Centre for Clinical Microbiology



Oxford Nanopore Technologies (ONT) MTB sequencing bioinformatics pipeline 2

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ONT MTB Bioinformatics Pipeline





TB-Profiler

- detect drug resistance-conferring mutations and predict drugresistant phenotypes.
- The pipeline is rabidly developed so make sure you use the latest version (currently v.4.3.0)
- Run

conda install -c bioconda tb-profiler

• Analysis pipelines is pretty much standardised; the database is manually curated database hosted on separate repository constantly updated, based on emergence of new evidence for the inclusion or exclusion of mutations affect the Accuracy of the AMR prediction.



Important! The mutations and resulting library files are in reference to the H37Rv (NC_000962.3/AL123456.3) reference genome



TB-profiler

Web-based

Standalone CLI

https://jodyphelan.github.io/TBProfiler/



This repository contains a complete rewrite of the web version of TBProfiler, described here. It allows the use of profiling through a command line interface and contains some additional functionality such as the ability to process minION data.

The pipeline aligns reads to the H37Rv reference using bowtie2, BWA or minimap2 and then calls variants using bcftools. These variants are then compared to a drug-resistance database. We also predict the number of reads supporting drug resistance variants as an insight into hetero-resistance (not applicable for minION data)

Keeping up to date

TBProfiler is under constant rapid development. If you plan to use the program in your work please make sure you are using the most up to date version! Similarly, the database is not static and is continuously being improved so make sure you are using the most latest version. If you use TBProfiler in your work please state the version of both the tool and the database as they are deveoped independantly from each other.

Detailed Manual: https://jodyphelan.gitbook.io/tb-profiler

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tlyA	c.125dupC	capreomycin	resistance	9	https://ww
tlyA	c.136dupG	capreomycin	resistance	ļ	https://www
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tlyA	c.311dupG	capreomycin	resistance	•	https://www
tlyA	c.315dupC	capreomycin	resistance	,	https://www

https://tbdr.lshtm.ac.uk/

TB-Profiler Home Upload SRA data



Welcome to the webserver of TB-Profiler - a pipeline which allows users to analyse M. tuberculosis whole genome sequencing data to predict lineage and drug resistance. Follow the instructions below to upload a new sample or view analysed runs.

How does it work?

The pipeline searches for small variants and big deletions associated with drug resistance. It will also report the lineage. By default it uses Trimmomatic to trim the reads, BWA (or minimap2 for nanopore) to align to the reference genome and GATK (open source v4) to call variants.



Find your results by entering you unique run ID directly into the search box below. ca9dfb9b-bc2f-4f93-905e-5bbb3b90db2f

Submit

=J 🔲 🕓

Pros

Simple UFI Interactive

Cons

Limit on the size of the files 1GB Batch analysis (ONT not supported) Stable Internet

TB-Profiler Home Upload SRA data

Upload your next generation sequencing data in **fastQ** format. Files will be processed using the tb-profiler pipeline with default parameters. You may select the technology used to generate the data (Illumina or Oxford Nanopore). Samples will be process with a first in first out policy so please be patient as there may be runs waiting to be processed before yours.

Please note: at the moment we can only accomodate uploads of under 1GB. If you have files which are larger or you require many isolates to be processed and have access to a linux or osX operating system then it might be worthwhile to run the commandline version of tb-profiler. For more information on this please visit the github repository.

Single sample

You can upload one or two (forward and reverse) fastq files. When you upload your data, the run will be be assigned a unique ID. Please take a note of this ID as you will need to to find your results later.

Fastq file 1:

Choose file No file chosen

Fastq file 2 (optional):

Choose file No file chosen

Illumina
 Oxford Nanopore

Batch upload

You can upload multiple samples together to batch process them. At the moment batch uploading only supports paried end reads. By default, files must use **_1.fastq.gz** and **_2.fastq.gz** as the file suffix in order for them to be paired correctly. The suffix can be changed in the advanced options.

Fastq files

Choose files No file chosen

Illumina

 \bigcirc Oxford Nanopore

Advanced options



Let's Install TB-profiler Please refer to Script_ONT.txt (line 206)

Meanwhile Lets try barcode10 on the Web-based version



Common File Types

✓ Fasta (.fna)
✓ Fastq (.fastq)
✓ Fast5

SAM/BAM

SAM

- The Sequence Alignment/Map file (.sam) is a file format to save alignment information of reads mapped against reference genome sequence
- It usually starts with a header section followed by alignment information as tab separated lines for each read

BAM

- The Binary Alignment/Map file (. bam) is the compressed binary version of a SAM file that is used to represent aligned sequences
- BAM file has an index file ".bam.bai"
- Not Human readable but you can open it on Artemis (Genome Viewer by Sanger) line 263 in the Script_ONT.txt



VCF

- Variant calling format (.vcf) (unzip it if it is zipped)
- Used to SNPs (Single Nucleotide Polymorphism) and Insertions and/or deletions (INDELs)
- Can be viewed in genome viewers or in Notepad
- Developed for large scale data storage



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41 #HORDMAT~CID=BCSQ, Number-, Type-Integer, Description="Bitmask of indexes to INFO/BCSQ, with interleaved first/second haplotype. Use \"bcftools query -f' 41 #HORDMAT~CID=BCSQ, Number-, Type-Integer, Description="Bitmask of indexes to INFO/BCSQ, with interleaved first/second haplotype. Use \"bcftools query -f' 41 #HORDMAT~CID=BCSQ, Number-, Type-Integer, Description="Bitmask of indexes to INFO/BCSQ, with interleaved first/second haplotype. Use \"bcftools query -f' 41 #HORDMAT~CID=BCSQ, Number-, Type-Integer, Description="Bitmask of indexes to INFO/BCSQ, with interleaved first/second haplotype. Use \"bcftools query -f' 41 Chromosome 101 RF ALT QUAL FILTER INFO FORMAT ERRIGE4619 42 Chromosome 7362 G C 225 PASS DP=46/VDB=0.682479/SBB=-0.693147/MQSB=1/MQOF=0/AC=2/AN=2/DF4=0, 0, 27, 31/MQ=60/BCSQ=missense gyrAlRv0006 prote 43 Chromosome 7582 A C 225 PASS DP=58/VDB=0.2639363/SBB=-0.693147/MQSB=1/MQOF=0/AC=2/AN=2/DF4=0, 0, 27, 31/MQ=60/BCSQ=missense gyrAlRv0006 prote 45 Chromosome 76198 G 225 PASS DP=48/VDB=0.261932/SBB=-0.693147/MQSB=1/MQOF=0/AC=2/AN=2/DF4=0, 0, 23, 21/MQ=60/BCSQ=missense gyrAlRv006 prote 54 Chromosome 76198 T C 225 PASS DP=46/VDB=0.2639363/MSB=1/MQOF=0/AC=2/AN=2/DF4=0, 0, 23, 21/MQ=60/BCSQ=missense gyrAlRv006 prote 54 Chromosome 76198 T C 225 PASS DP=47/VDB=0.063147	42	##INFO= <id=< td=""><td>BCSQ,Num</td><td>ber=</td><td>.,Ту</td><td>pe=S</td><td>tring,Desc</td><td>cription="Haplotype-aware consequence annotation from BCFtools/csq, see <u>http://samtools.github.io/bcftools/howto</u></td></id=<>	BCSQ , Num	ber=	., Ту	pe=S	tring,Desc	cription="Haplotype-aware consequence annotation from BCFtools/csq, see <u>http://samtools.github.io/bcftools/howto</u>
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47 Chromosome 7362 G C 225 PASS DP=467VDB=0.628247; SGB=-0.633147; MQSB=1; MQOP=0; AC=2; AN=2; DP4=0, 0, 27, 31; MQ=60; BCSQ=missensel gyrA [Rv0006] prote 48 Chromosome 7585 G C 225 PASS DP=467VDB=0.263147; MQSB=1; MQOP=0; AC=2; AN=2; DP4=0, 0, 27, 31; MQ=60; BCSQ=missensel gyrA [Rv0006] prote 49 Chromosome 7585 G C 225 PASS DP=467VDB=0.261952; SGB=-0.693147; MQSB=1; MQOP=0; AC=2; AN=2; DP4=0, 0, 22, 26; MQ=60; BCSQ=missensel gyrA [Rv0067] prote 51 Chromosome 761998 T C 228 PASS DP=457VDB=0.1693147; MQSB=1; MQDP=0; AC=2; AN=2; DP4=0, 0, 19, 16; MQ=60; BCSQ=missensel tryB Rv0667] prote 52 Chromosome 761998 T C 228 PASS DP=457VDB=0.19829; SGB=-0.693147; MQSB=1; MQDP=0; AC=2; AN=2; DP4=0, 0, 13, 21; MQ=60; BCSQ=missensel tryB Rv0667] prote 53 Chromosome 781395 T C 225 PASS DP=467VDB=0.484133; SGB=-0.693147; MQSB=1; MQDP=0; AC=2; AN=2; DP4=0, 0, 23, 21; MQ=60; BCSQ=missensel tryB Rv0667] prote 54 Chromosome 781395 T C 225 PASS DP=467VDB=0.484133; SGB=-0.693147; MQSB=1; MQDP=0; AC=2; AN=2; DP4=0, 0, 21, 10; MQ=60; BCSQ=missensel tryB Rv0667] prote Chromosome 167425 A G 225 PASS	46	Chromosome	6140	•	G	Т	225 PASS	DP=40;VDB=0.970148;SGB=-0.693145;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,18,22;MQ=60;BCSQ=missense gyrB Rv0005 prote
48 Chromosome 7582 A C 225 PASS DP=58; VDB=0.999003; SGB=-0.693147; MgSB=1; MgOF=0; AC=2; AN=2; DP4=0, 0, 27, 31; Mg=60; BCSQ=missensel gyrAl Rv0006 [prote 50 Chromosome 7515 . G 225 PASS DP=58; VDB=0.693147; MgSB=1; MgOF=0; AC=2; AN=2; DP4=0, 0, 27, 31; Mg=60; BCSQ=missensel gyrAl Rv0006 [prote 51 Chromosome 761155 . T 225 PASS DP=56; VDB=0.66238; SGB=-0.693147; MgSB=1; MgOF=0; AC=2; AN=2; DP4=0, 0, 22, 26; Mg=60; BCSQ=missensel gyrAl Rv0006 [prote 52 Chromosome 761998 T C 228 PASS DP=56; VDB=0.159622; SGB=-0.693147; MgSB=1; MgOF=0; AC=2; AN=2; DP4=0, 0, 33, 21; Mg=60; BCSQ=mynonymous [proc] Rv0660] Brote 53 Chromosome 761998 T C 228 PASS DP=54; VDB=0.6931467; MgSB=1; MgOF=0; AC=2; AN=2; DP4=0, 0, 33, 21; Mg=60; BCSQ=mynonymous [proc] Rv0660] Brote 54 Chromosome 714355 T C 225 PASS DP=54; VDB=0.6931467; MgSB=1; MgOF=0; AC=2; AN=2; DP4=0, 0, 23, 1; Mg=60; BCSQ=missensel [pASI, 0; A31; A31; A2, 0; A31; A31; A31; A31; A31; A31; A31; A31	47	Chromosome	7362	•	G	С	225 PASS	DP=46;VDB=0.682479;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,25,21;MQ=60;BCSQ=missense gyrA Rv0006 prote
49 Chromosome 7585 . G C 225 PASS DP=56;VDB=0.99970;G;SDB=-0.693147;MQSB=1;MQDF=0;AC=2;AN=2;DP4=0,0,22,26;MQ=60;BCSQ=missense gyAlRv0066 prote 50 Chromosome 761155 . C T 225 PASS DP=46;VDB=0.261952;SCB=-0.693137;MQSB=1;MQDF=0;AC=2;AN=2;DP4=0,0,22,26;MQ=60;BCSQ=missense gyAlRv0066 prote 51 Chromosome 76195 . C 225 PASS DP=56;VDB=0.159622;SCB=-0.693147;MQSB=1;MQDF=0;AC=2;AN=2;DP4=0,0,33,21;MQ=60;BCSQ=missense gyAlRv0066 prote 52 Chromosome 761995 . C 225 PASS DP=56;VDB=0.159622;SCB=-0.693147;MQSB=1;MQDF=0;AC=2;AN=2;DP4=0,0,33,21;MQ=60;BCSQ=synonymous rpoClRv0668 prot 54 Chromosome 781395 . T C 225 PASS DP=54;VDB=0.463146;MQSB=1;MQDF=0;AC=2;AN=2;DP4=0,0,33,21;MQ=60;BCSQ=non_coding rrs1 rNA GT:P12;DF:AD 1/1:255,93,0:31:0,31 55 Chromosome 1673425 . C T 225 PASS DP=3;VDB=0.42172;SCB=-0.693147;MQSB=1;MQDF=0;AC=2;AN=2;DP4=0,0,22,1;T/MQ=60;BCSQ=synonymous s11yA Rv1641 prote DF=3;VDB=0.860765;SCB=-0.693147;MQSB=1;MQDF=0;AC=2;AN=2;DP4=0,0,22,1;T/MQ=60;BCSQ=synonymous s11yA Rv1641 prote DF=3;VDB=0.860765;SCB=-0.693147;MQSB=1;MQDF=0;AC=2;AN=2;DP4=0,0,22,1;T/MQ=60;BCSQ=synonymous s11yA Rv1640 prot DF=3;VDB=0.8607655;SCB=-0.693131;MQSB=1;MQDF=0;AC=2;AN=2;DP4=0,0,22,2;T/MQ=60;BCSQ=	48	Chromosome	7582	•	А	С	225 PASS	DP=58;VDB=0.999803;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,27,31;MQ=60;BCSQ=missense gyrA Rv0006 prote
50 Chromosome 9304 . G A 225 PASS DP=48;VDB=0.26328;SB=-0.693147;MQSB=1;MQOP=0;AC=2;AN=2;DP4=0,0,22,26;MQ=60;BCSQ=missensel grpoBlRv0667]prote 51 Chromosome 761998 . T C 228 PASS DP=55;VDB=0.663288;SGB=-0.693147;MQSB=1;MQOP=0;AC=2;AN=2;DP4=0,0,33,21;MQ=60;BCSQ=missensel grpoBlRv0667]prote 52 Chromosome 761998 . T C 228 PASS DP=56;VDB=0.159622;SGB=-0.693147;MQSB=1;MQOP=0;AC=2;AN=2;DP4=0,0,33,21;MQ=60;BCSQ=monymouns lepClRv0668]prot 53 Chromosome 761998 . C C 225 PASS DP=45;VDB=0.9789;SGB=-0.693147;MQSB=1;MQOP=0;AC=2;AN=2;DP4=0,0,23;24;MQ=60;BCSQ=moymouns lepClRv0668]prot 54 Chromosome 1473246 A G 225 PASS DP=47;VDB=0.846133;SGB=-0.693147;MQSB=1;MQOP=0;AC=2;AN=2;DP4=0,0,22;71;MQ=60;BCSQ=missensel jnrAll*12;S5,03,0;31:0,31 DF=37;VDB=0.42172;SGB=-0.693147;MQSB=1;MQOP=0;AC=2;AN=2;DP4=0,0,22;17;MQ=60;BCSQ=missensel inhAlRv1484 proteinsensel inhAlRv1484 proteinsensel inhAlRv1484 proteinsensel inf38;MSB=1;AQOP=0;AC=2;AN=2;DP4=0,0,22;71;MQ=60;BCSQ=missensel inhAlRv1484 proteinsensel inhAlRv1484	49	Chromosome	7585	•	G	С	225 PASS	DP=58;VDB=0.999706;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,27,31;MQ=60;BCSQ=missense gyrA Rv0006 prote
51 Chromosome 761155 C T 225 PASS DP=35; VDB=0.62388; SGB=-0.693147; NgSE=1; MgSE=1; MgSE=0; ASS DP=43; VDB=0.15962; SGB=-0.693147; MgSE=1; MgSE=1; MgSE=1; MgSE=0; ASS DP=43; VDB=0.486133; SGB=-0.693147; MgSE=1; MgSE=1; MgSE=0; ASS DP=43; VDB=0; MSGSE=0; ASS DP=42; VDP=0; ASS DP=43; VDB=0; MSGSE=0; ASS DP=42; ASS DP=43; VDB=0; MSGSE=0; ASSS DP=42; ASS DP=43; VDB=0; MSGSE=0; ASSS DP=42; VDB=0; MSGSE=0; ASSS DP=43; VDB=0; MSGSE=0; ASSSSS	50	Chromosome	9304	•	G	А	225 PASS	DP=48;VDB=0.261952;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,22,26;MQ=60;BCSQ=missense gyrA Rv0006 prote
52 Chromosome 761998	51	Chromosome	761155	•	С	Т	225 PASS	DP=35;VDB=0.662388;SGB=-0.693136;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,19,16;MQ=60;BCSQ=missense rpoB Rv0667 prote
53 Chromosome 764995 . C G 225 PASS DP=54;VDB=0.998095;SDB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,33,21;MQ=60;BCSQ=synonymous rpoC Rv0668 pro 54 Chromosome 1473246 A G 225 PASS DP=47;VDB=0.846133;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,23,24;MQ=60;BCSQ=non_coding rs rRNA GT:PL:DP:AD 1/1:255,129,0:4310,4 56 Chromosome 1673425 C T 225 PASS DP=31;VDB=0.442172;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,22,17;MQ=60;BCSQ=missense inhA Rv1484 prote 57 Chromosome 1673425 T C 225 PASS DP=31;VDB=0.42172;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,22,15;MQ=60;BCSQ=missense inhA Rv1484 prote 58 Chromosome 1917972 A G 225 PASS DP=37;VDB=0.78866;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,22,27;MQ=60;BCSQ=missense pnA Rv2043c prote 59 Chromosome 3067464 A G 225 PASS DP=42;VDB=0.3538;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,22,27;MQ=60;BCSQ=missense pnA Rv2043c prote A 125 PAS DP=42;VDB=0.81664;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,22,27;MQ=60;BCSQ=missense pnA Rv2043c prote A C25 PASS DP=42;VVDB=0.516657;SGB=-0.693147;	52	Chromosome	761998	•	Т	С	228 PASS	DP=56;VDB=0.159622;SGB=-0.693147;RPB=1;MQB=1;MQSB=1;BQB=1;MQ0F=0;AC=2;AN=2;DP4=0,1,32,23;MQ=60;BCSQ=missense
54 Chromosome 781395 T C 225 PASS DP=43;VDB=0.7789;SGB=-0.693146;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,23,24;MQ=60;BCSQ=non_coding rs rRNA GT:PL:DP:AD 1/1:255,129,0:43:0,4 56 Chromosome 1673425 C T 225 PASS DP=47;VDB=0.846133;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,22,17;MQ=60;BCSQ=non_coding rs rRNA GT:PL:DP:AD 1/1:255,93,0:31:0,31 57 Chromosome 1674782 T C 225 PASS DP=37;VDB=0.442172;SGB=-0.693144;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,22,17;MQ=60;BCSQ=synonymous tlyA Rv1684 prote 58 Chromosome 1674782 T C 225 PASS DP=37;VDB=0.48266;SGB=-0.693144;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,22,17;MQ=60;BCSQ=synonymous tlyA Rv1684 prote 59 Chromosome 2067464 A G 225 PASS DP=35;VDB=0.78866;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,12,2;T;MQ=60;BCSQ=missense thX Rv2754c prote 61 Chromosome 3067464 A G 225 PASS DP=42;VDB=0.35383;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,12,2;MQ=60;BCSQ=missense thX Rv2754c prote 61 Chromosome 3067464 A G 225 PASS DP=42;VDB=0.35383;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,12,2;MQ=60;BCSQ=missense thX Rv27	53	Chromosome	764995	•	С	G	225 PASS	DP=54;VDB=0.998895;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,33,21;MQ=60;BCSQ=synonymous rpoC Rv0668 pro
55 Chromosome 1473246 A G 225 PASS DP=41;VDB=0.446133;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,21,10;MQ=60;GSCg=non_coding rrs rRNA GT:F 56 Chromosome 1673425 C T 225 PASS DP=31;VDB=0.442172;SGB=-0.693114;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,22,17;MQ=60;GSCg=nissense inhA RV14841prote 57 Chromosome 1917972 A G 225 PASS DP=3;VDB=0.64015;SGB=-0.693114;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,22,17;MQ=60;BCSQ=missense inhA RV14841prote 59 Chromosome 1917972 A G 225 PASS DP=3;VDB=0.680765;SGB=-0.693144;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,22,15;MQ=60;BCSQ=missense ncA Rv2043c prot 60 Chromosome 306744 A G 225 PASS DP=4;VDB=0.816864;SGB=-0.693146;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,22,27;MQ=60;BCSQ=missense ncA Rv2043c prot 61 Chromosome 306749 G A 225 PASS DP=4;VDB=0.816864;SGB=-0.693146;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,22,27;MQ=60;GCSQ=missense ncA Rv2043c prot 62 Chromosome 3067949 G A 225 PASS DP=4;VDB=0.816864;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,22,27;MQ=60;GCSQ=missense ncA Rv2043c prot A C252 PASS	54	Chromosome	781395	•	Т	С	225 PASS	DP=43;VDB=0.7789;SGB=-0.693146;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,19,24;MQ=60 GT:PL:DP:AD 1/1:255,129,0:43:0,4
56 Chromosome 1673425 C T 225 PASS DP=31; VDB=0.42172; SGB=-0.693114; MQSB=1; MQOF=0; AC=2; AN=2; DP4=0, 0, 22, 17; MQ=60; BCSQ=missense inAlRv1484 prote 57 Chromosome 1674782 T C 225 PASS DP=31; VDB=0.42172; SGB=-0.693114; MQSB=1; MQOF=0; AC=2; AN=2; DP4=0, 0, 22, 17; MQ=60; BCSQ=missense inAlRv1484 prote 58 Chromosome 1917972 A G 225 PASS DP=37; VDB=0.860765; SGB=-0.693141; MQSB=1; MQOF=0; AC=2; AN=2; DP4=0, 0, 22, 17; MQ=60; BCSQ=missense inAlRv1484 prote 59 Chromosome 3067464 A G 225 PASS DP=35; VDB=0.788686; SGB=-0.693146; MQSB=1; MQOF=0; AC=2; AN=2; DP4=0, 0, 22, 27; MQ=60; BCSQ=missense inAlRv2043c prot 60 Chromosome 3067464 A G 225 PASS DP=49; VDB=0.35383; SGB=-0.693146; MQSB=1; MQOF=0; AC=2; AN=2; DP4=0, 0, 12, 3; MQ=60 GT: PL: DP:AD 1/1:255, 126, 0:42 61 Chromosome 3086788 T C 225 PASS DP=49; VDB=0.3518057; SGB=-0.693146; MQSB=1; MQOF=0; AC=2; AN=2; DP4=0, 0, 24, 12; MQ=60; BCSQ=missense inAlRv1484 prote 62 Chromosome 3840719 T C 225 PASS DP=49; VDB=0.35383; SGB=-0.693147; MQSB=1; MQOF=0; AC=2; AN=2; DP4=0, 0, 24, 12; MQ=60; BCSQ=misse	55	Chromosome	1473246	•	А	G	225 PASS	DP=47;VDB=0.846133;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,23,24;MQ=60;BCSQ=non_coding rrs rRNA GT:F
57 Chromosome 1674782 T C 225 PASS DP=33;VDB=0.923491;SGB=-0.693144;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,22,1;MQ=60;BCSQ=missense inhA Rv1484 prote 58 Chromosome 1917972 A G 225 PASS DP=37;VDB=0.860765;SGB=-0.693141;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,22,1;MQ=60;BCSQ=missense pncA Rv2043c prot 59 Chromosome 3067464 A G 225 PASS DP=35;VDB=0.35383;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,22,27;MQ=60;BCSQ=missense pncA Rv2043c prot 61 Chromosome 3067464 A G 225 PASS DP=49;VDB=0.35383;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,22,27;MQ=60;BCSQ=missense thyX Rv2754c prote 61 Chromosome 3067464 A G 225 PASS DP=42;VDB=0.35383;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,19,23;MQ=60 GT:PL:DP:AD 1/1:255,126,0:42 62 Chromosome 3086788 T C 225 PASS DP=58;VDB=0.516057;SGB=-0.693146;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,24,12;MQ=60;BCSQ=synonymous a r Rv3423c prote 63 Chromosome 3840719 T C 225 PASS DP=44;VDB=0.853588;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,24,12;MQ=60;BCSQ=synonymous a r Rv3423c prote A C 225 <td>56</td> <td>Chromosome</td> <td>1673425</td> <td>•</td> <td>С</td> <td>Т</td> <td>225 PASS</td> <td>DP=31;VDB=0.442172;SGB=-0.69311;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,21,10;MQ=60 GT:PL:DP:AD 1/1:255,93,0:31:0,31</td>	56	Chromosome	1673425	•	С	Т	225 PASS	DP=31;VDB=0.442172;SGB=-0.69311;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,21,10;MQ=60 GT:PL:DP:AD 1/1:255,93,0:31:0,31
58 Chromosome 1917972 A G 225 PASS DP=37;VDB=0.860765;SGB=-0.693141;MQSE=1;MQOF=0;AC=2;AN=2;DP4=0,0,12,15;MQ=60;BCSQ=synonymous tjyA Rv1694 prot 59 Chromosome 2288868 A C 225 PASS DP=35;VDB=0.788666;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,12,27;MQ=60;BCSQ=missense pnc4 Rv2043c prot 60 Chromosome 3067464 A G 225 PASS DP=49;VDB=0.35383;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,22,7;MQ=60;BCSQ=missense thxX Rv2754c prot 61 Chromosome 306784 T C 225 PASS DP=49;VDB=0.35383;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,22,21;MQ=60;BCSQ=synonymous atr Rv3423c prot 62 Chromosome 3086788 T C 225 PASS DP=58;VDB=0.516057;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,24,12;MQ=60;BCSQ=synonymous atr Rv3423c prot 63 Chromosome 3841433 C G 225 PASS DP=49;VDB=0.377577;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,24,20;MQ=60;BCSQ=synonymous atr Rv3423c prot 64 Chromosome 3841433 C T 225 PASS DP=47;VDB=0.853888;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,24,20;MQ=60;BCSQ=synonymous atr Rv3423c prot 64 Chromosome	57	Chromosome	1674782	•	Т	С	225 PASS	DP=39;VDB=0.923491;SGB=-0.693144;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,22,17;MQ=60;BCSQ=missense inhA Rv1484 prote
59 Chromosome 2288868 A C 225 PASS DP=35;VDB=0./88686;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,12,2;NQ=60;BCSQ=missense pncA Rv2043c prote 60 Chromosome 3067464 A G 225 PASS DP=49;VDB=0.35383;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,12,2;NQ=60;BCSQ=missense pncA Rv2043c prote 61 Chromosome 3067464 A G 225 PASS DP=49;VDB=0.35383;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,19,23;MQ=60 GT:PL:DP:AD 1/1:255,126,0:42 62 Chromosome 3086788 T C 225 PASS DP=42;VDB=0.516057;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,33,25;MQ=60 GT:PL:DP:AD 1/1:255,175,0:58 63 Chromosome 3840719 T C 225 PASS DP=42;VDB=0.516057;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,24,20;MQ=60 GT:PL:DP:AD 1/1:255,175,0:58 64 Chromosome 3841433 C G 225 PASS DP=44;VDB=0.987756;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,24,20;MQ=60 GT:PL:DP:AD 1/1:255,132,0:44 65 Chromosome 4242643 C T 225 PASS DP=47;VDB=0.853588;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,22,20;MQ=60;BCSQ=missense embE Rv3795 prote <tr< td=""><td>58</td><td>Chromosome</td><td>1917972</td><td>•</td><td>A</td><td>G</td><td>225 PASS</td><td>DP=37;VDB=0.860765;SGB=-0.693141;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,22,15;MQ=60;BCSQ=synonymous t1yA Rv1694 pro</td></tr<>	58	Chromosome	1917972	•	A	G	225 PASS	DP=37;VDB=0.860765;SGB=-0.693141;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,22,15;MQ=60;BCSQ=synonymous t1yA Rv1694 pro
60 Chromosome 306/464 A G 225 PASS DP=49;VDB=0.35383;SGB=-0.69314/;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,22,27;MQ=60;BCSQ=missense thyx Rv2/54c prote 61 Chromosome 3067949 G A 225 PASS DP=42;VDB=0.816864;SGB=-0.693146;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,19,23;MQ=60 GT:PL:DP:AD 1/1:255,175,0:58 62 Chromosome 3086788 T C 225 PASS DP=58;VDB=0.516057;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,33,25;MQ=60 GT:PL:DP:AD 1/1:255,175,0:58 63 Chromosome 3841433 C G 225 PASS DP=42;VDB=0.377577;SGB=-0.693146;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,24,20;MQ=60 GT:PL:DP:AD 1/1:255,132,0:44 64 Chromosome 3841433 C G 225 PASS DP=44;VDB=0.987756;SGB=-0.693146;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,24,20;MQ=60 GT:PL:DP:AD 1/1:255,132,0:44 65 Chromosome 4242643 C T 225 PASS DP=42;VDB=0.278066;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,22,20;MQ=60 GT:PL:DP:AD 1/1:255,126,0:42 66 Chromosome 4247429 A G 225 PASS DP=42;VDB=0.278066;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,3,21;MQ=60;BCSQ=missense embB Rv3795 protei	59	Chromosome	2288868	•	A	С	225 PASS	DP=35;VDB=0.788686;SGB=-0.693136;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,17,18;MQ=60;BCSQ=missense pncA Rv2043c prot
61 Chromosome 306/949 . G A 225 PASS DP=42;VDB=0.816864;SGB=-0.693146;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,19,23;MQ=60 GT:PL:DP:AD 1/1:255,126,0:42 62 Chromosome 3086788 T C 225 PASS DP=58;VDB=0.516057;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,24,12;MQ=60 GT:PL:DP:AD 1/1:255,175,0:58 63 Chromosome 3841433 C G 225 PASS DP=36;VDB=0.377577;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,24,20;MQ=60 GT:PL:DP:AD 1/1:255,126,0:42 64 Chromosome 3841433 C G 225 PASS DP=44;VDB=0.987756;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,24,20;MQ=60 GT:PL:DP:AD 1/1:255,126,0:42 65 Chromosome 4242643 C T 225 PASS DP=47;VDB=0.853588;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,25,22;MQ=60;BCSQ=synonymous ehRv3793 pro 66 Chromosome 4243217 C T 225 PASS DP=42;VDB=0.278066;SGB=-0.693147;MQSB=1;MQOF=0;AC=2;AN=2;DP4=0,0,30,21;MQ=60;BCSQ=missense embB Rv3795 prote 68 67 Chromosome 4247429 A G 225 PASS DP=51;VDB=0.559817;SGB=-0.693147;MQSB	60	Chromosome	3067464	•	A	G	225 PASS	DP=49;VDB=0.35383;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,22,27;MQ=60;BCSQ=missense thyX Rv2754c prote
62 Chromosome 3086788 T C 225 PASS DP=58;VDB=0.576057;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,33,25;MQ=60 GT:PL:DP:AD 1/1:255,175,0158 63 Chromosome 3840719 T C 225 PASS DP=36;VDB=0.377577;SGB=-0.693139;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,24,12;MQ=60;BCSQ=synomymous alr Rv3423c pro 64 Chromosome 3841433 C G 225 PASS DP=44;VDB=0.987756;SGB=-0.693146;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,24,20;MQ=60;BCSQ=synomymous alr Rv3423c pro 64 Chromosome 4242643 C T 225 PASS DP=44;VDB=0.987756;SGB=-0.693146;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,24,20;MQ=60;BCSQ=synomymous alr Rv3423c pro 66 Chromosome 4242643 C T 225 PASS DP=42;VDB=0.278066;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,22,20;MQ=60;BCSQ=missense embE Rv3795 prote 67 Chromosome 4247429 A G 225 PASS DP=51;VDB=0.559817;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,30,21;MQ=60;BCSQ=missense embB Rv3795 prote 68 Chromosome 4247781 T C 225 PASS DP=45;VDB=0.99981;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,19,29;MQ=60;BCSQ=missense embB Rv3795 prote P=45;VDB=0.999981;SGB=-0.693147;MQSB=1;MQ0	61	Chromosome	3067949	•	G	A	225 PASS	DP=42;VDB=0.816864;SGB=-0.693146;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,19,23;MQ=60 GT:PL:DP:AD 1/1:255,126,0:42
63 Chromosome 3840719 T C 225 PASS DP=36; VDB=0.377577; SGB=-0.693139; MQSB=1; MQOF=0; AC=2; AN=2; DP4=0, 0, 24, 12; MQ=60; BCSQ=synonymous a1r Rv3423c pro 64 Chromosome 3841433 C G 225 PASS DP=44; VDB=0.987756; SGB=-0.693146; MQSB=1; MQOF=0; AC=2; AN=2; DP4=0, 0, 24, 20; MQ=60 GT: PL: DP: AD 1/1:255, 132, 0:44 65 Chromosome 4242643 C T 225 PASS DP=47; VDB=0.853588; SGB=-0.693147; MQSB=1; MQOF=0; AC=2; AN=2; DP4=0, 0, 25, 22; MQ=60; BCSQ=synonymous embC Rv3793 pro 66 Chromosome 4242643 C T 225 PASS DP=42; VDB=0.853588; SGB=-0.693147; MQSB=1; MQOF=0; AC=2; AN=2; DP4=0, 0, 22, 20; MQ=60; BCSQ=synonymous embC Rv3793 pro 66 Chromosome 4247429 A G 225 PASS DP=51; VDB=0.278066; SGB=-0.693147; MQSB=1; MQOF=0; AC=2; AN=2; DP4=0, 0, 30, 21; MQ=60; BCSQ=missense embB Rv3795 prote 68 67 Chromosome 4247781 T C 225 PASS DP=48; VDB=0.86667; SGB=-0.693147; MQSB=1; MQOF=0; AC=2; AN=2; DP4=0, 0, 19, 29; MQ=60; BCSQ=missense embB Rv3795 prote 69 69 Chromosome 4328127 G C 225 PASS DP=45; VDB=0.99981; SGB=-0.693147; MQSB=1; MQOF=0; AC=	62	Chromosome	3086788	•	Т	C	225 PASS	DP=58;VDB=0.516057;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,33,25;MQ=60 GT:PL:DP:AD 1/1:255,175,0:58
64 Chromosome 3841433 C G 225 PASS DP=44;VDB=0.987756;SGB=-0.693146;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,24,20;MQ=60 GT:PL:DP:AD 1/1:255,132,0:44 65 Chromosome 4242643 C T 225 PASS DP=47;VDB=0.853588;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,25,22;MQ=60;BCSQ=synonymous embC Rv3793 pro 66 Chromosome 4243217 C T 225 PASS DP=42;VDB=0.278066;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,22,20;MQ=60 GT:PL:DP:AD 1/1:255,126,0:42 67 Chromosome 4247429 A G 225 PASS DP=51;VDB=0.559817;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,30,21;MQ=60;BCSQ=missense embB Rv3795 prote 68 Chromosome 4247781 T C 225 PASS DP=45;VDB=0.86667;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,19,29;MQ=60;BCSQ=missense embB Rv3795 protei DP=45;VDB=0.99981;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,20,25;MQ=60;BCSQ=missense embB Rv3795 protei DP=45;VDB=0.99981;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,20,25;MQ=60;BCSQ=missense gid Rv3919c protei 69 Chromosome 4407965 C G 225 PASS DP=33;VDB=0.873953;SGB=-0.693127;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,12,21;MQ=60;BCSQ=missense gid Rv3919c protei DP=52;VDB=0.982744;SGB=-0.693147;	63	Chromosome	3840719	•	Т	C	225 PASS	DP=36;VDB=0.377577;SGB=-0.693139;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,24,12;MQ=60;BCSQ=synonymous a1r Rv3423c pro
65 Chromosome 4242643 C T 225 PASS DP=47;VDB=0.853588;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,25,22;MQ=60;BCSQ=synonymous embc Rv3793 pro 66 Chromosome 4243217 C T 225 PASS DP=42;VDB=0.278066;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,22,20;MQ=60 GT:PL:DP:AD 1/1:255,126,0:42 67 Chromosome 4247429 A G 225 PASS DP=51;VDB=0.559817;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,30,21;MQ=60;BCSQ=missense embB Rv3795 prote 68 Chromosome 4247781 T C 225 PASS DP=48;VDB=0.86667;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,19,29;MQ=60;BCSQ=missense embB Rv3795 protei 69 Chromosome 4328127 G C 225 PASS DP=45;VDB=0.99981;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,20,25;MQ=60;BCSQ=missense embB Rv3855 prot 70 Chromosome 4407965 C G 225 PASS DP=33;VDB=0.873953;SGB=-0.693127;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,12,21;MQ=60;BCSQ=missense gid Rv3919c prote 71 Chromosome 4408156 A C 225 PASS DP=52;VDB=0.982744;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,33,19;MQ=60;BCSQ=missense gid Rv3919c prote 71	64	Chromosome	3841433	•	C	G	225 PASS	DP=44;VDB=0.987756;SGB=-0.693146;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,24,20;MQ=60 GT:PL:DP:AD 1/1:255,132,0:44
66 Chromosome 4243217 C T 225 PASS DP=42;VDB=0.278066;SGB=-0.693146;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,22,20;MQ=60 GT:PL:DP:AD 1/1:255,126,0:42 67 Chromosome 4247429 A G 225 PASS DP=51;VDB=0.559817;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,30,21;MQ=60;BCSQ=missense embB Rv3795 prote 68 Chromosome 4247781 T C 225 PASS DP=48;VDB=0.86667;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,19,29;MQ=60;BCSQ=missense embB Rv3795 protei 69 Chromosome 4328127 G C 225 PASS DP=45;VDB=0.99981;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,20,25;MQ=60;BCSQ=missense embB Rv3795 protei 70 Chromosome 4407965 C G 225 PASS DP=33;VDB=0.873953;SGB=-0.693127;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,12,21;MQ=60;BCSQ=missense gid Rv3919c prote 71 Chromosome 4408156 A C 225 PASS DP=52;VDB=0.982744;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,33,19;MQ=60;BCSQ=missense gid Rv3919c prote	65	Chromosome	4242643	•	C	Т	225 PASS	DP=47;VDB=0.853588;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,25,22;MQ=60;BCSQ=synonymous embC RV3793 pro
67 Chromosome 4247429 A G 225 PASS DP=51;VDB=0.559817;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,30,21;MQ=60;BCSQ=missense embB Rv3795 prote 68 Chromosome 4247781 T C 225 PASS DP=48;VDB=0.86667;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,19,29;MQ=60;BCSQ=missense embB Rv3795 prote 69 Chromosome 4328127 G C 225 PASS DP=45;VDB=0.99981;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,20,25;MQ=60;BCSQ=missense embB Rv3795 prote 70 Chromosome 4407965 C G 225 PASS DP=33;VDB=0.873953;SGB=-0.693127;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,12,21;MQ=60;BCSQ=missense gid Rv3919c prote 71 Chromosome 4408156 A C 225 PASS DP=52;VDB=0.982744;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,33,19;MQ=60;BCSQ=missense gid Rv3919c prote	66	Chromosome	4243217	•	C	Т	ZZ5 PASS	DP=42;VDB=0.278066;SGB=-0.693146;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,22,20;MQ=60 GT:PL:DP:AD 1/1:255,126,0:42
60 Chromosome 4247781 1 C 225 PASS DP=48;VDB=0.86667;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,19,29;MQ=60;BCSQ=missense embB Rv3795 prote1 69 Chromosome 4328127 G C 225 PASS DP=45;VDB=0.99981;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,20,25;MQ=60;BCSQ=missense embB Rv3795 prote1 70 Chromosome 4407965 C G 225 PASS DP=33;VDB=0.873953;SGB=-0.693127;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,12,21;MQ=60;BCSQ=missense gid Rv3919c prote 71 Chromosome 4408156 A C 225 PASS DP=52;VDB=0.982744;SGB=-0.693147;MQSB=1;MQ0F=0;AC=2;AN=2;DP4=0,0,33,19;MQ=60;BCSQ=missense gid Rv3919c prote	67	Chromosome	424/429	•	A	G	ZZ5 PASS	DP=51;VDB=0.55981/;SGB=-0.69314/;MQSB=1;MQ0E=0;AC=2;AN=2;DP4=0,0,30,21;MQ=60;BCSQ=missense embB RV3/95 prote
09 Chromosome 4328127 G C 225 PASS DP=45; VDB=0.99981; SGB=-0.693147; MQSB=1; MQ0F=0; AC=2; AN=2; DP4=0, 0, 20, 25; MQ=60; BCSQ=synonymous/etnR/RV3855/prot 70 Chromosome 4407965 C G 225 PASS DP=33; VDB=0.873953; SGB=-0.693127; MQSB=1; MQ0F=0; AC=2; AN=2; DP4=0, 0, 12, 21; MQ=60; BCSQ=missense gid Rv3919c prote 71 Chromosome 4408156 A C 225 PASS DP=52; VDB=0.982744; SGB=-0.693147; MQSB=1; MQ0F=0; AC=2; AN=2; DP4=0, 0, 33, 19; MQ=60; BCSQ=missense gid Rv3919c prote	60	Chromosome	424//81	•	T	C	ZZ5 PASS	DF=48;VDB=0.8000/;SGB=-0.69314/;MQSB=1;MQUF=0;AC=2;AN=2;DF4=0,0,19,29;MQ=60;BCSQ=mlssense embB RV3/95 prote1
70 Chromosome 4407965 C G 225 PASS DP=53; VDB=0.873953; SGB=-0.693127; MQSB=1; MQ0F=0; AC=2; AN=2; DP4=0, 0, 12, 21; MQ=60; BCSQ=missense gid RV3919c prote 71 Chromosome 4408156 A C 225 PASS DP=52; VDB=0.982744; SGB=-0.693147; MQSB=1; MQ0F=0; AC=2; AN=2; DP4=0, 0, 33, 19; MQ=60; BCSQ=missense gid Rv3919c prote	70	Chromosome	4328127	•	G	C	ZZS PASS	DF=45; VD=0.33361; 5GB=-0.635147; mQ5B=1; mQ0F=0; AC=2; AN=2; DF4=0, 0, 20, 25; MQ=60; BC5Q=synonymous etnR RV3855 prot
Chromosome 4400150 . A C 225 PASS DP=52;VDB=0.982/44;SGB=-0.09314/;MQ5B=1;MQ0F=0;AC=2;AN=2;DP4=0,0,55,19;MQ=60;BC5Q=missense gid RV3919C prote	70	Chromosome	440/905	•	7	G	ZZO FASS	DP=53; VD=0.075955; SG=-0.095127; MQSB=1; MQ0F=0; AC=2; AN=2; DP4=0, 0, 12, 21; MQ=00; BCSQ=missense g1a RV5919C prote
	71	Chromosome	4408130	•	А	C	223 PASS	Dr - 32; VDD - 0.302/44; SGD = -0.03314/; MQSD = 1; MQ0r = 0; AC = 2; AN = 2; DP4 = 0, 0, 33, 13; MQ = 60; BCSQ = m1ssense g1d RV3919C prote v

Norm	mal text file Ln : 1 Col : 1 Pos : 1 Unix (LF) UTF-8 INS
<	>
35	<pre>##DCLUOUS_CONCalverSION=1.10.2+NLSIID=1.10.2 ##bcftools_concatCommand=concat _aD_nineline/callers/thnrofiler_test_run/TR-profiler/AsAcd95_3486_Asfc_af21_63affd161753 Chromosome A998 7267 wcf_cz_ni</pre>
34	<pre>###bcluous_lillerCommand=liller -t Unromosome:4990-7207 -e FMI/DFCIU -5UZ -0 pipeline/Callers/toproller_test_run/TB-proller/4e84Cd95-3480-4eIC-aIZ ##baftoola_gongstVergion=1_10_2/btglib_1_10_2</pre>
33	<pre>##pclloois_lillerversion=1.10.2+htslip=1.10.2 ##baftaola_filterCommand=filter_t_Chromogome:4000_7267_c_FMT/DD/10_SOz_c_pipeline/gallerg/therefiler_test_mum/TP_profiler/4c04cd05_2406_4cfg_sf2</pre>
32	<pre>2 ##polloois_normcommand=norm -1 /lustre/projects/com_snared_NG5_data/sylvia/.snakemake/conda/2c3a442eb14/4c51b4a96IIb80e4b315/share/tbprofiler/tbdb.fasta 2 ##bafteela_filterWargion=1 10 2/btglib 1 10 2</pre>
31	<pre>1 ##pcltools_normversion=1.10.2+htsiip=1.10.2 2 ##baftaola_normCommand=norm f /lustro/projects/CCM_shared_NCS_data/sulvia/_spakemake/sonda/2s3a442ab1474s51b4a06ffb90s4b215/share/throafiles/thdb_fasta</pre>
30	<pre>##portoous_carronumang=carr =mv; pate=weg sep 29 14:19:55 2021 ##bafteela_normVergion=1 10 2thtglib 1 10 2</pre>
29	<pre>##betcools_callversion=1.10.2+hcslip=1.10.2 ##beftools_callcommand=callmv. Date=Wed_Sep_20_14.10.35_2021</pre>
20	<pre>##INFO-CID-FQ,Number-I,Type-Integer,Description- Average mapping quarity > ##baftools_collVorsion=1_10_2ibtslib_1_10_2</pre>
20	<pre>##INFO-<id-dr4,number-4,type-integer,description= ,="" and="" att-forward="" att-reverse="" bases"="" high-quality="" number="" of="" ref-forward="" ref-reverse,=""> ##INFO-<id-mo_number-1_type-integer_description="average guality"="" mapping=""></id-mo_number-1_type-integer_description="average></id-dr4,number-4,type-integer,description=></pre>
20	<pre>##INFO-<id-an,number=1,type=integer,description= affects="" called="" genotypes="" in="" number="" of="" total=""> 7 ##INFO-<id-dp4 description="Number of high-guality ref_forward = ref_reverse = alt_forward and alt_reverse bases" number="4" type="Integer"> 7 ##INFO-<id-dp4 description="Number of high-guality ref_forward = ref_reverse = alt_forward and alt_reverse bases" number="4" type="Integer"> 7 ##INFO-<id-dp4 description="Number of high-guality ref_forward = ref_reverse = alt_forward and alt_reverse bases" number="4" type="Integer"> 7 ##INFO-<id-dp4 description="Number of high-guality ref_forward = ref_reverse = alt_forward and alt_reverse = bases" number="4" type="Integer"> 7 ##INFO-<id-dp4 description="Number of high-guality ref_forward = ref_reverse = alt_forward = ref_reverse = bases" number="4" type="Integer"> 7 ##INFO-<id-dp4 description="Number of high-guality ref_forward = ref_reverse = alt_forward = ref_reverse = bases" number="4" type="Integer"> 7 ##INFO-<id-dp4 description="Number of high-guality ref_forward = ref_reverse = alt_forward = ref_reverse = bases" number="4" type="Integer"> 7 ##INFO-<id-dp4 description="Number of high-guality ref_forward = ref_reverse = alt_forward = ref_reverse = bases" number="4" type="Integer"> 7 ##INFO-<id-dp4 =="" bases"="" number="4" type="Integer"> 7 ##INFO-</id-dp4></id-dp4></id-dp4></id-dp4></id-dp4></id-dp4></id-dp4></id-dp4></id-dp4></id-dp4></id-dp4></id-dp4></id-dp4></id-dp4></id-dp4></id-dp4></id-dp4></id-dp4></id-an,number=1,type=integer,description=></pre>
20	<pre>##INFO-<id-ac,number=a,type=integer,description= aff="" affete="" affete,="" as="" count="" each="" fisted="" for="" genotypes="" in="" order="" same="" the=""> 6 ##INFO-<id-an_number=1_type=integer_description="tetal alleles="" called="" genetypes"="" in="" number="" of=""></id-an_number=1_type=integer_description="tetal></id-ac,number=a,type=integer,description=></pre>
24	<pre>###INFO=<id=ac (smaller="" 1s="" better)="" description="bias" in="" noms="" number="" of="" the="" type="Float,"> ###INFO=<id=ac description="Allele count in genetypes for each ALT allele, in the same order as listed" number="3" type="Integer"> </id=ac></id=ac></pre>
23	<pre>##INFO-<id-hor (eigger="" coefficient="" description-="" detter)="" ethomiat="" is="" lest="" number-1.type-float="" thereading=""> 4 ##INFO-<id-hor (smaller="" better)"="" description-"bias="" homs="" in="" is="" number="" number-1="" of="" the="" type-float=""> 4</id-hor></id-hor></pre>
22	z ##ronnar-sid-oi,Number-1,Type-Stillg,Description- Genotype > 3 ##INEO-ZID-ICB Number-1 Type-Fleat Description-"Inbreeding Coefficient Binemial test (bigger is better)"\
	<pre>##FORMAT=<id=ad,number=k,type=integer,description= (high="quality" affeire="" bases)="" depths=""> ##FORMAT=<id=ct_number=1_tupe=string_description="constume"></id=ct_number=1_tupe=string_description="constume"></id=ad,number=k,type=integer,description=></pre>
20	<pre>##FORMAT-<id-df,number-i,type-integer,description= bases="" high-quality="" number="" of=""> ##FORMAT-<id-ad_number-p_type-integer_description="allolic_denths_(bigh-quality_bases)"\< pre=""></id-ad_number-p_type-integer_description="allolic_denths_(bigh-quality_bases)"\<></id-df,number-i,type-integer,description=></pre>
20	##FORMAT= <id=dp_number=1_tupe=integer_description="number bigb='guality_bases"' of=""></id=dp_number=1_tupe=integer_description="number>
10	##INFO-KID-Rgor, Number-I, Type-Float, Description- Flaction of Rgo Teads (Smaller is Detter) > 9 ##FORMAT=/ID=PL Number=G Type=Integer Description="List of Phred-scaled genotype likelihoods">
18	##INFO= <id=mode description="Fraction of MOD reads (smaller is better)" number="1" type="Float"></id=mode>
	<pre>##INFO=<id=ngsd,number=1,type=float,description= ##info="<ID=SGB" (bigger="" 0="" bias="" description="Segregation based metric " detter)="" is="" mann="Whitney" mapping="" number="1" of="" quarter="" strand="" test="" type="Float" vs=""></id=ngsd,number=1,type=float,description=></pre>
16	<pre>##INFO=<id=mose description="Mann-Whitney U test of Manning Ouality vs Strand Bias (bigger is better)" number="1" type="Float"> 6 ##INFO=<id=mose description="Mann-Whitney U test of Manning Ouality vs Strand Bias (bigger is better)" number="1" type="Float"> </id=mose></id=mose></pre>
15	<pre># ##INFO=<id=rqb,number=1,type=float description="Mann-Whitney U test of Base Quality Bias (bigger is better)"> 5 ##INFO=<id=bob description="Mann-Whitney U test of Base Quality Bias (bigger is better)" number="1" type="Float"> </id=bob></id=rqb,number=1,type=float></pre>
1.0	##INFO= <id=nid, <="" description="Mann-Whitney U test of Manning Ouality Bias (bigger is better)" number="1," td="" type="Float,"></id=nid,>
	2 ##INFO-CID-PDB,Number-1,Type-Float,Description-Variance Distance Dias for filtering spince-site arteracts in RNA-seq data (Digger is better),Version- 3 3 ##INFO-CID-PDB Number-1 Type-Float Description-"Mann-Whitney II test of Poad Desition Bias (bigger is better)"\
12	<pre>##INFO=<id=vdb (bigger="" artefacts="" better)"="" bias="" data="" denth"="" description="Variant Distance Bias for filtering splice-site artefacts in RNA-seg data (bigger is better)" distance="" filtering="" for="" in="" is="" number="1" raw="" read="" rna-seg="" splice-site="" type="Elost" variant="" varsion="3</pre></th></tr><tr><th>11</th><th>##INFO=<ID=DP Number=1 Type=Integer Description="></id=vdb></pre>
10	##INFO-CID-IMF Number-1.Type-Integer.Description- Maximum fraction of raw reads supporting an indel >
	<pre>##INFO=<id=indel,number=0,iype=flag,description= an="" indel.="" indicates="" is="" that="" the="" variant=""> </id=indel,number=0,iype=flag,description=></pre>
	/ ##ALI= <id=^,description= allete(s)="" observed.="" other="" represents="" than=""> ##INFO=/ID=INDFI Number=0 Type=Flag Description="Indicates that the variant is an INDFI "></id=^,description=>
	<pre>0 ##CONCLY=<id=chlonosonne,iengun=4411552 <br="">7 ##ALT=/ID=* Description="Perrosents allolo(s) other than observed "\</id=chlonosonne,iengun=4411552></pre>
5	<pre>##reference=fife;//fustre/projects/com_snared_NG5_data/sylvia/.snakemake/conda/2c3a442eb14/4c3fb4a9011b80e4b315/snare/tbprofiler/tbdb.fasta 6 ##gentig=/ID=Chromeseme_length=4411532></pre>
	<pre>4 ##pcitoolscommand=mplleup -1 /lustre/projects/CCM_shared_NGS_data/sylvia/.snakemake/conda/2c3a442ep14/4c51p4a9611b80e4p315/snare/toproilier/todo.lasta - 5 ##psference_files///lustre/projects/CCM_shared_NGS_data/sylvia/.snakemake/conda/2c3a442ep14/4c51p4a9611b80e4p315/snare/toproilier/todo.lasta - 5 ##psference_files///lustre/toproiests/CCM_shared_NGS_data/sylvia/.snakemake/conda/2c3a442ep14/4c51p4a9611b80e4p315/snare/toproilier/todo.lasta - 5 ##psference_files///lustre/toproilier/todo.lasta - 5 ##psference_files///lustre/toproilier/todo.lasta - 5 ##psference_files///lustre/toproilier/todo.lasta - 5 ##psference_files//lustre/toproilier/todo.lasta - 5 ##psference_files//lustre/toproilier/toproilie</pre>
3	
2	2 ##FILTER= <id=pass,description="all filters="" passed"=""></id=pass,description="all>
	##TILETORMAT=VCFV4.2

Drug class definitions

Samples can be classed into different types using the following definitions

Туре	Drugs resistance
Sensitive	No drug resistance
Pre-MDR	Rifampicin or isonisazid
MDR	Rifampicin and isoniazid
Pre-XDR	MDR and any fluoriquinolone
XDR	MDR and (any fluoriquinolone and any group A drug)
Other	Resistance to any drug but none of the above categories

Mutation format

Mutations must follow the HGVS nomenclature. Information on this format can be found here. The following types of mutations are currently allowed:

- Amino acid substitutions. *Example: S450L in rpoB would be p.Ser450Leu*
- Deletions in genes. Example: Deletion of nucleotide 758 in tlyA would be c.758del
- Insertion in genes. Example: Insertion of GT between nucleotide 1850 and 1851 in katG would be c.1850_1851insGT
- SNPs in non-coding RNAs. Example: A to G at position 1401 in rrs would be r.1401a>g
- SNPs in gene promoters. Example: A to G 7 bases 5' of the start codon in pncA c.-7A>G

Important! The mutations and resulting library files are in reference to the H37Rv (NC_000962.3/AL123456.3) reference genome

Depth is the amount of times a base within a genome has been sequenced. The greater the depth, the greater the confidence in the identity of the sequenced base



rpoB gene Coverage in 2 sequencing runs



Artemis: line 251



Let's Have a look at a TB-profiler output report

TB-profile Collate Script

Very Useful script to collate all data of multiple samples done in batches from .json files in a useful way in order to run queries on the whole batch.

Exercise

Let's Run the 12 fastq files in the directory fastq_ready through TB-profiler (Please refer to line 225 in Script_ONT.txt)

Then collate the data of the 12 isolates (Please refer to line 259 in Script_ONT.txt)

TB-profile Collate Script

It also produce 3 config files to annotate phylogenetic tree with

- Lineage
- Drug resistance classes (Sensitive, drug-resistant, MDR, XDR)
- Drug resistance calls for individual drugs (filled circles represent resistance)

Tree scale: 0.00001 🖂





ASANTE SANA!

