Next-Generation Anchor Based Phylogeny (NexABP): Constructing phylogeny from Next-generation sequencing data

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Supplementary Figures:

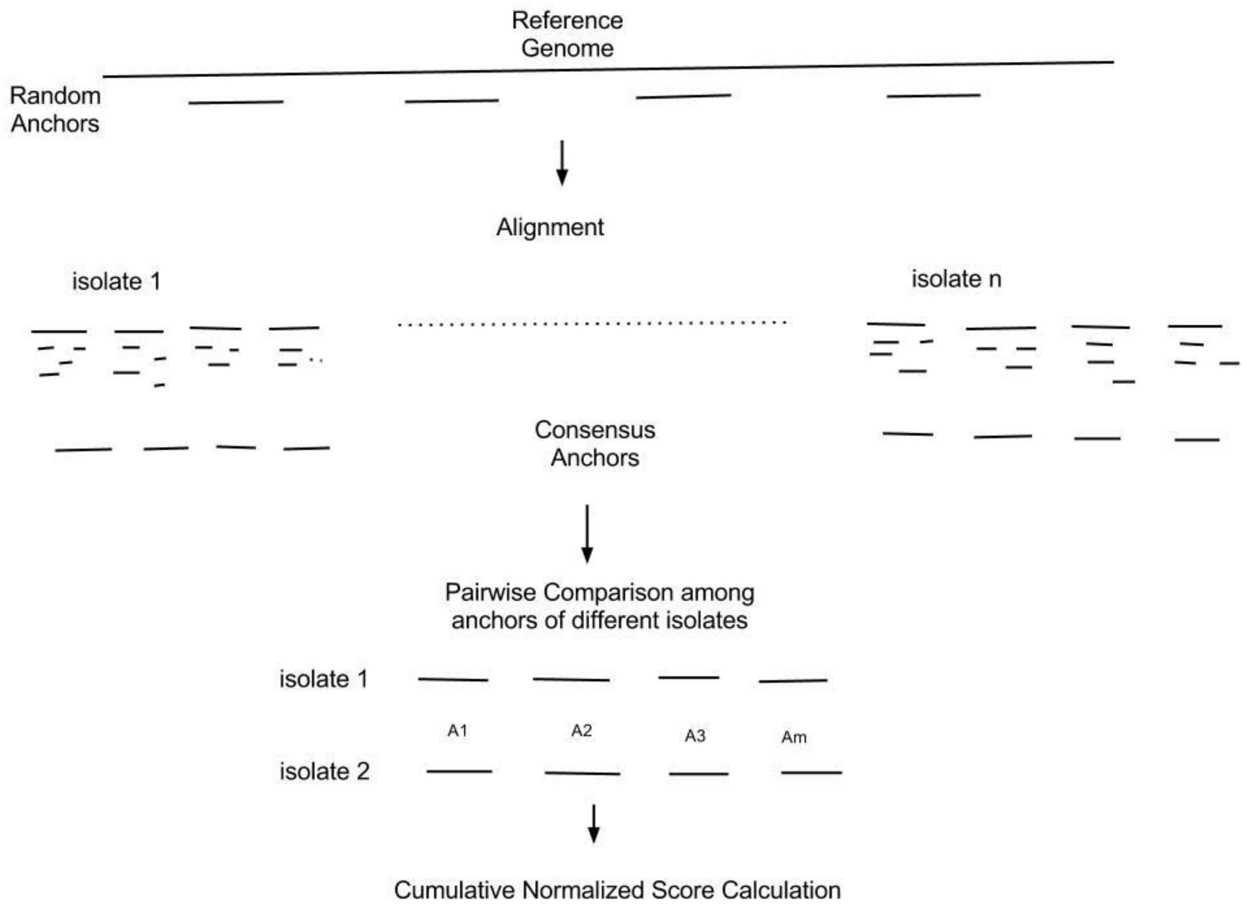

Figure S1: A pictorial representation of CNS calculation by NexABP.

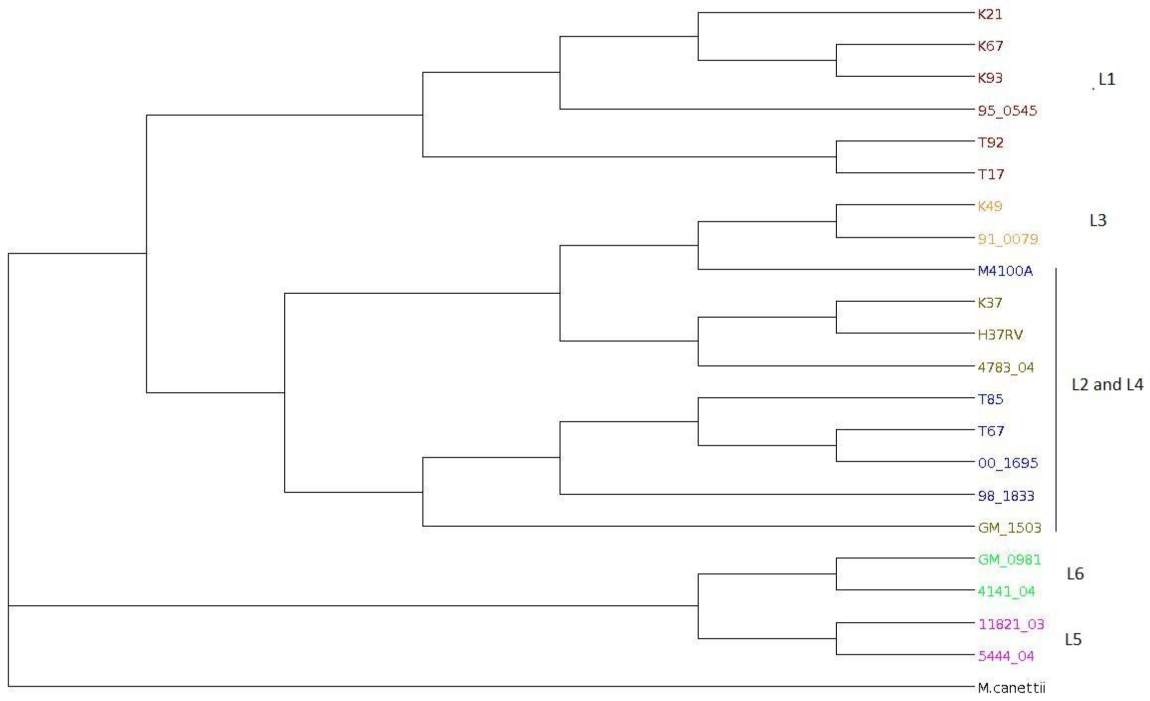

Figure S2: NexABP generated phylogenetic tree of *Mycobacterium tuberculosis* isolates. Six major lineages are represented by different colors. *Mycobacterium bovis* genome was used to pick random anchors.

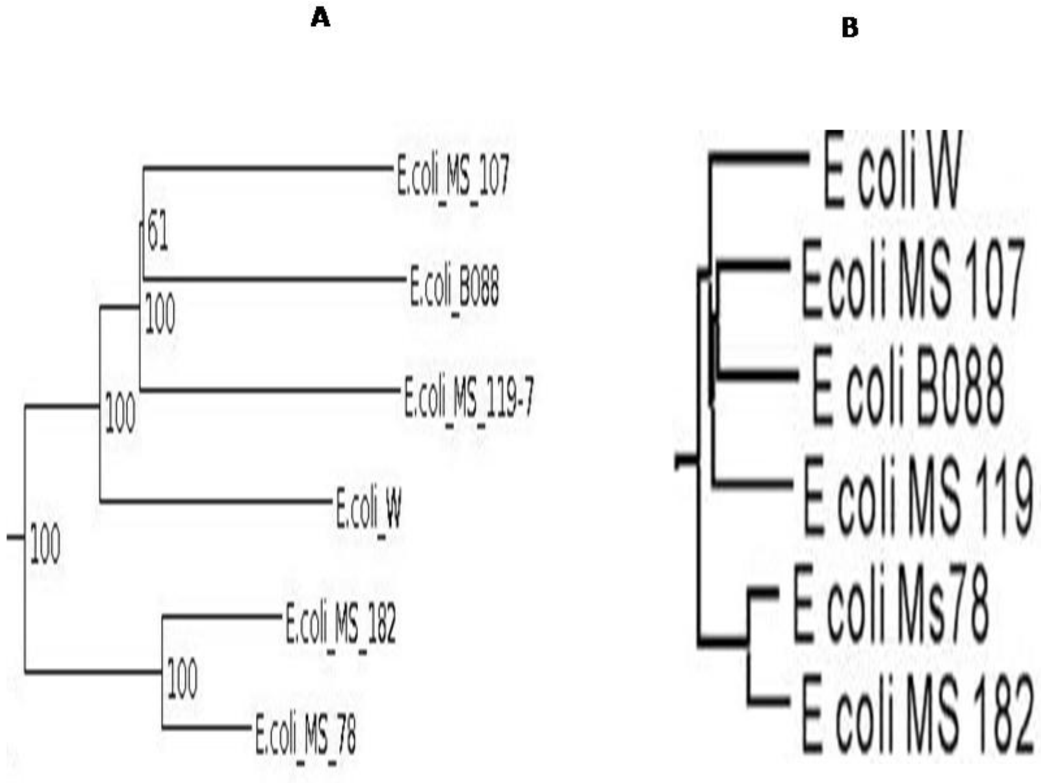

Figure S3: A screenshot from (A) NexABP and (B) Co-phylog generated phylogenetic tree of *E.coli*. Lengths of internal branches are much less in Co-phylog generated tree.

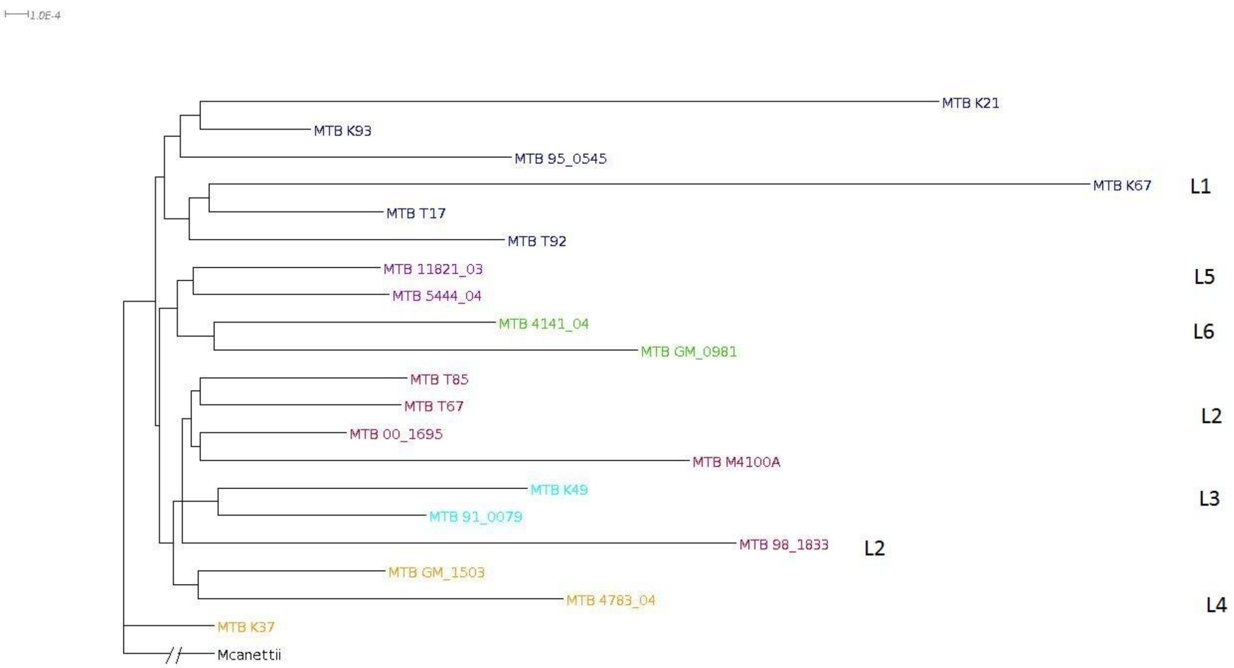

Figure S4: CO-phylog generated phylogenetic tree of *Mycobacterium tuberculosis* isolates. Six major lineages are represented by different colors.

Supplementary Tables:

Table S1: Tree topology test. The approximately unbiased (AU) test, bootstrap probability (BP), Unweighted and weighted (W) Kishino-Hasegawa (KH) and Shimodaira-Hasegawa (SH) tests were performed.

Tree 1: Tree generated by NexABP
Tree 2: Tree generated by Comas et.al.

Item	Obs	Au	Np	Bp	Pp	Kh	Sh	Wkh	wsh
Tree 1	-60.1	0.92	0.923	0.917	1.00	0.922	0.922	0.922	0.922
Tree 2	60.1	0.08	0.077	0.083	8e-27	0.078	0.078	0.078	0.078