Majority of the genomics resources in the public domain employ pre-existing annotation for comparative genomics analyses. However, due to the lack standards for genome annotation, there exist inconsistencies, which get propagated during comparative genomics studies leading to erroneous inferences. The present study is an effort to overcome the problem of varying annotation strategies by employing a uniform protocol of reannotation for the genomes of *Mycobacterium bovis* AF2122/97 (MB) and two strains of *Mycobacterium tuberculosis*, H37Rv (MTH) and CDC1551 (MTC). The reannotation procedure involves gene prediction using Glimmer and identification of orthologs amongst the three genomes along with their simultaneous functional annotation by search against non-redundant protein sequence database as well as 12-signature databases followed by manual curation. The re-annotation strategy resulted in the identification of 4102, 4098, 4040 putative ORFs of which 293, 275, 300 are novel ORFs in MTH, MTC and MB respectively. The above procedure helped in removing discrepancies in original annotation, for instance, in the original annotation of MTC, gene NirD, is absent. This study reveals that NirD gene is present in all the three genomes and shares 100% identity. Similarly, re-annotation revealed that all the three genomes contain six genes encoding CopG family DNA-binding protein, but two of them are missing in the original annotation of MTH and MB. Further comparative genome analyses revealed that 3573 genes across the three genomes are of identical length, of which 2175 genes have 100% sequence identity. 13% of the genes account for genomic variations, which involve polymorphism due to RD (Region of difference), PE and PPE family genes, insertion (IS) elements, inframe indels and frameshift/non-sense/mis-sense mutations, which may represent experimental artifacts like sequencing errors.