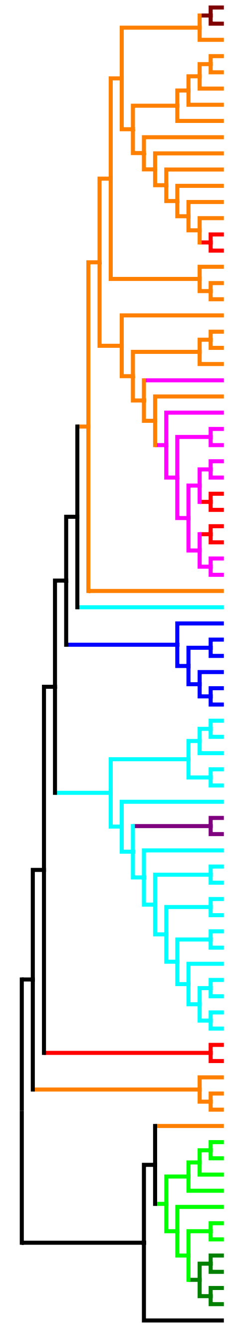
Table S1. Sequence types of the 82 *P. acnes* strains based on two MLST schemes.

Phylogenetic tree	Genome	RT	*RecA* type	Clade	eMLST by McDowell[13]											MLST by Lomholt[11]											
					Type	Clonal complexes (CC)	Sequence type	*aroE*	*atpD*	*gmk*	*guaA*	*lepA*	*sodA*	*tly*	*camp2*	Type	Clonal clusters (CC)	Sequence type	*cel*	*coa*	*fba*	*gms*	*lac*	*oxc*	*pak*	*recA*	*zno*
	HL036PA1	532	IA	IA-1	IA1	CC1	1	1	1	1	3	1	1	1	1	I-1a	CC18	8	5	9	2	8	4	3	3	5	5
	HL036PA2	532	IA	IA-1	IA1	CC1	1	1	1	1	3	1	1	1	1	I-1a	CC18	8	5	9	2	8	4	3	3	5	5
	HL036PA3	1	IA	IA-1	IA1	CC1	1	1	1	1	3	1	1	1	1	I-1a	CC18	8	5	9	2	8	4	3	3	5	5
	HL005PA3	1	IA	IA-1	IA1	CC1	16	1	1	10	3	1	1	1	1	I-1a	CC18	12	5	5	2	8	4	3	3	5	6
	HL005PA2	1	IA	IA-1	IA1	CC1	15	1	1	10	3	1	1	6	1	I-1a	CC18	12	5	5	2	8	4	3	3	5	6
	HL020PA1	1	IA	IA-1	IA1	CC1	9	1	1	1	3	1	1	4	1	I-1a	CC18	77	5	18	2	8	4	3	3	5	6
	HL027PA2	1	IA	IA-1	IA1	CC1	1	1	1	1	3	1	1	1	1	I-1a	CC18	12	5	5	2	8	4	3	3	5	6
	HL100PA1	1	IA	IA-1	IA1	CC1	1	1	1	1	3	1	1	1	1	I-1a	CC18	18	5	9	2	8	4	3	3	5	6
	266	1	IA	IA-1	IA1	CC1	20	5	1	1	3	1	1	1	1	I-1a	CC18	18	5	9	2	8	4	3	3	5	6
	HL013PA2	1	IA	IA-1	IA1	CC1	1	1	1	1	3	1	1	1	1	I-1a	CC18	18	5	9	2	8	4	3	3	5	6
	HL087PA2	1	IA	IA-1	IA1	CC1	1	1	1	1	3	1	1	1	1	I-1a	CC18	18	5	9	2	8	4	3	3	5	6
	HL063PA1	1	IA	IA-1	IA1	CC1	1	1	1	1	3	1	1	1	1	I-1a	CC18	18	5	9	2	8	4	3	3	5	6
	HL096PA3	1	IA	IA-1	IA1	CC1	8	1	1	1	3	1	1	3	1	I-1a	CC18	18	5	9	2	8	4	3	3	5	6
	J165	1	IA	IA-1	IA1	CC1	1	1	1	1	3	1	1	1	1	I-1a	CC18	18	5	9	2	8	4	3	3	5	6
	HL072PA2	5	IA	IA-1	IA1	CC1	1	1	1	1	3	1	1	1	1	I-1a	CC18	18	5	9	2	8	4	3	3	5	6
	HL072PA1	5	IA	IA-1	IA1	CC1	1	1	1	1	3	1	1	1	1	I-1a	CC18	18	5	9	2	8	4	3	3	5	6
	HL046PA2	1	IA	IA-1	IA1	CC1	1	1	1	1	3	1	1	1	1	I-1a	CC18	59	5	9	2	8	9	3	3	5	6
	HL002PA2	1	IA	IA-1	IA1	CC1	1	1	1	1	3	1	1	1	1	I-1a	CC18	59	5	9	2	8	9	3	3	5	6
	HL002PA3	1	IA	IA-1	IA1	CC1	1	1	1	1	3	1	1	1	1	I-1a	CC18	59	5	9	2	8	9	3	3	5	6
	HL078PA1	1	IA	NA	IA1	CC3	14	1	1	1	3	1	14	2	3	NA	Singleton	63	8	4	5	8	11	8	3	5	11
	SK137	1	IA	IA-2	IA1	CC3	18	8	1	1	3	1	1	2	5	I-1a	CC3	3	5	9	4	8	5	3	3	5	11
	SK182	1	IA	IA-2	IA1	CC3	29	1	13	1	3	1	1	2	5	I-1a	CC3	3	5	9	4	8	5	3	3	5	11
	HL106PA2	1	IA	IA-2	IA1	CC3	3	1	1	1	3	1	1	2	2	I-1a	CC3	3	5	9	4	8	5	3	3	5	11
	HL099PA1	4	IA	IA-2	IA1	CC3	3	1	1	1	3	1	1	2	2	I-1a	CC3	3	5	9	4	8	5	3	3	5	11
	HL083PA1	1	IA	IA-2	IA1	CC3	3	1	1	1	3	1	1	2	2	I-1a	CC3	3	5	9	4	8	5	3	3	5	11
	HL038PA1	4	IA	IA-2	IA1	CC3	10	1	1	1	3	1	1	2	4	I-1a	CC3	3	5	9	4	8	5	3	3	5	11
	HL005PA1	4	IA	IA-2	IA1	CC3	11	1	1	1	3	1	1	5	2	I-1a	CC3	3	5	9	4	8	5	3	3	5	11
	HL074PA1	4	IA	IA-2	IA1	CC3	3	1	1	1	3	1	1	2	2	I-1a	CC3	3	5	9	4	8	5	3	3	5	11
	HL007PA1	4	IA	IA-2	IA1	CC3	3	1	1	1	3	1	1	2	2	I-1a	CC3	3	5	9	4	8	5	3	3	5	11
	HL045PA1	4	IA	IA-2	IA1	CC3	17	1	10	1	3	1	1	2	2	I-1a	CC3	3	5	9	4	8	5	3	3	5	11
	HL096PA1	5	IA	IA-2	IA1	CC3	3	1	1	1	3	1	1	2	2	I-1a	CC3	3	5	9	4	8	5	3	3	5	11
	HL096PA2	5	IA	IA-2	IA1	CC3	3	1	1	1	3	1	1	2	2	I-1a	CC3	3	5	9	4	8	5	3	3	5	11
	HL043PA1	5	IA	IA-2	IA1	CC3	3	1	1	1	3	1	1	2	2	I-1a	CC3	58	10	9	4	8	5	3	3	5	11
	HL043PA2	5	IA	IA-2	IA1	CC3	3	1	1	1	3	1	1	2	2	I-1a	CC3	58	10	9	4	8	5	3	3	5	11
	HL053PA1	4	IA	IA-2	IA1	CC3	3	1	1	1	3	1	1	2	2	I-1a	CC3	3	5	9	4	8	5	3	3	5	11
	HL056PA1	4	IA	IA-2	IA1	CC3	3	1	1	1	3	1	1	2	2	I-1a	CC3	3	5	9	4	8	5	3	3	5	11
	HL025PA1	1	IB	NA	IA1	CC4	4	1	1	1	3	1	1	8	6	I-1a	CC28	27	5	9	4	6	4	3	3	2	11
	SK187	3	IB	NA	NA	Singleton	19	16	1	1	15	1	4	8	6	I-1a	CC28	67	5	9	4	3	4	3	3	2	11
	HL086PA1	8	IB	IB-1	IA1	CC4	4	1	1	1	3	1	1	8	6	I-1b	CC31	31	8	9	5	3	4	3	3	2	7
	HL082PA1	8	IB	IB-1	IA1	CC4	4	1	1	1	3	1	1	8	6	I-1b	CC31	31	8	9	5	3	4	3	3	2	7
	HL110PA2	8	IB	IB-1	IA1	CC4	21	1	1	1	1	1	1	8	6	I-1b	CC31	31	8	9	5	3	4	3	3	2	7
	HL053PA2	8	IB	IB-1	IA1	CC4	4	1	1	1	3	1	1	8	6	I-1b	CC31	31	8	9	5	3	4	3	3	2	7
	HL092PA1	8	IB	IB-1	IA1	CC4	4	1	1	1	3	1	1	8	6	I-1b	CC31	31	8	9	5	3	4	3	3	2	7
	HL110PA1	8	IB	IB-1	IA1	CC4	4	1	1	1	3	1	1	8	6	I-1b	CC31	31	8	9	5	3	4	3	3	2	7
	HL030PA2	3	IB	IB-2	IA2	Singleton	22	1	1	1	5	3	5	8	7	I-1a	CC28	66	9	9	4	3	4	3	3	2	11
	HL063PA2	3	IB	IB-2	IA2	Singleton	23	1	18	1	5	3	5	8	8	I-1a	CC28	70	7	9	4	3	4	3	3	2	11
	P.acn17	3	IB	IB-2	IA2	CC2	22	1	1	1	5	3	5	8	7	I-1a	CC28	70	7	9	4	3	4	3	3	2	11
	HL037PA1	3	IB	IB-2	IA2	CC2	2	1	1	1	5	1	4	8	2	I-1a	CC28	67	5	9	4	3	4	3	3	2	11
	P.acn31	3	IB	IB-2	IA2	CC2	36	1	1	1	13	1	4	8	2	I-1a	CC28	67	5	9	4	3	4	3	3	2	11
	P.acn33	3	IB	IB-2	IA2	CC2	2	1	1	1	5	1	4	8	2	NA	NA	NA	5	8	4	3	4	3	3	NA	11
	HL059PA1	16	IB	IB-2	IA2	CC2	2	1	1	1	5	1	4	8	2	I-1a	CC28	28	5	8	4	3	4	3	3	2	11
	HL059PA2	16	IB	IB-2	IA2	CC2	2	1	1	1	5	1	4	8	2	I-1a	CC28	28	5	8	4	3	4	3	3	2	11
	HL025PA2	3	IB	IB-2	IA2	CC2	2	1	1	1	5	1	4	8	2	I-1a	CC28	65	5	8	4	3	4	3	3	2	16
	HL005PA4	3	IB	IB-2	IA2	CC2	2	1	1	1	5	1	4	8	2	I-1a	CC28	28	5	8	4	3	4	3	3	2	11
	HL067PA1	3	IB	IB-2	IA2	CC2	24	1	1	1	5	1	4	8	9	I-1a	CC28	64	5	8	4	3	4	3	3	2	15
	HL002PA1	3	IB	IB-2	IA2	CC2	2	1	1	1	5	1	4	8	2	I-1a	CC28	28	5	8	4	3	4	3	3	2	11
	HL027PA1	3	IB	IB-2	IA2	CC2	2	1	1	1	5	1	4	8	2	I-1a	CC28	28	5	8	4	3	4	3	3	2	11
	HL046PA1	3	IB	IB-2	IA2	CC2	2	1	1	1	5	1	4	8	2	I-1a	CC28	28	5	8	4	3	4	3	3	2	11
	HL083PA2	3	IB	IB-2	IA2	CC2	2	1	1	1	5	1	4	8	2	I-1a	CC28	28	5	8	4	3	4	3	3	2	11
	HL013PA1	3	IB	IB-2	IA2	CC2	2	1	1	1	5	1	4	8	2	I-1a	CC28	28	5	8	4	3	4	3	3	2	11
	HL050PA1	3	IB	IB-2	IA2	Singleton	91	1	1	1	5	1	4	9	2	I-1a	CC28	28	5	8	4	3	4	3	3	2	11
	HL050PA3	3	IB	IB-2	IA2	CC2	2	1	1	1	5	1	4	8	2	I-1a	CC28	28	5	8	4	3	4	3	3	2	11
	HL087PA1	3	IB	IB-2	IA2	CC2	2	1	1	1	5	1	4	8	2	I-1a	CC28	28	5	8	4	3	4	3	3	2	11
	HL087PA3	3	IB	IB-2	IA2	CC2	2	1	1	1	5	1	4	8	2	I-1a	CC28	28	5	8	4	3	4	3	3	2	11
	HL097PA1	5	IA	IC	IC	Singleton	70	9	1	4	8	6	8	14	14	NA	Singleton	74	7	9	4	13	5	3	9	10	17
	PRP-38	5	IA	IC	IC	Singleton	70	9	1	4	8	6	8	14	14	NA	Singleton	74	7	9	4	13	5	3	9	10	17
	6609	1	IB	IB-3	IB	CC5	5	1	1	1	4	1	4	8	6	NA	NA	NA	5	9	3*	3	4	3	NA	2*	9*
	KPA171202	1	IB	IB-3	IB	CC5	5	1	1	1	4	1	4	8	6	I-2	CC36	36	5	9	3	3	4	3	5	2	9
	HL030PA1	1	IB	IB-3	IB	CC5	5	1	1	1	4	1	4	8	6	I-2	CC36	36	5	9	3	3	4	3	5	2	9
	HL050PA2	1	II	NA	II	Singleton	26	17	4	2	17	2	3	11	11	II	CC60	60	3	16	7	11	7	7	5	6	14
	HL060PA1	2	II	II	II	CC6	6	17	4	2	4	2	3	10	10	II	CC60	69	3	16	7	11	10	7	5	6	14
	HL103PA1	2	II	II	II	CC6	25	17	9	2	4	2	3	10	10	II	CC60	60	3	16	7	11	7	7	5	6	14
	HL082PA2	2	II	II	II	CC6	6	17	4	2	4	2	3	10	10	NA	Singleton	62	3	17	9	11	7	7	5	6	14
	HL001PA1	2	II	II	II	CC72	30	17	4	2	4	2	6	10	12	II	CC60	60	3	16	7	11	7	7	5	6	14
	HL106PA1	2	II	II	NA	NA	NA	18	4	2	4	2	6	10	12**	II	CC60	73	3	16	8	11	7	7	5	6	14
	J139	2	II	II	II	CC72	28	17	4	2	16	2	12	10	12	II	CC60	73	3	16	8	11	7	7	5	6	14
	ATCC11828	2	II	II	II	Singleton	27	17	4	2	4	9	12	10	13	II	CC60	73	3	16	8	11	7	7	5	6	14
	HL110PA4	6	II	II	II	CC6	7	15	4	2	4	2	3	10	10	II	CC60	73	3	16	8	11	7	7	5	6	14
	HL110PA3	6	II	II	II	CC6	7	15	4	2	4	2	3	10	10	II	CC60	73	3	16	8	11	7	7	5	6	14
	HL042PA3	6	II	II	II	CC6	7	15	4	2	4	2	3	10	10	II	CC60	73	3	16	8	11	7	7	5	6	14
	HL202PA1	6	II	II	II	CC6	7	15	4	2	4	2	3	10	10	NA	NA	NA	1	16	8	11	7	7	5	6	14
	HL201PA1	NA	III	III	NA	NA	NA	7	6	3	7	5	7**	12**	32**	NA	NA	NA	6	NA	6	10	NA	4	4	9	NA

NA: Not assigned or not available in the references due to novel sequence type or allele type.

* Sequence type or allele type was corrected from the one originally assigned in the references.

** closest allele