












Sequencing analysis Evomicrocomm

Introduction

We analyze genomic sequencing data derived from Philippe Piccardi's evolution experiment. In this experiment *Agrobacterium tumefaciens*, *Comamonas testosteroni*, *Microbacterium saperdae* and *Ochrobactrum anthropi* were evolved over 44 weeks either 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.

Treatment	Combination of species	Number of microcosms transfer 0 → transfer 44
1	 <i>A. tumefaciens</i>	5 → 2
2	 <i>C. testosteroni</i>	5 → 5
3	   <i>A. tumefaciens</i> + <i>C. testosteroni</i> + <i>M. saperdae</i>	5 → 5
4	    <i>A. tumefaciens</i> + <i>C. testosteroni</i> + <i>M. saperdae</i> + <i>O. anthropi</i>	5 → 5
5	 <i>M. saperdae</i>	5 → 0
6	 <i>O. anthropi</i>	5 → 0

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 [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 sound 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 [deletion_detection](#).

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

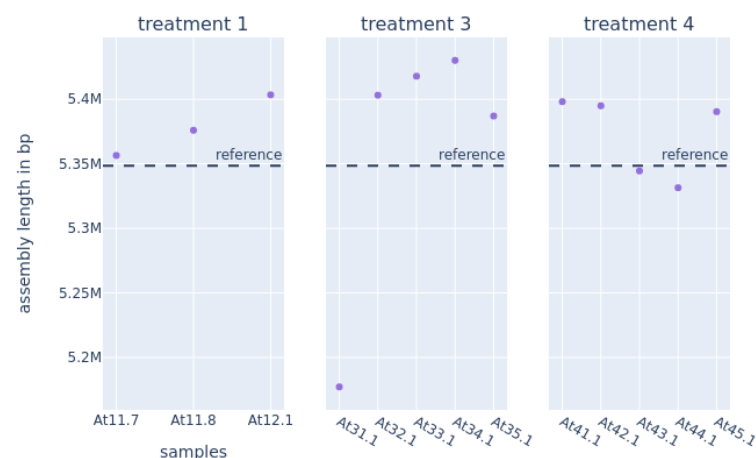
Lastly we look at how many contigs were generated by assembling the PacBio data. Even though this is very interesting, we need to be careful with interpretations for this data. While the assemblies are very accurate, thanks to the accurate and long PacBio reads, assemblers sometimes struggle to close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

The complete sample processing is implemented as Snakemake workflow and can be found here [pacbio workflow](#).

Agrobacterium tumefaciens

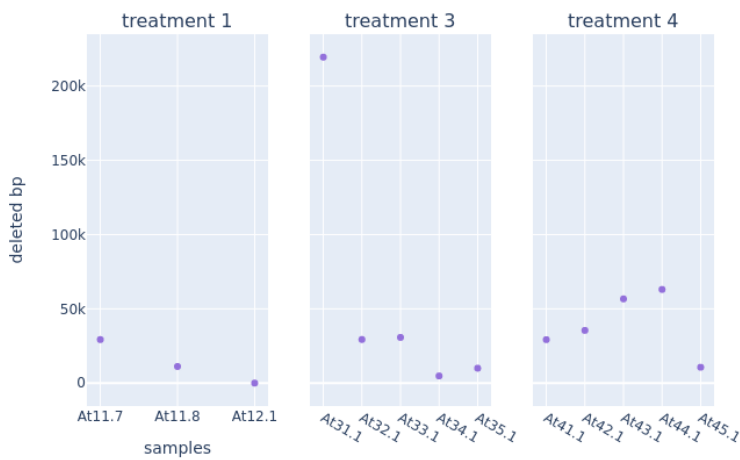
The plotted genome lengths below show that the genome size increased for most samples when compared to the assembly of the reference (dashed line).

Assembly length in *Agrobacterium tumefaciens*



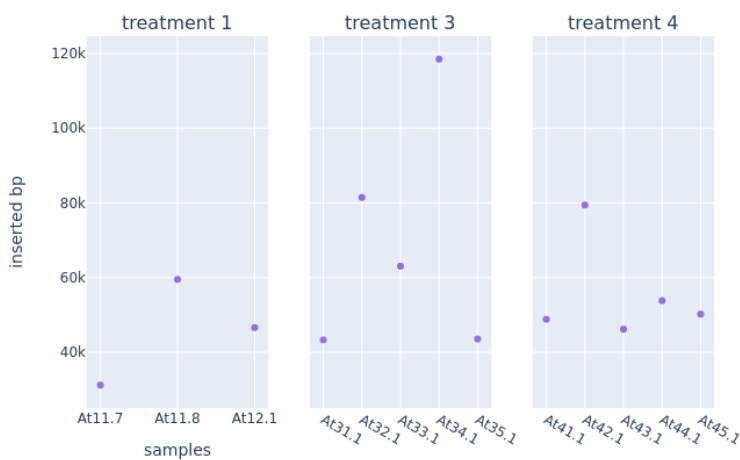
If we look at the sum of deleted bases we can see that the large deletion in At31.1 reflects in the assembled genome length.

Deleted bases in *Agrobacterium tumefaciens*



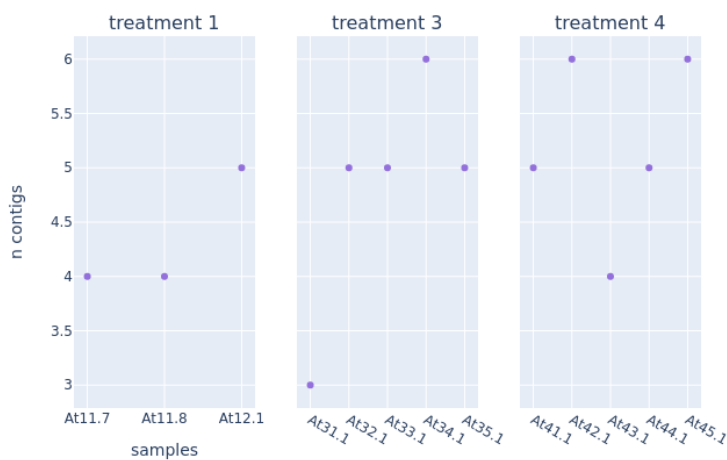
Looking at inserted bases we see that many samples have medium to large insertions. We can see for example that the large insertion in At34.1 again reflects in the assembled genome length.

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*



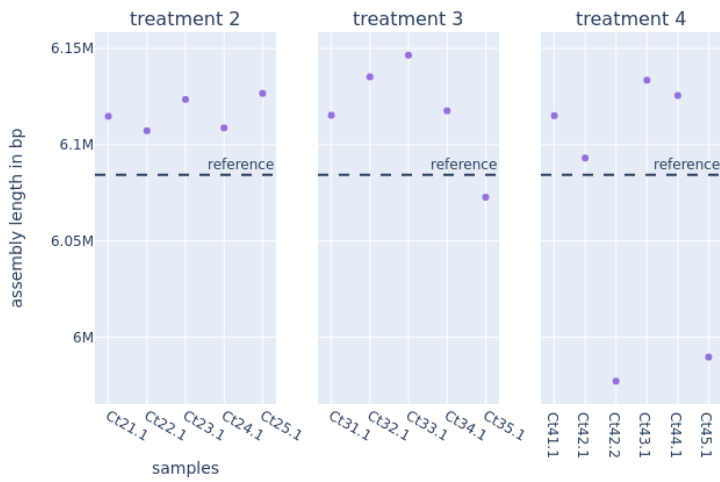
Since there is clearly rearrangement visible in the evolved genomes of *Agrobacterium tumefaciens* it might be interesting to look what products were affected deletions and insertions. This is unfortunately a pretty long list, because sometimes entire plasmids were deleted or taken up.

The list can be found in the [Appendix > Deleted and inserted products > Agrobacterium tumefaciens](#).

Comamonas testosteroni

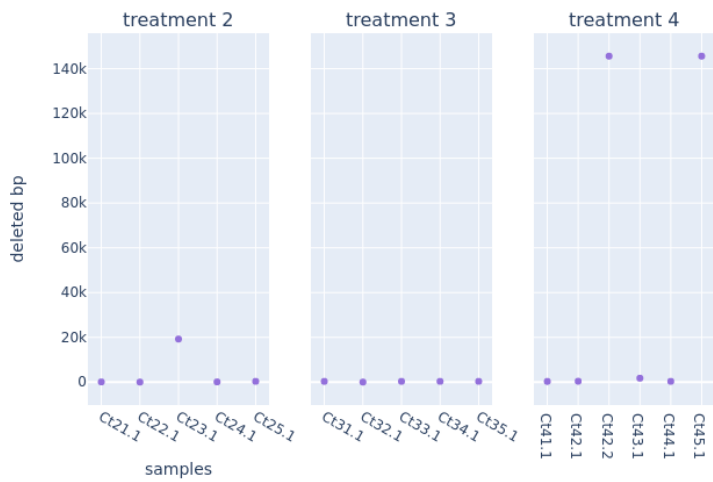
Except for three strains we can see again an increase in the genome size. Just as we observed for *Agrobacterium tumefaciens*, the variation in genome length can be explained by looking at the sum of deleted and inserted bases.

Assembly length in *Comamonas testosteroni*



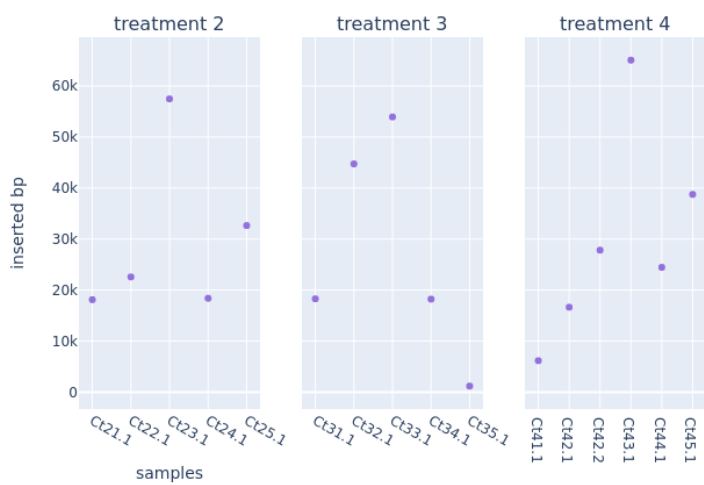
Only the samples Ct42.2 and Ct45.1 have large deletions.

Deleted bases in *Comamonas testosteroni*



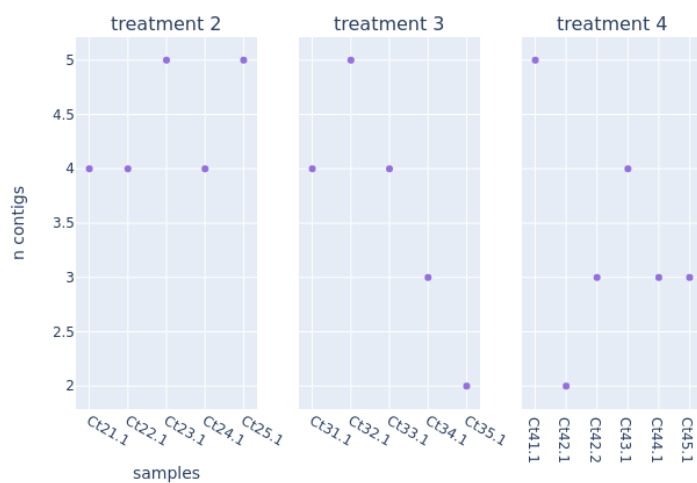
For almost all samples we observe inserted bases.

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

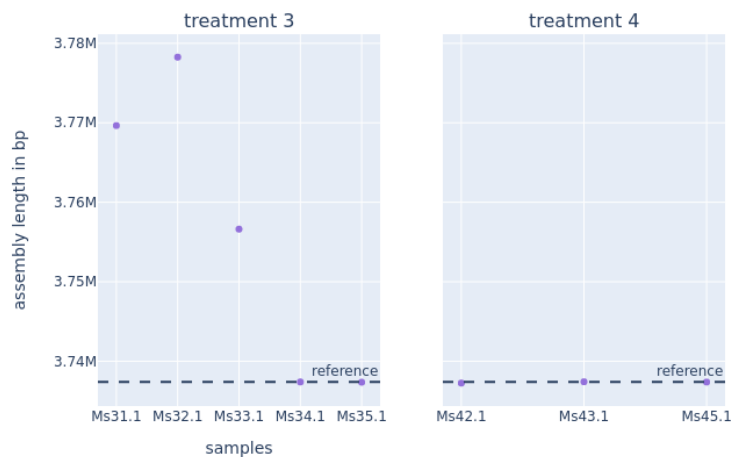


A list of deleted and inserted products can be found in the [Appendix > Deleted and inserted products > Comamonas testosteroni](#)

Microbacterium saperdae

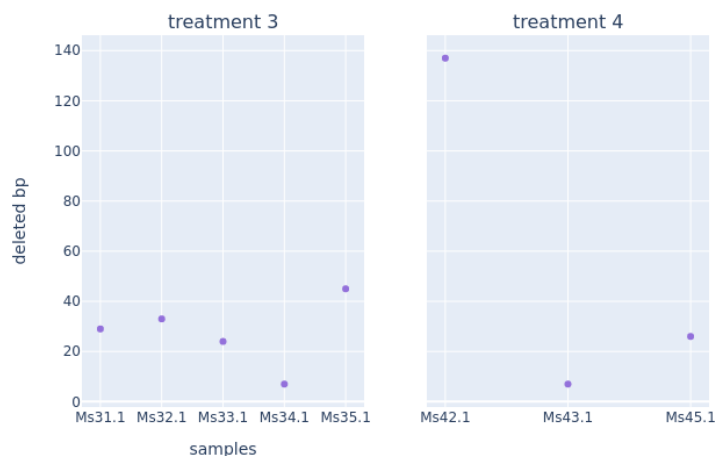
Microbacterium saperdae can not be grown in mono-culture which is why we only have treatment three and four. For once, the genome size of the majority of the assemblies remains similar compared to the wild-type assembly.

Assembly length in *Microbacterium saperdae*



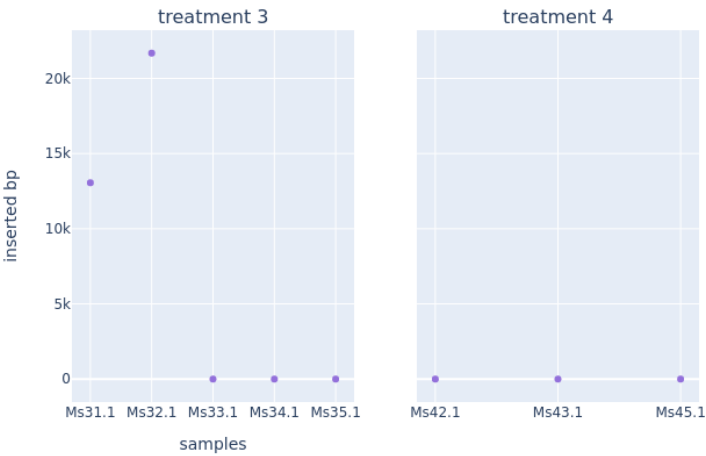
Also almost no deleted bases are visible for *Microbacterium saperdae*.

Deleted bases in *Microbacterium saperdae*



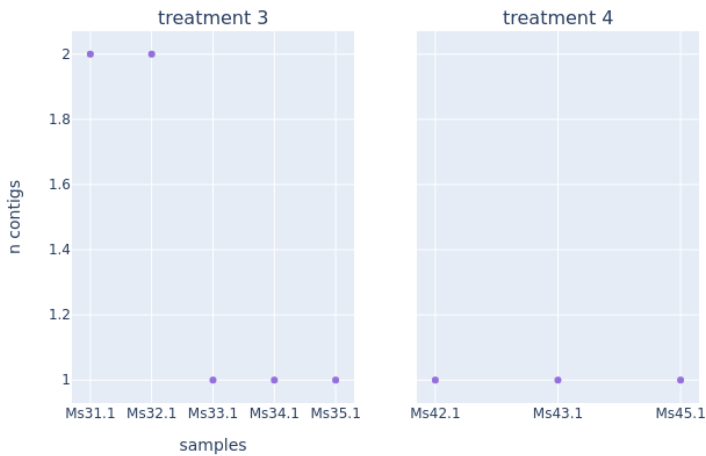
We can see how the insertions of Ms31.1 and Ms32.1 are causing the difference in the genome length.

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*



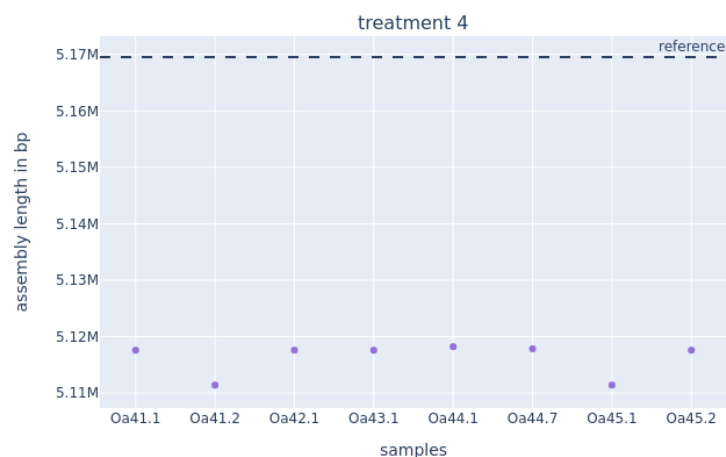
For *Microbacterium saperdae* no products were deleted.
Inserted products:

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

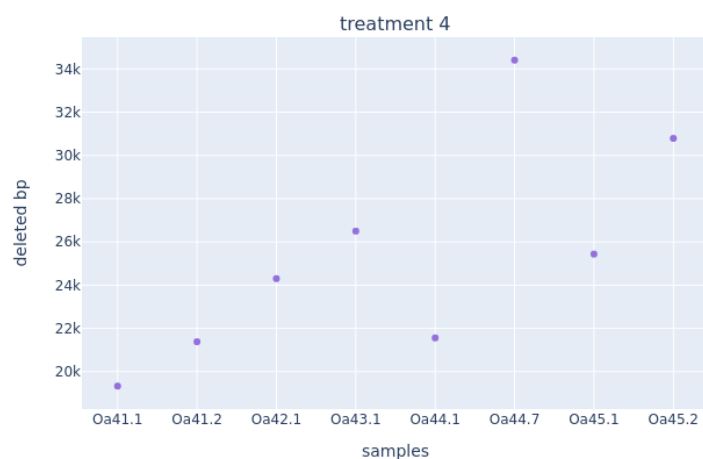
Just as *Microbacterium saperdae*, *Ochrobactrum anthropi* can not be grown in co-culture. Compared to most other strains, the genome of all samples of *Ochrobactrum anthropi* shrunk.

Assembly length in *Ochrobactrum anthropi*



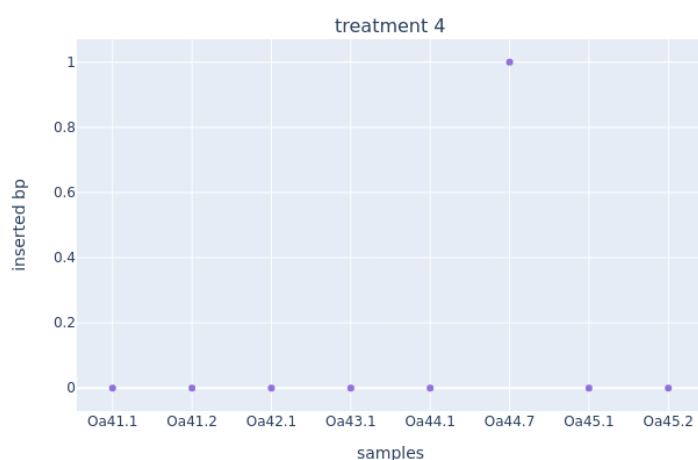
This is again very nicely in line with the observed sum of deleted basepairs.

Deleted bases in *Ochrobactrum anthropi*



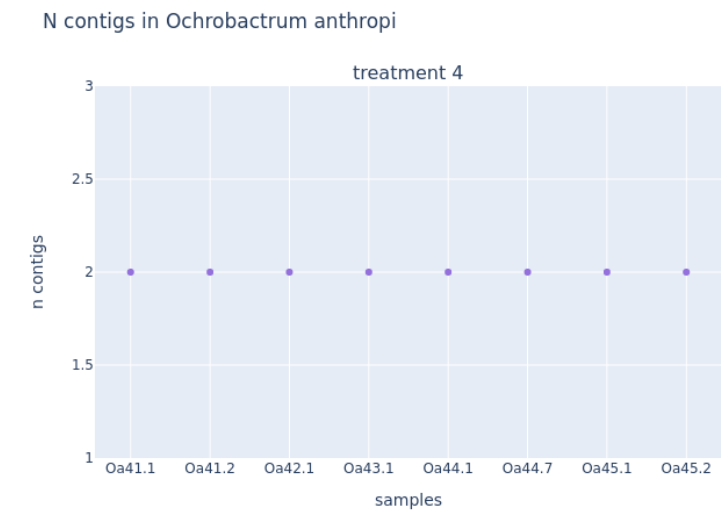
For once we can't observe any inserted bases.

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

see any insertions.



Deleted products observed in n microcosms:

product	treatment 4
30S ribosomal protein S20	8
DNA replication and repair protein RecF	8
Glucose-1-phosphate thymidyltransferase	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 adenyltransferase/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 BetI	2
3-deoxy-manno-octulosonate cytidyltransferase	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	T44.4.2	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](#).

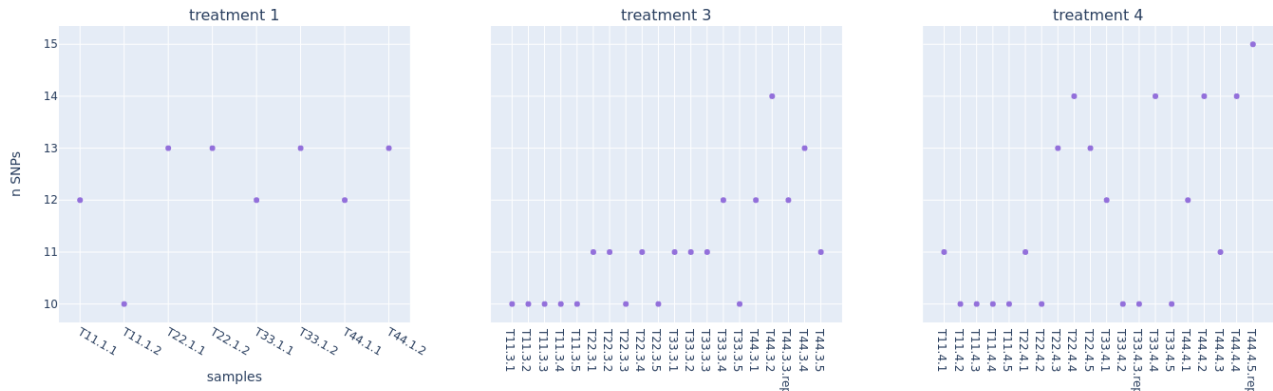
The complete sample processing is implemented as Snakemake workflow and can be found [here](#).

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

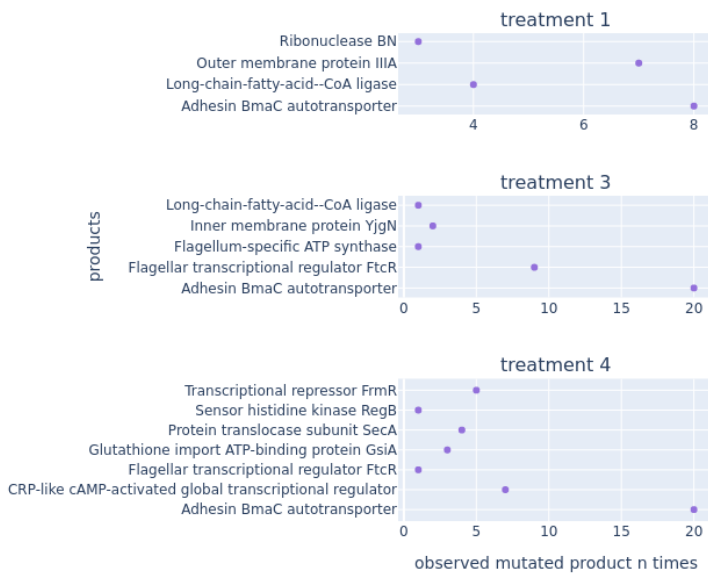
Below we compare the amount of SNPs over all time points and microcosms. The amount of SNPs seems to be independent of the treatment in *Agrobacterium tumefaciens*.

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



[bmaC](#) 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*:

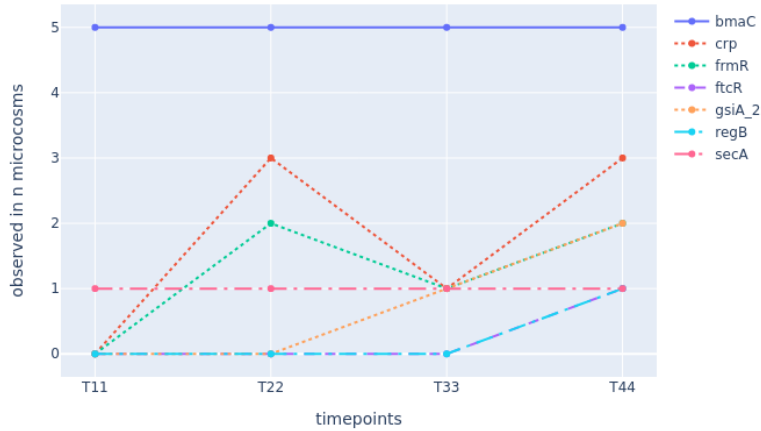
sample	CHROM	POS	TYPE	EFFECT	GENE
T22.4.3	AGTU001.0001.c01	2351459	del	frameshift_variant	crp
T22.4.4	AGTU001.0001.c01	2351324	del	frameshift_variant	crp
T22.4.5	AGTU001.0001.c01	2351347	snp	stop_gained	crp
T33.4.4	AGTU001.0001.c01	2351324	del	frameshift_variant	crp
T44.4.3	AGTU001.0001.c01	2351459	del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

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

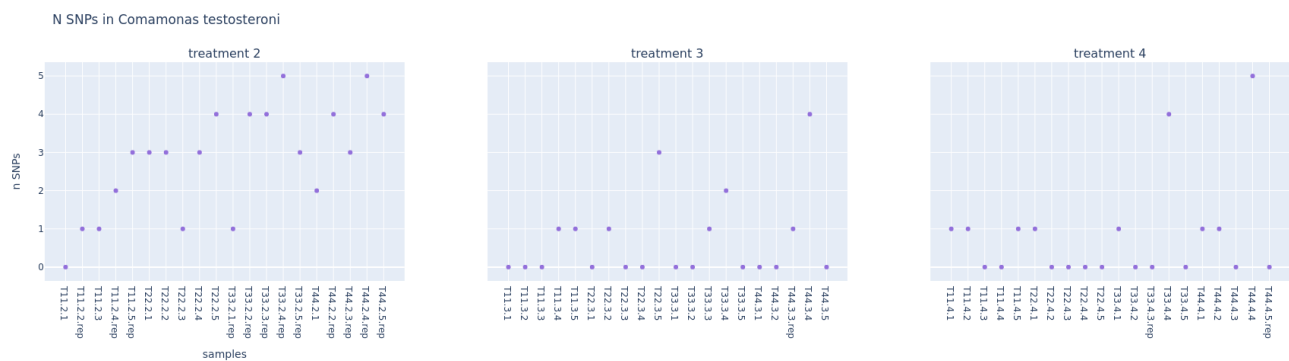
Below I plotted in how many microcosms a mutation came up during every time point for treatment four. The complete output of snippy can be found in the [Appendix > SNPs > Agrobacterium tumefaciens](#)

Mutated genes in *Agrobacterium tumefaciens* in treatment 4



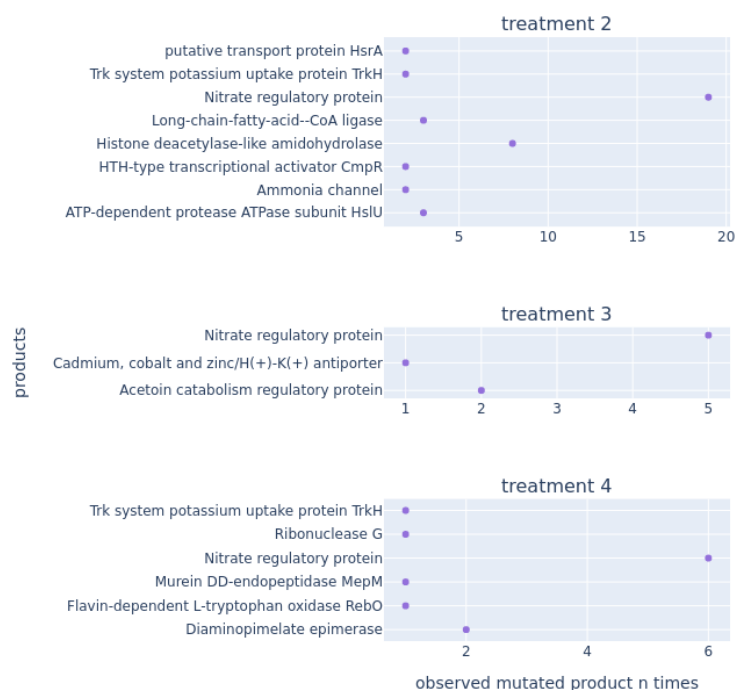
Comamonas testosteroni

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



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

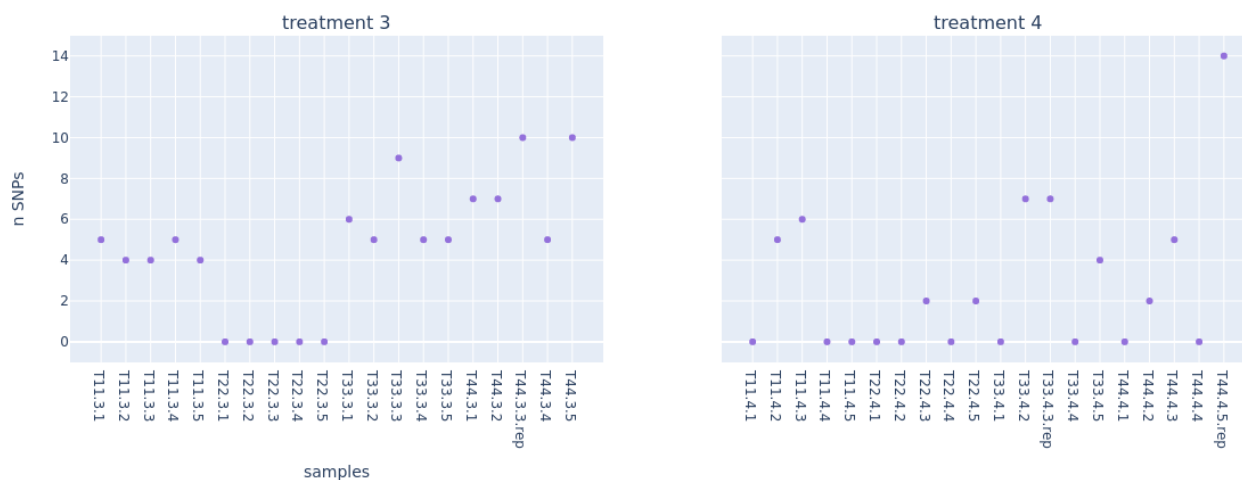
Products affected by mutations in *Comamonas testosteroni*



The complete output of snippy can be found in the [Appendix > SNPs > Comamonas testosteroni](#)

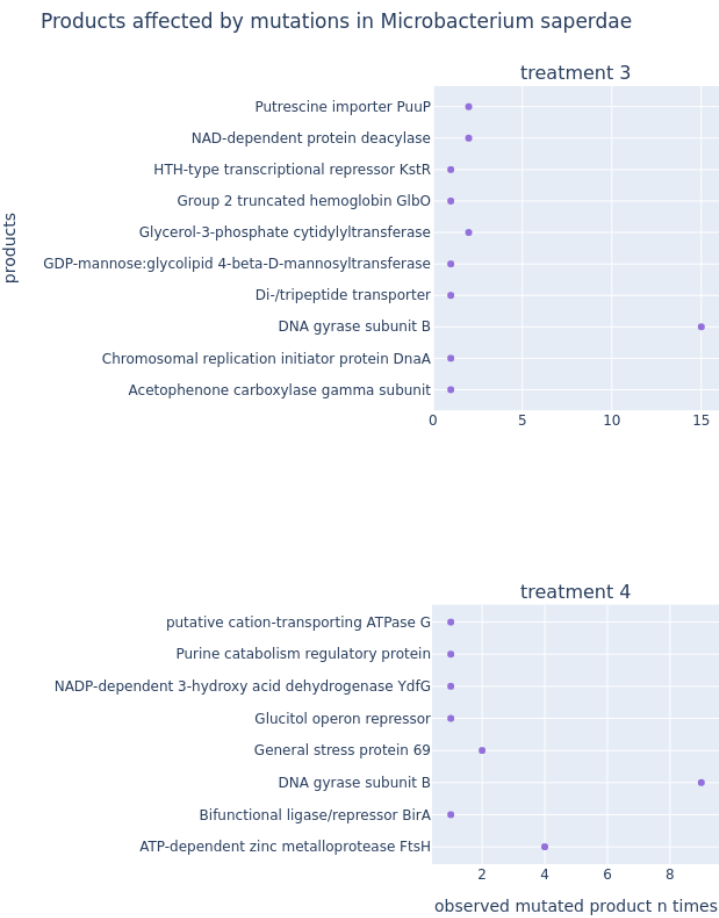
Microbacterium saperdae

N SNPs in *Microbacterium saperdae*



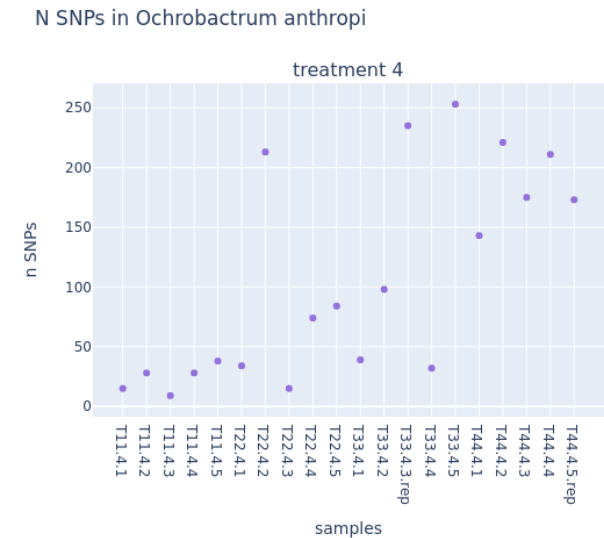
We can see that the DNA gyrase subunit B is mutated in many samples. This protein negatively supercoils DNA. Negative supercoiling favors strand separation and therefore DNA replication, transcription, recombination and repair. All mutations that we observe in the gene *gyrB_2* coding for this protein 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 defect DNA gyrase subunit B could cause that the transcription and

replication was reduced.



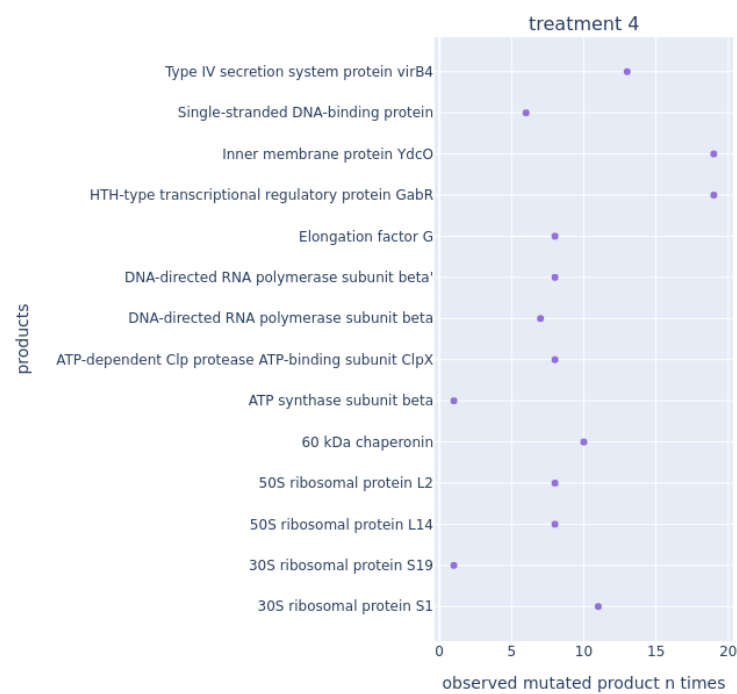
Ochrobactrum anthropi

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.



We see many changed ribosomal proteins. I checked the mutations 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 BdlA	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	
SCO1 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

Inserted products observed in n microcosms:

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

product	treatment 1	treatment 3	treatment 4
putative cyclic di-GMP phosphodiesterase PdeB	3		
Cold shock protein CspA	3		
Aerobic respiration control sensor protein ArcB	1		
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	1		
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		
Putrescine--pyruvate aminotransferase	2		
Leucine-responsive regulatory protein	2		
Succinate-semialdehyde dehydrogenase [NADP(+)] GabD	2		
ATM1-type heavy metal exporter	1		
Purine ribonucleoside efflux pump NepI	2		
Ubiquinone biosynthesis O-methyltransferase, mitochondrial	1		
Ectoine hydrolase	1		
Alanine dehydrogenase	1		
Taurine--pyruvate 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 ClC-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	
HTH-type transcriptional regulator NorG			1
Adhesin BmaC autotransporter			1
disulfide formation protein			1
Lipoprotein signal peptidase			1
HTH-type transcriptional regulator HmrR			1
Urocanate hydratase			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:

product	treatment 2	treatment 3	treatment 4
Gentisate transporter	1		
Acyl-CoA dehydrogenase	1		
1,2-epoxyphenylacetyl-CoA isomerase	1		
2,3-dehydrodipyl-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-methylmercaptopyrionyl-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
Transcriptional activator protein CzcR			2
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		
Phenylalanine--tRNA 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(Ile)-lysine synthase		1	
Acetyl-CoA acetyltransferase		1	
Phenylalanine--tRNA ligase alpha subunit		1	
Hydroxyacylglutathione hydrolase		1	
Cysteine--tRNA ligase		1	
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha		1	
Acyl-CoA dehydrogenase		1	
2-succinylbenzoate--CoA ligase		1	
HTH-type transcriptional regulator CueR		1	
Integration host factor subunit alpha		1	
UDP-2,3-diacylglucosamine hydrolase		1	
Arginine--tRNA ligase		1	
HTH-type transcriptional regulator DmlR		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 aminoacylate 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

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

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T11.4.1	c02	555455	snp	506/905	missense_variant c.1517G>T p.Gly506Val	secA	Protein translocase subunit SecA
T11.4.1	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T11.4.2	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T11.4.3	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T11.4.4	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T11.4.5	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T22.1.1	c01	83654	snp	275/569	missense_variant c.824G>A p.Cys275Tyr	fadD	Long-chain-fatty-acid--CoA ligase
T22.1.1	c01	703340	snp	66/348	stop_gained c.196C>T p.Gln66*	ropA_2	Outer membrane protein IIIA
T22.1.1	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T22.1.2	c01	83654	snp	275/569	missense_variant c.824G>A p.Cys275Tyr	fadD	Long-chain-fatty-acid--CoA ligase
T22.1.2	c01	703263	ins	41/348	frameshift_variant c.120dupC p.Asp41fs	ropA_2	Outer membrane protein IIIA
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 autotransporter
T22.3.1	c01	238024	del	201/223	disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del	ftcR	Flagellar transcriptional regulator FtcR
T22.3.1	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T22.3.2	c01	238024	del	201/223	disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del	ftcR	Flagellar transcriptional regulator FtcR
T22.3.2	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T22.3.3	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T22.3.4	c01	238024	del	201/223	disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del	ftcR	Flagellar transcriptional regulator FtcR
T22.3.4	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T22.3.5	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T22.4.1	c02	555455	snp	506/905	missense_variant c.1517G>T p.Gly506Val	secA	Protein translocase subunit SecA
T22.4.1	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T22.4.2	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T22.4.3	c01	2351459	del	60/151	frameshift_variant c.178delG p.Val60fs	crp	CRP-like cAMP-activated global transcriptional regulator
T22.4.3	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T22.4.4	c01	2351324	del	17/151	frameshift_variant c.49delT p.Ser17fs	crp	CRP-like cAMP-activated global transcriptional regulator
T22.4.4	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T22.4.4	p02	181352	snp	71/93	stop_gained c.211C>T p.Gln71*	frmR	Transcriptional repressor FrmR
T22.4.5	c01	2351347	snp	22/151	stop_gained c.65C>A p.Ser22*	crp	CRP-like cAMP-activated global transcriptional regulator
T22.4.5	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T22.4.5	p02	181297	snp	89/93	missense_variant c.266G>C p.Arg89Pro	frmR	Transcriptional repressor FrmR
T33.1.1	c01	703340	snp	66/348	stop_gained c.196C>T p.Gln66*	ropA_2	Outer membrane protein IIIA
T33.1.1	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T33.1.2	c01	83654	snp	275/569	missense_variant c.824G>A p.Cys275Tyr	fadD	Long-chain-fatty-acid--CoA ligase
T33.1.2	c01	703263	ins	41/348	frameshift_variant c.120dupC p.Asp41fs	ropA_2	Outer membrane protein 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 autotransporter
T33.3.1	c01	238024	del	201/223	disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del	ftcR	Flagellar transcriptional regulator FtcR
T33.3.1	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T33.3.2	c01	238024	del	201/223	disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del	ftcR	Flagellar transcriptional regulator FtcR
T33.3.2	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T33.3.3	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T33.3.4	c01	238024	del	201/223	disruptive_inframe_deletion c.603_614delGCGCAAGAAGCT p.Arg202_Leu205del	ftcR	Flagellar transcriptional regulator FtcR
T33.3.4	c01	2863371	snp	326/356	synonymous_variant c.978C>A p.Gly326Gly	yjgN	Inner membrane protein YjgN
T33.3.4	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T33.3.5	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T33.4.1	c01	2361041	snp	440/630	stop_gained c.1320T>G p.Tyr440*	gsiA_2	Glutathione import ATP-binding protein GsiA
T33.4.1	c02	555455	snp	506/905	missense_variant c.1517G>T p.Gly506Val	secA	Protein translocase subunit SecA
T33.4.1	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T33.4.2	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T33.4.3.rep	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T33.4.4	c01	2351324	del	17/151	frameshift_variant c.49delT p.Ser17fs	crp	CRP-like cAMP-activated global transcriptional regulator
T33.4.4	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter
T33.4.4	p02	181352	snp	71/93	stop_gained c.211C>T p.Gln71*	frmR	Transcriptional repressor FrmR
T33.4.5	c02	1946877	del	4/825	frameshift_variant c.10delG p.Val4fs	bmaC	Adhesin BmaC autotransporter

sample	CHROM	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-acid--CoA 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	filI	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-acid--CoA 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_213delAACGGCCCGCTG 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.MetGln163IleLys	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 HslU
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-acid--CoA 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.MetGln163IleLys	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 HslU

sample	CHROM	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-acid--CoA 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.MetGln163IleLys	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 HslU
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-acid--CoA 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.MetGln163IleLys	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	CHROM	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_111delCC 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_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T11.4.3	c01	699272	snp	520/666	missense_variant c.1559C>T p.Thr520Ile	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_111delCC 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.Ile176fs	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 KstR
T33.3.2	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T33.3.2	c01	1739320	del	37/411	frameshift_variant c.110_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T33.3.3	c01	657367	snp	55/151	missense_variant c.163A>C p.Thr55Pro	tagD	Glycerol-3-phosphate cytidyltransferase
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_111delCC 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.Thr520Ile	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 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_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T44.3.2	c01	660917	snp	366/665	missense_variant c.1096T>C p.Ser366Pro	gumI	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_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T44.3.2	c01	3382652	del	88/516	conservative_inframe_deletion c.262_285delCCCGAGGCGGTCTCGGGCGGCATC p.Pro88_Ile95del	dtpT	Di-/tripeptide transporter
T44.3.3.rep	c01	657367	snp	55/151	missense_variant c.163A>C p.Thr55Pro	tagD	Glycerol-3-phosphate cytidyltransferase
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.Thr520Ile	ftsH_1	ATP-dependent zinc metalloprotease FtsH
T44.4.3	c01	1739271	del	20/411	frameshift_variant c.59delA p.Asn20fs	gyrB_2	DNA gyrase subunit B
T44.4.3	c01	1739320	del	37/411	frameshift_variant c.110_111delCC p.Pro37fs	gyrB_2	DNA gyrase subunit B
T44.4.5.rep	c01	698447	snp	245/666	missense_variant c.734T>C p.Val245Ala	ftsH_1	ATP-dependent zinc metalloprotease FtsH
T44.4.5.rep	c01	804045	snp	222/651	synonymous_variant c.666C>T p.Gly222Gly	ctpG_2	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	srlR	Glucitol operon repressor

Ochrobactrum anthropi

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
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sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T11.4.1	c01	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ydcO_1	Inner membrane protein YdcO
T11.4.1	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ydcO_1	Inner membrane protein YdcO
T11.4.1	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	HTH-type transcriptional regulatory protein GabR
T11.4.2	c01	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ydcO_1	Inner membrane protein YdcO
T11.4.2	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ydcO_1	Inner membrane protein YdcO
T11.4.2	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	HTH-type transcriptional regulatory protein GabR
T11.4.3	c01	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ydcO_1	Inner membrane protein YdcO
T11.4.3	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ydcO_1	Inner membrane protein YdcO
T11.4.3	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	HTH-type transcriptional regulatory protein GabR
T11.4.4	c01	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ydcO_1	Inner membrane protein YdcO
T11.4.4	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ydcO_1	Inner membrane protein YdcO
T11.4.4	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	HTH-type transcriptional regulatory protein GabR
T11.4.5	c01	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ydcO_1	Inner membrane protein YdcO
T11.4.5	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ydcO_1	Inner membrane protein YdcO
T11.4.5	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	HTH-type transcriptional regulatory protein GabR
T11.4.5	c01	2022111	snp	309/840	synonymous_variant c.927C>A p.Ala309Ala	virB4_2	Type IV secretion system protein virB4
T22.4.1	c01	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ydcO_1	Inner membrane protein YdcO
T22.4.1	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ydcO_1	Inner membrane protein YdcO
T22.4.1	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	HTH-type transcriptional regulatory protein GabR
T22.4.1	c01	2022111	snp	309/840	synonymous_variant c.927C>A p.Ala309Ala	virB4_2	Type IV secretion system protein virB4
T22.4.2	c01	96441	snp	171/546	synonymous_variant c.513T>C p.Asn171Asn	groL	60 kDa chaperonin
T22.4.2	c01	96450	snp	174/546	synonymous_variant c.522G>C p.Val174Val	groL	60 kDa chaperonin
T22.4.2	c01	96456	snp	176/546	synonymous_variant c.528G>C p.Thr176Thr	groL	60 kDa chaperonin
T22.4.2	c01	96534	snp	202/546	synonymous_variant c.606T>C p.Pro202Pro	groL	60 kDa chaperonin
T22.4.2	c01	96543	snp	205/546	synonymous_variant c.615C>G p.Val205Val	groL	60 kDa chaperonin
T22.4.2	c01	96549	complex	207/546	synonymous_variant c.621_624delCCCTinsTCCG p.209	groL	60 kDa chaperonin
T22.4.2	c01	96567	snp	213/546	synonymous_variant c.639T>G p.Ala213Ala	groL	60 kDa chaperonin
T22.4.2	c01	96609	snp	227/546	synonymous_variant c.681C>T p.Leu227Leu	groL	60 kDa chaperonin
T22.4.2	c01	96624	complex	232/546	missense_variant c.696_699delTCTTinsCATG p.Leu233Met	groL	60 kDa chaperonin
T22.4.2	c01	96633	snp	235/546	synonymous_variant c.705G>T p.Pro235Pro	groL	60 kDa chaperonin
T22.4.2	c01	96639	snp	237/546	synonymous_variant c.711G>C p.Leu237Leu	groL	60 kDa chaperonin
T22.4.2	c01	96658	mnp	244/546	missense_variant c.730_731delITCinsGG p.Ser244Gly	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.813G>C p.Leu271Leu	groL	60 kDa chaperonin
T22.4.2	c01	96753	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.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.867C>G p.Leu289Leu	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.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.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.Ile326Val	virB4_2	Type IV secretion system protein virB4
T22.4.2	c01	2022206	complex	341/840	missense_variant c.1022_1031delCCGATGCCGCinsAGGACGCCCCG p.AlaAspAlaAla341GluAspAlaArg	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

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T22.4.2	c01	2022253	snp	357/840	missense_variant c.1069A>G p.Ile357Val	virB4_2	Type IV secretion system protein virB4
T22.4.2	c01	2022276	snp	364/840	synonymous_variant c.1092G>C p.Val364Val	virB4_2	Type IV secretion system protein virB4
T22.4.2	c01	2022318	snp	378/840	synonymous_variant c.1134C>G p.Ser378Ser	virB4_2	Type IV secretion system protein virB4
T22.4.2	c01	2022324	snp	380/840	synonymous_variant c.1140G>C p.Pro380Pro	virB4_2	Type IV secretion system protein virB4
T22.4.2	c01	2022330	complex	382/840	synonymous_variant c.1146_1149delCGCCinsTGCT p.384	virB4_2	Type IV secretion system protein virB4
T22.4.2	c01	2022339	snp	385/840	synonymous_variant c.1155A>C p.Ala385Ala	virB4_2	Type IV secretion system protein virB4
T22.4.2	c01	2022358	snp	392/840	missense_variant c.1174G>A p.Val392Ile	virB4_2	Type IV secretion system protein virB4
T22.4.2	c01	2023410	snp	742/840	synonymous_variant c.2226A>G p.Gln742Gln	virB4_2	Type IV secretion system protein virB4
T22.4.2	c01	2023416	complex	744/840	synonymous_variant c.2232_2233delCAinsGC p.746	virB4_2	Type IV secretion system protein virB4
T22.4.2	c01	2023443	snp	753/840	synonymous_variant c.2259C>T p.Gly753Gly	virB4_2	Type IV secretion system protein virB4
T22.4.2	c01	2023509	snp	775/840	synonymous_variant c.2325T>C p.Asp775Asp	virB4_2	Type IV secretion system protein virB4
T22.4.2	c01	2023515	snp	777/840	synonymous_variant c.2331C>A p.Leu777Leu	virB4_2	Type IV secretion system protein virB4
T22.4.2	c01	2023521	snp	779/840	synonymous_variant c.2337G>A p.Glu779Glu	virB4_2	Type IV secretion system protein virB4
T22.4.2	c02	436029	snp	508/1377	synonymous_variant c.1524T>A p.Ala508Ala	rpoB	DNA-directed RNA polymerase subunit beta
T22.4.2	c02	436035	snp	510/1377	synonymous_variant c.1530A>C p.Ala510Ala	rpoB	DNA-directed RNA polymerase subunit beta
T22.4.2	c02	436041	snp	512/1377	synonymous_variant c.1536G>T p.Val512Val	rpoB	DNA-directed RNA polymerase subunit beta
T22.4.2	c02	436047	snp	514/1377	synonymous_variant c.1542G>A p.Glu514Glu	rpoB	DNA-directed RNA polymerase subunit beta
T22.4.2	c02	436083	complex	526/1377	missense_variant c.1578_1584delTCAGACCinsCCAGGTG p.Thr528Val	rpoB	DNA-directed RNA polymerase subunit beta
T22.4.2	c02	436125	snp	540/1377	synonymous_variant c.1620C>T p.Leu540Leu	rpoB	DNA-directed RNA polymerase subunit beta
T22.4.2	c02	436143	snp	546/1377	synonymous_variant c.1638C>T p.Gly546Gly	rpoB	DNA-directed RNA polymerase subunit beta
T22.4.2	c02	439829	snp	329/1400	synonymous_variant c.987G>C p.Leu329Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	439856	snp	338/1400	synonymous_variant c.1014T>C p.Gly338Gly	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	439865	snp	341/1400	synonymous_variant c.1023T>C p.Arg341Arg	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	439874	snp	344/1400	synonymous_variant c.1032G>T p.Leu344Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	439910	snp	356/1400	synonymous_variant c.1068C>T p.Val356Val	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	439931	snp	363/1400	synonymous_variant c.1089C>G p.Leu363Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	439985	snp	381/1400	synonymous_variant c.1143A>G p.Pro381Pro	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	440172	snp	444/1400	missense_variant c.1330A>G p.Ile444Val	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	440186	snp	448/1400	synonymous_variant c.1344T>C p.Ala448Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	440198	snp	452/1400	synonymous_variant c.1356T>C p.His452His	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	440207	complex	455/1400	synonymous_variant c.1365_1368delTTGTinsCTGC p.457	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	440216	snp	458/1400	synonymous_variant c.1374G>C p.Ala458Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	440264	snp	474/1400	synonymous_variant c.1422G>C p.Leu474Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	440270	snp	476/1400	synonymous_variant c.1428C>G p.Leu476Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	440282	snp	480/1400	synonymous_variant c.1440T>G p.Leu480Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	c02	440288	snp	482/1400	synonymous_variant c.1446A>G p.Ala482Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T22.4.2	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.Ile756Ile	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_531delITCGinsCGCC 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_420delITGTGCCAinsCGTTCCC 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.Ile109Val	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

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
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.277T>C p.Gly9Gly	ssb_4	Single-stranded DNA-binding protein
T22.4.2	c02	2279055	complex	14/134	missense_variant c.40_41delGAlnsAC 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.Ile326Val	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.Ile326Val	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.Ile357Val	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
T22.4.5	c02	1909086	complex	242/566	missense_variant c.725_729delCCATCInsACATT p.Thr242Asn	rpsA	30S ribosomal protein S1

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T33.4.1	c01	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ycdO_1	Inner membrane protein YdcO
T33.4.1	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ycdO_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	snp	227/546	synonymous_variant c.681C>T p.Leu227Leu	groL	60 kDa chaperonin
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	ycdO_1	Inner membrane protein YdcO
T33.4.2	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ycdO_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.Ile326Val	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.Ile357Val	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 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	96741	snp	271/546	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
T33.4.3.rep	c01	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ycdO_1	Inner membrane protein YdcO
T33.4.3.rep	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ycdO_1	Inner membrane protein YdcO

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T33.4.3.rep	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	HTH-type transcriptional regulatory protein GabR
T33.4.3.rep	c01	2007281	snp	55/133	synonymous_variant c.165C>G p.Thr55Thr	ssb_1	Single-stranded DNA-binding protein
T33.4.3.rep	c01	2007330	complex	72/133	missense_variant c.214_216delCAAlnsGAG p.Gln72Glu	ssb_1	Single-stranded DNA-binding protein
T33.4.3.rep	c01	2007347	snp	77/133	synonymous_variant c.231T>C p.Gly77Gly	ssb_1	Single-stranded DNA-binding protein
T33.4.3.rep	c01	2007392	snp	92/133	synonymous_variant c.276C>G p.Thr92Thr	ssb_1	Single-stranded DNA-binding protein
T33.4.3.rep	c01	2021961	snp	259/840	synonymous_variant c.777G>C p.Ser259Ser	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2021973	complex	263/840	missense_variant c.789_793delTCTGAinsCCTGC p.Met265Leu	virB4_2	Type IV secretion system protein 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.Ile326Val	virB4_2	Type IV secretion system protein virB4
T33.4.3.rep	c01	2022206	complex	341/840	missense_variant c.1022_1031delCCGATGCCGCinsAGGACGCCCG p.AlaAspAlaAla341GluAspAlaArg	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.Ile357Val	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.Val392Ile	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	rpoB	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
T33.4.3.rep	c02	436083	complex	526/1377	missense_variant c.1578_1584delTCAGACCinsCCAGGTG p.Thr528Val	rpoB	DNA-directed RNA polymerase subunit beta

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T33.4.3.rep	c02	436125	snp	540/1377	synonymous_variant c.1620C>T p.Leu540Leu	rpoB	DNA-directed RNA polymerase subunit beta
T33.4.3.rep	c02	436143	snp	546/1377	synonymous_variant c.1638C>T p.Gly546Gly	rpoB	DNA-directed RNA polymerase subunit beta
T33.4.3.rep	c02	439856	snp	338/1400	synonymous_variant c.1014T>C p.Gly338Gly	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	439865	snp	341/1400	synonymous_variant c.1023T>C p.Arg341Arg	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	439874	snp	344/1400	synonymous_variant c.1032G>T p.Leu344Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	439910	snp	356/1400	synonymous_variant c.1068C>T p.Val356Val	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	439931	snp	363/1400	synonymous_variant c.1089C>G p.Leu363Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	439985	snp	381/1400	synonymous_variant c.1143A>G p.Pro381Pro	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	440144	snp	434/1400	synonymous_variant c.1302T>G p.Leu434Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	440156	snp	438/1400	synonymous_variant c.1314C>T p.Ala438Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	440165	complex	441/1400	missense_variant c.1323_1325delCACinsGAT p.Thr442Met	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	440172	snp	444/1400	missense_variant c.1330A>G p.Ile444Val	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	440186	snp	448/1400	synonymous_variant c.1344T>C p.Ala448Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	440198	snp	452/1400	synonymous_variant c.1356T>C p.His452His	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	440207	complex	455/1400	synonymous_variant c.1365_1368delTTGTinsCTGC p.457	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	440216	snp	458/1400	synonymous_variant c.1374G>C p.Ala458Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	440264	snp	474/1400	synonymous_variant c.1422G>C p.Leu474Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	440270	snp	476/1400	synonymous_variant c.1428C>G p.Leu476Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	440282	snp	480/1400	synonymous_variant c.1440T>G p.Leu480Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	440288	snp	482/1400	synonymous_variant c.1446A>G p.Ala482Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	441077	snp	745/1400	synonymous_variant c.2235C>A p.Ala745Ala	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	441101	complex	753/1400	synonymous_variant c.2259_2262delAACCinsGACG p.755	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	441110	snp	756/1400	synonymous_variant c.2268A>C p.Ile756Ile	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	441195	snp	785/1400	synonymous_variant c.2353T>C p.Leu785Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T33.4.3.rep	c02	441203	complex	787/1400	synonymous_variant c.2361_2364delTGCTinsGGCG p.789	rpoC	DNA-directed RNA polymerase subunit beta'
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	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.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.735_738delTGTinsGGTT 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_36delICGTTCGATinsTGTTGAC 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_126delGGTGTTCGinsCGTTTCC 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-binding subunit ClpX

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	mnf	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-binding subunit ClpX
T33.4.3.rep	c02	698627	snp	150/424	synonymous_variant c.450G>C p.Thr150Thr	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T33.4.3.rep	c02	698633	snp	148/424	synonymous_variant c.444A>G p.Thr148Thr	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T33.4.3.rep	c02	698639	snp	146/424	synonymous_variant c.438G>A p.Ala146Ala	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T33.4.3.rep	c02	698645	snp	144/424	synonymous_variant c.432C>G p.Ala144Ala	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T33.4.3.rep	c02	698657	complex	138/424	synonymous_variant c.414_420delGTGCCAinsCGTTCCC p.141	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T33.4.3.rep	c02	698675	snp	134/424	synonymous_variant c.402A>C p.Ala134Ala	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T33.4.3.rep	c02	698726	complex	116/424	missense_variant c.348_351delTCTTinsCATG p.Leu117Met	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T33.4.3.rep	c02	698752	snp	109/424	missense_variant c.325A>G p.Ile109Val	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T33.4.3.rep	c02	1908916	complex	185/566	synonymous_variant c.555_558delGGAinsCGAG 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_669delITCTCinsCCTG 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	mnf	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	mnf	244/546	missense_variant c.730_731delITCinsGG 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
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	c01	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_216delCAAGinsGAG 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.Ile326Val	virB4_2	Type IV secretion system protein virB4
T33.4.5	c01	2022206	complex	341/840	missense_variant c.1022_1031delCCGATGCCGinsAGGACGCCCG 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.Ile357Val	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.Val392Ile	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
T33.4.5	c02	436008	snp	501/1377	synonymous_variant c.1503T>C p.Asp501Asp	rpoB	DNA-directed RNA polymerase subunit beta

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T33.4.5	c02	436029	snp	508/1377	synonymous_variant c.1524T>A p.Ala508Ala	rpoB	DNA-directed RNA polymerase 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_1161delACGTCTTinsCCGCCTC 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.Ile444Val	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.Ile756Ile	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.Ile356Val	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
T33.4.5	c02	446154	snp	415/694	synonymous_variant c.1245T>G p.Ala415Ala	fusA	Elongation factor G
T33.4.5	c02	446174	snp	422/694	missense_variant c.1265C>G p.Ala422Gly	fusA	Elongation factor G

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T33.4.5	c02	451011	snp	243/277	synonymous_variant c.729T>C p.Arg243Arg	rplB	50S ribosomal protein L2
T33.4.5	c02	451017	complex	245/277	synonymous_variant c.735_738delTGTCinsGGTT p.247	rplB	50S ribosomal protein L2
T33.4.5	c02	451038	snp	252/277	synonymous_variant c.756T>C p.Pro252Pro	rplB	50S ribosomal protein L2
T33.4.5	c02	451051	complex	257/277	missense_variant c.769_777delAAGACGCGCinsCGCACCCGT p.Lys257Arg	rplB	50S ribosomal protein L2
T33.4.5	c02	453539	snp	13/122	synonymous_variant c.39C>T p.Asn13Asn	rplN	50S ribosomal protein L14
T33.4.5	c02	453590	complex	30/122	missense_variant c.90_96delGCGTTACinsCAAATAT p.Arg31Lys	rplN	50S ribosomal protein L14
T33.4.5	c02	453602	snp	34/122	synonymous_variant c.102C>T p.Ser34Ser	rplN	50S ribosomal protein L14
T33.4.5	c02	453620	complex	40/122	synonymous_variant c.120_126delGGTGTGCGinsCGTTTCC p.43	rplN	50S ribosomal protein L14
T33.4.5	c02	453659	snp	53/122	synonymous_variant c.159A>G p.Lys53Lys	rplN	50S ribosomal protein L14
T33.4.5	c02	453665	complex	55/122	synonymous_variant c.165_168delTGATinsCGAC p.57	rplN	50S ribosomal protein L14
T33.4.5	c02	698342	snp	245/424	synonymous_variant c.735C>G p.Leu245Leu	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T33.4.5	c02	698351	snp	242/424	synonymous_variant c.726G>C p.Thr242Thr	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T33.4.5	c02	698357	snp	240/424	synonymous_variant c.720C>T p.Asp240Asp	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T33.4.5	c02	698399	snp	226/424	synonymous_variant c.678A>G p.Gln226Gln	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T33.4.5	c02	698420	snp	219/424	synonymous_variant c.657C>G p.Thr219Thr	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T33.4.5	c02	698474	snp	201/424	synonymous_variant c.603C>T p.Arg201Arg	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T33.4.5	c02	698492	snp	195/424	synonymous_variant c.585T>C p.Asp195Asp	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T33.4.5	c02	698505	mnp	190/424	synonymous_variant c.570_572delCAGinsTTC p.192	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T33.4.5	c02	1908908	mnp	183/566	synonymous_variant c.547_548delAGinsTC p.184	rpsA	30S ribosomal protein S1
T33.4.5	c02	1908916	complex	185/566	synonymous_variant c.555_558delGGAAinsCGAG p.187	rpsA	30S ribosomal protein S1
T33.4.5	c02	1908928	snp	189/566	synonymous_variant c.567G>T p.Ser189Ser	rpsA	30S ribosomal protein S1
T33.4.5	c02	1908937	snp	192/566	synonymous_variant c.576C>T p.Val192Val	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.Gly198Gly	rpsA	30S ribosomal protein S1
T33.4.5	c02	1908961	snp	200/566	synonymous_variant c.600C>T p.Val200Val	rpsA	30S ribosomal protein S1
T33.4.5	c02	1908967	snp	202/566	missense_variant c.606A>C p.Glu202Asp	rpsA	30S ribosomal protein S1
T33.4.5	c02	1909027	complex	222/566	synonymous_variant c.666_669delTCTCinsCCTG p.224	rpsA	30S ribosomal protein S1
T33.4.5	c02	1909039	snp	226/566	synonymous_variant c.678G>T p.Val226Val	rpsA	30S ribosomal protein S1
T33.4.5	c02	1909072	snp	237/566	synonymous_variant c.711G>T p.Pro237Pro	rpsA	30S ribosomal protein S1
T33.4.5	c02	1909086	complex	242/566	missense_variant c.725_729delCCATCinsACATT p.Thr242Asn	rpsA	30S ribosomal protein S1
T33.4.5	c02	1909097	mnp	246/566	missense_variant c.736_737delACinsCA p.Thr246Gln	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.27T>C p.Gly9Gly	ssb_4	Single-stranded DNA-binding protein
T33.4.5	c02	2279055	complex	14/134	missense_variant c.40_41delGAGinsAC p.Asp14Thr	ssb_4	Single-stranded DNA-binding protein
T33.4.5	c02	2279075	complex	20/134	missense_variant c.60_61delCCinsTG p.Gln21Glu	ssb_4	Single-stranded DNA-binding protein
T33.4.5	c02	2279084	snp	23/134	synonymous_variant c.69C>T p.Gly23Gly	ssb_4	Single-stranded DNA-binding protein
T33.4.5	c02	2445232	snp	314/521	synonymous_variant c.942C>G p.Leu314Leu	atpD	ATP synthase subunit beta
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	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_731delTTCinsGG 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
T44.4.1	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
T44.4.1	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.Ile326Val	virB4_2	Type IV secretion system protein virB4
T44.4.1	c01	2022206	complex	341/840	missense_variant c.1022_1031delCCGATGCCGCinsAGGACGCCCCG p.AlaAspAlaAla341GluAspAlaArg	virB4_2	Type IV secretion system protein virB4
T44.4.1	c01	2022225	snp	347/840	missense_variant c.1041A>C p.Glu347Asp	virB4_2	Type IV secretion system protein virB4
T44.4.1	c01	2022253	snp	357/840	missense_variant c.1069A>G p.Ile357Val	virB4_2	Type IV secretion system protein virB4
T44.4.1	c01	2022276	snp	364/840	synonymous_variant c.1092G>C p.Val364Val	virB4_2	Type IV secretion system protein virB4
T44.4.1	c01	2022318	snp	378/840	synonymous_variant c.1134C>G p.Ser378Ser	virB4_2	Type IV secretion system protein virB4
T44.4.1	c01	2022324	snp	380/840	synonymous_variant c.1140G>C p.Pro380Pro	virB4_2	Type IV secretion system protein virB4
T44.4.1	c02	436083	complex	526/1377	missense_variant c.1578_1584delTCAGACCinsCCAGGTG p.Thr528Val	rpoB	DNA-directed RNA polymerase subunit beta
T44.4.1	c02	439910	snp	356/1400	synonymous_variant c.1068C>T p.Val356Val	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.1	c02	439931	snp	363/1400	synonymous_variant c.1089C>G p.Leu363Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.1	c02	441101	complex	753/1400	synonymous_variant c.2259_2262delAACCinsGACG p.755	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.1	c02	441110	snp	756/1400	synonymous_variant c.2268A>C p.Ile756Ile	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	rplB	50S ribosomal protein L2
T44.4.1	c02	451011	snp	243/277	synonymous_variant c.729T>C p.Arg243Arg	rplB	50S ribosomal protein L2
T44.4.1	c02	451017	complex	245/277	synonymous_variant c.735_738delTGTTCinsGGTT 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	rplB	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_126delGGTGTTCGinsCGTTTCC 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

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	snp	176/546	synonymous_variant c.528G>C p.Thr176Thr	groL	60 kDa chaperonin
T44.4.2	c01	96534	snp	202/546	synonymous_variant c.606T>C p.Pro202Pro	groL	60 kDa chaperonin
T44.4.2	c01	96543	snp	205/546	synonymous_variant c.615C>G p.Val205Val	groL	60 kDa chaperonin
T44.4.2	c01	96549	complex	207/546	synonymous_variant c.621_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	c01	96786	snp	286/546	synonymous_variant c.858A>G p.Lys286Lys	groL	60 kDa chaperonin
T44.4.2	c01	96795	snp	289/546	synonymous_variant c.867C>G p.Leu289Leu	groL	60 kDa chaperonin
T44.4.2	c01	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ydcO_1	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.Ile326Val	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2022206	complex	341/840	missense_variant c.1022_1031delCCGATGCCGCinsAGGACGCCCG p.AlaAspAlaAla341GluAspAlaArg	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2022225	snp	347/840	missense_variant c.1041A>C p.Glu347Asp	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2022253	snp	357/840	missense_variant c.1069A>G p.Ile357Val	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2022276	snp	364/840	synonymous_variant c.1092G>C p.Val364Val	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2022318	snp	378/840	synonymous_variant c.1134C>G p.Ser378Ser	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2022324	snp	380/840	synonymous_variant c.1140G>C p.Pro380Pro	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2022330	complex	382/840	synonymous_variant c.1146_1149delCGCCinsTGCT p.384	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2023443	snp	753/840	synonymous_variant c.2259C>T p.Gly753Gly	virB4_2	Type IV secretion system protein virB4
T44.4.2	c01	2023509	snp	775/840	synonymous_variant c.2325T>C p.Asp775Asp	virB4_2	Type IV secretion system protein 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	rpoB	DNA-directed RNA polymerase subunit beta
T44.4.2	c02	436083	complex	526/1377	missense_variant c.1578_1584delTCAGACCinsCCAGGTG p.Thr528Val	rpoB	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.Ile444Val	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.Ile756Ile	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
T44.4.2	c02	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_738delTGTCTinsGGTT 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_126delGGTGTCTGinsCGTTTCC 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	mnf	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	mnf	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.Ile326Val	virB4_2	Type IV secretion system protein virB4
T44.4.3	c01	2022206	complex	341/840	missense_variant c.1022_1031delCCGATGCCGcinsAGGACGCCCCG 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.Ile357Val	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.Ile756Ile	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_1125delITGCAinsCGCC 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	rplB	50S ribosomal protein L2

sample	CHROM	POS	TYPE	AA_POS	EFFECT	GENE	PRODUCT
T44.4.3	c02	451051	complex	257/277	missense_variant c.769_777delAAGACGCGCinsCGCACCCGT p.Lys257Arg	rplB	50S ribosomal protein L2
T44.4.3	c02	453539	snp	13/122	synonymous_variant c.39C>T p.Asn13Asn	rplN	50S ribosomal protein L14
T44.4.3	c02	453590	complex	30/122	missense_variant c.90_96delGCGTTACinsCAAATAT p.Arg31Lys	rplN	50S ribosomal protein L14
T44.4.3	c02	453602	snp	34/122	synonymous_variant c.102C>T p.Ser34Ser	rplN	50S ribosomal protein L14
T44.4.3	c02	453620	complex	40/122	synonymous_variant c.120_126delGGTGTGCinsCGTTTCC p.43	rplN	50S ribosomal protein L14
T44.4.3	c02	698399	snp	226/424	synonymous_variant c.678A>G p.Gln226Gln	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T44.4.3	c02	698420	snp	219/424	synonymous_variant c.657C>G p.Thr219Thr	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T44.4.3	c02	698474	snp	201/424	synonymous_variant c.603C>T p.Arg201Arg	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T44.4.3	c02	698492	snp	195/424	synonymous_variant c.585T>C p.Asp195Asp	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T44.4.3	c02	1908928	snp	189/566	synonymous_variant c.567G>T p.Ser189Ser	rpsA	30S ribosomal protein S1
T44.4.3	c02	1908937	snp	192/566	synonymous_variant c.576C>T p.Val192Val	rpsA	30S ribosomal protein S1
T44.4.3	c02	1908946	snp	195/566	synonymous_variant c.585T>C p.Leu195Leu	rpsA	30S ribosomal protein S1
T44.4.3	c02	1908955	snp	198/566	synonymous_variant c.594T>C p.Gly198Gly	rpsA	30S ribosomal protein S1
T44.4.3	c02	1908961	snp	200/566	synonymous_variant c.600C>T p.Val200Val	rpsA	30S ribosomal protein S1
T44.4.3	c02	1908967	snp	202/566	missense_variant c.606A>C p.Glu202Asp	rpsA	30S ribosomal protein S1
T44.4.3	c02	1909027	complex	222/566	synonymous_variant c.666_669delTCTCinsCCTG p.224	rpsA	30S ribosomal protein S1
T44.4.3	c02	1909039	snp	226/566	synonymous_variant c.678G>T p.Val226Val	rpsA	30S ribosomal protein S1
T44.4.3	c02	1909072	snp	237/566	synonymous_variant c.711G>T p.Pro237Pro	rpsA	30S ribosomal protein S1
T44.4.3	c02	1909086	complex	242/566	missense_variant c.725_729delCCATCinsACATT p.Thr242Asn	rpsA	30S ribosomal protein S1
T44.4.3	c02	1909097	mnp	246/566	missense_variant c.736_737delACinsCA p.Thr246Gln	rpsA	30S ribosomal protein S1
T44.4.3	c02	1909108	snp	249/566	synonymous_variant c.747G>T p.Val249Val	rpsA	30S ribosomal protein S1
T44.4.4	c01	96450	snp	174/546	synonymous_variant c.522G>C p.Val174Val	groL	60 kDa chaperonin
T44.4.4	c01	96456	snp	176/546	synonymous_variant c.528G>C p.Thr176Thr	groL	60 kDa chaperonin
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.615C>G p.Val205Val	groL	60 kDa chaperonin
T44.4.4	c01	96549	complex	207/546	synonymous_variant c.621_624delCCCTinsTCCG p.209	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.681C>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	96633	snp	235/546	synonymous_variant c.705G>T p.Pro235Pro	groL	60 kDa chaperonin
T44.4.4	c01	96639	snp	237/546	synonymous_variant c.711G>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	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	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ydcO_1	Inner membrane protein YdcO
T44.4.4	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ydcO_1	Inner membrane protein YdcO
T44.4.4	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	HTH-type transcriptional regulatory protein GabR
T44.4.4	c01	2021961	snp	259/840	synonymous_variant c.777G>C p.Ser259Ser	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2021973	complex	263/840	missense_variant c.789_793delTCTGAinsCCTGC p.Met265Leu	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2021999	snp	272/840	missense_variant c.815G>A p.Arg272Lys	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2022018	snp	278/840	synonymous_variant c.834C>T p.Arg278Arg	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2022111	snp	309/840	synonymous_variant c.927C>A p.Ala309Ala	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2022120	mnp	312/840	missense_variant c.936_938delTGCinsGCT p.Ala313Leu	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2022133	snp	317/840	missense_variant c.949C>A p.Leu317Met	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2022138	complex	318/840	synonymous_variant c.954_957delGCTAinsCTTG p.320	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2022160	complex	326/840	missense_variant c.976_978delATCinsGTG p.Ile326Val	virB4_2	Type IV secretion system protein virB4
T44.4.4	c01	2022206	complex	341/840	missense_variant c.1022_1031delCCGATGCCGCinsAGGACGCCCG p.AlaAspAlaAla341GluAspAlaArg	virB4_2	Type IV secretion system protein virB4

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.Ile357Val	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	rpoB	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.Ile444Val	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.Ile756Ile	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_738delGTGCinsGGTT 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_96delICGTTACinsCAAATAT 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_126delGGTGTTCGinsCGTTTCC 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-binding subunit ClpX
T44.4.4	c02	698399	snp	226/424	synonymous_variant c.678A>G p.Gln226Gln	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T44.4.4	c02	698420	snp	219/424	synonymous_variant c.657C>G p.Thr219Thr	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
T44.4.4	c02	698474	snp	201/424	synonymous_variant c.603C>T p.Arg201Arg	clpX	ATP-dependent Clp protease ATP-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.Thr246Gln	rpsA	30S ribosomal protein S1
T44.4.4	c02	1909108	snp	249/566	synonymous_variant c.747G>T p.Val249Val	rpsA	30S ribosomal protein S1
T44.4.4	c02	2279042	snp	9/134	synonymous_variant c.27T>C p.Gly9Gly	ssb_4	Single-stranded DNA-binding protein
T44.4.4	c02	2279055	complex	14/134	missense_variant c.40_41delGAinsAC p.Asp14Thr	ssb_4	Single-stranded DNA-binding protein
T44.4.4	c02	2279075	complex	20/134	missense_variant c.60_61delCCinsTG p.Gln21Glu	ssb_4	Single-stranded DNA-binding protein
T44.4.4	c02	2279084	snp	23/134	synonymous_variant c.69C>T p.Gly23Gly	ssb_4	Single-stranded DNA-binding protein
T44.4.5.rep	c01	96456	snp	176/546	synonymous_variant c.528G>C p.Thr176Thr	groL	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
T44.4.5.rep	c01	96633	snp	235/546	synonymous_variant c.705G>T p.Pro235Pro	groL	60 kDa chaperonin
T44.4.5.rep	c01	96639	snp	237/546	synonymous_variant c.711G>C p.Leu237Leu	groL	60 kDa chaperonin
T44.4.5.rep	c01	96658	mnp	244/546	missense_variant c.730_731delTCinsGG p.Ser244Gly	groL	60 kDa chaperonin
T44.4.5.rep	c01	96732	snp	268/546	synonymous_variant c.804C>T p.Arg268Arg	groL	60 kDa chaperonin
T44.4.5.rep	c01	96741	snp	271/546	synonymous_variant c.813G>C p.Leu271Leu	groL	60 kDa chaperonin
T44.4.5.rep	c01	96753	snp	275/546	synonymous_variant c.825T>C p.Ala275Ala	groL	60 kDa chaperonin
T44.4.5.rep	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
T44.4.5.rep	c01	96786	snp	286/546	synonymous_variant c.858A>G p.Lys286Lys	groL	60 kDa chaperonin
T44.4.5.rep	c01	1008848	del	218/239	frameshift_variant c.653delG p.Gly218fs	ydcO_1	Inner membrane protein YdcO
T44.4.5.rep	c01	1008861	del	214/239	frameshift_variant c.640delC p.Arg214fs	ydcO_1	Inner membrane protein YdcO
T44.4.5.rep	c01	1010254	del	2/429	frameshift_variant c.4delG p.Ala2fs	gabR_1	HTH-type transcriptional regulatory protein GabR
T44.4.5.rep	c01	2007330	complex	72/133	missense_variant c.214_216delCAAGinsGAG p.Gln72Glu	ssb_1	Single-stranded DNA-binding protein
T44.4.5.rep	c01	2007347	snp	77/133	synonymous_variant c.231T>C p.Gly77Gly	ssb_1	Single-stranded DNA-binding protein
T44.4.5.rep	c01	2021961	snp	259/840	synonymous_variant c.777G>C p.Ser259Ser	virB4_2	Type IV secretion system protein virB4
T44.4.5.rep	c01	2021973	complex	263/840	missense_variant c.789_793delTCTGAinsCCTGC p.Met265Leu	virB4_2	Type IV secretion system protein virB4
T44.4.5.rep	c01	2021999	snp	272/840	missense_variant c.815G>A p.Arg272Lys	virB4_2	Type IV secretion system protein virB4
T44.4.5.rep	c01	2022018	snp	278/840	synonymous_variant c.834C>T p.Arg278Arg	virB4_2	Type IV secretion system protein virB4
T44.4.5.rep	c01	2022111	snp	309/840	synonymous_variant c.927C>A p.Ala309Ala	virB4_2	Type IV secretion system protein virB4
T44.4.5.rep	c01	2022120	mnp	312/840	missense_variant c.936_938delTGCinsGCT p.Ala313Leu	virB4_2	Type IV secretion system protein virB4
T44.4.5.rep	c01	2022133	snp	317/840	missense_variant c.949C>A p.Leu317Met	virB4_2	Type IV secretion system protein virB4
T44.4.5.rep	c01	2022138	complex	318/840	synonymous_variant c.954_957delGCTAinsCTTG p.320	virB4_2	Type IV secretion system protein virB4
T44.4.5.rep	c01	2022160	complex	326/840	missense_variant c.976_978delATCinsGTG p.Ile326Val	virB4_2	Type IV secretion system protein virB4
T44.4.5.rep	c01	2022206	complex	341/840	missense_variant c.1022_1031delCCGATGCCGCinsAGGACGCCCG p.AlaAspAlaAla341GluAspAlaArg	virB4_2	Type IV secretion system protein virB4
T44.4.5.rep	c01	2022225	snp	347/840	missense_variant c.1041A>C p.Glu347Asp	virB4_2	Type IV secretion system protein virB4
T44.4.5.rep	c01	2022253	snp	357/840	missense_variant c.1069A>G p.Ile357Val	virB4_2	Type IV secretion system protein virB4
T44.4.5.rep	c01	2022276	snp	364/840	synonymous_variant c.1092G>C p.Val364Val	virB4_2	Type IV secretion system protein virB4
T44.4.5.rep	c01	2022318	snp	378/840	synonymous_variant c.1134C>G p.Ser378Ser	virB4_2	Type IV secretion system protein virB4
T44.4.5.rep	c01	2022324	snp	380/840	synonymous_variant c.1140G>C p.Pro380Pro	virB4_2	Type IV secretion system protein virB4
T44.4.5.rep	c01	2023443	snp	753/840	synonymous_variant c.2259C>T p.Gly753Gly	virB4_2	Type IV secretion system protein virB4
T44.4.5.rep	c01	2023509	snp	775/840	synonymous_variant c.2325T>C p.Asp775Asp	virB4_2	Type IV secretion system protein virB4
T44.4.5.rep	c01	2023515	snp	777/840	synonymous_variant c.2331C>A p.Leu777Leu	virB4_2	Type IV secretion system protein virB4
T44.4.5.rep	c01	2023521	snp	779/840	synonymous_variant c.2337G>A p.Glu779Glu	virB4_2	Type IV secretion system protein virB4
T44.4.5.rep	c02	439856	snp	338/1400	synonymous_variant c.1014T>C p.Gly338Gly	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.5.rep	c02	439865	snp	341/1400	synonymous_variant c.1023T>C p.Arg341Arg	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.5.rep	c02	439874	snp	344/1400	synonymous_variant c.1032G>T p.Leu344Leu	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.5.rep	c02	439910	snp	356/1400	synonymous_variant c.1068C>T p.Val356Val	rpoC	DNA-directed RNA polymerase subunit beta'
T44.4.5.rep	c02	439931	snp	363/1400	synonymous_variant c.1089C>G p.Leu363Leu	rpoC	DNA-directed RNA polymerase 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.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 subunit beta'

sample	CHROM	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.Ile756Ile	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_1125delITGCAinsCGCC p.376	fusA	Elongation factor G
T44.4.5.rep	c02	451038	snp	252/277	synonymous_variant c.756T>C p.Pro252Pro	rplB	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_126delGGTGTGCGinsCGTTTCC 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