Table S1, Blast-results of 81 AFLP-markers

							blastn (*S. aureus*)	
Marker (Fig. 1)	**Fig. S1**	**Frag. length**	**Mu50 code**	**Mu50 gene**	**Mu50 protein**	**Mu50 localization**	**Alignment score**	**Blast**
Block A								
1	A1	166	SAV0939	-	conserved hypothetical protein	981091	231	95%
2	A2	263	SAV1856	-	conserved hypothetical protein	1987628	414	97%
3		181	-	-	-	2 hits	161	90%
4	A3	159	SAV2157	-	hypothetical protein, similar to transcription antiterminator BglG family	2284038	244	98%
5	A4	288	SAV1791	pckA	phosphoenolpyruvate carboxykinase	1923388	494	99%
Block B								
1		305	-	-	-	-	-	-
2		403	-	-	-	-	-	-
3	B1	401	SAV1276	spoIIIE	sporulation-related protein SpoIIIE homologue	1348144	692	99%
4	B2	177	SAV0553	-	hypothetical protein, similar to UDP-glucose 4-epimerase related protein	623082	277	100%
5	B3	160	SAV2157	-	hypothetical protein, similar to transcription antiterminator BglG family	2284038	231	96%
6	B4	200	SAV0131	-	hypothetical protein, similar to capsular polysaccharide synthesis protein 14H	145461	294	98%
7	B5	147	SAV1184	div1b	cell division protein	1239814	198	96%
8	B6	121	SAV1417	-	conserved hypothetical protein	1501679	162	97%
9		129	-	-	-	-	-	-
Block C								
1	C1	488	SAV1808	-	type I restriction enzyme EcoR124II M protein homolog	1937059	319	90%
2		234	-	-	-	-	-	-
3	C2	117	SAV0244	-	hypothetical protein, similar to BglG antiterminator family	287246	142	95%
4		154	-	-	-	-	98	88%
5	C3	159	SAV0841	-	conserved hypothetical protein	911403	212	95%
6	C4	267	SAV2633	arcD	arginine/oirnithine antiporter	2786871	316	92%
7	C5	321	SAV2221	-	hypothetical protein, similar to ABC transporter ATP-binding protein	2362564	354	89%
8		388	2 hits	-	hypothetical protein, similar to bacteriophage terminase small subunit	2 hits	310	93%
9	C6	282	SAV1171	-	conserved hypothetical protein	1225308	358	97%
10		188	-	-	-	-	-	-
11	C7	278	SAV0264	-	hypothetical protein, similar to transcription regulator GntR family	308322	327	90%
12	C8	236	SAV0783	-	hypothetical protein, similar to excisionase	868515	383	99%

							blastn (*S. aureus*)	
Marker (Fig. 1)	**Fig. S1**	**Frag. length**	**N315 code**	**N315 gene**	**N315 protein**	**N315 localization**	**Alignment score**	**Blast**
Block A								
1	A1	166	SA0800	-	conserved hypothetical protein	904783	231	95%
2	A2	263	SA1673	-	conserved hypothetical protein	1909764	414	97%
3		181	-	-	-	2 hits	161	90%
4	A3	159	SA1961	-	hypothetical protein, similar to transcription antiterminator BglG family	2214248	244	98%
5	A4	288	SA1609	pckA	phosphoenolpyruvate carboxykinase	1845526	494	99%
Block B								
1		305	-	-	-	-	-	-
2		403	-	-	-	-	-	-
3	B1	401	SA1119	spoIIIE	sporulation-related protein SpoIIIE homologue	1271752	692	99%
4	B2	177	SA0511	-	hypothetical protein, similar to UDP-glucose 4-epimerase related protein	598834	277	100%
5	B3	160	SA1961	-	hypothetical protein, similar to transcription antiterminator BglG family	2214248	231	96%
6	B4	200	SA0126	-	hypothetical protein, similar to capsular polysaccharide synthesis protein 14H	145496	294	98%
7	B5	147	SA1027	div1b	cell division protein, FtsQ homolog	1163424	198	96%
8	B6	121	SA1250	-	conserved hypothetical protein	1425198	162	97%
9		129	-	-	-	-	-	-
Block C								
1	C1	488	SA1626	-	type I restriction enzyme EcoR124II M protein homolog	1859197	319	90%
2		234	-	-	-	-	-	-
3	C2	117	SA0235	-	hypothetical protein, similar to BglG antiterminator family	287282	142	95%
4		154	-	-	-	-	98	88%
5	C3	159	SA0773	-	conserved hypothetical protein	879575	212	95%
6	C4	267	SA2426	arcD	arginine/oirnithine antiporter	2723648	316	92%
7	C5	321	SA2020	-	hypothetical protein, similar to ABC transporter ATP-binding protein	2292994	354	89%
8		388	SA1820	-	hypothetical protein, similar to bacteriophage terminase small subunit	2061937 (1 hit)	302	93%
9	C6	282	SA1014	-	conserved hypothetical protein	1148919	358	97%
10		188	-	-	-	-	-	-
11	C7	278	SA0254	-	hypothetical protein, similar to transcription regulator GntR family	308358	327	90%
12	C8	236	-	-	-	-	-	-

							blastn (*S. aureus*)	
Marker (Fig. 1)	**Fig. S1**	**Frag. length**	**MW2 code**	**MW2 gene**	**MW2 protein**	**MW2 localization**	**Alignment score**	**Blast**
Block A								
1	A1	166	MW0821	-	conserved hypothetical protein	904695	231	95%
2	A2	263	MW1797	-	conserved hypothetical protein	1951797	414	97%
3		181	-	-	-		109	85%
4	A3	159	MW2083	-	hypothetical protein, similar to transcription antiterminator BglG family	2234185	239	97%
5	A4	288	MW1729	pckA	phosphoenolpyruvate carboxykinase	1881717	481	98%
Block B								
1		305	-	-	-	-	-	-
2		403	-	-	-	-	-	-
3	B1	401	MW1159	spoIIIE	hypothetical protein, similar to sporulation-related protein SpoIIIE DNA translocas	1271886	698	99%
4	B2	177	MW0508	-	hypothetical protein, similar to UDP-glucose 4-epimerase related protein	589393	277	100%
5	B3	160	MW2083	-	hypothetical protein, similar to transcription antiterminator BglG family	2234185	225	96%
6	B4	200	MW0105	-	hypothetical protein, similar to capsular polysaccharide synthesis protein 14H	122959	294	98%
7	B5	147	MW1067	div1b	cell division protein, FtsQ homolog	1163198	204	97%
8	B6	121	MW1306	-	conserved hypothetical protein	1427964	162	97%
9		129	-	-	-	-	-	-
Block C								
1	C1	488	MW1751	hsdM	type I restriction enzyme EcoR124II M protein homolog	1901785	319	90%
2		234	-	-	-	-	-	-
3	C2	117	MW0220	-	hypothetical protein, similar to BglG antiterminator family	265266	154	96%
4		154	-	-	-	-	90	87%
5	C3	159	MW0794	-	conserved hypothetical protein	881218	212	95%
6	C4	267	MW2554	arcD	arginine/oirnithine antiporter	2725847	310	91%
7	C5	321	MW2140	-	hypothetical protein, similar to ABC transporter ATP-binding protein	2304399	360	89%
8		388	2 hits	-	hypothetical protein, similar to bacteriophage terminase small subunit	2 hits	244	93%
9	C6	282	MW1052	-	conserved hypothetical protein	1148686	364	98%
10		188	-	-	-	-	-	-
11	C7	278	MW0240	-	hypothetical protein, similar to transcription regulator GntR family	286942	327	90%
12	C8	236	MW0745	int	hypothetical protein, similar to integrase	839734	152	80%

Marker (Fig. 1)	Fig. S1	Frag. length	blastn (all organisms) Blast to other genome	Alignment score
Block A				
1	A1	166		
2	A2	263		
3		181		
4	A3	159		
5	A4	288		
Block B				
1		305	Staphylococcus aureus TY4, ETB plasmid DNA	450
2		403	Bacteriophage phi ETA DNA	611
3	B1	401		
4	B2	177		
5	B3	160		
6	B4	200		
7	B5	147		
8	B6	121		
9		129	no significant similarity	
Block C				
1	C1	488		
2		234	EMRSA-16	335
3	C2	117		
4		154		
5	C3	159		
6	C4	267		
7	C5	321		
8		388		
9	C6	282		
10		188	no significant similarity	
11	C7	278		
12	C8	236		

Marker (Fig. 1)	Fig. S1	Frag. length	Mu50 code	Mu50 gene	Mu50 protein	Mu50 localization	Alignment score	Blast
Block D								
1	D1	471	SAV2705	-	hypothetical protein	2870193	448	92%
2	D2	206	SAV0023	-	hypothetical protein	32870	269	96%
3		265	-	-	-	-	-	-
4	D3	455	SAV2202	hysA	hyaluronate lyase precursor	2344109	389	92%
5		217	-	-	-	5 hits	260	96%
6	D4	340	SAV2471	-	conserved hypothetical protein	2607876	198	94%
7	D5	105	SAV0306	-	hypothetical protein, similar to branched-chain amino acid uptake carrier	349224	127	94%
8		434	-	-	-	-	-	-
9	D6	410	SAV2511	-	conserved hypothetical protein	2652422	521	91%
10	D7	397	SAV2582	-	hypothetical protein, similar to cobalamin synthesis related protein CobW	2727811	504	95%
11	D8	332	SAV0179	-	hypothetical protein, similar to surfactin synthetase	201142	544	98%
12	D9	328	SAV2384	gltT	proton/ sodium-glutamate symport protein	2511738	494	96%
13	D10	192	SAV0238	-	conserved hypothetical protein	278888	210	91%
14	D11	185	SAV2156	mtlF	mannitol IIBC component of PTS system	2282748	227	95%
15	D12	162	SAV2368	-	hypothetical protein, similar to TpgX protein	2494575	202	92%
Block E								
1	E1	104	SAV0564	-	hypothetical protein, similar to poly (glycerol-phosphate) alpha-glucosyltransfer	641455	137	97%
2	E2	291	SAV1262	-	conserved hypothetical protein	1327689	223	99%
3	E3	317	SAV0363	-	hypothetical protein, similar to GTP-binding protein	410336	364	89%
4	E4	252	SAV1652	-	hypothetical protein, similar to transporter PAB2175 from Pyrococcus abyssi	1760330	390	98%
5	E5	478	SAV1017	-	hypothetical protein, similar to cell wall synthesis protein	1067328	863	100%
6	E6	338	SAV1639	tgt	tRNA-guanine transglycosylase	1751303	596	100%
7	E7	356	SAV1139	pheT	Phe-tRNA synthetase beta chain	1192752	631	100%
8	E8	351	SAV2156	mtlF	mannitol IIBC component of PTS system	2282562	621	100%
9	E9	198	SAV0458	-	hypothetical protein, similar to sodium-dependent transporter	503915	300	95%
10	E10	167	SAV0939	-	conserved hypothetical protein	981091	225	95%
11	E11	139	SAV0562	sdrD	Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein	636698	216	100%
Block F								
1	F1	101	SAV0465	-	hypothetical protein	509658	133	97%
2	F2	115	SAV1595	-	conserved hypothetical protein	1704576	171	100%
3	F3	313	SAV0773	pgk	phosphoglycerate kinase	858592	550	100%
4	F4	119	SAV1285	recA	RecAprotein	1357916	160	96%
Block G								
1	G1	90	SAV1093	pdhA	pyruvate dehydrogenase E1 component alpha subunit	1148021	114	96%
2	G2	271	SAV2688	drp35	Drp35	2854751	467	100%
3	G3	317	SAV2679	hisG	ATP phosphoribosyltransferase	2845964	471	98%
4	G4	245	SAV2612	betA	choline dehydrogenase	2758932	419	100%

Marker (Fig. 1)	Fig. S1	Frag. length	N315 code	N315 gene	N315 protein	N315 localization	Alignment score	Blast
Block D								
1	D1	471	SA2495	-	hypothetical protein	2806969	448	92%
2	D2	206	SA0022	-	hypothetical protein, similar to 5'-nucleotidase	32869	269	96%
3		265	-	-	-	-	-	-
4	D3	455	SA2003	hysA	hyaluronate lyase precursor	2274539	389	92%
5		217	-	-	-	5 hits	260	96%
6	D4	340	SA2259	-	conserved hypothetical protein	2537173	198	94%
7	D5	105	SA0294	-	hypothetical protein, similar to branched-chain amino acid uptake carrier	349312	109 (nblast)	94%
8		434	-	-	-	-	-	-
9	D6	410	SA2299	-	conserved hypothetical protein	2582487	466	91%
10	D7	397	SA2368	-	hypothetical protein, similar to cobalamin synthesis related protein CobW	2657876	504	95%
11	D8	332	SA0173	-	hypothetical protein, similar to surfactin synthetase	201177	544	98%
12	D9	328	SA2172	gltT	proton/ sodium-glutamate symport protein	2441211	494	96%
13	D10	192	SA0230	-	conserved hypothetical protein	278924	210	91%
14	D11	185	SA1960	mtlF	mannitol IIBC component of PTS system	2212958	227	95%
15	D12	162	SA2158	-	hypothetical protein, similar to TpgX protein	2425567	202	92%
Block E								
1	E1	104	SA0522	-	hypothetical protein, similar to poly (glycerol-phosphate) alpha-glucosyltransferas	617206	137	97%
2	E2	291	SA1105	-	conserved hypothetical protein	1251297	223	99%
3	E3	317	SA0351	-	hypothetical protein, similar to GTP-binding protein	410374	364	89%
4	E4	252	SA1478	-	hypothetical protein, similar to transporter PAB2175 from Pyrococcus abyssi	1683848	390	98%
5	E5	478	SA0875	-	hypothetical protein, similar to cell wall synthesis protein	991016	863	100%
6	E6	338	SA1465	tgt	tRNA-guanine transglycosylase	1674821	596	100%
7	E7	356	SA0986	pheT	Phe-tRNA synthetase beta chain	1116409	631	100%
8	E8	351	SA1960	mtlF	mannitol IIBC component of PTS system	2212772	621	100%
9	E9	198	SA0417	-	hypothetical protein, similar to sodium-dependent transporter	479395	300	95%
10	E10	167	SA0800	-	conserved hypothetical protein	904783	225	95%
11	E11	139	SA0520	sdrD	Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein	612449	210	99%
Block F								
1	F1	101	SA0423	-	hypothetical protein, similar to autolysin N-acetylmuramoyl-L-alanine amidase	485139	133	97%
2	F2	115	SA1423	-	conserved hypothetical protein	1628096	171	100%
3	F3	313	SA0728	pgk	phosphoglycerate kinase	834398	550	100%
4	F4	119	SA1128	recA	RecAprotein	1281524	160	96%
Block G								
1	G1	90	SA0943-1	pdhA	pyruvate dehydrogenase E1 component alpha subunit	1071676	114	96%
2	G2	271	SA2480	drp35	Drp35	2791526	467	100%
3	G3	317	SA2471	hisG	ATP phosphoribosyltransferase	2782741	471	98%
4	G4	245	SA2405	betA	choline dehydrogenase	2695709	419	100%

Marker (Fig. 1)	Fig. S1	Frag. length	MW2 code	MW2 gene	MW2 protein	MW2 localization	Alignment score	Blast
Block D								
1	D1	471	MW2624	-	hypothetical protein	2812767	454	93%
2	D2	206	MW0023	-	hypothetical protein, similar to 5'-nucleotidase	32866	262	95%
3		265	-	-	-	-	-	-
4	D3	455	MW2129	hysA	hyaluronate lyase precursor	2295348	379	93%
5		217	-	-	-	7 hits	260	96%
6	D4	340	-	-	-	-	-	
7	D5	105	MW0283	-	hypothetical protein, similar to branched-chain amino acid uptake carrier	329207	127	94%
8		434	-	-	-	-	-	-
9	D6	410	MW2429	-	conserved hypothetical protein	2591195	458	90%
10	D7	397	MW2502	-	hypothetical protein, similar to cobalamin synthesis related protein CobW	2667088	510	96%
11	D8	332	MW0153	-	hypothetical protein, similar to surfactin synthetase	179569	550	98%
12	D9	328	MW2304	gltT	proton/ sodium-glutamate symport protein	2454617	494	96%
13	D10	192	MW0214	-	conserved hypothetical protein	256911	204	90%
14	D11	185	MW2082	mtlT	mannitol IIBC component of PTS system	2232895	227	95%
15	D12	162	MW2289	-	hypothetical protein, similar to TpgX protein	2437358	214	93%
Block E								
1	E1	104	MW0519	-	hypothetical protein, similar to poly (glycerol-phosphate) alpha-glucosyltransferas	607656	137	97%
2	E2	291	MW1145	-	conserved hypothetical protein	1251428	229	100%
3	E3	317	MW0339	-	hypothetical protein, similar to GTP-binding protein	390116	542	99%
4	E4	252	MW1603	-	hypothetical protein, similar to transporter PAB2175 from Pyrococcus abyssi	1729581	390	98%
5	E5	478	MW0898	-	hypothetical protein, similar to cell wall synthesis protein	990983	846	99%
6	E6	338	MW1589	tgt	tRNA-guanine transglycosylase	1720297	596	100%
7	E7	356	MW1022	pheT	Phe-tRNA synthetase beta chain	1117840	631	100%
8	E8	351	MW2082	mtlT	mannitol IIBC component of PTS system	2232709	615	99%
9	E9	198	MW0413	-	hypothetical protein, similar to sodium-dependent transporter	464770	294	95%
10	E10	167	MW0821	-	conserved hypothetical protein	904695	219	94%
11	E11	139	MW0517	sdrD	Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein	602901	204	98%
Block F								
1	F1	101	MW0419	-	hypothetical protein, similar to autolysin N-acetylmuramoyl-L-alanine amidase	470516	133	97%
2	F2	115	MW1546	-	conserved hypothetical protein	1673747	171	100%
3	F3	313	MW0735	pgk	phosphoglycerate kinase	829614	550	100%
4	F4	119	MW1168	recA	RecAprotein	1281661	160	96%
Block G								
1	G1	90	MW0976	-	pyruvate dehydrogenase E1 component alpha subunit	1073103	114	96%
2	G2	271	MW2608	drp35	Drp35	2794744	467	97%
3	G3	317	MW2598	hisG	ATP phosphoribosyltransferase	2785629	471	98%
4	G4	245	MW2531	betA	choline dehydrogenase	2696816	419	100%

Marker (Fig. 1)	Fig. S1	Frag. length	Blast to other genome	Alignment score
Block D				
1	D1	471		
2	D2	206		
3		265	EMRSA-16	294
4	D3	455		
5		217		
6	D4	340		
7	D5	105		
8		434	EMRSA-16 (bbp gene)	644
9	D6	410		
10	D7	397		
11	D8	332		
12	D9	328		
13	D10	192		
14	D11	185		
15	D12	162		
Block E				
1	E1	104		
2	E2	291		
3	E3	317		
4	E4	252		
5	E5	478		
6	E6	338		
7	E7	356		
8	E8	351		
9	E9	198		
10	E10	167		
11	E11	139		
Block F				
1	F1	101		
2	F2	115		
3	F3	313		
4	F4	119		
Block G				
1	G1	90		
2	G2	271		
3	G3	317		
4	G4	245		

Marker (Fig. 1)	Fig. S1	Frag. length	Mu50 code	Mu50 gene	Mu50 protein	Mu50 localization	Alignment score	Blast
Remaining								
1		447	10 hits	tnp	transposase	10 hits	806	100%
2		134	SAV1317	-	cardiolipin synthetase homolog	1392901	208	100%
3		151	SAV2593	-	hypothetical protein, similar to transcriptional regulator tetR-family	2737748	241	100%
4		88	SAV0974	-	hypothetical protein, similar to lipopolysaccharide modification acyltransferase	1021631	117	100%
5		114	SAV1732	fhs	formyltetrahydrofolate synthetase	1857166	169	100%
6		158	SAV2320	-	hypothetical protein, similar to phosphoglycolate phosphatase	2443654	252	100%
7		352	SAV2054	ilvB	acetolactate synthase large subunit	2177289	623	100%
8		248	SAV0452	ndhF	NADH dehydrogenase subunit 5	496038	425	100%
9		145	SAV1683	thrS	threonyl-tRNA synthetase 1	1792249	227	100%
10		143	SAV0316	-	hypothetical protein, similar to glucokinase	361078	223	100%
11		121	SAV1782	-	hypothetical protein	1915903	181	100%
12		227	SAV0010	-	hypothetical protein, similar to amino acid permease	15111	383	100%
13		238	SAV1904	nnlJ	DNA ligase	2046571	406	100%
14		110	SAV1843	-	conserved hypothetical protein	1975069	160	100%
15		173	SAV1740	murC	UDP-N-Aacerylmuramate-alanine ligase	1868566	283	100%
16		198	SAV0374	-	conserved hypothetical protein	417876	329	100%
17		174	SAV1307	-	hypothetical protein, similar to GTP-binding proteinase modulator homolog ynb	1381152	285	100%
18		144	SAV1183	murD	UDP-N-acetylmuramoylalanine-D-glutamate ligase	1238883	225	100%
19		165	SAV0501	rplY	50S ribosomal protein L25	554034	266	100%
20		183	SAV0771	gapR	glycolytic operon regulator	855701	300	100%
21		149	SAV1864	gsaB	glutamate-1-semialdehyde aminotransferase	2005471	235	100%

🟦 = sequence determined by computer analysis

<u>Supplementary data</u>

Table S1. Blast-results of 81 AFLP-markers.

Blast-results of 81 AFLP-markers against the three completed genome sequences of *S. aureus* (Mu50, N315, MW2). The BLAST value (in %) gives the percentage of correct blast identities (nucleotides) of the marker sequence with the (three) completed genome sequences of *S. aureus*.

Figure S1. Localization of the cluster-defining AFLP-markers on the *S. aureus* chromosome.

The localization is shown for 48 AFLP-markers on the three completed *S. aureus* genomes (Mu50, N315 and MW2). The different characters (A through G) correspond with the different cluster-defining blocks in Figure 1. The numbering of the characters (markers) correspond with the order of the markers in the horizontal dendrogram in Figure 1.