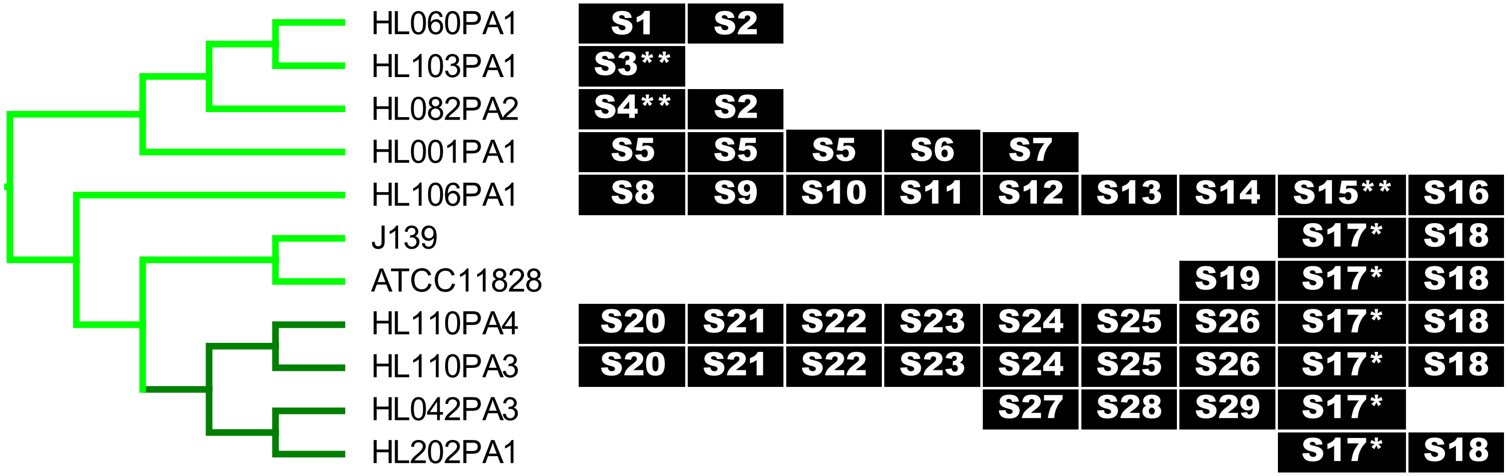

* CRISPR spacers that match to the sequence in locus 2, which is highly homologous to the sequence in *Clostridium leptum.*

** CRISPR spacers that match to the sequence in locus 3, which is highly homologous to the sequence in *Clostridium leptum.*

Figure S4. CRISPR spacer sequences in RT2 and RT6 strains. A total of 48 CRISPR spacer sequences were found in 11 *P. acnes* genomes, 29 of which were unique. Some CRISPR spacers were found in multiple strains. For example, spacer 2 (S2) was shared by HL060PA1 and HL082PA2. Spacer 17 (S17) was shared by J139, ATCC11828, HL110PA3, HL110PA4, HL042PA3 and HL202PA1. Spacer 18 (S18) was shared by J139, ATCC11828, HL110PA3, HL110PA4, and HL202PA1. The tree was from Figure 2 constructed based on the 123,223 SNPs in the core regions.