

Figure S2. Location of protospacers in the *parA* gene of the TAD locus

One gene within the TAD locus harbors 4 protospacer sequences. This gene encodes a putative plasmid partitioning protein (Soj/ParA family protein). 3 regions (in yellow) in the coding strand of *parA* in “*P. humerusii*” P08 (P.hum) are identical to spacers no. 8, 22, 23. An alignment of *parA* of “*P. humerusii*” and of *P. acnes* 15.1.R1 is shown. There is one additional protospacer (no. 17, in cyan) in the antisense strand of the *parA* gene of *P. acnes* 15.1.R1 (with one mismatch).

P.hum	1	ATGACCTCGACCAGACCGATTGACCGATCCCCGTTGACCGCACCATCGCGGTATGGAAC	60	
151R1	1	ATGACCTCGACCAGACCGATTGACCGATCCCCGTTGACCGCACTATTGCGGTGTGGAAC	60	
P.hum	61	CACAAAGGGGGCAGCTTCAAGACGTCCGTGCGGAACCTGGGATACCTGTTGCGCGCC	120	
151R1	61	CACAAAGGGGGCAGCTTCAAGACGTCCGTGCGGAACCTGGGATACCTGTTGCGCGCC	120	
P.hum	121	GGTGGCAACAAGGTGCTGATGGTCGACATGGACCCCAAGCCAATCTCGACATTGACTTC	180	
151R1	121	GGTGGCAACAAGGTGCTGCTGGTCGACATGGACCCCAAGCCAATCTCGACATTGACTTC	180	Spacer no. 17
P.hum	181	GGTATACCCGCGGGAGAACCTGAACGGGGCATGGGATTAGCCGAGGCGCTACGTGAGGGG	240	Spacer no. 8
151R1	181	GGTATACCCGCGGGAGAACCTGAACGGGGCATGGGATTAGCCGAGGCGCTACGTGAGGGG	240	
P.hum	241	ACGGCCCTTCCCCACCGC-GTCATCTCAGCGAAAACCTTCACCTGGTCAGTGGCGGCC	299	
151R1	241	ACGGCCCTTCCCCACCGCAG-CATCTCAGCGAAAACCTTCACCTGGTCAGTGGCGGCC	299	
P.hum	300	GGCCCTCCACGAGTTCACCGACCCCGCTCCCTAGCGGCCATCCTCGAGCGGGTCACTAC	359	
151R1	300	TGCTCTCAACGAGTTCACCGACCCCGCATCTTAGCGGCCATCCTCGACCGAGTCACTAC	359	
P.hum	360	CGCACGCTACGACCTGCTGGCCAGGCCCTCGCACCCTGGCCTGGGACTACGACCTTAT	419	
151R1	360	CGCACGCTACGACCTGCTAGCTCAGGCCCTTGCCCCGCTGGCCTGGGACTATGACCTCAT	419	
P.hum	420	CCTT-ATCGATTCCGGGCGGGCCAGACTGTGCTGTCCAGACCATCCTTGGAGTAGCCC	478	
151R1	420	C-TTCATCGACTCCGGGCGGGCACAACTCTGCTGTCCAGACCATCCTTGGAGTAGCCC	478	
P.hum	479	GTTACCTGGTGGTGGCCACCCGCTCCGATAACGCTCGATCACCGGGCTGGTCGGCGTTC	538	Spacer no. 23
151R1	479	GCTGGCTGGTAGTGCCACCCGACCCGATAACGCCTCAATCACTGGCCTCGTCACGTTT	538	
P.hum	539	AGGACGCCATCGATGAGGTCGCCGACTGCAACCCCGGCCTG-AACCTGCTCGGTGTTGTG	597	
151R1	539	AAGACGCCATCGACGGGGTGCCTCCTGCAACCCCTGACCTTCAAC-TACTCGGCGTTGTC	597	
P.hum	598	CTGGCTGGTGTGGGCACTCAGGCCACCCGGATCGGGGCCGATAAACGCAAGGCCATTGAC	657	
151R1	598	CTAGCCGGCGTGGGGGCCCGGCCACCCGGATCGCCGAGATAAACGCCACGCCATCGAC	657	
P.hum	658	ACGGT-CTTGGGGG-AGGGGACCGTCTTCGAGGCGATCATTTCACTACTCCGAAAAAGTGG	715	
151R1	658	ACAGTGCT-GGGGGCAGGA-ACCGTTTTCGATGCGGTATCCACTACTCCGAGAAGGTGT	715	
P.hum	716	CCGTGCTCGCACGCCAGCAGGGTAAGACCGTCGCCGAGTTGGCTGGCGAATACCACCACA	775	
151R1	716	CCGTGCTCGCACGCCAGCAGGGCAAGACCGTCGCCGAGCTAGCCAACGAGTACCACAACA	775	
P.hum	776	CCCAGCCCGCCTACACCTACCTAGCCAGGGCAAAAAGGTTCCCAACGTCGCTAAGGCGG	835	
151R1	776	CCCAGCCCGCCTACACCTACCTAGCTAAAGGCCAGAATCCCCAACGTCGCCAAGGCAG	835	
P.hum	836	CCGTC-GCCATTGAAACCGACTACCT-ACGGTTGGCCACCGAAATCAGTGACCGCATGTT	893	Spacer no. 22
151R1	836	CCGTCAGC-ATCGAAACTGATTATCTGA-GGCTGGCCACCGAGATCAGCGACCGCATGTT	893	
P.hum	894	CGCCGGCGACGAGCAGGAG	912	
151R1	894	CACCAGCGACGAGCAGGAG	912	