

Supplementary Fig. S1

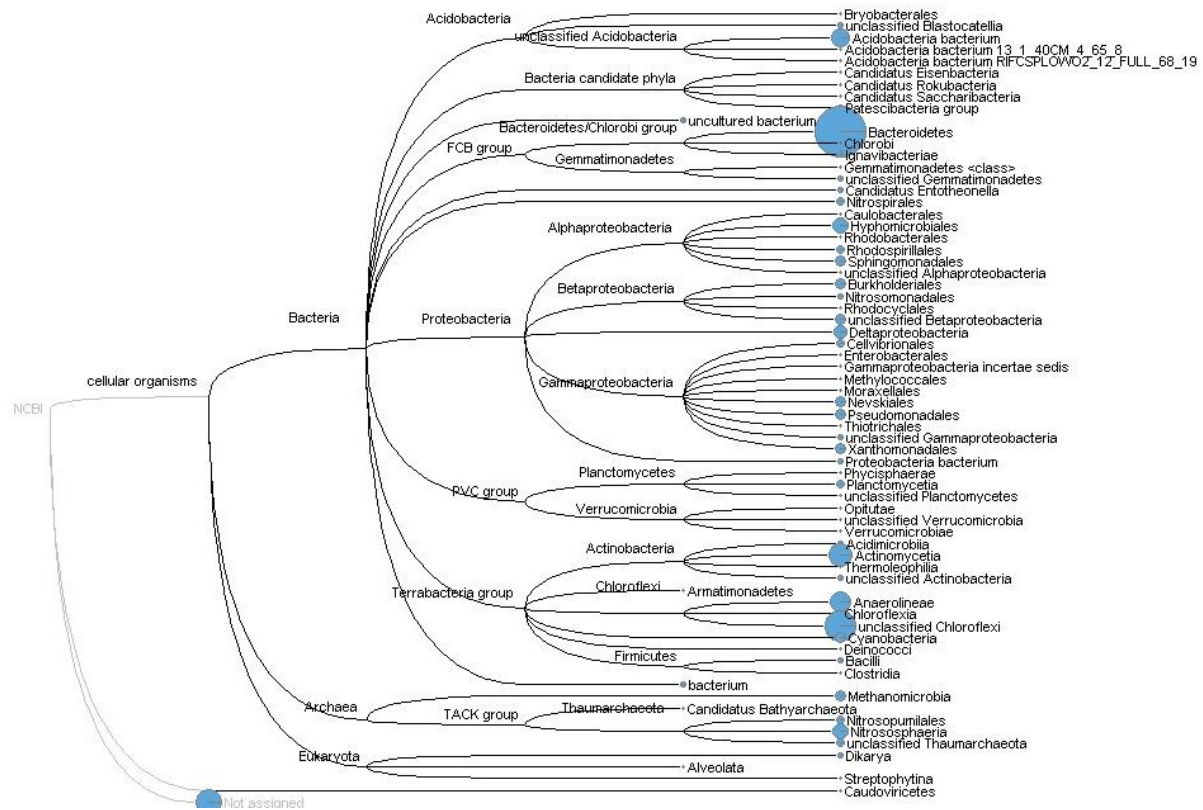


Figure S1. The operational taxonomic units identified after metagenomics analysis. The phyloge-237 netic tree of major microbial groups (OTUs) identified by metagenomic analysis after *Jeevamrit* ap-238 plication in the ZBNF field.

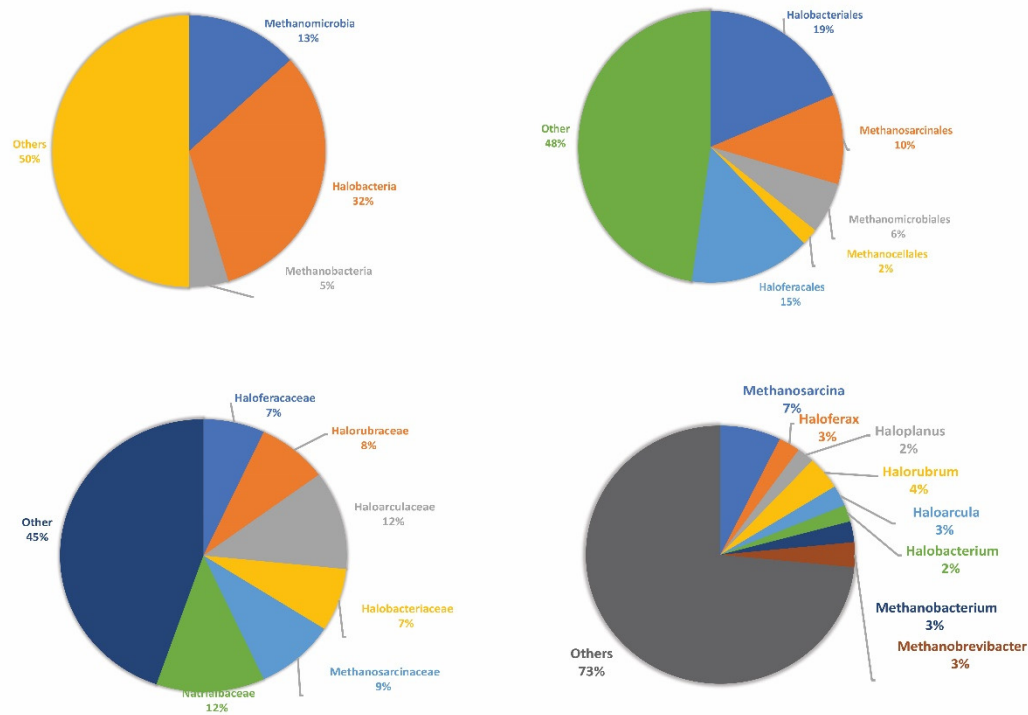


Figure S2. Abundance of various Archaea phyla, order, group, genus, and family present in ZBNF soil. Halobacteria, Methanomicrobia, Methanobacteria, Methanocarsina were the major phylum, order, group, genus and family in the ZBNF soil.

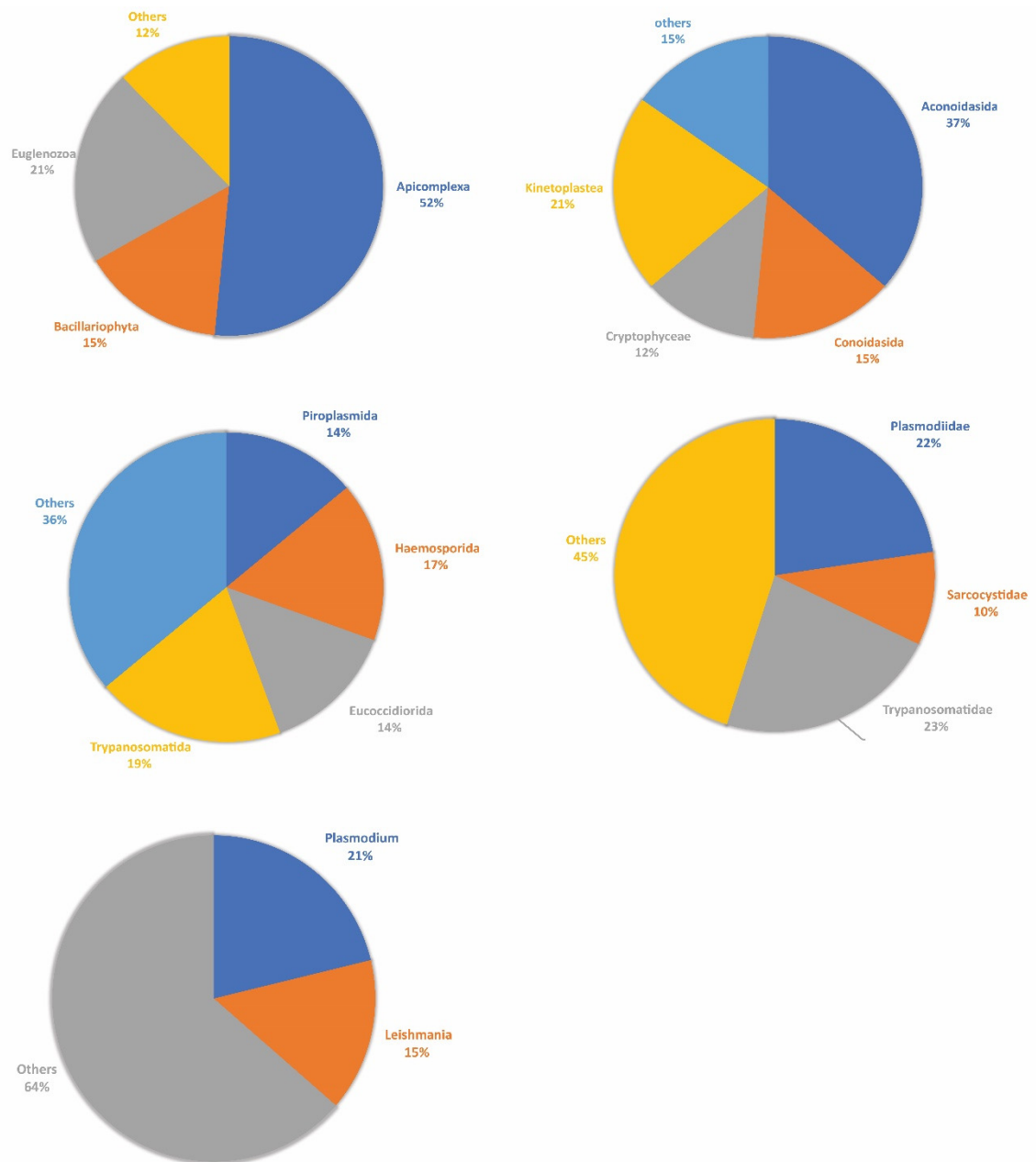


Figure S3. Abundance of various Plasmodium phyla, order, group, genus and family present in ZBNF soil. Apicomplexa, Aconoidasida, Trypanosomatida, Trypanosomatidae, Plasmodium was the major phylum, class, order, family, genus, and species respectively.

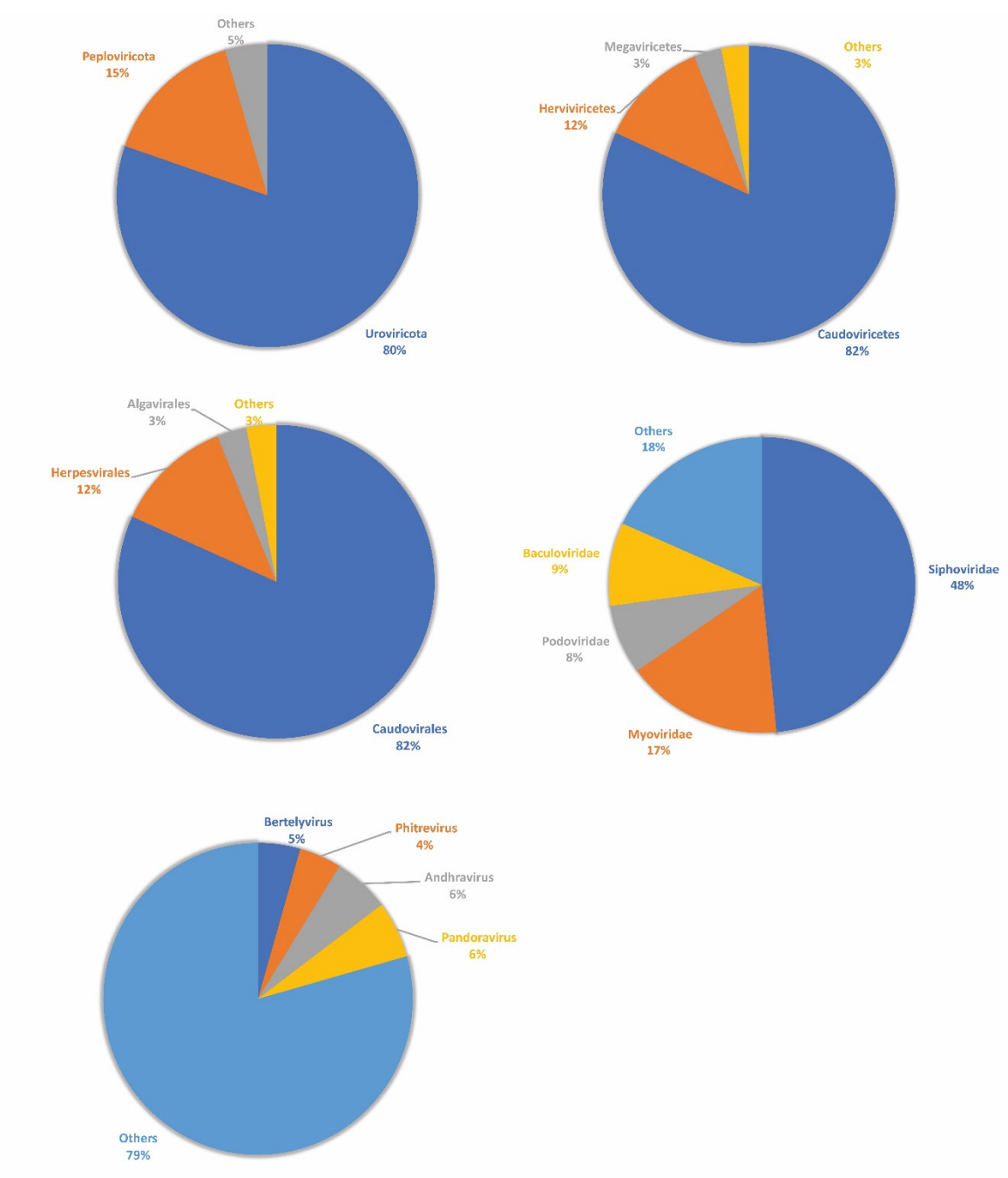


Figure S4. Abundance of various viral phyla, order, group, genus and family present in ZBNF soil. Uroviricota, Caudoviricetes, Caudovirales, Siphoviridae, Andhravirus and Pandoravirus respectively.

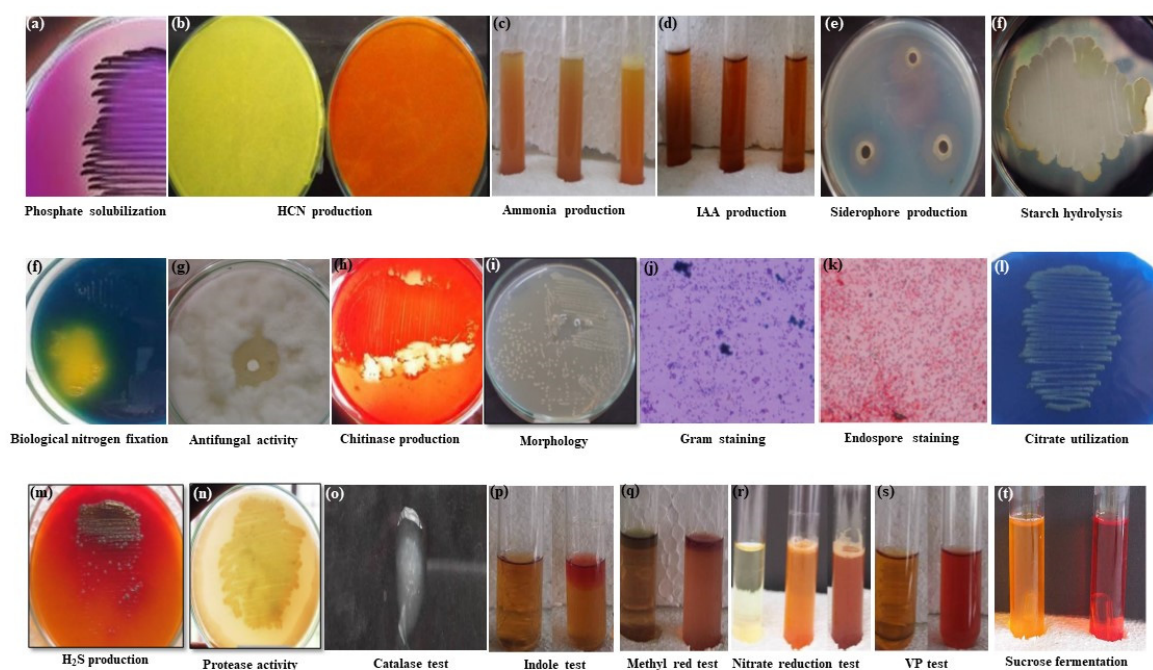


Figure S5. Plant growth promoting activities reported in the different bacteria and fungi isolated from ZBNF soil.

Supplementary Tables

Supplementary Table S1. The statistical information of the reads received after metagenomic analysis. Raw reads were filtered from for low quality and adapter sequences

Attributes	Before filtering	After filtering
total reads:	12.426664 M	12.012484 M
total bases:	1.876426 G	1.751104 G
Q20 bases:	1.812328 G	1.712364 G
Q30 bases:	1.732979 G	1.646039 G
GC content:	62.42%	63.01%
Reads passed filters:	96.667006%	
Reads with low quality:	3.146556%	
Reads with too many N:	0.030805%	
Reads too short:	0.155633%	