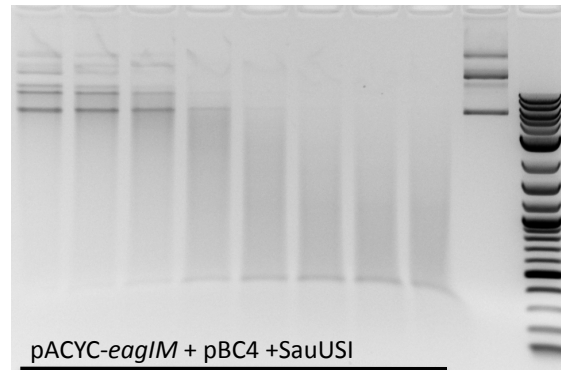
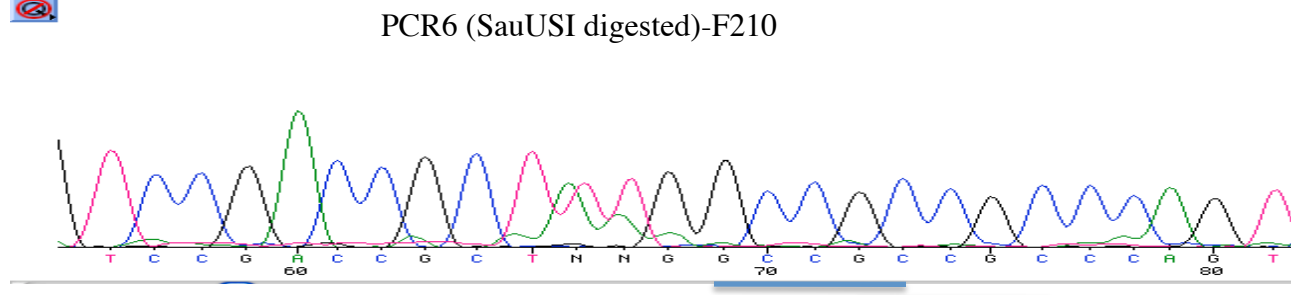
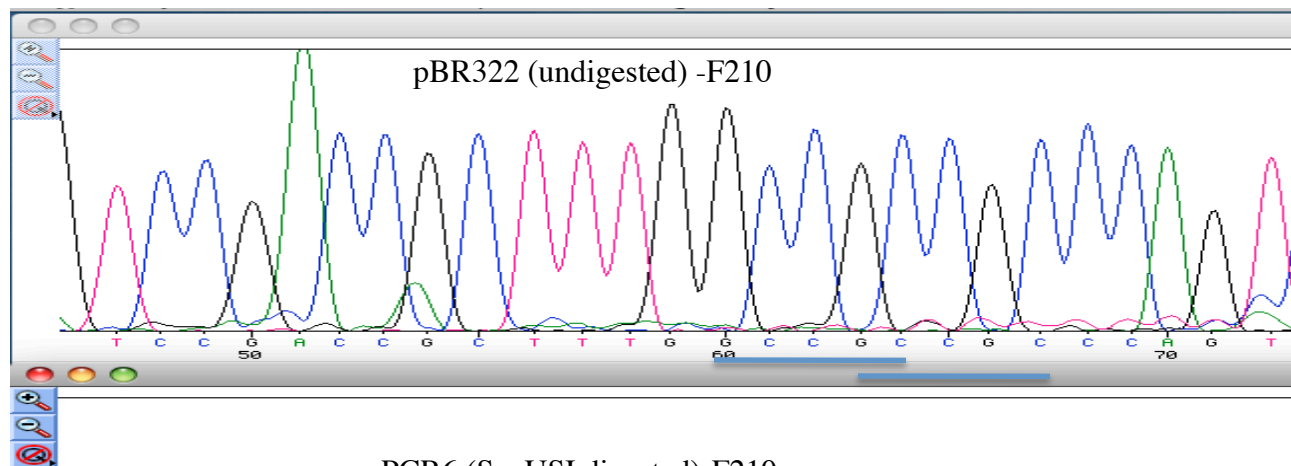


Supplementary **Figure S1**

Min: 2 4 6 10 20 30 40 60 - L



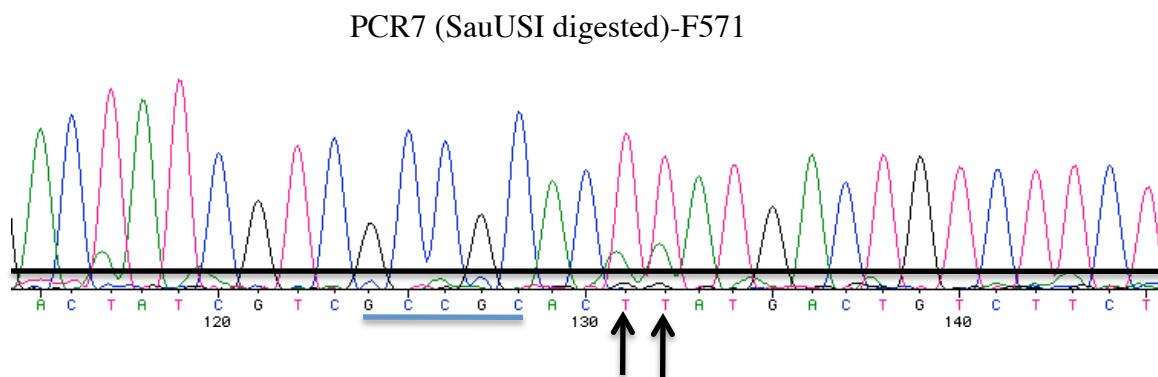
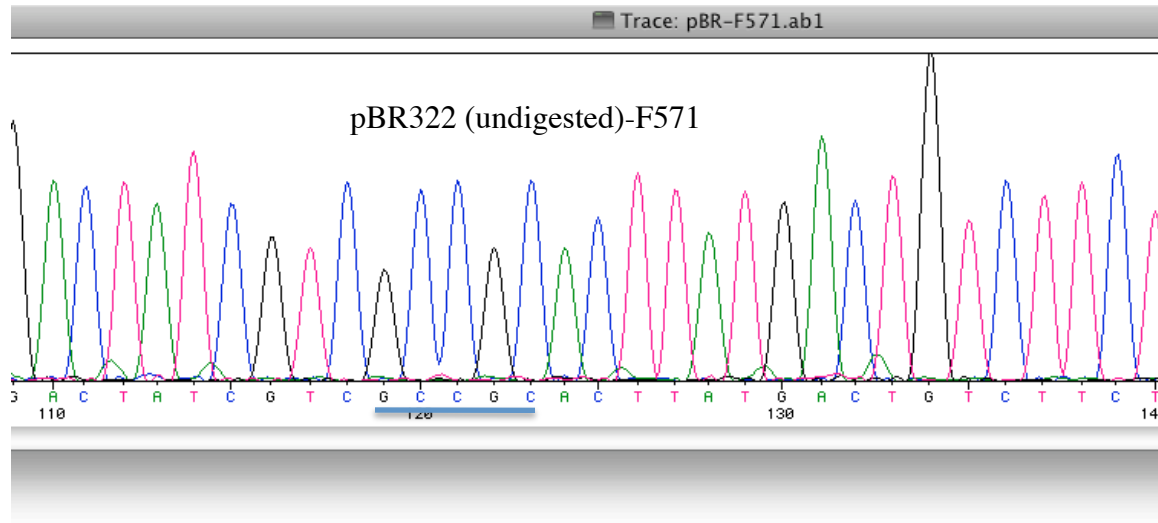
Supplementary **Figure S2**



Primer  
 F210 → 5' TCCGACCGCTWWG**CGGCC**CGCCCAGT 3' (sequencing read)  
 3' AGGCTGGCGAAAC**CGGCC**GCGGGTCA 5' (template strand)

↑↑

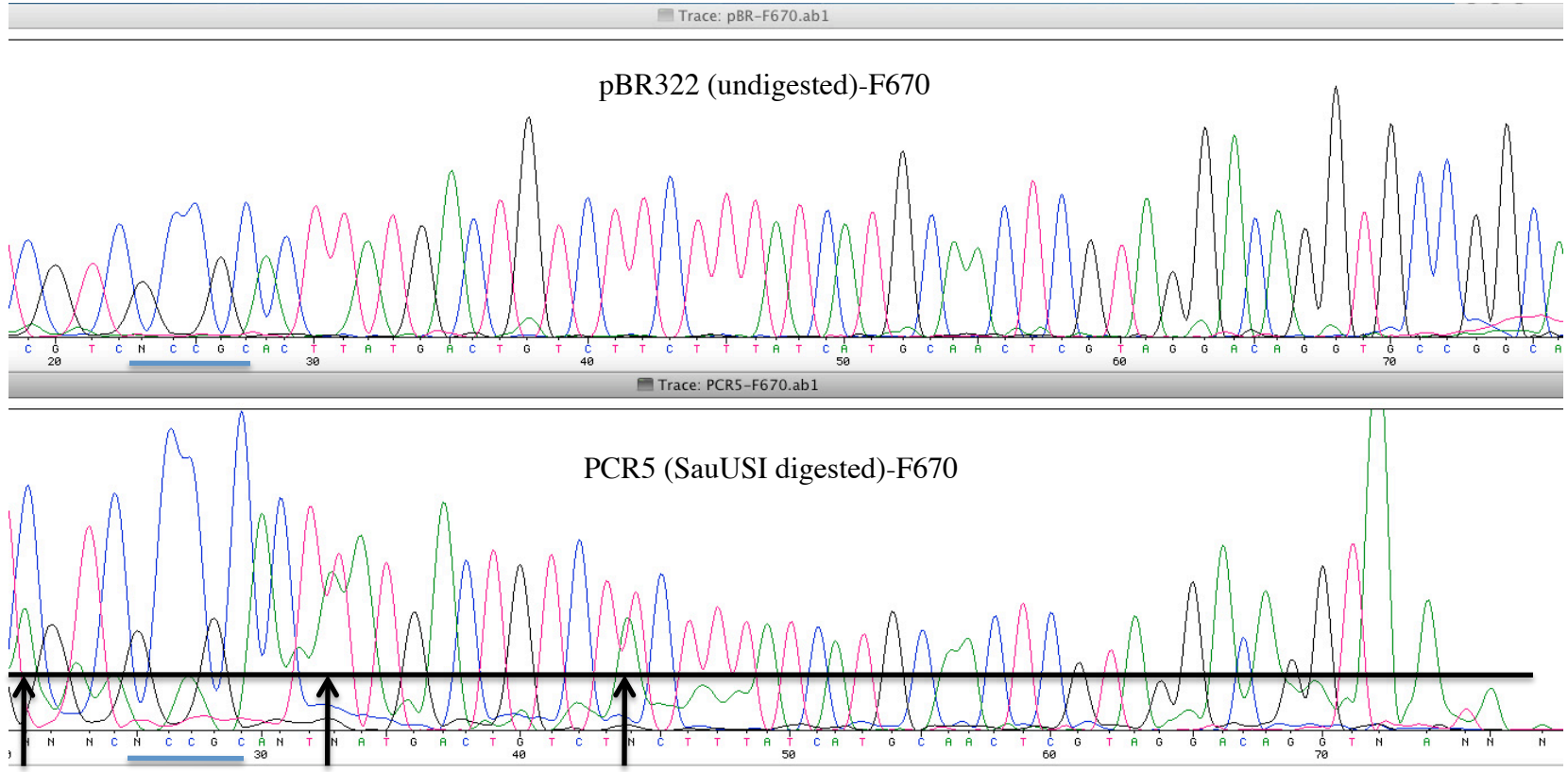
Supplementary Figure S3



5' ACTATCGT**C****GGCGC**ACWWATGACTGTCTTCT 3' (Sequencing read)  
 3' TGATAGCAG**CGGCGT**GAATACTGACAGAAGA 5' (template strand)

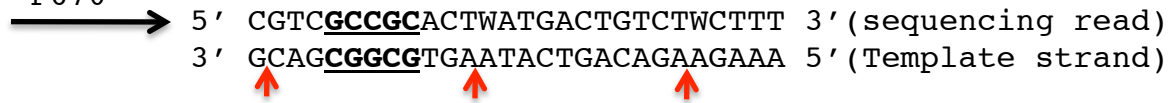
↑↑

Supplementary Figure S4

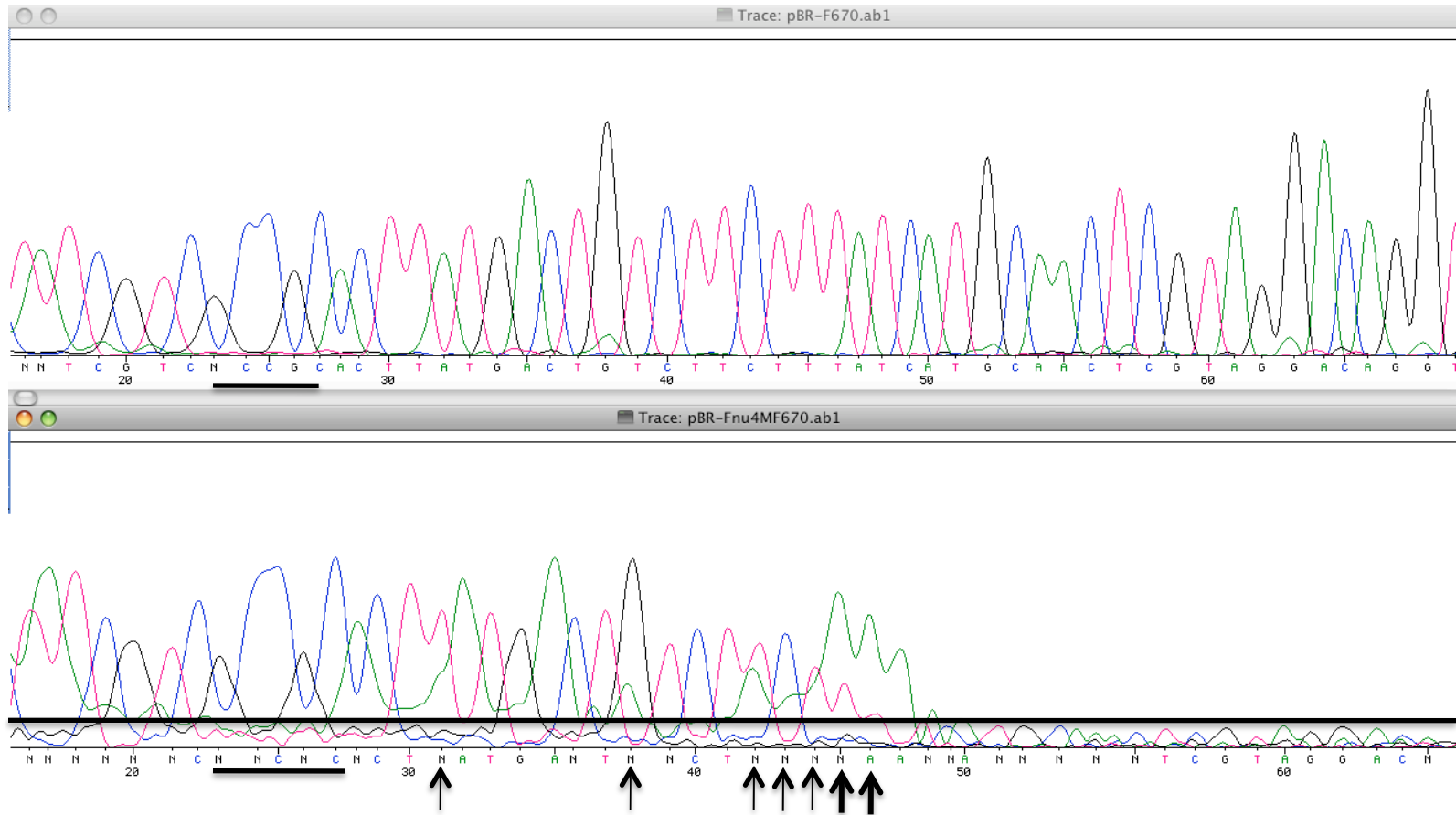


Primer

F670



Supplementary Figure S5



Primer F670

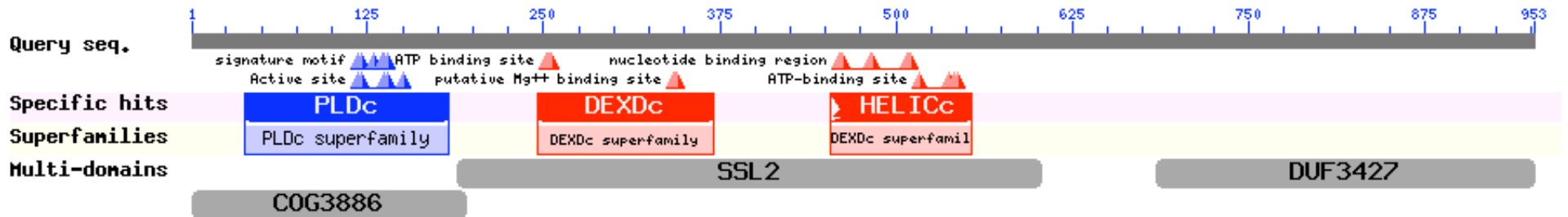


5' TATCGTCGCCGCACTWATGACTRTCCTWCWWW 3' (sequencing read)

3' ATAGCAGCGGCGTGAATACTGACAGAAGAAA 5'



Supplementary Figure S6



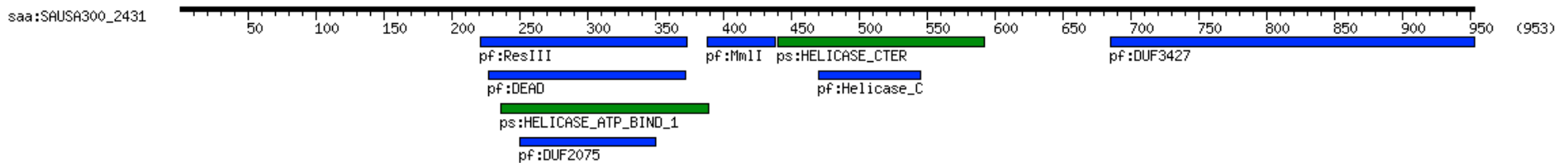
Organism : *S.aureus\_USA300*

Gene : SAUSA300\_2431

Definition : putative helicase

Motif id	From	To	Definition	E value	Score
pf:ResIII	221	373	Type III restriction enzyme, res subunit	1e-33	-
pf:DEAD	227	372	DEAD/DEAH box helicase	3.6e-05	-
ps:HELICASE_ATP_BIND_1	236	389	Superfamilies 1 and 2 helicase ATP-binding type-1 domain profile.	-	2231
pf:DUF2075	250	350	Uncharacterized conserved protein (DUF2075)	0.0014	-
pf:MmII	388	438	Methylmuconolactone methyl-isomerase	0.082	-
ps:HELICASE_CTER	440	592	Superfamilies 1 and 2 helicase C-terminal domain profile.	-	2678
pf:Helicase_C	470	545	Helicase conserved C-terminal domain	2.5e-13	-
pf:DUF3427	685	953	Domain of unknown function (DUF3427)	1.6e-72	-

Search GENES with the same motifs



Supplementary Figure S7