${\bf S7\ Table:\ Variants\ detected\ in\ CP56\ chitinase\ mutants\ and\ BLASTp\ results\ with\ predicted\ impacts.}$

Strain(s)	OrfID	Genbank accession	% identity	Description	Extra info
				Iron-containing alcohol	
	FHMOEFBK_00914	WP_110083220.1	100	dehydrogenase	Catalyses oxidation of ethanol to acetaldehyde
	FUN 40 FFRU 04000		400	ABC transporter ATP-	Regulating the import and export of substances across plasma
	FHMOEFBK_01293	WP_003456102.1	100	binding protein	membranes
CP56∆chiA1	FHMOEFBK 01743	WP 003455172.1	100	Nucleotide exchange factor GrpE	Regulation of protein folding, heat shock
	TTIWOLIBK_01743	W1_003433172.1	100	S66 peptidase family	Regulation of protein folding, fleat shock
	FHMOEFBK 02364	WP 078209983.1	100	protein	LD-carboxypeptidases, bacterial antibiotic resistance
				DUF1667 domain-	
	FHMOEFBK_03168	WP_003450903.1	100	containing protein	Potential metal-binding proteins
CP56Δ <i>chiA2</i>	FUN 40 FFRU 04 CO4	50755400544	00.05	Type IA DNA	E at the Louis India
	FHMOEFBK_01691	EGT5618054.1	99,86	topoisomerase	Function in transcription and DNA replication
	FHMOEFBK 01878	ELC8349289.1	97,78	Zn-dependent exopeptidase M28	Bacterial leucyl aminopeptidases, release N-terminal AA residues from polypeptides
	FHIVIUEFBK_U10/8	ELC0349209.1	97,78	ехорершаѕе мі28	пош розурершиех
	FHMOEFBK_02207	WP_011009793.1	100	Carbonic anhydrase	pH regulation
				Peptidylprolyl	Interconverts the cis and trans isomers of peptide bonds with the
	FHMOEFBK_02477	WP_003456782.1	100	isomerase	amino acid proline
CI SOLITIME	FUN 40 FFRU 00000		400	Mechanosensitive ion	
	FHMOEFBK_02990	WP_004458069.1	100	channel family protein	Osmotic balance
	FHMOEFBK_03023	WP_110083405.1	100	Arylsulfatase	Cleavage sulphate-containing fats
				Branched-chain amino	
				acid transport system 2	Diffusion of sugars, amino acids, and nucleosides across
	FHMOEFBK_03131	WP_003458178.1	100	carrier	membrane
				MIP/aquaporin family	Aqueous pores, passive transport of their solute(s) across the
CP56∆chiB1	FHMOEFBK_00530	WP_004457307.1	100	protein	membrane
				Putative manganese-	
	FUNADEEDIK 04764	MAD 0044570404	100	dependent inorganic	Control biomethodic continue that another Dai DNA conthacia
	FHMOEFBK_01764	WP_004457849.1	100	diphosphatase	Controls biosynthetic reactions that produce Ppi, RNA synthesis
				CoA-substrate-specific	Provide a reactive electron that their cognate enzyme requires for
	FHMOEFBK 00810	VTQ57712.1	99,8	enzyme activase	activity
	111110E1BK_00010	71007712.1	33,0	DUF4091 domain-	Domain with uncharacterised function, often conserved in N-
	FHMOEFBK 00922	WP 110083215.1	100	containing protein	acetylgalactosaminidases
	_			V-type ATP synthase	Produces ATP from ADP in the presence of a proton gradient
	FHMOEFBK_01347	WP_003449648.1	100	subunit A	across the membrane
				50S ribosomal protein	
	FHMOEFBK_01431	WP_003449428.1	100	L32	Binds/regulates splicing and translation of transcript
				Alpha/beta fold	Catalyze bond cleavages by reaction with water, break down
	FHMOEFBK_01947	WP_224391477.1	100	hydrolase	nutrients for digestion
	FUNDOTERK 01040	WD 079200064.4	100	IS110 family	Dinding/estal restion transposes to DNA
CP56∆chiB2	FHMOEFBK_01949	WP_078209964.1	100	transposase	Binding/catalysation transposon to DNA Hydrolyzing glycosidic bonds in peptidoglycans, function
	FHMOEFBK 02166	WP 057230598.1	100	GH25 family lysozyme	debatable
	THINIOELDK 02100	WF_U3/23U330.1	100	DNA-directed RNA	uevatavie
				polymerase subunit	
	FHMOEFBK 02803	WP 224361666.1	99,92	beta'	RNA synthesis
		.71_22-301000.1	33,32	500	11111 1 3 7 11 11 12 13