Supplementary figure 1. Phylogenetic analysis of 16S rRNA genes from all species of the genus Treponema presently recognised along with isolate RCC2812T using Neighbour-joining method : the evolutionary history was inferred using the Neighbour-Joining method(36). The optimal tree with the sum of branch length = 1.73380729 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches(37). The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Jukes-Cantor method(38) and are in the units of the number of base substitutions per site. The rate variation among sites was modelled with a gamma distribution (shape parameter = 1). The analysis involved 30 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 1242 positions in the final dataset. Evolutionary analyses were conducted in MEGA7(39).