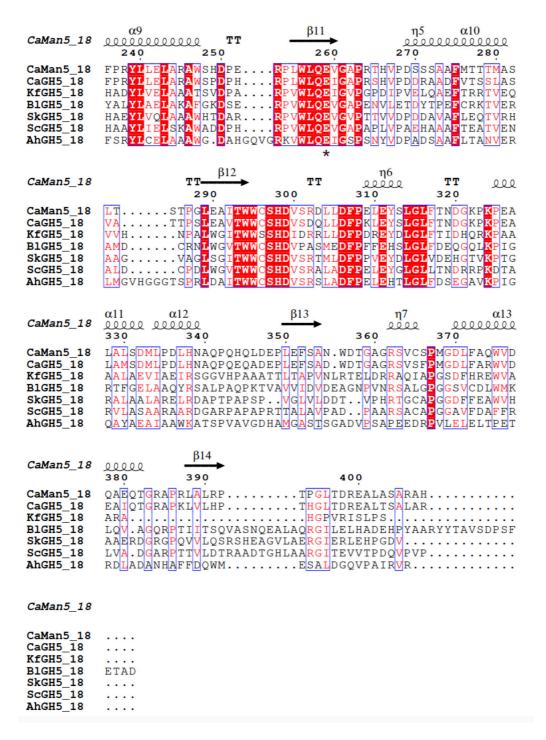
## S4 Fig. Sequence alignment of CaMan5\_18 and family GH5\_18 homologs.

		В1	n1	α1	β2
CaMan5_18	1	10	20	α1 000000000000000000000000000000000000	10
CaMan5_18 CaGH5_18 KfGH5_18 B1GH5_18 SkGH5_18 ScGH5_18 AhGH5_18	MLSDPATPRFMKFMRF	GVNHTPSQG GANYVPSSG GVNYTPSHG GVNYTPRVG GVNYTPSVG	WFHSWLDLD WFHSWLDLD WFYSWLDYD WFHAWLDPD WFHAWLDHD WFHHWLDFD	IDATRRDFEGI IDATRRDFEAI GDAVRRDLADL WDGIDNDLKQI RDAVRRDLEQV LDSVRADLDSI	AQLGLDHVRLFP ARLGLDHVRIFP AGLGLDHVRVFP SELGMDHVRIFP AALDLDHVRIFP AALDVDHVRVFP AGLGLDHVRIFP
CaMan5_18	α2 0000 TT 50	60	α3 00000000 <b>70</b>	-β3 80	β4 <b>TT</b> → Ω
CaMan5_18 CaGH5_18 KfGH5_18 B1GH5_18 SkGH5_18 ScGH5_18 AhGH5_18	LWPLLQPNRG VWPWIQPNRA IWPYLQPNRT LWDLVQPNRG LWPYFQPNRT	LVRPRALDD IIRQRAVDD WINKKGVAD HIRPAALAA LIRERAVED	VVSVVRA <mark>A</mark> G LLDTIDAAA VRRMVHIAG VADVVDAAA LVALVDAAG	EFDLEVT <mark>VD</mark> AL EHGLTVAVDLV EHGLDAYVDVF EVGLDVNVDAL ERGLDVNVDGL	NGHLSSYDFLPP NGHLSSYDFLPS QGHLSSFDFLPS QGHLSSFDFLPS QGHLSSFDYLPA QGHLSSFDYLPA QGHLSSFDYLPS
CaMan5_18	η2 η3 ου ουο 100	TT 000000	α4 000000000 12 <b>9</b>	000 TT <u>β</u>	6 η4 20000 *140
CaMan5_18 CaGH5_18 KfGH5_18 B1GH5_18 SkGH5_18 ScGH5_18 AhGH5_18	WVVTWHESNI WALTWHKASI WLVTWHAGNM WLTTWHERNM WTRTWHRRNI	FTDPLVKAG FEDSTVRAG FTDADAVAA FTDPDALAG FTDPDVVEG	QTELIIQLV LTAYCAAVA ERELVKTMT EEAYLRALG QAAYLRTLA	TRLREE <mark>P</mark> NVTG GAVSSRPNVFA DELSKE <mark>P</mark> AFKG ETLRGRPNLMG AALAGRPNFLG	MTVGNEFPQYAA MTVGNEFPQYAA ITLGNEVNNLWP LTLGNEVNQLSD LTLGNEVNQFAA MTLGNEVNQFSA LSLGNEFIQFAA
CaMan5 18	β7 β8 <b>TT T T T T T</b>	00000	α5	0000	_β9
Camalis_18	150	160	170	180	_
CaMan5_18 CaGH5_18 KfGH5_18 B1GH5_18 SkGH5_18 ScGH5_18 AhGH5_18	LAPGHHHP TR DSSTTP RPHPTK RPHPRP GPHPDP	SGCTIDEAQ ATST MSATDRQID HEIDADQAE DRATSAOID	TWLETMLGT AWAQELLTT AWLDALLPT AWLRRLLGA AWLERMLAA	MRD QWPD VKKAAPD AAGEGHN AREGLLGTEGA CEEGAPG	
CaMan5_18	<ul><li>α6</li><li>190</li></ul>	200	α7 210 <b>–</b>	β10 220	α8 000 230
CaMan5_18 CaGH5_18 KfGH5_18 B1GH5_18 SkGH5_18 ScGH5_18 AhGH5_18	WFGFDDDLWF LHSIFDDAWY LYSVNDGTWF THAAYDATWY LHAEYDATWY	VDDHPFTPR RPDHPFSPV IDGHPFTPV DERQPFLPR QDDQPFTPA	.HAVTL <mark>G</mark> SST DVVDLGELS QSATKGDMT .HAAELGDQT .QAARQGAVT	TIHSWVFAQVG TVHSWVFNGVS VIHSWVFNGIA VVHSWVFNGAA AVHSWVFNGTA	PRFCEGHPALTW PHFCEGHPALTW RVDCPLGPATLT QGYCATSEECSS QRHCGLGTGSVR QRHCRTSVPSEH PRFCAGTPQLEW



Sequence alignment using Clustal Omega (https://www.ebi.ac.uk/Tools/msa/clustalo). Strictly conserved and highly conserved residues are highlighted with red boxes and red lettering, respectively. Secondary-structure elements are shown on top as spirals and arrows for α-helices and β-strands, respectively. Solid stars indicate the active-site residues that are conserved. The GenBank accession numbers are as follows: CaMan5\_18 (AEE72695); CaGH5\_18 from *Cutibacterium avidum* 44067 (AGJ77370); KfGH5\_18 from *Kribbella flavida* DSM 17836 (ADB34475); BlGH5\_18 from *Bifidobacterium longum* subsp. infantis 157F (BAJ71452); SkGH5\_18 from *Sanguibacter keddieii* DSM 10542 (ACZ21418); ScGH5\_18 from *Streptomyces coelicolor* A3(2) (CAB61915) and AhGH5\_18 from *Arcanobacterium haemolyticum* DSM 20595 ADH91800). The figure was prepared with ESPript3 (http://espript.ibcp.fr/ESPript/ESPript/).