TABLE S1. Propionibacteria consumed glucose and produced several products during fermentation.

	Strain[1]				
Product[2]	*C. gran.*	*C. acnes*	*A. acid.*	*P. freud.*	SEM[3]
			mmol/L media		
Glucose	-6.75	-9.04	-9.03	-6.18	0.34
Formate	-0.25	-0.18	-0.18	-0.18	0.01
Acetate	4.38	2.77	3.53	4.25	0.07
Propionate	9.29	6.99	10.03	7.37	0.15
Butyrate	-0.02	0.00	-0.03	-0.02	0.02
Isobutyrate	0.58	0.44	0.63	0.77	0.06
Isovalerate	0.00	0.03	-0.02	-0.01	0.02
D-Lactate	-0.48	-0.20	-0.69	-0.74	0.01
L-Lactate	-1.03	-0.38	-0.98	-1.03	0.03
Succinate	2.37	1.00	0.56	2.76	0.06

[1] Abbreviations: *A. acid.*, *Acidipropionibacterium acidipropionici*; *C. acnes*, *Cutibacterium acnes*; *C. gran.*, *Cutibacterium granulosum*; and *P. freud*, *Propionibacterium freudenreichii*.

[2] Products with negative values were consumed from the media

[3] Standard error of the mean

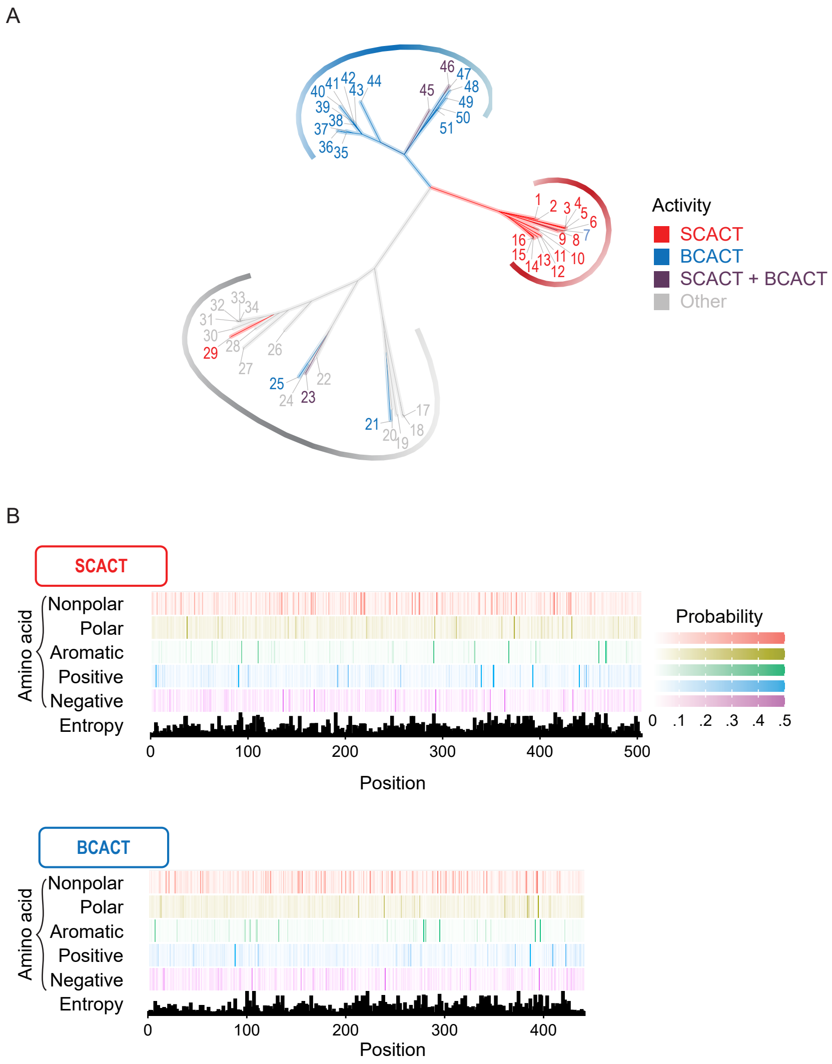

Fig. S1. ***See legend on next page***

Fig. S1. A large number of proteins was used to build and test profile hidden Markov models (pHMMs) for SCACT. **A.** Phylogenetic tree of protein sequences, highlighted by their activity. **B.** pHMMs for SCACT and BCACT. Protein sequences are 1. *Clostridium kluyveri*, 2. *Acinetobacter baumannii*, 3. *Trichomonas vaginalis*, 4. *Saccharomyces cerevisiae*, 5. *Aspergillus nidulans*, 6. *Escherichia coli* (homolog 1), 7. *Porphyromonas gingivalis* (homolog 3), 8. *Bacteroides fragilis*, 9. *Moraxella catarrhalis*, 10. *Snodgrassella alvi*, 11. *Acetobacter aceti*, 12. *Acetobacter cerevisiae*, 13. *Corynebacterium diphtheriae*, 14. *Propionibacterium freudenreichii*, 15. *Cutibacterium granulosum*, 16. *Acidipropionibacterium acidipropionici*, 17. *Mycobacterium tuberculosis*, 18. *Rhodococcus jostii*, 19. *Myxococcus xanthus*, 20. *Pseudomonas knackmussii*, 21. *Acidaminococcus fermentans*, 22. *Acetobacterium woodii*, 23. *Ralstonia eutropha*, 24. *Clostridium propionicum*, 25. *Escherichia coli* (homolog 2), 26. *Clostridium acetobutylicum*, 27. *Pseudomonas putida*, 28. *Helicobacter pylori*, 29. *Trypanosoma brucei* (homolog 1), 30. *Drosophila melanogaster*, 31. *Homo sapiens*, 32. *Sus scrofa*, 33. *Mus musculus*, 34. *Rattus norvegicus*, 35. *Anaerostipes* sp. 494a, 36. *Anaerostipes caccae* (homolog 1), 37. *Anaerostipes* sp. 992a, 38. *Butyricicoccus* sp. BB10, 39. *Intesimonas butyriciproducens*, 40. *Peptoniphilus* sp. 35-6-1, 41. *Roseburia hominis*, 42. *Roseburia* sp. 831b, 43. *Roseburia* sp. 499, 44. *Megasphaera elsdenii*, 45. *Yersinia pestis*, 46. *Fasciola hepatica*, 47. *Artemia franciscana*, 48. *Porphyromonas gingivalis* (homolog 2), 49. *Clostridium aminobutyricum*, 50. *Anaerostipes caccae* (homolog 2), 51. *Porphyromonas gingivalis* (homolog 1). Full information on proteins is in Dataset S2. For SCACT, HMMs were built using sequences of enzymes 1-6 and 8-16. For BCACT, they were build using sequences of enzymes 35-51. Amino acids were grouped as non-polar (G, A, P, V, L, I, M), polar (S, T, C, N, Q), aromatic (F, Y, W), positive (K, H, R), or negative (D, E). Entropy refers to bits of information. Abbreviations: BCACT, butyryl-CoA:acetate CoA-transferase; and SCACT, succinyl-CoA:acetate CoA-transferase.

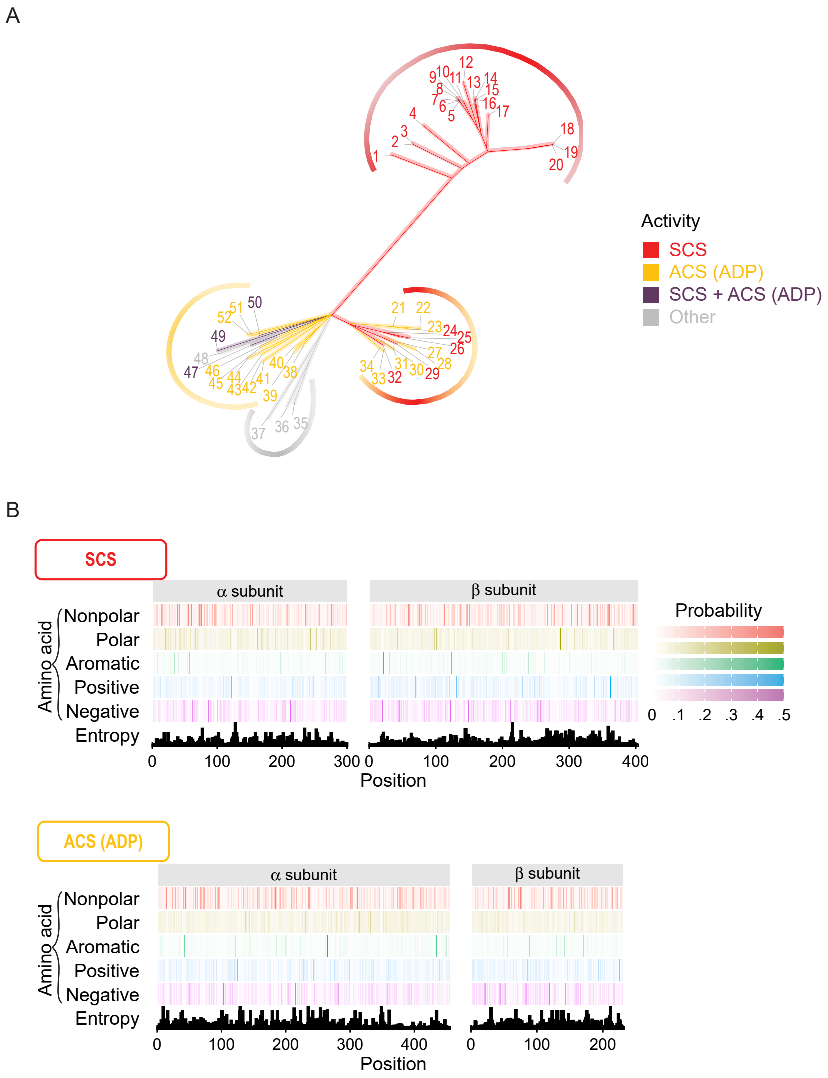

Fig. S2. ***See legend on next page***

Fig. S2. A large number of proteins was used to build and test profile hidden Markov models (pHMMs) for SCS. As Fig. S1, except sequences are for proteins with SCS activity and their homologs. Protein sequences are 1. *Korarchaeum cryptofilum* (homolog 4), 2. *Thermus aquaticus*, 3. *Thermus thermophilus*, 4. *Cutibacterium granulosum*, 5. *Sus scrofa* (homolog 2), 6. *Columba livia* (homolog 1), 7. *Sus scrofa* (homolog 1), 8. *Homo sapiens* (homolog 2), 9. *Columba livia* (homolog 2), 10. *Mus musculus*, 11. *Homo sapiens* (homolog 1), 12. *Saccharomyces cerevisiae*, 13. *Solanum lycopersicum* (homolog 1), 14. *Solanum lycopersicum* (homolog 2), 15. *Blastocystis* sp., 16. *Toxoplasma gondii*, 17. *Advenella mimigardefordensis*, 18. *Pseudomonas aeruginosa*, 19. *Escherichia coli*, 20. *Alcanivorax borkumensis*, 21. *Pyrococcus furiosus* (homolog 4), 22. *Pyrococcus furiosus* (homolog 3), 23. *Thermococcus kodakarensis* (homolog 2), 24. *Pyrococcus furiosus* (homolog 6), 25. *Thermococcus kodakarensis* (homolog 1), 26. *Pyrococcus furiosus* (homolog 5), 27. *Pyrococcus furiosus* (homolog 8), 28. *Pyrococcus furiosus* (homolog 7), 29. *Thermococcus kodakarensis* (homolog 4), 30. *Pyrococcus furiosus* (homolog 10), 31. *Pyrococcus furiosus* (homolog 9), 32. *Thermococcus kodakarensis* (homolog 3), 33. *Pyrococcus furiosus* (homolog 1), 34. *Pyrococcus furiosus* (homolog 2), 35. *Ralstonia eutropha* (homolog 2), 36. *Ralstonia eutropha* (homolog 1), 37. *Delftia acidovorans*, 38. *Korarchaeum cryptofilum* (homolog 3), 39. *Korarchaeum cryptofilum* (homolog 1), 40. *Korarchaeum cryptofilum* (homolog 2), 41. *Entamoeba histolytica* (homolog 1), 42. *Entamoeba histolytica* (homolog 2), 43. *Pyrobaculum aerophilum*, 44. *Methanosarcina mazei*, 45. *Haloarcula marismortui*, 46. *Chloroflexus aurantiacus*, 47. *Giardia lamblia*, 48. *Nitrosopumilus maritimus* (homolog 1), 49. *Archaeoglobus fulgidus* (homolog 2), 50. *Archaeoglobus fulgidus* (homolog 1), 51. *Methanocaldococcus jannaschii*, and 52. *Nitrosopumilus maritimus* (homolog 2). Full information on proteins is in Dataset S3. For SCS, pHMMs were built using sequences of enzymes 1-20, 24-26, 29, and 32. For ACS, they were built using sequences of enzymes 21-23, 27-28, 30-31, 33-34, 38-47, and 49-52. Abbreviations: ACS (ADP), acetyl-CoA synthetase (ADP-forming); and SCS, succinyl-CoA synthetase (ADP-forming).