

Supporting Information for

Identification of a domain critical for *Staphylococcus aureus* LukED receptor targeting and lysis of erythrocytes

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Running title: Characterization of the LukED-DARC interaction

Materials Included:

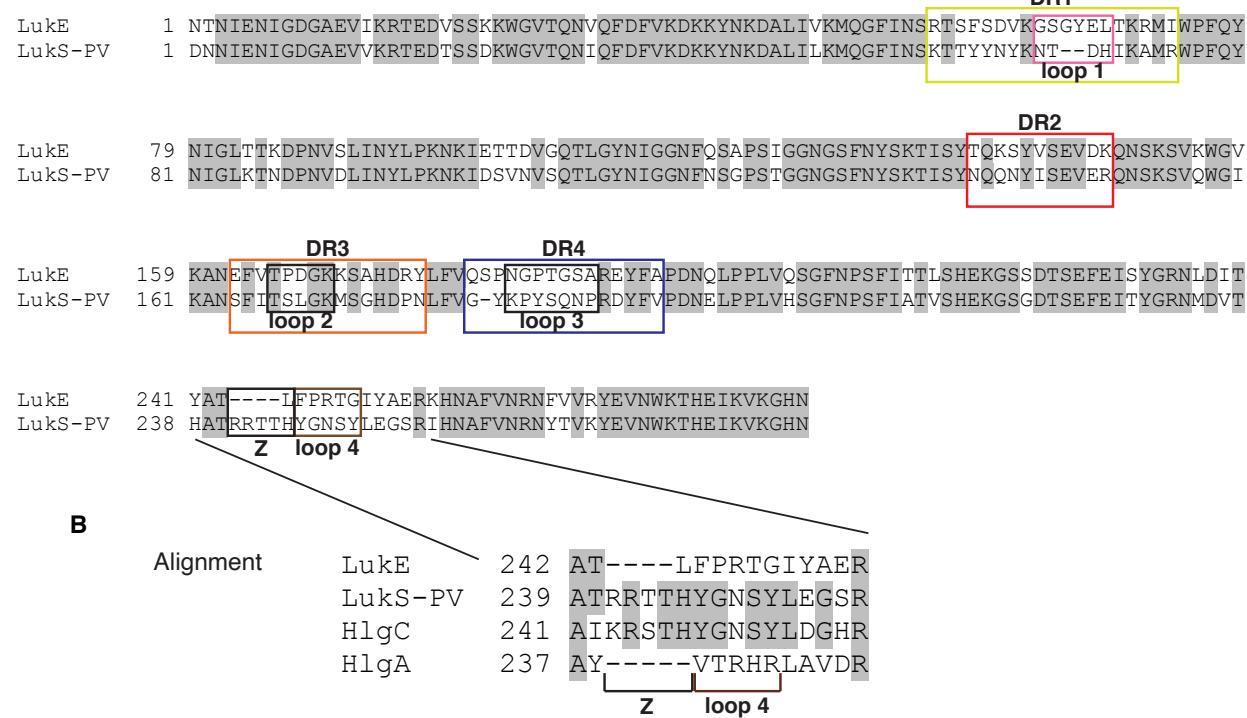
Table S1

Figure S1

Figure S2

Table S1. Primers used in this study.

Primer	Primer Sequence
VJT629	5' CCCGGATCCAATACTAATATTGAAAATATTGGTGATG 3'
VJT629	5' CCCGGATCCAATACTAATATTGAAAATATTGGTGATG 3'
VJT903	5' CTATATGGTTATATCCAACAAATAATCTATCATGCGCAGA 3'
VJT914	5' GACTATTTGTTCCAGACAATCAATTGCCACCTTAGTTCAAAG 3'
VJT1114	5' CCCCTGCAGTTAATTATGTCCTTCACTTTAATTCG 3'
VJT1117	5' CCCCTGCAGTTAATTATGTCCTTCACTTTAATTCG 3'
VJT1186	5' CTGAAAATGAAGTTCTTGAATTGATAAAACCTG 3'
VJT1187	5' AGAACTTCATTTTCAGATGTGAAGGGTAGTGGATATGAATTAACAAACGAATGATT 3'
VJT1188	5' AATCATTGCTTAGTTAATTCATATCCACTACCCTTCACATCTGAAAATGAAGTTCT 3'
VJT1189	5' GCAAGGTTTATCAATTCAAGAACCTTCATTTTCAG 3'
VJT1190	5' CATAACTCTTTGGGTATAACTAATTGTTTTG 3'
VJT1191	5' ACCCAAAAGAGTTATGTCAGTGAAGTAGACAAG 3'
VJT1192	5' CTTGTCTACTTCACTGACATAACTCTTTGGGT 3'
VJT1193	5' CAGTGAAGTAGACAAGCAAAATTCAAAAAGTGTTC 3'
VJT1194	5' CATCAGGCGTAACAAATTCTTACAGCTTTATTCCCC 3'
VJT1195	5' GAATTGTTACGCCTGATGGAAAAAAATCTGCGCATGATAGATAT 3'
VJT1196	5' ATATCTATCATGCGCAGATTTTTCCATCAGGCGTAACAAATTTC 3'
VJT1197	5' CTGCGCATGATAGATATTGTTGGATATAAC 3'
VJT1198	5' GGACCATTGGACTTGAACAAATAATTGGATC 3'
VJT1199	5' CAAAGTCCAATGGTCCAACAGGTTCAGCAAGAGAATATTGCT 3'
VJT1200	5' AGCAAAATATTCTCTGCTGAACCTGTTGGACCATTGGACTTG 3'
VJT1208	5' GCGCGGATCCGATAACAATTGAGAATATTGG 3'

A**B**

Alignment	LukE	LukS-PV
	242 AT --- LF P R T GIYAER	
	239 AT R RT T HY G NSY L E G SR	
	241 AIKR S THY G NSY L D G HR	
	237 AY --- VTRH R LA V DR	
	Z loop 4	

C

Realignment	LukE	LukS-PV
	242 AT L F P R T ---G-IYAE--R	
	239 AT--RR T THY G NSY L E G SR	
	241 AI--KR S THY G NSY L D G HR	
	237 AYV-T R HR-----LAVDR	
	T in basic context	

Figure S1. Alignment of LukE and LukS-PV.

A, Alignment of the mature sequences of LukE and LukS-PV, as in (8). Amino acids highlighted in gray are identical. Regions of low amino acid identity between the two toxins (referred to as divergence regions or DRs) from (8) are noted, as are the loops from (16). *B*, Magnification of alignment from (16) of residues 242-254 of LukE and aligned sections of the other S subunits. *C*, Realignment to highlight shared threonine and basic residues.

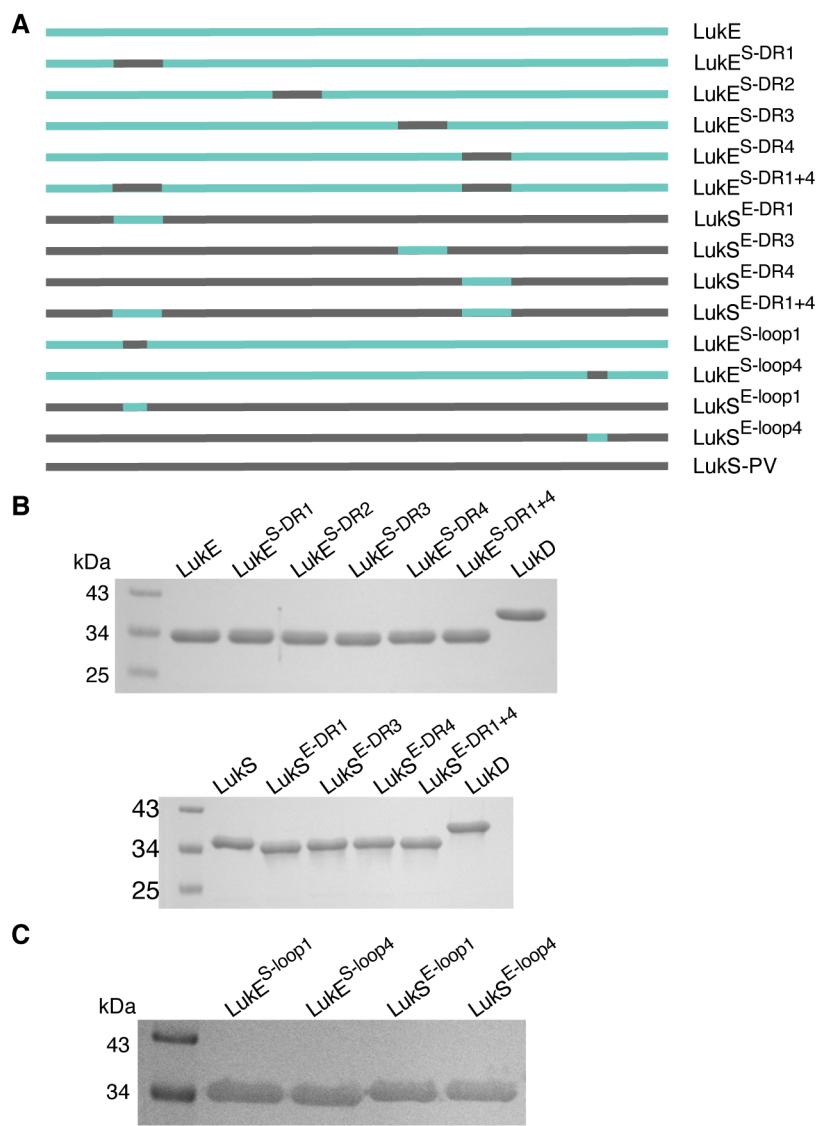


Figure S2. Toxin chimeras used in this study.

A, Diagram of toxin chimeras used. *B*, Coomasie-blue stained SDS-PAGE gels of 2 µg purified LukE and LukS chimeras. *C*, Coomasie-blue stained SDS-PAGE gel of 2 µg purified LukE and LukS loop chimeras as in (16).