Large-scale statistical analysis of *Mycobacterium tuberculosis* genome sequences identifies compensatory mutations associated with multi-drug resistance

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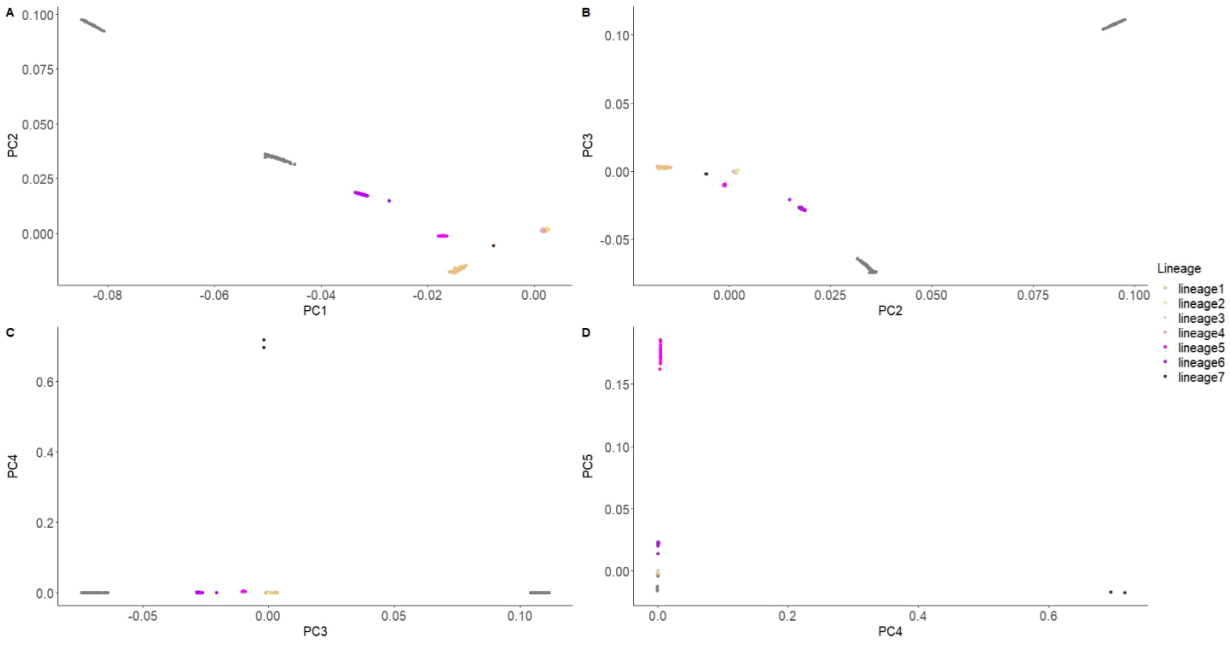
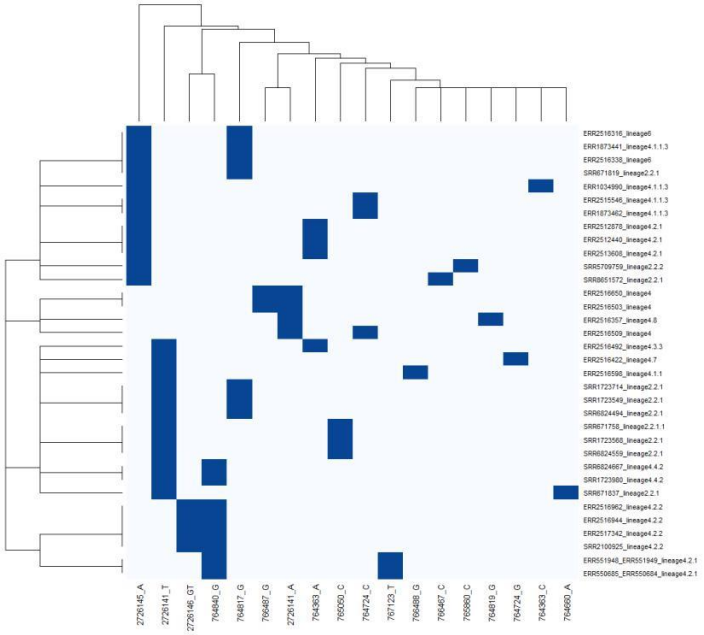
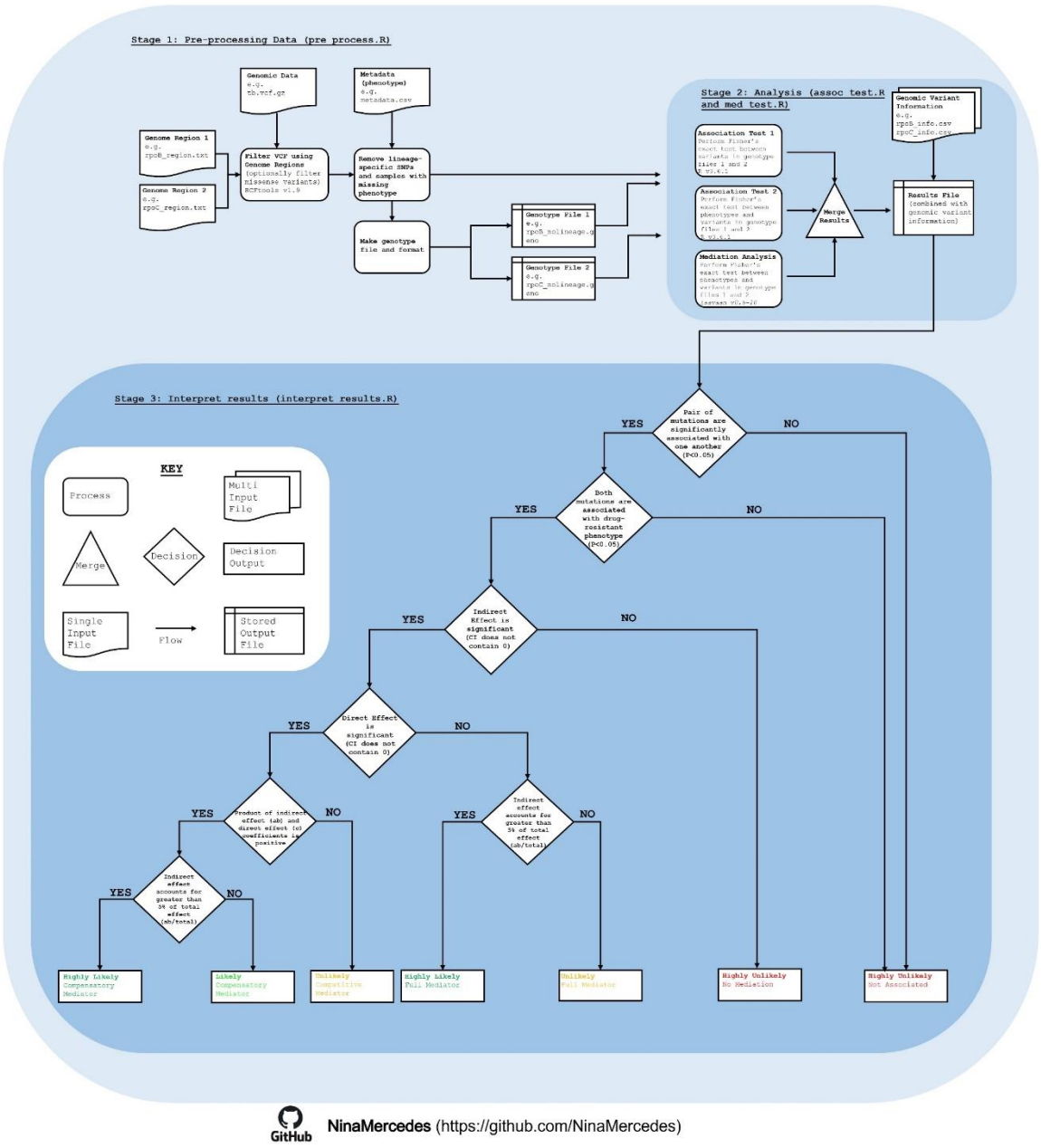
Supplementary Figures



Supplementary Figure S1. Principal Component Analysis of the global *M. tuberculosis* dataset. Principal components (PC) 1-5 are plotted for 18,396 isolates in the dataset and are colour coded by lineage. PCA was carried out using PLINK (v1.90) software.



Supplementary Figure S2. Co-occurring putative compensatory mutations in MDR isolates. MDR isolates with more than one putative compensatory mutation are shown alongside their respective mutations. The lineage of each sample is also shown.



Supplementary Figure S3. Overview of systematic framework to identify compensatory mutations.
Flow diagram summarises three stages of analysis and the key is shown.