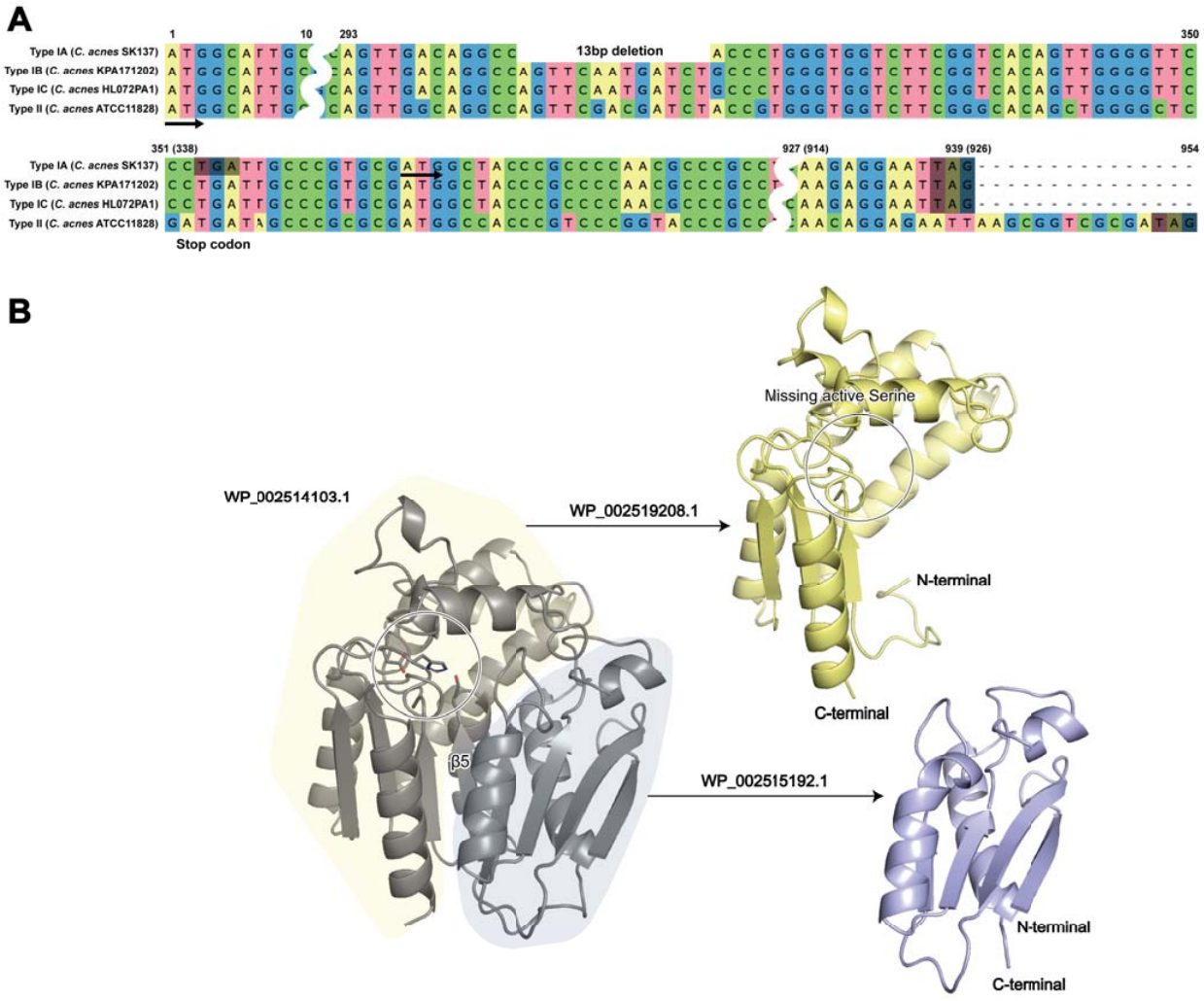
Supplemental Table S1.

Type IA				Type IB	Type IC	Type II	Length (aa)	
SK137	**266**	**J165**	**HL072PA1**	**KPA171202**	**HL097PA1**	**ATCC11828**		
WP_002515192.1	**WP_002515192.1**	**WP_002515192.1**	**WP_002515192.1**	**AAT82349.1 (312 aa)**	**EGE72844.1 (312 aa)**	**WP_002514103.1 (317 aa)**	**113**	**317**
WP_002519208.1	**WP_002519208.1**	**WP_002519208.1**	**WP_002519208.1**				**190**	
WP_002515422.1	WP_002515422.1	WP_002515422.1	WP_002515422.1	WP_002515422.1			318	
	WP_002516281.1	WP_002516281.1	WP_002516281.1				807	
WP_002515849.1	WP_002515849.1	WP_002515849.1	WP_002515849.1	WP_002515849.1			823	
	WP_002515392.1	WP_002515392.1	WP_002515392.1			WP_002515392.1	761	
	AEE73342.1	AEE73342.1	AEE73342.1				237	
WP_002515431.1	WP_002515431.1	WP_002515431.1	WP_002515431.1				407	
WP_002515878.1	WP_002515878.1	WP_002515878.1	WP_002515878.1				309	
	WP_002516320.1	WP_002516320.1	WP_002516320.1				339	
WP_002515456.1	WP_002515456.1	WP_002515456.1	WP_002515456.1	WP_002515456.1			387	

Supplemental Table S1. Conserved potential lipase genes in Type IA *C. acnes*

Conserved lipase genes in type IA *C. acnes* genomes based on the annotations of SK137, 266, J165, and HL072PA1. KPA171202, HL097PA1, and ATCC11828 are shown as examples of type IB, IC and II. Relatively short proteins are only detected in type IA *C. acnes* and these two proteins are highly conserved within a single protein in other types. The sequence homologies of combined type IA proteins (WP_002515192.1 and WP_002519208.1) with type IB AAT82349.1 is 97%, type IC *C. acnes* EGE72844.1 is 96%, and type II WP_002514103 is 83%. This high homology indicates protein on the top column originated from a common ancestor.

Supplemental Figure S1.

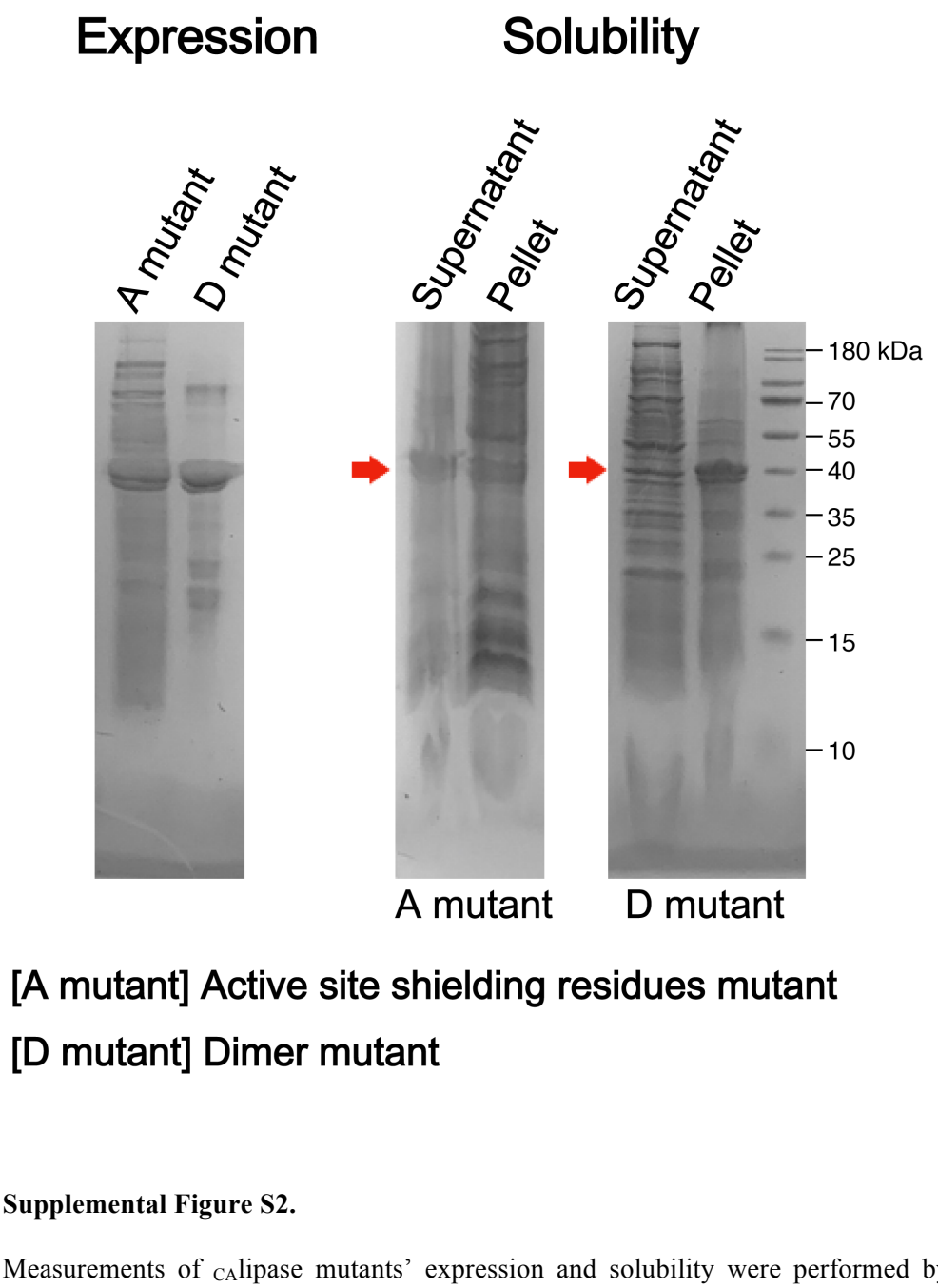


Supplemental Figure S1.

A) Deletions and frameshift observed in type IA lipase ORF. The lipase ORF for conserved lipase proteins that are highlighted in Supplemental Table S1. The nucleotide numbers are indicated above. Type IA strains show 13 nucleotides deletion, leading to a frameshift and introduction of a stop codon.

B) The structures of two short hydrolases from type I *C. acnes* are modeled using SWISS-MODEL workspace (coloured as yellow and blue) based on $_{CA}$lipase structure (coloured as grey). Both structures are considered unstable. Hydrophobic residues are exposed to solvent areas and loops do not support whole structured regions.

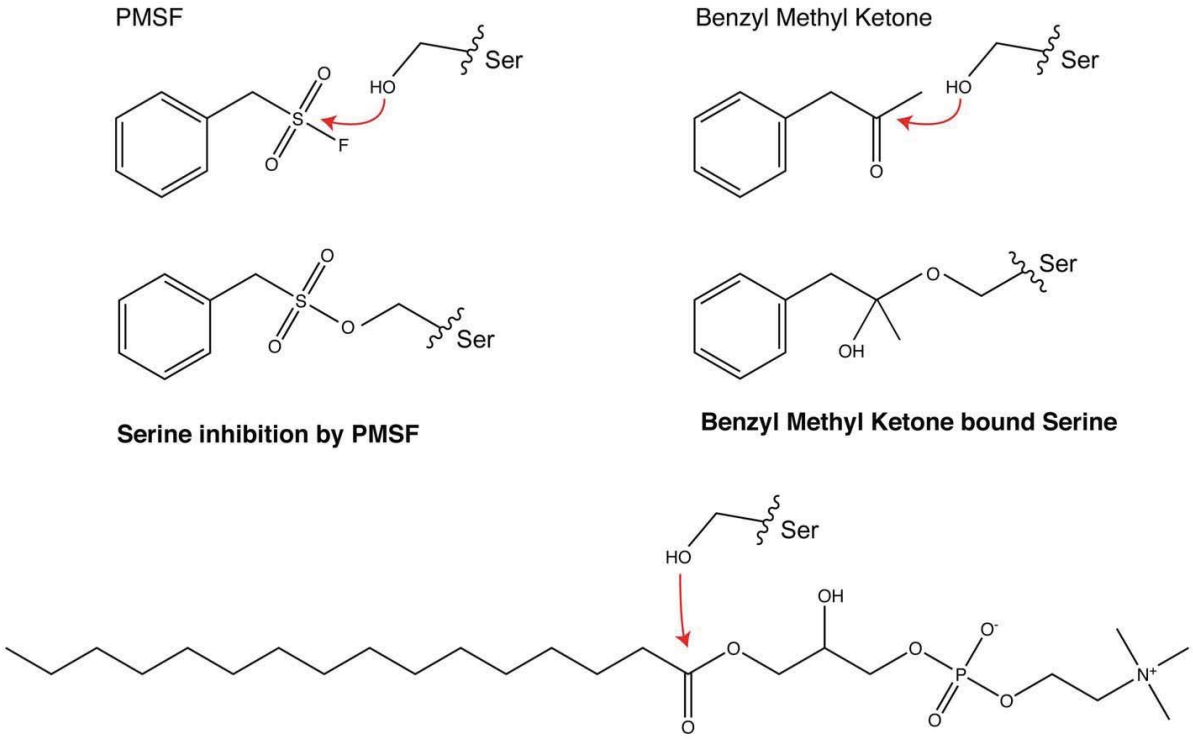
Supplemental Figure S2.



Supplemental Figure S2.

Measurements of $_{CA}$lipase mutants' expression and solubility were performed by SDS-PAGE. *E. coli* BL21 (DE3) cells (Agilent, U.S.A.) were used for all expression experiments. The active site shielding resides mutant (F176F179W192F211A) was successfully expressed in soluble state, but dimer mutant (E5D54D202K205D206A) was produced as inclusion bodies.

Supplemental Figure S3.



Serine nucleophile attacks carbonyl group of lysophosphatidyl Choline (16:0)

Supplemental Figure S3.

Nucleophilic serine attacks carbonyl group of the substrate. The serine becomes covalently attached to the substrate. For the comparison, similar process of serine protease inhibitor, PMSF is shown.