

Figure S1

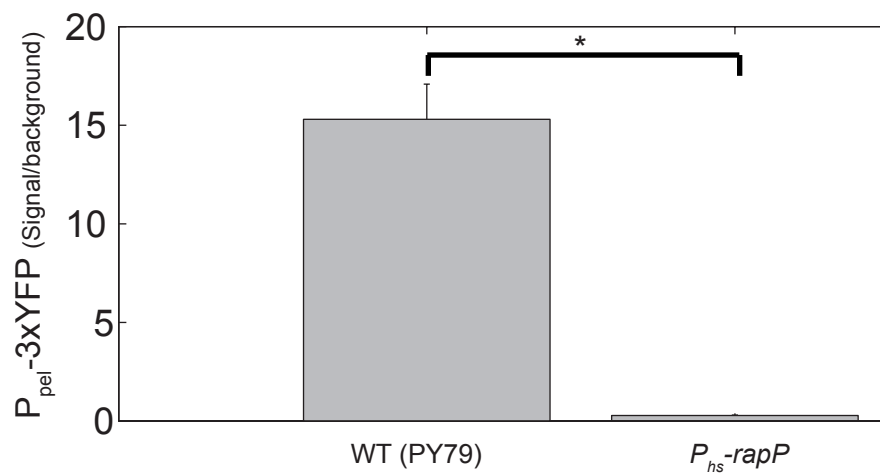


Figure S1: **RapP represses the pel promoter.** (a) Shown are the YFP expression levels of two strains carrying the P_{pel} -3xyfp reporter in the following backgrounds: wild-type PY79 (AES1418), P_{hs} -rapP (AES1445). All measurements were performed at an OD600 of one. The inducible promoter was induced with 10 μ M of IPTG.

Figure S2

#	Protein GI number	Aligned Sequence			#	Protein GI number	Aligned Sequence		
		226	236	246			226	236	246
1	443344996	lpltesfalf	n	lgvcferqkm	54	472329183	ndrfiaisll	n	iansydrsgd
2	443348859	denllchayy	n	lgflkatekk	55	351469170	ndrfiaisll	n	iansydrsgd
3	384177276	denllchayy	n	lgflkatekk	56	449093399	ndrfiaisll	n	iansydrsgd
4	472332020	denllchayy	n	lgflkatekk	57	321314410	ndrfiaisll	n	iansydrsgd
5	428281256	denllchayy	n	lgflkatekk	58	255767178	ndrfiaisll	n	iansydrsgd
6	430756569	denllchayy	n	lgflkatekk	59	497652574	ndrfiaisll	n	iansydrsgd
7	16080691	denllchayy	n	lgflkatekk	60	428278168	ndrfiaisll	n	iansydrsgd
8	321313185	denllchayy	n	lgflkatekk	61	350267934	qprligsaly	n	igncyddkge
9	305676255	ddnllchayy	n	lgflkatekk	62	443348902	qprligsaly	n	igncyddkge
10	296151383	ddnllchayy	n	lgflkatekk	63	305676292	qprligsaly	n	igncyddkge
11	350267898	denllchayy	n	lgflkatekk	64	384177312	qprligsaly	n	igncyddkge
12	16078951	deflkaqlfh	n	lsivysdwnk	65	449096120	qprligsaly	n	igncyddkge
13	384175679	deflkaqlfh	n	lsivysdwnk	66	428281290	qprligsaly	n	igncyddkge
14	443345550	defleaqlyh	n	lsivysdwnk	67	430756535	qprligsaly	n	igncyddkge
15	428278738	dkffeaqihh	n	lsitysaanr	68	16080722	qprligsaly	n	igncyddkge
16	305676690	dhffeaqllh	n	fgllhaqsgk	69	443345493	khkligasly	n	lgnicyymke
17	296153004	dhffeaqllh	n	fgllhaqsgk	70	443347386	msrligssly	n	lglcyfaeea
18	350268321	dhffeaqllh	n	fgllhaqsgk	71	50346533	kaqlvgrayy	n	lglcyynqel
19	443349311	dhffeaqllh	n	fgllhaqsgk	72	443346068	kaqlvgrayy	n	lglcyynqel
20	430757872	dhffeaqllh	n	fgllhaqsgk	73	50346536	kaqlvgrayy	n	lglcyynqel
21	384177691	dhffeaqllh	n	fgllhaqsgk	74	321314047	kaqlvgrayy	n	lglcyynqdl
22	428281704	dhffeaqllh	n	fgllhaqsgk	75	50363103	kaqlvgrayy	n	lglcyynqdl
23	16081082	dhffeaqllh	n	fgllhaqsgk	76	16077445	kaqlvgrayy	n	lglcyynqdl
24	351471787	dhffeaqllh	n	fgllhaqsgk	77	449093073	kaqlvgrayy	n	lglcyynqdl
25	1305514	hdyittkgl1	n	lgnfcnkqdd	78	351468784	kaqlvgrayy	n	lglcyynqdl
26	10956495	nkymlakall	n	lgdsyknmgd	79	402774618	kaqlvgrayy	n	lglcyynqdl
27	10956510	hsp1kakall	n	mgnsynqmg	80	430758593	kaqlvgrayy	n	lglcyynqdl
28	321314404	nkriyqgalf	n	lgnicylkmge	81	350264625	kaqlvgrayy	n	lglcyynqdl
29	443346532	nkriyqgalf	n	lgnicylkmge	82	305673084	kaqlvgrayy	n	lglcyynqdl
30	321312077	nthyataaff	n	lgnicyhkmdn	83	350268020	qpqlmgtly	n	lglcknsqsq
31	255767596	nthyataaff	n	lgnicyhkmdn	84	449096201	qpqlmgtly	n	lglcknsqsq
32	351471102	nthyataaff	n	lgnicyhkmdn	85	472332133	qpqlmgtly	n	lglcknsqsq
33	1217880	nthyataaff	n	lgnicyhkmdn	86	430755657	qpqlmgtly	n	lglcknsqsq
34	350266788	nthyataaff	n	lgnicyhkmdn	87	321313296	qpqlmgtly	n	lglcknsqsq
35	321314985	nprlissaly	n	lgnicykmge	88	428281376	qpqlmgtly	n	lglcknsqsq
36	407964200	nprlissaly	n	lgnicykmge	89	16080798	qpqlmgtly	n	lglcknsqsq
37	407956931	nprlissaly	n	lgnicykmge	90	384177394	qpqlmgtly	n	lglcknsqsq
38	39931	nprlissaly	n	lgnicykmge	91	305676373	qpqlmgtly	n	lglcknsqsq
39	305673952	nprlissaly	n	lgnicykmge	92	443348987	qpqlmgtly	n	lglcknsqsq
40	430755744	nprlissaly	n	lgnicykmge	93	321313952	eaymiaaayy	n	vghckyslgd
41	16078308	nprlissaly	n	lgnicykmge	94	449092977	eaymiaaayy	n	vghckyslgd
42	449093941	nprlissaly	n	lgnicykmge	95	351468559	eaymiaaayy	n	vghckyslgd
43	443346866	nprlissaly	n	lgnicykmge	96	384173932	eaymiaaayy	n	vghckyslgd
44	350264321	hdr1issaly	n	lgecyhymgq	97	16077351	eaymiaaayy	n	vghckyslgd
45	384176217	nkr1issaly	n	lgtnfadsgd	98	350264524	eaymiaaahy	n	vghckyslgd
46	472330992	nkr1issaly	n	lgtnfadsgd	99	305672983	eaymiaaahy	n	vghckyslgd
47	428280076	nkr1issaly	n	lgtnfadsgd	100	443345670	eaymiaaahy	n	vghckyslgd
48	443348016	nkr1issaly	n	lgtnfadsgd	101	16077568	ieh1iamshm	n	igicydelke
49	430756340	nkr1issaly	n	lgtnfadsgd	102	428277959	ieh1iamshm	n	igicydelke
50	305673899	nkr1issaly	n	lgtnfadrgd	103	443346203	ieh1iamshm	n	igicydelke
51	443346524	ndrfiaisll	n	iansydrsgd	104	428278423	idyligmahi	n	igicfdelkd
52	305673386	ndrfiaisll	n	iansydrsgd	105	323651054	eqh1igsahf	n	vglcynnlee
53	430757219	ndrfiaisll	n	iansydrsgd	106	350265475	eqh1igsahf	n	vglcynnlee
					107	323651061	ydkpitkiyh	n	lglvhwqkgs

Figure S2: Alignment of 107 Rap genes of *B. subtilis* strains show perfect conservation of the RapP asparagine residue in position 236. Using Blast, 107 sequences of Rap proteins of *B. subtilis* strains that show a difference in amino-acid sequence were identified and aligned. Shown are the alignment results for the region corresponding to amino-acids 226-246 of RapP³⁶¹⁰. Each protein sequence is marked by its NCBI GI number. Note that RapP³⁶¹⁰ is not shown. Residue 236 is specifically emphasized by spaces on both sides. The asparagine in this residue is 100% conserved.

Figure S3

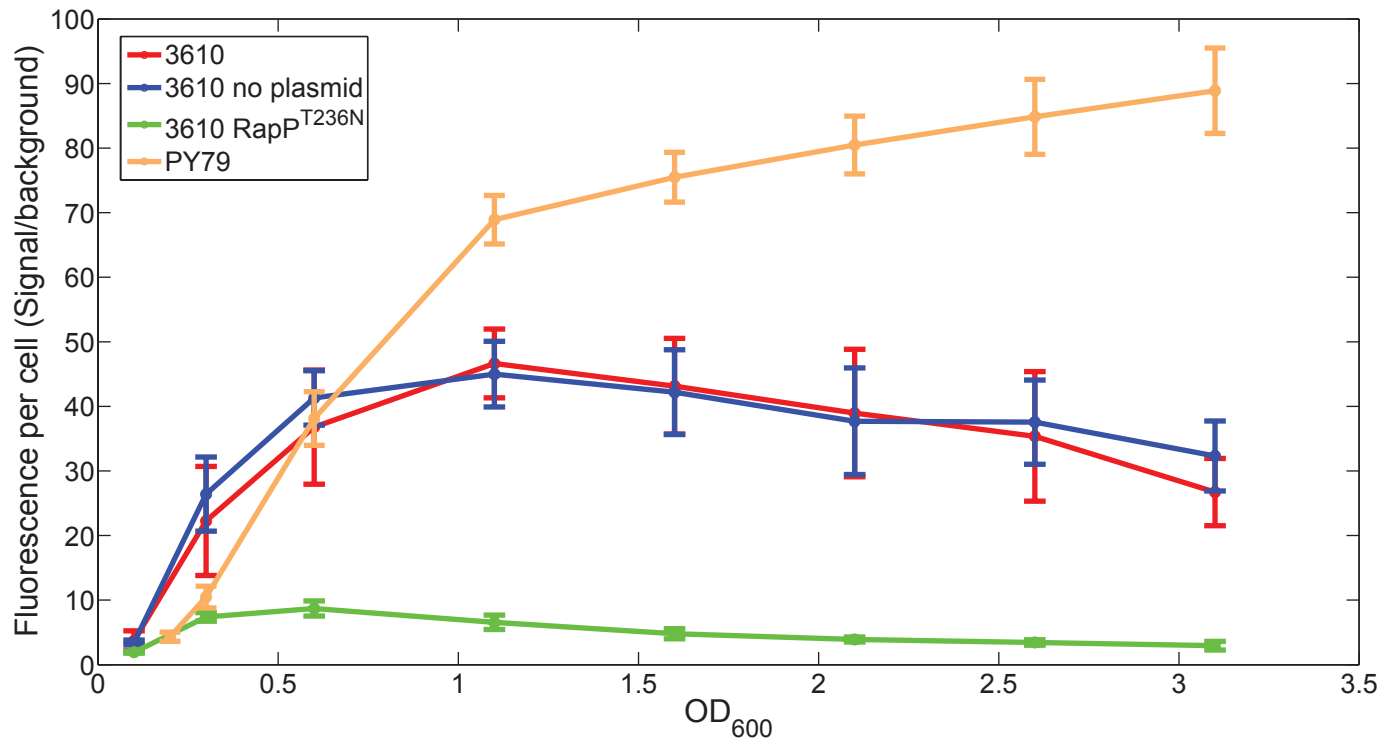


Figure S3: P_{srfA} -3xyfp expression as a function of time for strain 3610 derivatives and strain PY79. YFP expression levels of P_{srfA} -3xYFP as a function of optical density during growth in SMM for the following backgrounds: 3610;plasmid free strain (AES1605, blue), 3610;*rap*^{PT236N}-*phrP* strain (AES1873, green), strain 3610 (3610;*rap*^{P3610}-*phrP*, AES1336, red) and strain PY79 (AES1334, orange).