

TB3qc_mykrobe

```
{
  "species": {
    "susceptibility": {
      "Ofloxacin": {
        "predict": "R"
      }
    }
  },
  "called_by": {
    "gyrA_A90V-GCG7569GTG": {
      "variant": null,
      "genotype": [
        1,
        1
      ],
      "genotype_likelihoods": [
        -4290.611436662613,
        -99999999,
        -46.94967162259618
      ],
      "info": {
        "coverage": {
          "reference": {
            "percent_coverage": 0.0,
            "median_depth": 0,
            "min_non_zero_depth": 0,
            "kmer_count": 0,
            "klen": 21
          },
          "alternate": {
            "percent_coverage": 100.0,
            "median_depth": 34,
            "min_non_zero_depth": 30,
            "kmer_count": 645,
            "klen": 20
          }
        },
        "expected_depths": [
          39
        ],
        "contamination_depths": [],
        "filter": [],
        "conf": 4244
      },
      "_cls": "Call.VariantCall"
    }
  }
}
```

```

    }

    gyrA_S91P-TCG7572CCG": {
      "variant": null,
      "genotype": [
        1,
        1
      ],
      "genotype_likelihoods": [
        -4337.755190291881,
        -99999999,
        -43.144937925898645
      ],
      "info": {
        "coverage": {
          "reference": {
            "percent_coverage": 0.0,
            "median_depth": 0,
            "min_non_zero_depth": 0,
            "kmer_count": 0,
            "klen": 21
          },
          "alternate": {
            "percent_coverage": 100.0,
            "median_depth": 33,
            "min_non_zero_depth": 28,
            "kmer_count": 665,
            "klen": 21
          }
        },
        "expected_depths": [
          39
        ],
        "contamination_depths": [],
        "filter": [],
        "conf": 4295
      },
      "_cls": "Call.VariantCall"
    }
  }
}

Moxifloxacin": {
  "predict": "R

```

```

called_by": {
  "gyrA_A90V-GCG7569GTG": {
    "variant": null,
    "genotype": [
      1,
      1
    ],
    "genotype_likelihoods": [
      -4290.611436662613,
      -99999999,
      -46.94967162259618
    ],
    "info": {
      "coverage": {
        "reference": {
          "percent_coverage": 0.0,
          "median_depth": 0,
          "min_non_zero_depth": 0,
          "kmer_count": 0,
          "klen": 21
        },
        "alternate": {
          "percent_coverage": 100.0,
          "median_depth": 34,
          "min_non_zero_depth": 30,
          "kmer_count": 645,
          "klen": 20
        }
      },
      "expected_depths": [
        39
      ],
      "contamination_depths": [],
      "filter": [],
      "conf": 4244
    },
    "_cls": "Call.VariantCall"
  }
}

```

```

gyrA_S91P-TCG7572CCG": {
  "variant": null,
  "genotype": [
    1,
    1
  ],
  "genotype_likelihoods": [
    -4337.755190291881,
    -99999999,
    -43.144937925898645
  ],
  "info": {
    "coverage": {
      "reference": {
        "percent_coverage": 0.0,
        "median_depth": 0,
        "min_non_zero_depth": 0,
        "kmer_count": 0,
        "klen": 21
      },
      "alternate": {
        "percent_coverage": 100.0,
        "median_depth": 33,
        "min_non_zero_depth": 28,
        "kmer_count": 665,
        "klen": 21
      }
    },
    "expected_depths": [
      39
    ],
    "contamination_depths": [],
    "filter": [],
    "conf": 4295
  },
  "_cls": "Call.VariantCall"
}
}
}
Isoniazid": {
  "predict": "R

```

```

called_by": {
  "katG_S315G-GCT2155167GGT": {
    "variant": null,
    "genotype": [
      1,
      1
    ],
    "genotype_likelihoods": [
      -4672.233848007324,
      -99999999,
      -30.903794845738865
    ],
    "info": {
      "coverage": {
        "reference": {
          "percent_coverage": 0.0,
          "median_depth": 0,
          "min_non_zero_depth": 0,
          "kmer_count": 0,
          "klen": 21
        },
        "alternate": {
          "percent_coverage": 100.0,
          "median_depth": 39,
          "min_non_zero_depth": 32,
          "kmer_count": 741,
          "klen": 20
        }
      },
      "expected_depths": [
        39
      ],
      "contamination_depths": [],
      "filter": [],
      "conf": 4641
    },
    "_cls": "Call.VariantCall"
  }
}
}
Kanamycin": {
  "predict": "S

```

```

    }
    Ethambutol": {
      "predict": "R

called_by": {
  "embB_Q497R-CAG4248002CGG": {
    "variant": null,
    "genotype": [
      1,
      1
    ],
    "genotype_likelihoods": [
      -5204.863923415898,
      -999999999,
      -25.15674404283727
    ],
    "info": {
      "coverage": {
        "reference": {
          "percent_coverage": 10.0,
          "median_depth": 0,
          "min_non_zero_depth": 1,
          "kmer_count": 2,
          "klen": 21
        },
        "alternate": {
          "percent_coverage": 100.0,
          "median_depth": 48,
          "min_non_zero_depth": 42,
          "kmer_count": 910,
          "klen": 20
        }
      },
      "expected_depths": [
        39
      ],
      "contamination_depths": [],
      "filter": [],
      "conf": 5180
    },
    "_cls": "Call.VariantCall
  }
}

```

```

    }
    Streptomycin": {
      "predict": "R

called_by": {
  "rpsL_K43R-AAG781686AGG": {
    "variant": null,
    "genotype": [
      1,
      1
    ],
    "genotype_likelihoods": [
      -2914.920854490103,
      -99999999,
      -129.77218775526921
    ],
    "info": {
      "coverage": {
        "reference": {
          "percent_coverage": 30.0,
          "median_depth": 0,
          "min_non_zero_depth": 5,
          "kmer_count": 36,
          "klen": 21
        },
        "alternate": {
          "percent_coverage": 100.0,
          "median_depth": 23,
          "min_non_zero_depth": 11,
          "kmer_count": 440,
          "klen": 20
        }
      },
      "expected_depths": [
        39
      ],
      "contamination_depths": [],
      "filter": [],
      "conf": 2785
    },
    "_cls": "Call.VariantCall
  }
}

```

```

    }
  Ciprofloxacin": {
    "predict": "R

called_by": {
  "gyrA_A90V-GCG7569GTG": {
    "variant": null,
    "genotype": [
      1,
      1
    ],
    "genotype_likelihoods": [
      -4290.611436662613,
      -99999999,
      -46.94967162259618
    ],
    "info": {
      "coverage": {
        "reference": {
          "percent_coverage": 0.0,
          "median_depth": 0,
          "min_non_zero_depth": 0,
          "kmer_count": 0,
          "klen": 21
        },
        "alternate": {
          "percent_coverage": 100.0,
          "median_depth": 34,
          "min_non_zero_depth": 30,
          "kmer_count": 645,
          "klen": 20
        }
      },
      "expected_depths": [
        39
      ],
      "contamination_depths": [],
      "filter": [],
      "conf": 4244
    },
    "_cls": "Call.VariantCall
  }
}

```



```

gyrA_S91P-TCG7572CCG": {
  "variant": null,
  "genotype": [
    1,
    1
  ],
  "genotype_likelihoods": [
    -4337.755190291881,
    -999999999,
    -43.144937925898645
  ],
  "info": {
    "coverage": {
      "reference": {
        "percent_coverage": 0.0,
        "median_depth": 0,
        "min_non_zero_depth": 0,
        "kmer_count": 0,
        "klen": 21
      },
      "alternate": {
        "percent_coverage": 100.0,
        "median_depth": 33,
        "min_non_zero_depth": 28,
        "kmer_count": 665,
        "klen": 21
      }
    },
    "expected_depths": [
      39
    ],
    "contamination_depths": [],
    "filter": [],
    "conf": 4295
  },
  "_cls": "Call.VariantCall"
}
}
}
Pyrazinamide": {
  "predict": "r

```

```

called_by": {
  "pncA_D12G-GTC2289206GCC": {
    "variant": null,
    "genotype": [
      0,
      1
    ],
    "genotype_likelihoods": [
      -1903.656725557816,
      -158.99583713302795,
      -276.22421683691135
    ],
    "info": {
      "coverage": {
        "reference": {
          "percent_coverage": 100.0,
          "median_depth": 8,
          "min_non_zero_depth": 4,
          "kmer_count": 132,
          "klen": 21
        },
        "alternate": {
          "percent_coverage": 100.0,
          "median_depth": 27,
          "min_non_zero_depth": 24,
          "kmer_count": 525,
          "klen": 20
        }
      },
      "expected_depths": [
        39
      ],
      "contamination_depths": [],
      "filter": [],
      "conf": 1745
    },
    "_cls": "Call.VariantCall"
  }
}
}
Rifampicin": {
  "predict": "R

```

```

called_by": {
  "rpoB_S450L-TCG761154TTG": {
    "variant": null,
    "genotype": [
      1,
      1
    ],
    "genotype_likelihoods": [
      -4404.478230939082,
      -999999999,
      -40.687503862340144
    ],
    "info": {
      "coverage": {
        "reference": {
          "percent_coverage": 0.0,
          "median_depth": 0,
          "min_non_zero_depth": 0,
          "kmer_count": 0,
          "klen": 21
        },
        "alternate": {
          "percent_coverage": 100.0,
          "median_depth": 35,
          "min_non_zero_depth": 31,
          "kmer_count": 674,
          "klen": 20
        }
      },
      "expected_depths": [
        39
      ],
      "contamination_depths": [],
      "filter": [],
      "conf": 4364
    },
    "_cls": "Call.VariantCall"
  }
}
}
Amikacin": {
  "predict": "S

```

```

    }
    Capreomycin": {
      "predict": "r

called_by": {
  "rrs_C1402X-C1473247A": {
    "variant": null,
    "genotype": [
      0,
      1
    ],
    "genotype_likelihoods": [
      -1899.0356937696108,
      -778.6609519775338,
      -5231.24598764316
    ],
    "info": {
      "coverage": {
        "reference": {
          "percent_coverage": 100.0,
          "median_depth": 42,
          "min_non_zero_depth": 39,
          "kmer_count": 1416,
          "klen": 21
        },
        "alternate": {
          "percent_coverage": 100.0,
          "median_depth": 31,
          "min_non_zero_depth": 23,
          "kmer_count": 602,
          "klen": 21
        }
      },
      "expected_depths": [
        39
      ],
      "contamination_depths": [],
      "filter": [],
      "conf": 1120
    },
    "_cls": "Call.VariantCall
  }
}

```

TB3qc_mykrobe

```

    }
  }
  phylogenetics": {
    "phylo_group": {
      "Mycobacterium_tuberculosis_complex": {
        "percent_coverage": 99.564,
        "median_depth": 39
      }
    },
    "sub_complex": {
      "Unknown": {
        "percent_coverage": -1,
        "median_depth": -1
      }
    },
    "species": {
      "Mycobacterium_tuberculosis": {
        "percent_coverage": 98.514,
        "median_depth": 34
      }
    },
    "lineage": {
      "lineage": [
        "lineage2.2"
      ]
    }
  },
  calls_summary": {
    "lineage2.2": {
      "good_nodes": 2,
      "tree_depth": 2,
      "genotypes": {
        "lineage2": 1,
        "lineage2.2": 1
      }
    }
  },
  "calls": {
    "lineage2.2": {
      "lineage2": {
        "G497491A": {
          "variant": "ref-G497491A?var_name=G497491A&num_alts=1&ref=NC_000962.3&enum=0&gene=NA&mut=G497491A"
        }
      }
    }
  }
}

```

```

genotype": [
  1,
  1
],
"genotype_likelihoods": [
  -4601.386515514585,
  -99999999,
  -32.50342569218019
],
"info": {
  "coverage": {
    "reference": {
      "percent_coverage": 0.0,
      "median_depth": 0,
      "min_non_zero_depth": 0,
      "kmer_count": 0,
      "klen": 21
    },
    "alternate": {
      "percent_coverage": 100.0,
      "median_depth": 39,
      "min_non_zero_depth": 25,
      "kmer_count": 732,
      "klen": 21
    }
  },
  "expected_depths": [
    39
  ],
  "contamination_depths": [],
  "filter": [],
  "conf": 4569
},
"_cls": "Call.VariantCall
}
}
lineage2.2": {
  "G2505085A": {
    "variant": "ref-G2505085A?var_name=G2505085A&num_alts=2&ref=NC_000962.3&enum=0&gene=NA&mut=G2505085A

```

```

    "genotype": [
      1,
      1
    ],
    "genotype_likelihoods": [
      -4423.608355834194,
      -999999999,
      -38.93836579595363
    ],
    "info": {
      "coverage": {
        "reference": {
          "percent_coverage": 0.0,
          "median_depth": 0,
          "min_non_zero_depth": 0,
          "kmer_count": 0,
          "klen": 21
        },
        "alternate": {
          "percent_coverage": 100.0,
          "median_depth": 34,
          "min_non_zero_depth": 32,
          "kmer_count": 687,
          "klen": 21
        }
      },
      "expected_depths": [
        39
      ],
      "contamination_depths": [],
      "filter": [],
      "conf": 4385
    },
    "_cls": "Call.VariantCall"
  }
}
}
}
}
}
}

```

TB3qc_mykrobe

```
kmer": 21,  
  "probe_sets": [  
    "/home/idowu/miniconda3/lib/python3.6/site-packages/mykrobe/data/tb/tb-species-170421.fasta.gz  
/home/idowu/miniconda3/lib/python3.6/site-packages/mykrobe/data/tb/tb-hunt-probe-set-jan-03-2019.fasta.gz  
/home/idowu/miniconda3/lib/python3.6/site-packages/mykrobe/data/tb/tb.lineage.20200930.probes.fa.gz  
  ]  
files": [  
  "TB3qc_R1.fastq.gz  
TB3qc_R2.fastq.gz  
  ]  
version": {  
  "mykrobe-predictor": "v0.9.0  
mykrobe-atlas": "v0.9.0  
  }  
genotype_model": "kmer_count  
  }  
}
```