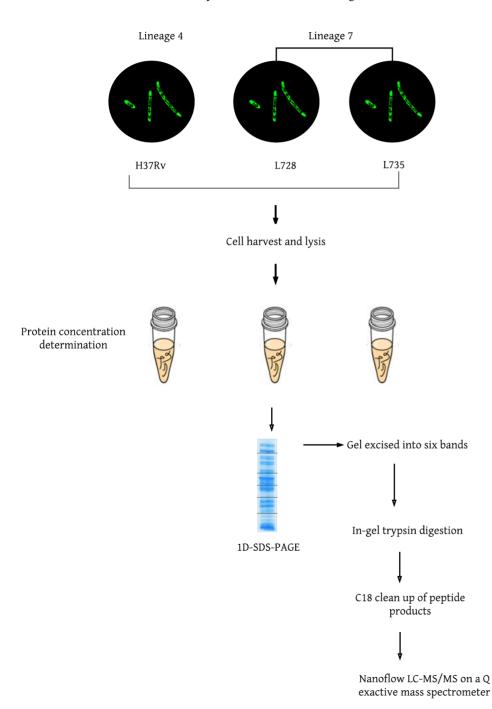
## Mycobacterium tuberculosis Lineages



Three biological protein samples from Lineage 4 and two clinical isolates of Lineage 7

Peptide products of each biological sample injected three times (27 LC-MS/MS runs)

A total of 2867 protein groups identified

1. Log 2 transformation of LFQ and iBAQ intensities

2. Protein abundances ranking based on iBAQ intensities

Quantitative analysis criteria

A total of 1946 protein qualify the criteria

- 2. Imputation for missing values
- 3. Two tailed t-test (permutation based-FDR 0.05,  $S_0$ = 2) and fold change cutoff 2

1. Filter at least two valid value per biological replicates in each lineage

125 proteins with significant abundance changes

- 4. Gene ontology
- 5. Unsupervised Hierarchical clustering analysis
- 6. KEGG enrichement analysis