	440270	snp	476/1400	synonymous_variant c.1428C>G p.Leu476Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.3	c02	441101	complex	753/1400	synonymous_variant c.2259_2262delAACCinsGACG p.755	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.3	c02	441110	snp	756/1400	synonymous_variant c.2268A>C p.lle756lle	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.3	c02	445987	snp	360/694	synonymous_variant c.1078T>C p.Leu360Leu	fusA	Elongation factor G
T44.4.3	c02	446031	complex	374/694	synonymous_variant c.1122_1125delTGCAinsCGCC p.376	fusA	Elongation factor G
T44.4.3	c02	446133	complex	408/694	missense_variant c.1224_1227delGGATinsCGAG p.Asp409Glu	fusA	Elongation factor G
T44.4.3	c02	446142	complex	411/694	missense_variant c.1233_1239delTATCGAAinsCATCCAG p.Glu413Gln	fusA	Elongation factor G
T44.4.3	c02	446154	snp	415/694	synonymous_variant c.1245T>G p.Ala415Ala	fusA	Elongation factor G
T44.4.3	c02	451038	snp	252/277	synonymous_variant c.756T>C p.Pro252Pro	rpIB	50S ribosomal protein L2

T44.4.3 c2	Γ
144.4.3 COZ 45590 Complex 4072 Sprongmout_variant c. 1200-1 p. 200420 Complex 4072 Complex 4072 Sprongmout_variant c. 1200-1 p. 200420 Complex 4072 Co	.2
144.4.3	14
144.4.3 027	14
TAME 1998 1999 1996	14
14.4.4.3 0.02 0.08470 0.09 0.09470 0.09 0.09470 0.09 0.09470 0.09 0.09470 0.09 0.09470 0.09 0.09470 0.09 0.09470 0.09 0.09470 0.09 0.09470 0.0	14
Fig. 4.3 OZ 99847 Spp 219424 Spp 2194	tease ATP-
14.4.4.3 COZ 006414 STD 201444 STD 20	tease ATP-
144.4.3 C2	tease ATP-
144.43 02	tease ATP-
T44.4.3 CO	 31
TAME	 31
T44.4.3 CO	
TA44.4.3 CO2 1908881 orp 2005688 Symptymous_variant c.800C>T p.ValD00Val rps.A 305 ribasomal protein ST TA4.4.3 CO2 1908977 orp 2009888 missense variant c.800EA-D p.CalD20Asp p.A 305 ribasomal protein ST TA4.4.3 CO2 1909072 orp 2275688 sympymous_variant c.87667-T p.Val226Val p.A 305 ribasomal protein ST TA4.4.3 CO2 1909072 orp 227568 sympymous_variant c.87667-T p.Val226Val p.A 305 ribasomal protein ST TA4.4.3 CO2 1909087 orp 247568 sympymous_variant c.77767-T p.Pa2277Po p.B 305 ribasomal protein ST TA4.4.3 CO2 1909087 orp 247568 sympymous_variant c.77767-T p.Pa2277Po p.Da2277Po p.Da2277Po </td <td></td>	
T44.4.3 C92	
T44.4.3 CO2 1999077 Complex 22/1560 Symonymous_variant c.666_669datTCTCinsCCTG p.224 rpsA 305 ribosomal protein ST T44.4.3 CO2 1999076 app 22/1560 rpsA 305 ribosomal protein ST T44.4.3 CO2 1999076 app 27/1560 rpsA 305 ribosomal protein ST T44.4.3 CO2 1999086 complex 24/1560 researce_variant c.736.73 page 127.73 real. Complex 24/1560 researce_variant_c.736.73 page 127.73 real. Complex 24/1560 researce_variant_c.736.73 page 127.73 real. Complex 24/1560 researce_variant_c.736.73 page 127.73 real. Complex 24/1560 real. real	
T44.4.3 C02	
T44.4.3 C02	
T44.4.3 CO2	
T44.4.3 C62 1909097 mp. 246/568 missense_variant c.736.7374elACinsCA.p.Thr246Gin 7ps.A 306 ribosomal protein ST T44.4.3 c62 1909108 spp. 249/568 synonymous_variant c.7376.7 p.Val249val rps.A 306 ribosomal protein ST T44.4.4 c01 98480 spp. 176/546 synonymous_variant c.5260-C p.Na174Val grol. 60 Kba chaperonin T44.4.4 c01 98534 spp. 205/546 synonymous_variant c.6017-C p.Pro2020ra grol. 60 Kba chaperonin T44.4.4 c01 98534 spp. 205/546 synonymous_variant c.6018-C p.Pro2020ra grol. 60 Kba chaperonin T44.4.4 c01 98567 spp. 207/546 synonymous_variant c.6180-C p.Pro2020ra grol. 60 Kba chaperonin T44.4.4 c01 98567 spp. 213/546 synonymous_variant c.6318-C p.Pro2027reu grol. 60 Kba chaperonin T44.4.4 c01 98633 spp. 233/546 synonymous_variant c.8180-C p.Leu231Met grol. 60 Kba chaperonin <	
T44.4.3 C62 1009108 snp 249/566 synonymous_variant c.7470-T p.Vai249Val rpsA 305 ribosomal protein ST T44.4.4 c01 98456 snp 174/546 synonymous_variant c.5280-C p.Val17Val grol. 60 Kba chaperonin T44.4.4 c01 98543 snp 202/546 synonymous_variant c.5280-C p.Val17Val grol. 60 Kba chaperonin T44.4.4 c01 98543 snp 202/546 synonymous_variant c.618C>G p.Nal20SVal grol. 60 Kba chaperonin T44.4.4 c01 98543 snp 205/546 synonymous_variant c.618C>G p.Nal20SVal grol. 60 Kba chaperonin T44.4.4 c01 98677 snp 213/546 synonymous_variant c.618C>G p.Nal20SVal grol. 60 Kba chaperonin T44.4.4 c01 98624 complex 232/546 synonymous_variant c.681C>T p.Leu227Leu grol. 60 Kba chaperonin T44.4.4 c01 98633 snp 237/546 synonymous_variant c.730-73 tept.2023Met grol. 60 Kba chaperonin T44.4.4	
T44.4.4 CO1 96450 rpp 174/546 yyronymous_variant c.5220-C p.Vait7AVal grol. 60 kDa chaperonin T44.4.4 cO1 98458 spp 16/646 yronymous_variant c.5280-C p.Thr1761br grol. 60 kDa chaperonin T44.4.4 cO1 98534 spp 205/546 syronymous_variant c.6087-C p.Pro202Pro grol. 60 kDa chaperonin T44.4.4 cO1 98549 complex 207/546 syronymous_variant c.8165C-Q p.Vai2OSVal grol. 60 kDa chaperonin T44.4.4 cO1 98569 spp 217/546 syronymous_variant c.8167-C p.Nai22SVal grol. 60 kDa chaperonin T44.4.4 cO1 98687 spp 221/546 syronymous_variant c.8167-C p.Leu22Tval grol. 60 kDa chaperonin T44.4.4 cO1 98633 spp 237/546 syronymous_variant c.730-CFT p.Leu22Tval grol. 60 kDa chaperonin T44.4.4 cO1 98633 spp 237/546 syronymous_variant c.730-CFT p.Leu22Tval grol. 60 kDa chaperonin T44.4.4	31
T44.4.4 c01 96456 snp 178/546 synonymous_variant c.9280>C p.Thr176Thr grol. 60 kDa chaperonin T44.4.4 c01 96534 snp 202/546 synonymous_variant c.680T>C p.Pre202Pre grol. 60 kDa chaperonin T44.4.4 c01 96549 snp 205/546 synonymous_variant c.680T>C p.Pre202Pre grol. 60 kDa chaperonin T44.4.4 c01 96567 snp 213/546 synonymous_variant c.68162PdedeCCTInsTCCG p.209 grol. 60 kDa chaperonin T44.4.4 c01 96567 snp 213/546 synonymous_variant c.6816.994edCCTTInsCCGG p.209 grol. 60 kDa chaperonin T44.4.4 c01 96639 snp 227/546 synonymous_variant c.680.699edeTTTInsCCTG p.Leu227Leu grol. 60 kDa chaperonin T44.4.4 c01 96633 snp 237/546 synonymous_variant c.705-T p.Pre237Ere grol. 60 kDa chaperonin T44.4.4 c01 96639 snp 237/546 synonymous_variant c.706-T p.Arg237Leu grol. 60 kDa chaperonin T4	
T44.4.4 c01 96534 snp 202/546 synonymous, variant c.606T>C p.Pro202Pro grol. 60 kDa chaperonin T44.4.4 c01 96543 snp 205/546 synonymous, variant c.652-G p.Na/205Val grol. 60 kDa chaperonin T44.4.4 c01 96569 complex 207/546 synonymous, variant c.632-G p.Na/205Val grol. 60 kDa chaperonin T44.4.4 c01 96697 snp 213/546 synonymous, variant c.6381C>T p.Leu227Leu grol. 60 kDa chaperonin T44.4.4 c01 96693 snp 223/546 missense_variant c.688C>T p.Leu227Leu grol. 60 kDa chaperonin T44.4.4 c01 96633 snp 237/546 synonymous_variant c.700C>T p.Pro235Fro grol. 60 kDa chaperonin T44.4.4 c01 96658 mp 244/546 missense_variant c.730-731deff clinsGo p.Ser/244Gby grol. 60 kDa chaperonin T44.4.4 c01 96732 snp 248/546 synonymous_variant c.710-C p.Leu271Leu grol. 60 kDa chaperonin T44.4.4	
T44.4.4 c01 96543 spn 205/546 synonymous_variant c.615C>G_P.Val205Val grol 60 kDa chaperonin T44.4.4 c01 96549 complex 207/546 synonymous_variant c.631C>G_P.Val205Val grol 60 kDa chaperonin T44.4.4 c01 96699 snp 21/546 synonymous_variant c.631C>T_P.Leu22TLeu grol 60 kDa chaperonin T44.4.4 c01 96699 snp 227/546 synonymous_variant c.631C>T_P.Leu22TLeu grol 60 kDa chaperonin T44.4.4 c01 96693 snp 232/546 synonymous_variant c.7050>T_P.Pr0235Pro grol 60 kDa chaperonin T44.4.4 c01 96633 snp 237/546 synonymous_variant c.7050>T_P.Pr0235Pro grol 60 kDa chaperonin T44.4.4 c01 96638 mp 274/546 synonymous_variant c.804C>T_P.Arg258Arg grol 60 kDa chaperonin T44.4.4 c01 96731 snp 289/546 synonymous_variant c.836>C_P.Leu271Leu grol 60 kDa chaperonin T44.4.4 c01	
T44.4.4 C01 96549 complex 207/546 synonymous_variant c.621,624detCCCTinsTCCG p.209 grol. 60 kDa chaperonin T44.4.4 C01 96567 snp 213/546 synonymous_variant c.6381~5 p.Ale213Ala grol. 60 kDa chaperonin T44.4.4 C01 96624 complex 232/546 synonymous_variant c.698(-699delTCTTinsCATG p.Leu233Met grol. 60 kDa chaperonin T44.4.4 C01 96633 snp 233/546 synonymous_variant c.7965-7 p.Pro235Pro grol. 60 kDa chaperonin T44.4.4 C01 96638 snp 237/546 synonymous_variant c.71G>C p.Leu237Leu grol. 60 kDa chaperonin T44.4.4 C01 96658 mp 244/546 missense_variant c.73G>T-1detTCinsGQ p.Ser244Gly grol. 60 kDa chaperonin T44.4.4 c01 96731 snp 274/546 synonymous_variant c.813G>C p.Leu27Leu grol. 60 kDa chaperonin T44.4.4 c01 96751 snp 278/546 synonymous_variant c.813G>C p.Leu27Leu grol. 60 kDa chaperonin	
T44.4.4 C01 96567 snp 213/546 synonymous_variant c.639T>G p.Ala213Ala groL 60 kDa chaperonin T44.4.4 C01 96609 snp 227/546 synonymous_variant c.881C>T p.Leu227Leu groL 60 kDa chaperonin T44.4.4 C01 96624 complex 232/546 sissense_variant c.705G>T p.Pro235Pro groL 60 kDa chaperonin T44.4.4 C01 96633 snp 235/546 synonymous_variant c.710G>C p.Leu237Leu groL 60 kDa chaperonin T44.4.4 C01 96658 mnp 244/546 missense_variant c.730_731delTCinsGG p.Ser244Gly groL 60 kDa chaperonin T44.4.4 C01 96732 snp 288/546 synonymous_variant c.8136>C p.Leu271Leu groL 60 kDa chaperonin T44.4.4 C01 96731 snp 271/546 synonymous_variant c.8362>C p.Leu271Leu groL 60 kDa chaperonin T44.4.4 C01 96732 snp 275/546 synonymous_variant c.825T>C p.Ala275Ala groL 60 kDa chaperonin T44.4.4 C01	
T44.4.4 C01 96609 snp 227/546 synonymous_variant c.6816.>T p.Leu227Leu groL 60 kDa chaperonin T44.4.4 C01 96624 complex 232/546 missense_variant c.696.699delTCTTinsCATG p.Leu233Met groL 60 kDa chaperonin T44.4.4 C01 96638 snp 237/546 synonymous_variant c.7052-T p.Pro235Pro groL 60 kDa chaperonin T44.4.4 C01 96638 snp 237/546 synonymous_variant c.7052-T p.Pro235Pro groL 60 kDa chaperonin T44.4.4 C01 96638 snp 237/546 synonymous_variant c.7052-T p.Pro235Pro groL 60 kDa chaperonin T44.4.4 C01 96732 snp 268/546 synonymous_variant c.8040-T p.Arg268Arg groL 60 kDa chaperonin T44.4.4 C01 96731 snp 27/546 synonymous_variant c.8267-D p.Leu271Leu groL 60 kDa chaperonin T44.4.4 C01 96756 snp 238/546 synonymous_variant c.8257-D p.Arg275Ala groL 60 kDa chaperonin T44.4.4 <	
T44.4.4 CO1 96624 complex 232/546 missense_variant c.696_699delTCTTinsCATG p.Leu233Met groL 60 kDa chaperonin T44.4.4 cO1 96833 snp 235/546 synonymous_variant c.705G>T p.Pro235Pro groL 60 kDa chaperonin T44.4.4 cO1 96839 snp 237/546 synonymous_variant c.71G>C p.Leu237Leu groL 60 kDa chaperonin T44.4.4 cO1 96858 mnp 244/546 missense_variant c.730_731delTCinsGQ p.Ser244Gly groL 60 kDa chaperonin T44.4.4 cO1 96731 snp 288/546 synonymous_variant c.804C>T p.Arg268Arg groL 60 kDa chaperonin T44.4.4 cO1 96753 snp 275/546 synonymous_variant c.825T>C p.Ala275Ala groL 60 kDa chaperonin T44.4.4 cO1 96763 snp 275/546 synonymous_variant c.849T>C p.Asp283Asp groL 60 kDa chaperonin T44.4.4 cO1 96786 snp 286/546 synonymous_variant c.876C>G p.Leu28Bleu groL 60 kDa chaperonin T44.4.4	
T44.4.4 c01 96833 snp 235/546 synonymous_variant c.7056>T p.Pro235Pro groL 60 kDa chaperonin T44.4.4 c01 96839 snp 237/546 synonymous_variant c.71G>C p.Leu237Leu groL 60 kDa chaperonin T44.4.4 c01 96868 mmp 244/546 missense_variant c.730_731delTcinsG0 p.Ser244Gly groL 60 kDa chaperonin T44.4.4 c01 96732 snp 268/546 synonymous_variant c.804C>T p.Arg26Barg groL 60 kDa chaperonin T44.4.4 c01 96731 snp 275/546 synonymous_variant c.836>C p.Leu271Leu groL 60 kDa chaperonin T44.4.4 c01 96773 snp 283/546 synonymous_variant c.849T>C p.Asp283Asp groL 60 kDa chaperonin T44.4.4 c01 96786 snp 286/546 synonymous_variant c.858A>Q p.Lys286Lys groL 60 kDa chaperonin T44.4.4 c01 96785 snp 286/546 synonymous_variant c.858A>Q p.Lys286Lys groL 60 kDa chaperonin T44.4.4 c01 <td></td>	
T44.4.4 C01 96639 spp 237/546 synonymous_variant c.711G>C p.Leu237Leu grol 60 kDa chaperonin T44.4.4 C01 96658 mmp 244/546 missense_variant c.730_731delTCinsGG p.Ser244Gly grol 60 kDa chaperonin T44.4.4 C01 96732 snp 268/546 synonymous_variant c.8304C>T p.Arg268Arg grol 60 kDa chaperonin T44.4.4 C01 96731 snp 271/546 synonymous_variant c.8332C p.Leu271Leu grol 60 kDa chaperonin T44.4.4 C01 96753 snp 275/546 synonymous_variant c.8257>C p.Leu271Leu grol 60 kDa chaperonin T44.4.4 c01 96786 snp 288/546 synonymous_variant c.858Acp p.Lys286Lys grol 60 kDa chaperonin T44.4.4 c01 96795 snp 288/546 synonymous_variant c.858Acp p.Lys286Lys grol 60 kDa chaperonin T44.4.4 c01 96795 snp 288/546 synonymous_variant c.858Acp p.Lys286Lys grol 60 kDa chaperonin T44.4.4 c01<	
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T44.4.4 c01 96732 snp 268/546 synonymous_variant c.804C>T p.Arg268Arg grol. 60 kDa chaperonin T44.4.4 c01 96741 snp 271/546 synonymous_variant c.813G>C p.Leu271Leu grol. 60 kDa chaperonin T44.4.4 c01 96753 snp 275/546 synonymous_variant c.825T>C p.Ala275Ala grol. 60 kDa chaperonin T44.4.4 c01 96777 snp 283/546 synonymous_variant c.849T>C p.Asp283Asp grol. 60 kDa chaperonin T44.4.4 c01 96786 snp 286/546 synonymous_variant c.858A>G p.Lys286Lys grol. 60 kDa chaperonin T44.4.4 c01 96795 snp 289/546 synonymous_variant c.867C>G p.Leu289Leu grol. 60 kDa chaperonin T44.4.4 c01 1008861 del 218/239 frameshift_variant c.867C>G p.Leu289Leu grol. 60 kDa chaperonin T44.4.4 c01 1008861 del 214/239 frameshift_variant c.867C>G p.Leu289Leu grol. 60 kDa chaperonin T44.4.4 c0	
T44.4.4 c01 96741 snp 271/546 synonymous_variant c.813G>C p.Leu271Leu grol 60 kDa chaperonin T44.4.4 c01 96753 snp 275/546 synonymous_variant c.825T>C p.Ala275Ala grol 60 kDa chaperonin T44.4.4 c01 96777 snp 283/546 synonymous_variant c.849T>C p.Asp283Asp grol 60 kDa chaperonin T44.4.4 c01 96786 snp 286/546 synonymous_variant c.8567C>G p.Leu289Leu grol 60 kDa chaperonin T44.4.4 c01 96795 snp 289/546 synonymous_variant c.867C>G p.Leu289Leu grol 60 kDa chaperonin T44.4.4 c01 1008848 del 218/239 frameshift_variant c.633delG p.Gly218fs ydcO_1 Inner membrane protein N T44.4.4 c01 1010254 del 21/239 frameshift_variant c.74delG p.Ala2fs gabR_1 HTH-type transcriptional protein GabR T44.4.4 c01 2021961 snp 259/840 synonymous_variant c.777G>C p.Ser259Ser vir84_2 Type IV secretion system virB4	
T44.4.4 c01 96753 snp 275/546 Synonymous_variant c.825T>C p.Ala275Ala grol 60 kDa chaperonin T44.4.4 c01 96777 snp 283/546 synonymous_variant c.849T>C p.Asp283Asp grol 60 kDa chaperonin T44.4.4 c01 96786 snp 286/546 synonymous_variant c.858A>G p.Lys286Lys grol 60 kDa chaperonin T44.4.4 c01 96795 snp 289/546 synonymous_variant c.867C>G p.Leu289Leu grol 60 kDa chaperonin T44.4.4 c01 1008848 del 218/239 frameshift_variant c.653delG p.Gly218fs ydc0_1 Inner membrane protein N T44.4.4 c01 1008861 del 214/239 frameshift_variant c.46elG p.Ala2fs gabR_1 HTH-type transcriptional protein GabR T44.4.4 c01 2021961 snp 259/840 synonymous_variant c.777G>C p.Ser259Ser virB4_2 Type IV secretion system virB4 T44.4.4 c01 2021993 snp 272/840 missense_variant c.815G>A p.Arg272Lys virB4_2 Type IV secretion system virB4 <	
T44.4.4 C01 96777 snp 283/546 synonymous_variant c.849T>C p.Asp283Asp grol. 60 kDa chaperonin T44.4.4 C01 96786 snp 286/546 synonymous_variant c.858A>G p.Lys286Lys grol. 60 kDa chaperonin T44.4.4 C01 96795 snp 289/546 synonymous_variant c.857C>G p.Leu289Leu grol. 60 kDa chaperonin T44.4.4 C01 1008848 del 218/239 frameshift_variant c.653delG p.Gly218fs ydcO_1 Inner membrane protein of the protein of th	
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T44.4.4 c01 96786 snp 286/546 synonymous_variant c.858A>G p.Lys286Lys grol 60 kDa chaperonin T44.4.4 c01 96795 snp 289/546 synonymous_variant c.867C>G p.Leu289Leu grol 60 kDa chaperonin T44.4.4 c01 1008848 del 218/239 frameshift_variant c.653delG p.Gly218fs ydcO_1 Inner membrane protein of the protein o	
T44.4.4 c01 96795 snp 289/546 synonymous_variant c.867C>G p.Leu289Leu grol 60 kDa chaperonin T44.4.4 c01 1008848 del 218/239 frameshift_variant c.630delG p.Gly218fs ydcO_1 Inner membrane protein N T44.4.4 c01 1008861 del 214/239 frameshift_variant c.640delC p.Arg214fs ydcO_1 Inner membrane protein N T44.4.4 c01 1010254 del 2/429 frameshift_variant c.4delG p.Ala2fs gabR_1 HTH-type transcriptional protein GabR T44.4.4 c01 2021961 snp 259/840 synonymous_variant c.777G>C p.Ser259Ser virB4_2 Type IV secretion system virB4 T44.4.4 c01 2021973 complex 263/840 missense_variant c.789_793delTCTGAinsCCTGC p.Met265Leu virB4_2 Type IV secretion system virB4 T44.4.4 c01 2021999 snp 272/840 missense_variant c.815G>A p.Arg272Lys virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022118 snp 278/840 synonymous_variant c.834C>T p.Arg278Arg vi	
T44.4.4 c01 1008848 del 218/239 frameshift_variant c.653delG p.Gly218fs ydcO_1 Inner membrane protein N T44.4.4 c01 1008861 del 214/239 frameshift_variant c.640delC p.Arg214fs ydcO_1 Inner membrane protein N T44.4.4 c01 1010254 del 2/429 frameshift_variant c.4delG p.Ala2fs gabR_1 HTH-type transcriptional protein GabR T44.4.4 c01 2021961 snp 259/840 synonymous_variant c.777G>C p.Ser259Ser virB4_2 Type IV secretion system virB4 T44.4.4 c01 2021973 complex 263/840 missense_variant c.789_793delTCTGAinsCCTGC p.Met265Leu virB4_2 Type IV secretion system virB4 T44.4.4 c01 2021999 snp 272/840 missense_variant c.815G>A p.Arg272Lys virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022018 snp 278/840 synonymous_variant c.834C>T p.Arg278Arg virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022111 snp 309/840 synonymous_variant c.936_938delTGCinsGCT	
T44.4.4 c01 1008861 del 214/239 frameshift_variant c.640delC p.Arg214fs ydcO_1 Inner membrane protein N T44.4.4 c01 1010254 del 2/429 frameshift_variant c.4delG p.Ala2fs gabR_1 HTH-type transcriptional protein GabR T44.4.4 c01 2021961 snp 259/840 synonymous_variant c.777G>C p.Ser259Ser virB4_2 Type IV secretion system virB4 T44.4.4 c01 2021973 complex 263/840 missense_variant c.789_793delTCTGAinsCCTGC p.Met265Leu virB4_2 Type IV secretion system virB4 T44.4.4 c01 2021999 snp 272/840 missense_variant c.815G>A p.Arg272Lys virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022018 snp 278/840 synonymous_variant c.834C>T p.Arg278Arg virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022111 snp 309/840 synonymous_variant c.927C>A p.Ala309Ala virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022120 mnp 312/840 missense_variant c.949C>A p.Leu317	
T44.4.4 c01 1010254 del 2/429 frameshift_variant c.4delG p.Ala2fs gabR_1 HTH-type transcriptional protein GabR T44.4.4 c01 2021961 snp 259/840 synonymous_variant c.777G>C p.Ser259Ser virB4_2 Type IV secretion system virB4 T44.4.4 c01 2021973 complex 263/840 missense_variant c.789_793delTCTGAinsCCTGC p.Met265Leu virB4_2 Type IV secretion system virB4 T44.4.4 c01 2021999 snp 272/840 missense_variant c.815G>A p.Arg272Lys virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022018 snp 278/840 synonymous_variant c.834C>T p.Arg278Arg virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022111 snp 309/840 synonymous_variant c.927C>A p.Ala309Ala virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022120 mnp 312/840 missense_variant c.936_938delTGCinsGCT p.Ala313Leu virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022133 snp 317/840 missense_variant	
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T44.4.4 c01 2021999 snp 272/840 missense_variant c.815G>A p.Arg272Lys virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022018 snp 278/840 synonymous_variant c.834C>T p.Arg278Arg virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022111 snp 309/840 synonymous_variant c.927C>A p.Ala309Ala virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022120 mnp 312/840 missense_variant c.936_938delTGCinsGCT p.Ala313Leu virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022133 snp 317/840 missense_variant c.949C>A p.Leu317Met virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022138 complex 318/840 synonymous_variant c.949C>A p.Leu317Met virB4_2 Type IV secretion system virB4	m protein
T44.4.4 c01 2022018 snp 278/840 synonymous_variant c.834C>T p.Arg278Arg virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022111 snp 309/840 synonymous_variant c.927C>A p.Ala309Ala virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022120 mnp 312/840 missense_variant c.936_938delTGCinsGCT p.Ala313Leu virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022133 snp 317/840 missense_variant c.949C>A p.Leu317Met virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022138 complex 318/840 synonymous variant c.949 PS7/delGCTAinsCTTG p.320 virB4_2 Type IV secretion system virB4	m protein
T44.4.4 C01 2022110 snp 309/840 synonymous_variant c.92/CSA p.Aia309Aia VirB4_2 virB4_2 virB4_2 T44.4.4 c01 2022120 mnp 312/840 missense_variant c.936_938delTGCinsGCT p.Ala313Leu virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022133 snp 317/840 missense_variant c.949C>A p.Leu317Met virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022138 complex 318/840 synonymous variant c.954_957delGCTAinsCTTG p.320 virB4_2 Type IV secretion system	m protein
T44.4.4 c01 2022120 mnp 312/840 missense_variant c.936_938delTGCinsGCT p.Ala313Leu virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022133 snp 317/840 missense_variant c.949C>A p.Leu317Met virB4_2 Type IV secretion system virB4 T44.4.4 c01 2022138 complex 318/840 synonymous variant c.954_957delGCTAinsCTTG p.320 virB4_2 Type IV secretion system virB4	m protein
T44.4.4 c01 2022133 snp 317/840 missense_variant c.949C>A p.Leu317Met virB4_2 Type IV secretion system virB4 TA4.4.4 c01 2022138 complex 318/840 synonymous variant c.954 957delGCTAinsCTTG p.320 virB4 2 Type IV secretion system	m protein
TA4.4.4 c01 2022138 complex 318/840 synonymous variant c 954 957delGCTAinsCTTG n 220 vir.4.2 Type IV secretion system	m protein
	m protein
T44.4.4 c01 2022160 complex 326/840 missense_variant c.976_978delATCinsGTG p.lle326Val virB4_2 Type IV secretion system virB4	m protein
T44.4.4 c01 2022206 complex 341/840 missense_variant c.1022_1031delCCGATGCCGCinsAGGACGCCCG virB4_2 Type IV secretion system virB4_2	m protein

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T44.4.4	c01	2022225	snp	347/840	missense_variant c.1041A>C p.Glu347Asp	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2022253	snp	357/840	missense_variant c.1069A>G p.lle357Val	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2022276	snp	364/840	synonymous_variant c.1092G>C p.Val364Val	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2022318	snp	378/840	synonymous_variant c.1134C>G p.Ser378Ser	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2022324	snp	380/840	synonymous_variant c.1140G>C p.Pro380Pro	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2022330	complex	382/840	synonymous_variant c.1146_1149delCGCCinsTGCT p.384	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2022339	snp	385/840	synonymous_variant c.1155A>C p.Ala385Ala	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2023443	snp	753/840	synonymous_variant c.2259C>T p.Gly753Gly	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2023509	snp	775/840	synonymous_variant c.2325T>C p.Asp775Asp	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2023515	snp	777/840	synonymous_variant c.2331C>A p.Leu777Leu	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2023521	snp	779/840	synonymous_variant c.2337G>A p.Glu779Glu	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2023532	complex	783/840	missense_variant c.2348_2352delACGGTinsGCGGC p.Asp783Gly	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2023545	complex	787/840	synonymous_variant c.2361_2364delTGCAinsCGCT p.789	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2023554	snp	790/840	synonymous_variant c.2370C>G p.Leu790Leu	virB4_2	Type IV secretion system protein virB4
T44.4.4	c02	436029	snp	508/1377	synonymous_variant c.1524T>A p.Ala508Ala	rpoB	DNA-directed RNA polymerase subunit beta
T44.4.4	c02	436035	snp	510/1377	synonymous_variant c.1530A>C p.Ala510Ala	rpoB	DNA-directed RNA polymerase subunit beta
T44.4.4	c02	436041	snp	512/1377	synonymous_variant c.1536G>T p.Val512Val	гроВ	DNA-directed RNA polymerase subunit beta
T44.4.4	c02	436047	snp	514/1377	synonymous_variant c.1542G>A p.Glu514Glu	rpoB	DNA-directed RNA polymerase subunit beta
T44.4.4	c02	436083	complex	526/1377	missense_variant c.1578_1584delTCAGACCinsCCAGGTG p.Thr528Val	rpoB	DNA-directed RNA polymerase subunit beta
T44.4.4	c02	436125	snp	540/1377	synonymous_variant c.1620C>T p.Leu540Leu	rpoB	DNA-directed RNA polymerase subunit beta
T44.4.4	c02	436143	snp	546/1377	synonymous_variant c.1638C>T p.Gly546Gly	rpoB	DNA-directed RNA polymerase subunit beta
T44.4.4	c02	439856	snp	338/1400	synonymous_variant c.1014T>C p.Gly338Gly	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.4	c02	439865	snp	341/1400	synonymous_variant c.1023T>C p.Arg341Arg	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.4	c02	439874	snp	344/1400	synonymous_variant c.1032G>T p.Leu344Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.4	c02	439910	snp	356/1400	synonymous_variant c.1068C>T p.Val356Val	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.4	c02	439931	snp	363/1400	synonymous_variant c.1089C>G p.Leu363Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.4	c02	439985	snp	381/1400	synonymous_variant c.1143A>G p.Pro381Pro	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.4	c02	440172	snp	444/1400	missense_variant c.1330A>G p.lle444Val	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.4	c02	440186	snp	448/1400	synonymous_variant c.1344T>C p.Ala448Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.4	c02	440198	snp	452/1400	synonymous_variant c.1356T>C p.His452His	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.4	c02	440207	complex	455/1400	synonymous_variant c.1365_1368delTTGTinsCTGC p.457	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.4	c02	440216	snp	458/1400	synonymous_variant c.1374G>C p.Ala458Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.4	c02	440264	snp	474/1400	synonymous_variant c.1422G>C p.Leu474Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.4	c02	440270	snp	476/1400	synonymous_variant c.1428C>G p.Leu476Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.4	c02	441065	snp	741/1400	synonymous_variant c.2223T>C p.Arg741Arg	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.4	c02	441071	snp	743/1400	synonymous_variant c.2229T>G p.Leu743Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.4	c02	441077	snp	745/1400	synonymous_variant c.2235C>A p.Ala745Ala	rpoC	DNA-directed RNA polymerase subunit beta'

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T44.4.4	c02	441101	complex	753/1400	synonymous_variant c.2259_2262delAACCinsGACG p.755	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.4	c02	441110	snp	756/1400	synonymous_variant c.2268A>C p.lle756lle	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.4	c02	441195	snp	785/1400	synonymous_variant c.2353T>C p.Leu785Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.4	c02	441203	complex	787/1400	synonymous_variant c.2361_2364delTGCTinsGGCG p.789	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.4	c02	446031	complex	374/694	synonymous_variant c.1122_1125delTGCAinsCGCC p.376	fusA	Elongation factor G
T44.4.4	c02	446133	complex	408/694	missense_variant c.1224_1227delGGATinsCGAG p.Asp409Glu	fusA	Elongation factor G
T44.4.4	c02	446142	complex	411/694	missense_variant c.1233_1239delTATCGAAinsCATCCAG p.Glu413Gln	fusA	Elongation factor G
T44.4.4	c02	446154	snp	415/694	synonymous_variant c.1245T>G p.Ala415Ala	fusA	Elongation factor G
T44.4.4	c02	451011	snp	243/277	synonymous_variant c.729T>C p.Arg243Arg	rplB	50S ribosomal protein L2
T44.4.4	c02	451017	complex	245/277	synonymous_variant c.735_738delTGTCinsGGTT p.247	rplB	50S ribosomal protein L2
T44.4.4	c02	451038	snp	252/277	synonymous_variant c.756T>C p.Pro252Pro	rplB	50S ribosomal protein L2
T44.4.4	c02	451051	complex	257/277	missense_variant c.769_777delAAGACGCGCinsCGCACCCGT p.Lys257Arg	rplB	50S ribosomal protein L2
T44.4.4	c02	453539	snp	13/122	synonymous_variant c.39C>T p.Asn13Asn	rplN	50S ribosomal protein L14
T44.4.4	c02	453590	complex	30/122	missense_variant c.90_96delGCGTTACinsCAAATAT p.Arg31Lys	rplN	50S ribosomal protein L14
T44.4.4	c02	453602	snp	34/122	synonymous_variant c.102C>T p.Ser34Ser	rplN	50S ribosomal protein L14
T44.4.4	c02	453620	complex	40/122	synonymous_variant c.120_126delGGTGTCGinsCGTTTCC p.43	rplN	50S ribosomal protein L14
T44.4.4	c02	698357	snp	240/424	synonymous_variant c.720C>T p.Asp240Asp	clpX	ATP-dependent Clp protease ATP-
T44.4.4	c02	698399	snp	226/424	synonymous_variant c.678A>G p.Gln226Gln	clpX	binding subunit ClpX ATP-dependent Clp protease ATP-
			<u>'</u>	-			binding subunit ClpX ATP-dependent Clp protease ATP-
T44.4.4	c02	698420	snp	219/424	synonymous_variant c.657C>G p.Thr219Thr	clpX	binding subunit ClpX ATP-dependent Clp protease ATP-
T44.4.4	c02	698474	snp	201/424	synonymous_variant c.603C>T p.Arg201Arg	clpX	binding subunit ClpX
T44.4.4	c02	698492	snp	195/424	synonymous_variant c.585T>C p.Asp195Asp	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.4	c02	698505	complex	190/424	synonymous_variant c.570_572delCAGinsTTC p.192	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.4	c02	1908916	complex	185/566	synonymous_variant c.555_558delGGAAinsCGAG p.187	rpsA	30S ribosomal protein S1
T44.4.4	c02	1908928	snp	189/566	synonymous_variant c.567G>T p.Ser189Ser	rpsA	30S ribosomal protein S1
T44.4.4	c02	1908937	snp	192/566	synonymous_variant c.576C>T p.Val192Val	rpsA	30S ribosomal protein S1
T44.4.4	c02	1908946	snp	195/566	synonymous_variant c.585T>C p.Leu195Leu	rpsA	30S ribosomal protein S1
T44.4.4	c02	1908955	snp	198/566	synonymous_variant c.594T>C p.Gly198Gly	rpsA	30S ribosomal protein S1
T44.4.4	c02	1908961	snp	200/566	synonymous_variant c.600C>T p.Val200Val	rpsA	30S ribosomal protein S1
T44.4.4	c02	1908967	snp	202/566	missense_variant c.606A>C p.Glu202Asp	rpsA	30S ribosomal protein S1
T44.4.4	c02	1909027	complex	222/566	synonymous_variant c.666_669delTCTCinsCCTG p.224	rpsA	30S ribosomal protein S1
T44.4.4	c02	1909039	snp	226/566	synonymous_variant c.678G>T p.Val226Val	rpsA	30S ribosomal protein S1
T44.4.4	c02	1909072	snp	237/566	synonymous_variant c.711G>T p.Pro237Pro	rpsA	30S ribosomal protein S1
T44.4.4	c02	1909086	complex	242/566	missense_variant c.725_729delCCATCinsACATT p.Thr242Asn	rpsA	30S ribosomal protein S1
T44.4.4	c02	1909097	complex	246/566	missense_variant c.736_737delACinsCA p.Thr246GIn	rpsA	30S ribosomal protein S1
T44.4.4	c02	1909108 2279042	snp	249/566 9/134	synonymous_variant c.747G>T p.Val249Val synonymous_variant c.27T>C p.Gly9Gly	rpsA ssb_4	30S ribosomal protein S1 Single-stranded DNA-binding
T44.4.4	c02	2279055	complex	14/134	missense_variant c.40_41delGAinsAC p.Asp14Thr	ssb_4	protein Single-stranded DNA-binding
T44.4.4	c02	2279075	complex	20/134	missense_variant c.60_61delCCinsTG p.Gln21Glu	ssb_4	protein Single-stranded DNA-binding
T44.4.4	c02	2279084	snp	23/134	synonymous_variant c.69C>T p.Gly23Gly	ssb_4	protein Single-stranded DNA-binding
T44.4.5.rep	c01	96456	snp	176/546	synonymous_variant c.528G>C p.Thr176Thr	groL	protein 60 kDa chaperonin
T44.4.5.rep	c01	96534	snp	202/546	synonymous_variant c.606T>C p.Pro202Pro	groL	60 kDa chaperonin
T44.4.5.rep	c01	96543	snp	205/546	synonymous_variant c.615C>G p.Val205Val	groL	60 kDa chaperonin
T44.4.5.rep	c01	96549	complex	207/546	synonymous_variant c.621_624delCCCTinsTCCG p.209	groL	60 kDa chaperonin
T44.4.5.rep	c01	96567	snp	213/546	synonymous_variant c.639T>G p.Ala213Ala	groL	60 kDa chaperonin
T44.4.5.rep	c01	96609	snp	227/546	synonymous_variant c.681C>T p.Leu227Leu	groL	60 kDa chaperonin
T44.4.5.rep	c01	96624	complex	232/546	missense_variant c.696_699delTCTTinsCATG p.Leu233Met	groL	60 kDa chaperonin
		96633	snp	235/546	synonymous_variant c.705G>T p.Pro235Pro	groL	60 kDa chaperonin
T44.4.5.rep	c01				synonymous_variant c.711G>C p.Leu237Leu	groL	60 kDa chaperonin
T44.4.5.rep	c01	96639	snp	237/546	'', '' '' '' ''	J .	
		96639 96658	snp mnp	237/546 244/546	missense_variant c.730_731delTCinsGG p.Ser244Gly	groL	60 kDa chaperonin
T44.4.5.rep	c01					<u> </u>	·
T44.4.5.rep	c01	96658	mnp	244/546	missense_variant c.730_731delTCinsGG p.Ser244Gly	groL	60 kDa chaperonin
T44.4.5.rep T44.4.5.rep T44.4.5.rep	c01 c01 c01	96658 96732	mnp	244/546 268/546	missense_variant c.730_731delTCinsGG p.Ser244Gly synonymous_variant c.804C>T p.Arg268Arg	groL groL	60 kDa chaperonin 60 kDa chaperonin

TAKALENION COLUMNIA	sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
	T44.4.5.rep	c01	96786	snp	286/546	synonymous_variant c.858A>G p.Lys286Lys	groL	60 kDa chaperonin
	· ·						-	·
Part	T44.4.5.rep	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ydcO_1	·
New York 1965 1967 196	T44.4.5.rep	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	protein GabR
	T44.4.5.rep	c01	2007330	complex	72/133	missense_variant c.214_216delCAAinsGAG p.Gln72Glu	ssb_1	-
144.4.5.mg 101 2019/37 2019/	T44.4.5.rep	c01	2007347	snp	77/133	synonymous_variant c.231T>C p.Gly77Gly	ssb_1	
TALLA SUMP CON	T44.4.5.rep	c01	2021961	snp	259/840	synonymous_variant c.777G>C p.Ser259Ser	virB4_2	
Table 10	T44.4.5.rep	c01	2021973	complex	263/840	missense_variant c.789_793delTCTGAinsCCTGC p.Met265Leu	virB4_2	, ,
TALLASING COL 202211 Page 209840 Sympymmox_primate_20220-A p.Asignation Page	T44.4.5.rep	c01	2021999	snp	272/840	missense_variant c.815G>A p.Arg272Lys	virB4_2	
TALA 1.5.	T44.4.5.rep	c01	2022018	snp	278/840	synonymous_variant c.834C>T p.Arg278Arg	virB4_2	
T44.4.5.rep Corp.	T44.4.5.rep	c01	2022111	snp	309/840	synonymous_variant c.927C>A p.Ala309Ala	virB4_2	
TAMALS.Nep Col 2027/35 sep	T44.4.5.rep	c01	2022120	mnp	312/840	missense_variant c.936_938delTGCinsGCT p.Ala313Leu	virB4_2	
T44.4.5.rep C01 2022160 Complex 316/840 Misserne_variant c.1978_976escu.hamscu.frg p.18-326 Wr84_2 Wr84_2 Wr84_3 Wr84_4 Type If Vacretion system protein	T44.4.5.rep	c01	2022133	snp	317/840	missense_variant c.949C>A p.Leu317Met	virB4_2	, ,
T44.4.5.rep c01 202225 and 347840 synchymous_variant c109A>C p.Pu386Prio vir84.2 vir84.2 vir84 vir84.5.rep c01 202226 and 347840 synchymous_variant c109A>C p.Pu386Prio vir84.2 vir84.2 vir84.5.rep c01 202233 and 378840 synchymous_variant c109A>C p.Pu386Prio vir84.2 vir84.2 vir84.2 vir84.2 vir84.2 vir84.2 vir84.2 vir84.3 vir84.4 single color vir84.2	T44.4.5.rep	c01	2022138	complex	318/840	synonymous_variant c.954_957delGCTAinsCTTG p.320	virB4_2	
T44.4.5.rep C01 202225 Sinp 347/840 missense.variant c.1041A>C.p.Glus474sp viril	T44.4.5.rep	c01	2022160	complex	326/840	missense_variant c.976_978delATCinsGTG p.lle326Val	virB4_2	
14.4.5.frep COI 2022253 Stp 347/840 missense_variant c.1069A>-0 p.lle357val VirB4.2 VirB4.2 VirB4.2 VirB4 virB4 T.44.4.5.frep COI 2022253 snp 357/840 missense_variant c.1069A>-0 p.lle357val virB4.2 Type IV secretion system protein virB4 T.44.4.5.frep COI 2022218 snp 378/840 synonymous_variant c.1140G>C p.Pro380Pro virB4.2 Type IV secretion system protein virB4 T.44.4.5.frep COI 2022224 snp 380/840 synonymous_variant c.1140G>C p.Pro380Pro virB4.2 Type IV secretion system protein virB4 T.44.4.5.frep COI 2023443 snp 753/840 synonymous_variant c.2326T>C p.Asp775Asp virB4.2 Type IV secretion system protein virB4 T.44.4.5.frep COI 2023509 snp 775/840 synonymous_variant c.2326T>C p.Asp775Asp virB4.2 Type IV secretion system protein virB4 T.44.4.5.frep COI 2023515 snp 777/840 synonymous_variant c.2326T>C p.Asp775Asp virB4.2 Type IV secretion system protein virB4 virB4.2 Type IV secretion system protei	T44.4.5.rep	c01	2022206	complex	341/840		virB4_2	
T44.4.5.rep c01 202321 snp 775/840 synonymous_variant c.10926>C p.Vai364Val vir64.2 Type IV secretion system protein vir64 street for the first secretion system protein vir64	T44.4.5.rep	c01	2022225	snp	347/840	missense_variant c.1041A>C p.Glu347Asp	virB4_2	
14.4.5.rep CO1 2022318 snp 358/840 synonymous_variant c.103425 c. p.sca348s ViRS4.2 vir84.2	T44.4.5.rep	c01	2022253	snp	357/840	missense_variant c.1069A>G p.lle357Val	virB4_2	
T44.4.5.rep C01 2022334 snp 380/840 synonymous_variant c.1140G>C p.Fro380Pro Vir84_2 Type IV secretion system protein vir84 vir84 T44.4.5.rep C01 2023343 snp 753/840 synonymous_variant c.2259C>T p.Gly753Gly vir84_2 Type IV secretion system protein vir84 vir84 T44.4.5.rep C01 2023509 snp 775/840 synonymous_variant c.233TC>A p.Leu777Leu vir84_2 Type IV secretion system protein vir84 T44.4.5.rep C01 2023515 snp 777/840 synonymous_variant c.233TC>A p.Leu777Leu vir84_2 Type IV secretion system protein vir84 T44.4.5.rep C01 2023525 snp 779/840 synonymous_variant c.233TC>A p.Eu77756u Vir84_2 Type IV secretion system protein vir84 T44.4.5.rep C02 438856 snp 338/1400 synonymous_variant c.1014T>C p.Gly338Gly TpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep C02 439865 snp 344/1400 synonymous_variant c.1032G>T p.Leu344Leu TpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep C02 439910 <td>T44.4.5.rep</td> <td>c01</td> <td>2022276</td> <td>snp</td> <td>364/840</td> <td>synonymous_variant c.1092G>C p.Val364Val</td> <td>virB4_2</td> <td></td>	T44.4.5.rep	c01	2022276	snp	364/840	synonymous_variant c.1092G>C p.Val364Val	virB4_2	
144.4.5.rep C01 2022.343 snp selleau synonymous_variant c.12459Cp_ProseptPro VIRB-2 virB4 virB4 144.4.5.rep C01 2023433 snp 753/840 synonymous_variant c.2259Cp_T p.Gly753Gly virB4.2 Type IV secretion system protein virB4 144.4.5.rep C01 2023515 snp 777/840 synonymous_variant c.2331C>A p.Leu777Leu virB4.2 Type IV secretion system protein virB4 144.4.5.rep C01 2023521 snp 778/840 synonymous_variant c.2337C>A p.Glu779Glu virB4.2 Type IV secretion system protein virB4 144.4.5.rep C01 2023521 snp 778/840 synonymous_variant c.1014T>C p.Gly338Gly rpo DNA-directed RNA polymerase subunit beta' 144.4.5.rep C02 439876 snp 341/1400 synonymous_variant c.1023T>C p.Arg341Arg rpoC DNA-directed RNA polymerase subunit beta' 144.4.5.rep C02 439874 snp 344/1400 synonymous_variant c.1032G>T p.Leu344Leu rpoC DNA-directed RNA polymerase subunit beta' 144.4.5.rep C02 439981 snp <td>T44.4.5.rep</td> <td>c01</td> <td>2022318</td> <td>snp</td> <td>378/840</td> <td>synonymous_variant c.1134C>G p.Ser378Ser</td> <td>virB4_2</td> <td></td>	T44.4.5.rep	c01	2022318	snp	378/840	synonymous_variant c.1134C>G p.Ser378Ser	virB4_2	
144.4.5.rep COI 2023494 ssp 75/840 synonymous_variant c.229tCy p.5ij/S/Sdiy vir84.2 Type IV secretion system protein vir84.7 T44.4.5.rep c01 2023509 snp 775/840 synonymous_variant c.2325T>C p.Asp775Asp vir84.2 Type IV secretion system protein vir84 T44.4.5.rep c01 2023515 snp 777/840 synonymous_variant c.2337G>A p.Glu779Glu vir84.2 Type IV secretion system protein vir84 T44.4.5.rep c02 439856 snp 338/1400 synonymous_variant c.104T>C p.Gly33BGly TpoC DNA-directed RNA polymerase subunit betal T44.4.5.rep c02 439865 snp 341/1400 synonymous_variant c.1032G>T p.Leu344Leu TpoC DNA-directed RNA polymerase subunit betal T44.4.5.rep c02 439874 snp 346/1400 synonymous_variant c.1088C>T p.Val356Val rpoC DNA-directed RNA polymerase subunit betal T44.4.5.rep c02 439910 snp 356/1400 synonymous_variant c.1088C>T p.Val356Val rpoC DNA-directed RNA polymerase subunit betal T44.4.5.rep c02 439985	T44.4.5.rep	c01	2022324	snp	380/840	synonymous_variant c.1140G>C p.Pro380Pro	virB4_2	
144.4.5.rep CO1 2023515 snp 779/840 Synonymous_variant c.2331C>A p.Leu777Leu VirB4.2 Type IV secretion system protein virB4 T44.4.5.rep CO1 2023521 snp 779/840 synonymous_variant c.2337G>A p.Glu779Glu VirB4.2 Type IV secretion system protein virB4 T44.4.5.rep CO2 439856 snp 338/1400 synonymous_variant c.1014T>C p.Gly338Gly rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 439865 snp 341/1400 synonymous_variant c.1023T>C p.Arg341Arg rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 439874 snp 344/1400 synonymous_variant c.1032G>T p.Leu344Leu rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 439910 snp 365/1400 synonymous_variant c.1089C>G p.Leu363Leu rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 439985 snp 381/1400 synonymous_variant c.1143A>G p.Pro381Pro rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 440186	T44.4.5.rep	c01	2023443	snp	753/840	synonymous_variant c.2259C>T p.Gly753Gly	virB4_2	
144.4.5.rep COI 2023515 snp 7/7/840 synonymous_variant c.2337C>A p.Get/7/Leu virB4.2 virB4.2 virB4.2 Type IV secretion system protein virB4.2 T44.4.5.rep c02 439856 snp 338/1400 synonymous_variant c.1014T>C p.Gly338Gly rpc DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 439865 snp 341/1400 synonymous_variant c.1023T>C p.Arg341Arg rpc DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 439874 snp 344/1400 synonymous_variant c.1032G>T p.Leu344Leu rpc DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 439910 snp 356/1400 synonymous_variant c.1086C>T p.Val356Val rpc DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 439931 snp 363/1400 synonymous_variant c.1089C>G p.Leu363Leu rpc DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 439985 snp 381/1400 synonymous_variant c.1343>G p.Pro381Pro rpc DNA-directed RNA polymerase subunit beta' T44.4.5.rep	T44.4.5.rep	c01	2023509	snp	775/840	synonymous_variant c.2325T>C p.Asp775Asp	virB4_2	
144.4.5.rep c01 2023521 snp 7/9/840 synonymous_variant c.10417>C p.Gly338Gly rpoC DNA-directed RNA polymerase subunit beta' rpoC DNA-direct	T44.4.5.rep	c01	2023515	snp	777/840	synonymous_variant c.2331C>A p.Leu777Leu	virB4_2	
144.4.5.rep CO2 439856 snp 338/1400 synonymous_variant c.1041>C p.diy338Giy rpoC subunit beta' T44.4.5.rep CO2 439865 snp 341/1400 synonymous_variant c.1023T>C p.Arg341Arg rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 439874 snp 344/1400 synonymous_variant c.1032G>T p.Leu344Leu rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 439910 snp 356/1400 synonymous_variant c.1088C>G p.Leu363Leu rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 439931 snp 363/1400 synonymous_variant c.1089C>G p.Leu363Leu rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 439985 snp 381/1400 synonymous_variant c.1343AP>G p.Pro381Pro rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 440186 snp 452/1400 synonymous_variant c.1344T>C p.Ala448Ala rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 440207 complex <t< td=""><td>T44.4.5.rep</td><td>c01</td><td>2023521</td><td>snp</td><td>779/840</td><td>synonymous_variant c.2337G>A p.Glu779Glu</td><td>virB4_2</td><td>, ,</td></t<>	T44.4.5.rep	c01	2023521	snp	779/840	synonymous_variant c.2337G>A p.Glu779Glu	virB4_2	, ,
144.4.5.rep CO2 439865 snp 341/1400 synonymous_variant c.102375c p.Arg.341Arg rpoC subunit beta' T44.4.5.rep cO2 439874 snp 344/1400 synonymous_variant c.10326>T p.Leu344Leu rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep cO2 439910 snp 356/1400 synonymous_variant c.1088C>G p.Leu363Leu rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep cO2 439985 snp 381/1400 synonymous_variant c.1143A>G p.Pro381Pro rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep cO2 440186 snp 448/1400 synonymous_variant c.1344T>C p.Ala448Ala rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep cO2 440198 snp 452/1400 synonymous_variant c.1356T>C p.His452His rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep cO2 440207 complex 455/1400 synonymous_variant c.1366HTGTinsCTGC p.457 rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep cO2 440264 snp	T44.4.5.rep	c02	439856	snp	338/1400	synonymous_variant c.1014T>C p.Gly338Gly	rpoC	
144.4.5.rep 602 4398/4 snp 344/1400 synonymous_variant c.10326>T p.Val326Val rpoC subunit beta' 144.4.5.rep c02 439910 snp 356/1400 synonymous_variant c.1089C>G p.Leu363Leu rpoC DNA-directed RNA polymerase subunit beta' 144.4.5.rep c02 439931 snp 381/1400 synonymous_variant c.1143A>G p.Pro381Pro rpoC DNA-directed RNA polymerase subunit beta' 144.4.5.rep c02 440186 snp 448/1400 synonymous_variant c.1344T>C p.Ala448Ala rpoC DNA-directed RNA polymerase subunit beta' 144.4.5.rep c02 440198 snp 452/1400 synonymous_variant c.1356T>C p.His452His rpoC DNA-directed RNA polymerase subunit beta' 144.4.5.rep c02 440207 complex 455/1400 synonymous_variant c.1365_1368delTTGTinsCTGC p.457 rpoC DNA-directed RNA polymerase subunit beta' 144.4.5.rep c02 440216 snp 458/1400 synonymous_variant c.1374G>C p.Ala458Ala rpoC DNA-directed RNA polymerase subunit beta' 144.4.5.rep c02 440284 snp	T44.4.5.rep	c02	439865	snp	341/1400	synonymous_variant c.1023T>C p.Arg341Arg	rpoC	
144.4.5.rep CO2 439910 Snp 356/1400 synonymous_variant c.1088C>I p.Val356Val rpoC subunit beta' T44.4.5.rep CO2 439931 Snp 363/1400 synonymous_variant c.1089C>G p.Leu363Leu rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 439985 Snp 381/1400 synonymous_variant c.1343A>G p.Pro381Pro rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 440186 Snp 448/1400 synonymous_variant c.1344T>C p.Ala448Ala rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 440198 Snp 452/1400 synonymous_variant c.1356T>C p.His452His rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 440207 complex 455/1400 synonymous_variant c.1365_1368delTTGTinsCTGC p.457 rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 440216 Snp 458/1400 synonymous_variant c.1374G>C p.Leu474Leu rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 440270 Snp	T44.4.5.rep	c02	439874	snp	344/1400	synonymous_variant c.1032G>T p.Leu344Leu	rpoC	
144.4.5.rep c02 439931 snp 363/1400 synonymous_variant c.1089C>G p.Leu363Leu rpoC subunit beta' T44.4.5.rep c02 439985 snp 381/1400 synonymous_variant c.1143A>G p.Pro381Pro rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 440186 snp 448/1400 synonymous_variant c.1344T>C p.Ala448Ala rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 440198 snp 452/1400 synonymous_variant c.1356T>C p.His452His rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 440207 complex 455/1400 synonymous_variant c.1365_1368delTTGTinsCTGC p.457 rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 440216 snp 458/1400 synonymous_variant c.1374G>C p.Leu474Leu rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 440264 snp 476/1400 synonymous_variant c.1428C>G p.Leu476Leu rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 440270 snp	T44.4.5.rep	c02	439910	snp	356/1400	synonymous_variant c.1068C>T p.Val356Val	rpoC	
144.4.5.rep CO2 439985 Srip 381/1400 Synonymous_variant c.1344T>C p.Ala448Ala rpoc DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 440186 snp 452/1400 synonymous_variant c.1344T>C p.Ala448Ala rpoc DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 440198 snp 452/1400 synonymous_variant c.1356T>C p.His452His rpoc DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 440207 complex 455/1400 synonymous_variant c.1365_1368delTTGTinsCTGC p.457 rpoc DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 440216 snp 458/1400 synonymous_variant c.1374G>C p.Ala458Ala rpoc DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 440264 snp 474/1400 synonymous_variant c.1422G>C p.Leu474Leu rpoc DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 440270 snp 476/1400 synonymous_variant c.1428C>G p.Leu476Leu rpoc DNA-directed RNA polymerase subunit beta'	T44.4.5.rep	c02	439931	snp	363/1400	synonymous_variant c.1089C>G p.Leu363Leu	rpoC	
144.4.5.rep CO2 440186 Srip 446/1400 Sylonymous_variant c.134417C p.Ala446Ala rpoc subunit beta' T44.4.5.rep CO2 440198 snp 452/1400 synonymous_variant c.1356T>C p.His452His rpoc DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 440207 complex 455/1400 synonymous_variant c.1365_1368delTTGTinsCTGC p.457 rpoc DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 440216 snp 458/1400 synonymous_variant c.1374G>C p.Ala458Ala rpoc DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 440264 snp 474/1400 synonymous_variant c.1422G>C p.Leu474Leu rpoc DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 440270 snp 476/1400 synonymous_variant c.1428C>G p.Leu476Leu rpoc DNA-directed RNA polymerase subunit beta' T44.4.5.rep CO2 440282 snp 480/1400 synonymous_variant c.1440T>G p.Leu480Leu rpoc DNA-directed RNA polymerase	T44.4.5.rep	c02	439985	snp	381/1400	synonymous_variant c.1143A>G p.Pro381Pro	rpoC	
144.4.5.rep C02 440198 snp 452/1400 synonymous_variant c.13561>C p.His452His rpoC subunit beta' T44.4.5.rep c02 440207 complex 455/1400 synonymous_variant c.1365_1368delTTGTinsCTGC p.457 rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 440216 snp 458/1400 synonymous_variant c.1374G>C p.Ala458Ala rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 440264 snp 474/1400 synonymous_variant c.1422G>C p.Leu474Leu rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 440270 snp 476/1400 synonymous_variant c.1428C>G p.Leu476Leu rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 440282 snp 480/1400 synonymous_variant c.1440T>G p.Leu480Leu rpoC DNA-directed RNA polymerase	T44.4.5.rep	c02	440186	snp	448/1400	synonymous_variant c.1344T>C p.Ala448Ala	rpoC	
T44.4.5.rep c02 440207 complex 455/1400 synonymous_variant c.1365_1368del11G1insC1GC p.457 rpoC subunit beta' T44.4.5.rep c02 440216 snp 458/1400 synonymous_variant c.1374G>C p.Ala458Ala rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 440264 snp 474/1400 synonymous_variant c.1422G>C p.Leu474Leu rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 440270 snp 476/1400 synonymous_variant c.1428C>G p.Leu476Leu rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 440282 snp 480/1400 synonymous_variant c.1440T>G p.Leu480Leu rpoC DNA-directed RNA polymerase	T44.4.5.rep	c02	440198	snp	452/1400	synonymous_variant c.1356T>C p.His452His	rpoC	
T44.4.5.rep C02 440216 snp 458/1400 synonymous_variant c.1374GSC p.Ala458Ala rpoC subunit beta' T44.4.5.rep c02 440264 snp 474/1400 synonymous_variant c.1422GSC p.Leu474Leu rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 440270 snp 476/1400 synonymous_variant c.1428CSG p.Leu476Leu rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 440282 snp 480/1400 synonymous_variant c.1440TSG p.Leu480Leu rpoC DNA-directed RNA polymerase	T44.4.5.rep	c02	440207	complex	455/1400	synonymous_variant c.1365_1368delTTGTinsCTGC p.457	rpoC	
T44.4.5.rep c02 440264 snp 4/4/1400 synonymous_variant c.1428C>C p.Leu4/4Leu rpoC subunit beta' T44.4.5.rep c02 440270 snp 476/1400 synonymous_variant c.1428C>G p.Leu476Leu rpoC DNA-directed RNA polymerase subunit beta' T44.4.5.rep c02 440282 snp 480/1400 synonymous_variant c.1440T>G p.Leu480Leu rpoC DNA-directed RNA polymerase	T44.4.5.rep	c02	440216	snp	458/1400	synonymous_variant c.1374G>C p.Ala458Ala	rpoC	
144.4.5.rep	T44.4.5.rep	c02	440264	snp	474/1400	synonymous_variant c.1422G>C p.Leu474Leu	rpoC	
1 144.4.5.rep 1 CUZ	T44.4.5.rep	c02	440270	snp	476/1400	synonymous_variant c.1428C>G p.Leu476Leu	rpoC	
	T44.4.5.rep	c02	440282	snp	480/1400	synonymous_variant c.1440T>G p.Leu480Leu	rpoC	

sample	СНКОМ	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T44.4.5.rep	c02	441101	complex	753/1400	synonymous_variant c.2259_2262delAACCinsGACG p.755	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.5.rep	c02	441110	snp	756/1400	synonymous_variant c.2268A>C p.lle756lle	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.5.rep	c02	441195	snp	785/1400	synonymous_variant c.2353T>C p.Leu785Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.5.rep	c02	446031	complex	374/694	synonymous_variant c.1122_1125delTGCAinsCGCC p.376	fusA	Elongation factor G
T44.4.5.rep	c02	451038	snp	252/277	synonymous_variant c.756T>C p.Pro252Pro	rpIB	50S ribosomal protein L2
T44.4.5.rep	c02	453539	snp	13/122	synonymous_variant c.39C>T p.Asn13Asn	rplN	50S ribosomal protein L14
T44.4.5.rep	c02	453590	complex	30/122	missense_variant c.90_96delGCGTTACinsCAAATAT p.Arg31Lys	rplN	50S ribosomal protein L14
T44.4.5.rep	c02	453602	snp	34/122	synonymous_variant c.102C>T p.Ser34Ser	rplN	50S ribosomal protein L14
T44.4.5.rep	c02	453620	complex	40/122	synonymous_variant c.120_126delGGTGTCGinsCGTTTCC p.43	rplN	50S ribosomal protein L14
T44.4.5.rep	c02	698399	snp	226/424	synonymous_variant c.678A>G p.Gln226Gln	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.5.rep	c02	698420	snp	219/424	synonymous_variant c.657C>G p.Thr219Thr	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.5.rep	c02	698474	snp	201/424	synonymous_variant c.603C>T p.Arg201Arg	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.5.rep	c02	698492	snp	195/424	synonymous_variant c.585T>C p.Asp195Asp	clpX	ATP-dependent Clp protease ATP- binding subunit ClpX
T44.4.5.rep	c02	1908928	snp	189/566	synonymous_variant c.567G>T p.Ser189Ser	rpsA	30S ribosomal protein S1
T44.4.5.rep	c02	1908937	snp	192/566	synonymous_variant c.576C>T p.Val192Val	rpsA	30S ribosomal protein S1
T44.4.5.rep	c02	1908946	snp	195/566	synonymous_variant c.585T>C p.Leu195Leu	rpsA	30S ribosomal protein S1
T44.4.5.rep	c02	1908955	snp	198/566	synonymous_variant c.594T>C p.Gly198Gly	rpsA	30S ribosomal protein S1
T44.4.5.rep	c02	1908961	snp	200/566	synonymous_variant c.600C>T p.Val200Val	rpsA	30S ribosomal protein S1
T44.4.5.rep	c02	1908967	snp	202/566	missense_variant c.606A>C p.Glu202Asp	rpsA	30S ribosomal protein S1
T44.4.5.rep	c02	1909027	complex	222/566	synonymous_variant c.666_669delTCTCinsCCTG p.224	rpsA	30S ribosomal protein S1
T44.4.5.rep	c02	1909039	snp	226/566	synonymous_variant c.678G>T p.Val226Val	rpsA	30S ribosomal protein S1
T44.4.5.rep	c02	1909072	snp	237/566	synonymous_variant c.711G>T p.Pro237Pro	rpsA	30S ribosomal protein S1
T44.4.5.rep	c02	1909086	complex	242/566	missense_variant c.725_729delCCATCinsACATT p.Thr242Asn	rpsA	30S ribosomal protein S1
T44.4.5.rep	c02	1909097	mnp	246/566	missense_variant c.736_737delACinsCA p.Thr246Gln	rpsA	30S ribosomal protein S1