*M. tuberculosis* WGS report

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| --- | --- |
| **Date** | {{ d[‘timestamp’] }} |
| **Software version** | TB-Profiler v{{ d[‘pipeline’][‘software\_version’] }} |
| **Database version** | {{ d[‘pipeline’][‘db\_version’][‘name’] }} - {{ d[‘pipeline’][‘db\_version’][‘commit’] }} |
| **Sample ID** | {{ d[‘id’] }} |
| **Median coverage** | {{ d[‘qc’][‘target\_median\_depth’] }} |
| **Strain type** | {{ d[‘sub\_lineage’] }} |
| **Drug resistance** | {{ d[‘drtype’] }} |
| **Result summary**: {{ result\_summary }} | |
| **Notes**: {{ notes }} | |

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| Mutation Report  All mutations in target genes are reported if they have been assigned a confidence value of *Assoc. w R* or *Assoc. w R – Interim* according to the WHO mutation catalogue 2nd edition or if there is there is evidence from the literature. | | | | |
| **Drug** | **Gene** | **Mutation** | **Frequency** | **Confidence** |
| {%tr for r in rows %} | | | | |
| {{ r[‘drug’] }} | {% if r[‘qc’]>=99 %} l {% else %} l {% endif %} *{{ r[‘gene’] }}* | {{ r[‘change’] }} | {{ r[‘freq’] }} | {{ r[‘confidence’] }} {{ r[‘comment’] }} |
| {%tr endfor %} | | | | |
| Footnotes: {% for c in comments %}  {{ loop.index }} {{ c }}  {%- endfor %}  Gene QC:  l Sufficient coverage across >=99% of gene  l Sufficient coverage across <99% of gene | | | | |

| QC failed variants  This table lists mutations in target genes that have been assigned a confidence value of *Assoc. w R* or *Assoc. w R – Interim* according to the WHO mutation catalogue 2nd or have evidence from the literature **but fall below the confident detection threshold**. This may be due to low coverage data or a low frequency variant. | | | | | |
| --- | --- | --- | --- | --- | --- |
| **Gene** | **Mutation** | **Drug** | **Confidence** | **Depth** | **Frequency** |
| {%tr for r in fail\_variants %} | | | | | |
| {% if r[‘qc’]>=99 %} l {% else %} l {% endif %} *{{ r[‘gene’] }}* | {{ r[‘change’] }} | {{ r[‘drug’] }} | {{ r[‘confidence’] }} {{ r[‘comment’] }} |  |  |
| {%tr endfor %} | | | | | |
| Footnotes: {% for c in fail\_comments %}  {{ loop.index }} {{ c }}  {%- endfor %}  Gene QC:  l Sufficient coverage across >=99% of gene  l Sufficient coverage across <99% of gene | | | | | |

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| Other variants  This table lists mutations in target genes that **have not** been assigned a confidence value of *Assoc. w R* or *Assoc. w R – Interim* according to the WHO mutation catalogue 2nd edition. | | | | | |
| Gene | Mutation | Depth | Frequency | **Drug** | **Confidence** |
| {%tr for r in other\_variants %} | | | | | |
| {% if r[‘qc’]>=99 %} l {% else %} l {% endif %} *{{ r[‘gene’] }}* | {{ r[‘change’] }} | {{ r[‘depth’] }} | {{ r[‘freq’] }} | {{ r[‘drug’] }} | {{ r[‘confidence’] }} {{ r[‘comment’] }} |
| {%tr endfor %} | | | | | |
| Footnotes: {% for c in fail\_comments %}  {{ loop.index }} {{ c }}  {%- endfor %}  Gene QC:  l Sufficient coverage across >=99% of gene  l Sufficient coverage across <99% of gene | | | | | |