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Supplementary Materials for:

Proposal to reclassify *Propionibacterium acnes* type I as *Propionibacterium acnes* subsp. *acnes* subsp. nov. and *Propionibacterium acnes* type II as *Propionibacterium acnes* subsp. *defendens* subsp. nov.

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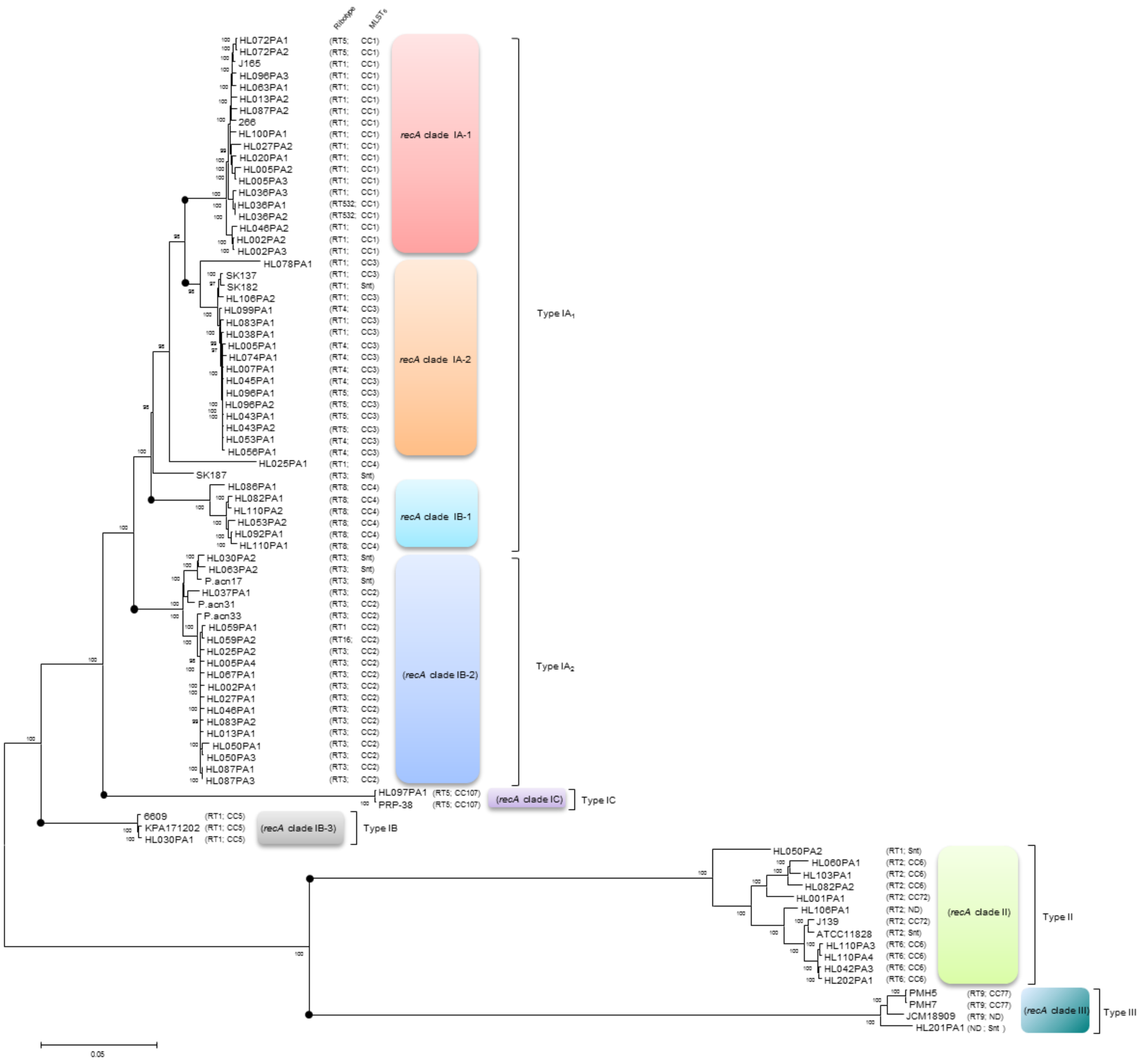
Ribotype
MLST₈
HL072PA1 (RT5; CC1)
HL072PA2 (RT5; CC1)
J165 (RT1; CC1)
HL096PA3 (RT1; CC1)
HL063PA1 (RT1; CC1)
HL013PA2 (RT1; CC1)
HL087PA2 (RT1; CC1)
266 (RT1; CC1)
HL100PA1 (RT1; CC1)
HL027PA2 (RT1; CC1)
HL020PA1 (RT1; CC1)
HL005PA2 (RT1; CC1)
HL005PA3 (RT1; CC1)
HL036PA3 (RT1; CC1)
HL036PA1 (RT532; CC1)
HL036PA2 (RT532; CC1)
HL046PA2 (RT1; CC1)
HL002PA2 (RT1; CC1)
HL002PA3 (RT1; CC1)
recA clade IA-1
HL078PA1 (RT1; CC3)
SK137 (RT1; CC3)
SK182 (RT1; Snt)
HL106PA2 (RT1; CC3)
HL099PA1 (RT4; CC3)
HL083PA1 (RT1; CC3)
HL038PA1 (RT1; CC3)
HL005PA1 (RT4; CC3)
HL074PA1 (RT4; CC3)
HL007PA1 (RT4; CC3)
HL045PA1 (RT4; CC3)
HL096PA1 (RT5; CC3)
HL096PA2 (RT5; CC3)
HL043PA1 (RT5; CC3)
HL043PA2 (RT5; CC3)
HL053PA1 (RT4; CC3)
HL056PA1 (RT4; CC3)
recA clade IA-2
HL025PA1 (RT1; CC4)
SK187 (RT3; Snt)
HL086PA1 (RT8; CC4)
HL082PA1 (RT8; CC4)
HL110PA2 (RT8; CC4)
HL053PA2 (RT8; CC4)
HL092PA1 (RT8; CC4)
HL110PA1 (RT8; CC4)
recA clade IB-1
Type IA₁
HL030PA2 (RT3; Snt)
HL063PA2 (RT3; Snt)
P.acn17 (RT3; Snt)
HL037PA1 (RT3; CC2)
P.acn31 (RT3; CC2)
P.acn33 (RT3; CC2)
HL059PA1 (RT1 CC2)
HL059PA2 (RT16; CC2)
HL025PA2 (RT3; CC2)
HL005PA4 (RT3; CC2)
HL067PA1 (RT3; CC2)
HL002PA1 (RT3; CC2)
HL027PA1 (RT3; CC2)
HL046PA1 (RT3; CC2)
HL083PA2 (RT3; CC2)
HL013PA1 (RT3; CC2)
HL050PA1 (RT3; CC2)
HL050PA3 (RT3; CC2)
HL087PA1 (RT3; CC2)
HL087PA3 (RT3; CC2)
(recA clade IB-2)
Type IA₂
HL097PA1 (RT5; CC107)
PRP-38 (RT5; CC107)
(recA clade IC)
Type IC
6609 (RT1; CC5)
KPA171202 (RT1; CC5)
HL030PA1 (RT1; CC5)
(recA clade IB-3)
Type IB
HL050PA2 (RT1; Snt)
HL060PA1 (RT2; CC6)
HL103PA1 (RT2; CC6)
HL082PA2 (RT2; CC6)
HL001PA1 (RT2; CC72)
HL106PA1 (RT2; ND)
J139 (RT2; CC72)
ATCC11828 (RT2; Snt)
HL110PA3 (RT6; CC6)
HL110PA4 (RT6; CC6)
HL042PA3 (RT6; CC6)
HL202PA1 (RT6; CC6)
(recA clade II)
Type II
PMH5 (RT9; CC77)
PMH7 (RT9; CC77)
JCM18909 (RT9; ND)
HL201PA1 (ND ; Snt)
(recA clade III)
Type III
0.05

Fig S1. Whole genome neighbour-joining phylogenetic tree (MEGA v5.0) based on the p-distances between each of 85 concatenated SNP sequences. Briefly, core regions were calculated by mapping 84 genome sequences against the reference genome KPA171202 using Nucmer [Kurtz et al. (2004). Versatile and open software for comparing large genomes. *Genome Biol* **5**: R12). Regions of KPA171202 that aligned with all 84 genomes were identified within the 84 ".coords" output files, and the corresponding aligned regions in all 85 genomes were extracted. A total of 124,731 SNPs relative to KPA171202 were identified and concatenated into a single sequence for analysis. The bootstrap tree was inferred from 200 replicates. Bootstrap values (≥70%) are shown on the arms of the tree. Horizontal bar represents genetic distance. Snt = singleton; CC = clonal complex (MLST$_8$ analysis).

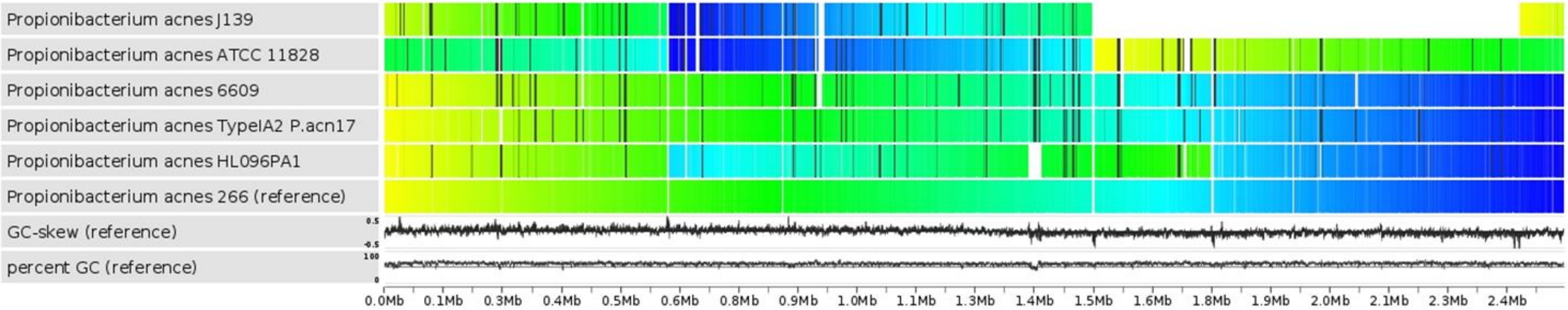

Fig S2. Visualisation of synteny between representative type I and type II genomes using the new *P. acnes* Sybil database. Type II specific inversions within the strains ATCC11828 (ST27) and J139 (ST28) can be clearly seen versus type I strains 266 (IA$_1$; ST20), P.acn17 (IA$_{2;}$ ST22) and 6609 (IB; ST5). Note: the type IA$_1$ strain HL096PA1 (ST3) has a distinct verified inversion while those in the type II strains remained to be confirmed. Strain J139 is currently not closed and is represented by a large contig which results in a white section in the alignment [Scholz et al. (2016). Genome stability of *Propionibacterium acnes*: a comprehensive study of indels and homopolymeric tracts. *Sci Rep,* **6,** 20662]. ST designations relate to MLST$_8$ analysis (http://pubmlst.org/pacnes/).