Fig. S1. Comparative analyses of total bacterial community (A to C) and Mycobacteria (D to F) in oral and upper respiratory tract per subject. Richness (A), evenness (B), and Shannon diversity (C) indices of total bacterial community per subjects. Richness (D), evenness (E), and Shannon diversity (F) indices of Mycobacterial-specific community where based on total number of positive PCR products: For subjects 1, 2, 5 and 6 (n=3); subjects 3, 4 and 8 (n=4); subjects 7, 9, and 10 (n=2) (see Fig. 1G). Shown P-value was calculated using Kruskal-Wallis test.
**Fig. S2. Correlations between Actinobacteria and Firmicutes phyla from libraries sequenced with universal primers.** A) Stacked bar plots show relative abundance of main families in nostrils; B) Linear regression between the relative prevalence (percentages of the total community) in nostrils of members of the phylum Firmicutes and Actinobacteria, where dashed lines indicate 95% confidence.