

SUPPLEMENTAL MATERIAL

Thomer et al., <http://www.jem.org/cgi/content/full/jem.20150074/DC1>

Table S1. **Attributes of mAbs raised against Coa_{Newman}**

mAb ^a	Isotype ^b	Affinity (nM ⁻¹) ^c						
		Coa	D1-D2	D1	D1 _{Δ1-18}	D2	L	R
5D5	IgG1	5.02	5.4	4.09	1.32	<	<	<
3B3	IgG1	7.58	<	<	<	<	<	8.03

^aMouse monoclonal antibodies were purified from isolated hybridoma clones.

^bImmunoglobulin call and subclass of mAbs.

^cAffinity was determined by ELISA as the association constant (K_a) in nM⁻¹ for the coagulase protein (Coa) from strain Newman. Mapping of mAb binding sites was performed by using either the full-length Coa or its sub-domains D1-D2, D1, D1_{Δ1-18}, D2, linker (L), and repeat (R) domains.

Table S2. **Affinity of mAbs toward Coa proteins of different strains**

mAb ^a	Domain ^b	Affinity (nM ⁻¹) ^c					
		Coa _{NM}	Coa _{USA300}	Coa _{N315}	Coa _{MRSA252}	Coa _{85/2082}	Coa _{WIS}
5D5	D1	5.02	5.20	<	<	<	4.00
3B3	R	7.58	6.55	7.20	6.76	7.41	6.75

^aMouse monoclonal antibodies were purified from isolated hybridoma clones.

^bCoa subdomains D1 or R recognized by mAb 5D5 and 3B3, respectively as shown in Table S1.

^cAffinity was determined by ELISA as the association constant (K_a) in nM⁻¹ for each protein domain.

Table S3. **Phagocytosis and OPK of MRSA USA300 LAC in human blood**

Donor ^a	Serum IgG titer ^b			Without CD		With CD ^c		Agglutinated ^d	OPK ^e	Category ^f
	Hla	D1-D2 _{ST}	R _{N12D}	Mock (% total) ^g	SK (% inoculum) ^h	Mock (% total) ^g	SK (% inoculum) ^h			
A	2599	320	716	64.62 (±20.53)	48.96 (±4.48)	2.08 (±0.31)	145.59 (±32.82)	35.38	51.04	K
B	1936	546	245	63.16 (±8.01)	124.77 (±6.02)	5.07 (±0.57)	236.51 (±6.14)	36.84	0	P
C	3176	1550	276	31.28 (±0.53)	90.4 (±2.95)	3.98 (±2.81)	87.65 (±18.98)	68.72	9.60	K
D	1134	85	134	37.79 (±6.30)	139.97 (±5.78)	1.90 (±0.21)	218.46 (±5.15)	62.79	0	P
E	1365	278	226	39.40 (±3.42)	115.52 (±30.84)	3.83 (±1.06)	246.74 (±39.85)	60.60	0	C
F	6849	4470	2905	14.35 (±1.23)	130.93 (±11.2)	2.1 (±1.79)	117.08 (±22.04)	85.65	0	P
G	8688	2308	2760	21.93 (±1.94)	99.68 (±8.25)	2.58 (±0.47)	149.60 (±18.75)	78.07	0.32	C
H	3541	553	167	72.35 (±8.22)	117.51 (±9.59)	7.05 (±1.09)	321.39 (±24.81)	27.65	0	P
I	1680	245	250	14.25 (±1.74)	204.42 (±29.76)	10.49 (±0.75)	174.60 (±1.95)	85.75	0	P
J	554	281	178	48.12 (±0.60)	177.97 (±3.19)	5.59 (±0.44)	218.06 (±11.31)	51.88	0	P
K	2066	383	520	85.24 (±3.36)	122.63 (±28.2)	17.45 (±0.78)	300.6 (±14.15)	14.76	0	C
L	2333	185	667	63.17 (±6.08)	176.42 (±29.9)	3.00 (±0.08)	354.94 (±19.19)	36.83	0	P
M	955	1343	1940	75.56 (±1.23)	173.73 (±2.73)	7.49 (±0.80)	392.53 (±68.16)	24.44	0	P
N	2109	575	323	77.61 (±12.31)	149.42 (±9.46)	16.43 (±9.36)	308.80 (±30.28)	22.39	0	P
O	1881	148	216	66.91 (±14.36)	195.00 (±28.06)	9.10 (±2.92)	310.92 (±6.27)	33.09	0	P
P	459	80	57	65.30 (±0.55)	110.80 (±8.02)	4.36 (±0.46)	355.53 (±33.92)	34.70	0	C
Q	2469	1156	414	39.26 (±10.55)	203.63 (±17.23)	13.30 (±2.08)	196.19 (±38.14)	60.74	0	P
R	5934	1114	907	26.77 (±0.04)	241.30 (±23.59)	12.97 (±0.16)	342.54 (±17.54)	73.23	0	P
S	4070	225	300	66.06 (±8.19)	113.39 (±21.00)	10.89 (±5.89)	132.24 (±18.5)	33.94	0	C
T	1878	319	507	55.32 (±0.72)	90.86 (±3.65)	7.99 (±2.94)	292.10 (±46.85)	44.68	9.14	K

^aBlood from human volunteers was anticoagulated with 10 µg/ml desirudin, dispensed into 0.5-ml aliquots, and inoculated with 5 × 10⁶ CFU USA300 LAC. The inoculum was enumerated by lysing blood with 0.5 ml PBS (with 0.5% saponin, 100 U SK K, 50 µg trypsin, 1 µg DNase, and 5 µg RNase) prior to plating on agar for CFU enumeration.

^bSerum from coagulated blood of human volunteers was examined by ELISA for the half-maximal IgG titer against purified recombinant proteins derived from of *S. aureus* Newman genome sequence: α-hemolysin (Hla), D1-D2 domain (D1-D2), or a tandem repeat of the R domain carrying the N12D substitution.

^cBlood was pretreated with 10 µg CD/ml prior to infection with 5 × 10⁶ CFU USA300 LAC.

^dAgglutination (%) was calculated from the percent mock-treated CFU after 60 min (without CD) and the staphylococcal load enumerated with SK treatment.

^eOPK (%) was calculated as the Δ0-60-min load in SK-treated blood without CD treatment.

^fHuman blood samples were categorized as killer (K), controllers (C), or prey (P) of MRSA isolate USA300 LAC.

^gBlood samples were lysed after 60 min at 37°C with 0.5 ml PBS (0.5% saponin, 1 µg DNase, and 5 µg RNase), followed by CFU enumeration. Data were averaged from two independent determinations. SEM and percent amount of total (60-min SK-treated sample) were calculated.

^hBlood samples were lysed after 60 min at 37°C with 0.5 ml PBS (0.5% saponin, 100 U SK, 50 µg trypsin, 1 µg DNase, and 5 µg RNase), followed by CFU enumeration. Data were averaged from two independent determinations, and SEM and percentage of inoculum (0 min = 5 × 10⁶ CFU) were calculated.