

**Supplementary Figure 1(a).** Alignment of the O-Antigen ligase domain-containing predicted proteins for each of the types assigned for *wa* Region 1.

```

olc1_piscicola_  -----MPIRCLYL-----LDKTTTALFALT-----I
olc2_salmonicid -----MSIRSLEL-----LDKATTALFALV-----I
olc22_tecta      -----MSIKPLEI-----LDKVTTAVFALT-----I
olc4_veronii_Hm  -----MAQNSRKLCLEIKVISKNAISMERFALLIFSCT-----L
olc5_popoffi     -----MT-----L
olc6_enteropelo  -----MNMTQY-----FHRLNVLIFSCT-----L
olc21_taiwanens  -----MPINSKIL-----LVRMTIGLFSLS-----I
olc20_veronii_A  -----MTIEKVTEYFFALT-----I
olc11_veronii_A  MI-----TICKNKKI-----VSYMLHAYYLLP-----M
olc25_sp_ZOR000  -----M-----M
olc7_veronii_B5  -----MAICSPLI-----MPFRSHLTHNLVQTS-----A
olc12_caviae_42  -----MILASPII-----LPLRINILHNLVQVS-----A
olc13_media_423  -----MTLASPII-----LPLRINILHNLVQVS-----A
olc14_media_ws   -----MTLASPII-----LPLRINILHNLVQVS-----A
olc15_allosacch  -----MFLGNKLFMTPTHNIF-----LSWRDNATHNLVQVG-----A
olc9_allosaccha  -----
olc19_sobria_42  -----
olc24_salmonici  -----
olc23_145        VT-----SYKKYLRINIIVQFA-----A
olc17_jandaei_4  -----MQEIMMV-----LFSKEKFVPMVQAS-----A
olc18_sp_EERV15  MCSGCGVKSVMGIMFLES--EKRRKMMV-----LVNKERFVPLVVQTS-----A
olc26_enceleleia -----MYLGSK--MYPTISII-----PTKRAELLPWLVLQLS-----A
olc8_bv_sobria_  MFSENNVAVEKQMSLEKN--PTIIGSHF-----FLNRRNIFPLLVLQLS-----A
olc10_caviae_83  MSSENKVVVEERMPMQTE--SPPNQGAF-----GLVHDQALPLLVLQLS-----A
olc28_caviae_42  -----
olc3_caviae_A23  -----MTDH--DSSTSDYFL-----R-----IFHGQAFGNFI
olc27_simiae     MLL-----LDIFKSH-W-----PSGRRQVESVLRYGGLAC--L
olc16_diversa    -----MFSE--NEKKSTGF-----NCLMIEKILVGIFSAS-----I
olc29_veronii_1  -----MKEKKM-----NYKKIETYLLCLLAAS-----I

```

```

olc1_piscicola_  IF----SFCGLFLVPAGQSIESNLLAVTGIFGLL---NYFVGKQQDVGLKD--RRILWGL
olc2_salmonicid  LF----SFCGLFLVPAGQTILSNLLVVASVFGLL---NYFVGKKRDVGLED--RRILWVL
olc22_tecta      AF----SFCGLFLVPSGQSILSNLLVSGVLGLL---NYFIGGKKEVLFTD--RRLIWIF
olc4_veronii_Hm  IF----AFSVMFFFTDGKTYLSNLIVVASIIGMV---SFYI-HRYPVGFKN--RHIIWVL
olc5_popoffi     FF----TLCGLFIVPLGQHYLTKLVLSSIIGVI---NYFVGKNKELIGVSA--KNLYWCV
olc6_enteropelo  FF----TLCGLFLVPQGNHYLSKLLVLSSIVGFI---NYFIGNKDKLGVSA--KNLYACV
olc21_taiwanens  IF----LFCGLFIVPSGTSYMSTLIVLSCFFGVV---NFFTGDKTSVGLRD--KRLLEAF
olc20_veronii_A  FF----AFGFLYASARGHSYLSIFVVISIILGAI---NLIY-NKEIGTLKSGCGFLKIT
olc11_veronii_A  LI----LSCLAFNTEDGKHYISRLVVAMFIIISLFTARKILWSNLNPEI---KRIMFFW
olc25_sp_ZOR000  LI----LSCLTFTTFDGKHYISRLVVVMFVISCVFCRNTIINNIIKAEV---RRILFFG
olc7_veronii_B5  FF----FGALCLAIPSGYSYGPVLLSIMSLFVFW-RADYWLAMSREA-----KILFWIF
olc12_caviae_42  FL----FGALALTIPSGYSYGPAILLLASITVCW-RPFYVWNMPREV-----KILALIF
olc13_media_423  FL----FGALTLAIPSGYSYGPAILLLASLTVCW-RPSYWMNMPREV-----KILALIF
olc14_media_ws   FL----FGALTLAIPSGYSYGPAILLLASLTVCW-RPSYWMNMPREV-----KILALIF
olc15_allosacch  FL----FGALSLAIPSGYSYGPAILLAVSLTVCW-RPLYWLRMPKEV-----KMLALFF
olc9_allosaccha  -----MSSEV-----KILSYIF
olc19_sobria_42  -----MSSEA-----RILSYIF
olc24_salmonici  -----MSSEV-----KILSYIF
olc23_145        FL----FGAIVLTVPSGYGYGPSILVLASFFVFW-RKKYYLAMSESA-----KTLLYIF
olc17_jandaei_4  FL----FGALALAVPSGYSYGPALLAVVSLFVFW-RKDYL SAMEKEH-----KIIASLL
olc18_sp_EERV15  FL----FGALALAVPSGYSYGPALLAIVSLFVFW-RKEYLSAMEKEH-----KIIASLL
olc26_enceleleia FS----FGALAIAIPSGYSYGPALLAIVSLFVFW-RKEYLDCLTKEH-----KVVAALL
olc8_bv_sobria_  FL----FGALALTMPSGYSYGPGLLLLAGLGFIICKRSSALS LPFEL-----KIISLAF
olc10_caviae_83  FL----FGALALSVPSGYSYGPALLLLASLCFFAVRRLNWV-LPREL-----KFIGLGL
olc28_caviae_42  -----MPREL-----KLIGLGL
olc3_caviae_A23  FLNILGYTLFKDSIQLIADVCQTIIIVLATLMAFYVERAFFTRNRIF-----QLLCLAL
olc27_simiae     FL----YALSRLALPGLGKGLEIGYVLAGAILLFGWRRELLGSIYI-----KLLLLAL
olc16_diversa    FV-----SKPAITISMAVLVGFSLFYFKDGEYRSALRG-----DAIVSS
olc29_veronii_1  FT-----SKPAIYISSALMIVFFIGRCIFDRDYNNVVKR-----NIVLWGP

```

:

olc1\_piscicola\_ VVYAAMIFVNRLI---HGDQYGVMRGLFYVVIFALMMP-----RKPILLMLGYLAIVLG  
 olc2\_salmonici AAYAAMIFVNRLI---HGDQYGVMRGLFYVVVFALMIP-----RKPVLLTLGYAAIVTG  
 olc22\_tecta VFYATVILINRII---HGDQYGVMRDLFYVSVFSLMMP-----RKILFSVGCIAILIG  
 olc4\_veronii\_Hm LFYAIYLFVNRQI---HGDQYGIMRAIYVIVFFTFLLIP-----RNVFLLKAGCYGVILG  
 olc5\_popoffi LIYIVAIGISRLV---HDDSWLIRNLILYLAFFLLMP-----REAVLVSFVKLGSLVG  
 olc6\_enteropelo LIYIAAIGASRLV---HDDSWLIRNLILYLVFFLFIP-----REAVIRALKLGLALIG  
 olc21\_taiwanens LAYALVILVNRQI---HGDASWIMRNILYVIVFSFFLP-----RERIIINIGVLSVIMG  
 olc20\_veronii\_A LMYGIVMIFNRLS---HGEDSALIRITLFFTAFFVFFVP-----KTELIKKYAIYGAITG  
 olc11\_veronii\_A ILIAVVFAGYHIF---RGEVFSAPRAILVSLLYLLVVP-----WHRIQKQMVLLLVILFG  
 olc25\_sp\_ZOR000 FSVVVFSLYSIF---RGEQFSMPRTILVSLLYIVIVP-----WQMISLNVRLSIVLG  
 olc7\_veronii\_B5 IFYFMVQAISISL---DNGALKELDRPSRALMAAIIPLLL---SKHRVHLVSIMSGFALG  
 olc12\_caviae\_42 FAYVFVQGLSIWL---DGGKLRFDPRSRVLMAAITLPLL---SRYPVRLVSLIFGVAVG  
 olc13\_media\_423 FAYVFVQGLSIWL---DGGKLRFDPRSRVLMAAMTLPLL---SRYPARLVSLIFGFAVG  
 olc14\_media\_ws FAYVFVQGLSIWL---DGGKLRFDPRSRVLMAAMTLPLL---SRYPARLVSLIFGFAVG  
 olc15\_allosacch ILYALVQGLSILL---DNGSVREFDRPSRVIMATLILPLL---VQNPVRPITISLGVAVG  
 olc9\_allosaccha VSFFVIQAVSIGI---DGGTLKELDRPSRLLMAAMTLPLL---SVFPININVLIAGLSIG  
 olc19\_sobria\_42 ISFFIIQAVSVWV---DGGVLKELDRPSRLLMAAMTLPLL---SLFPVININVLLAGLSIG  
 olc24\_salmonici IAFFIIQAVSIWI---DGGTLKELDRPSRLLMAAITLPLL---SALPININVLIAGLSIG  
 olc23\_145 IAFFITQAIISIWI---DDGSLKELDRPSRLLMAAMILPLL---SVFPVININFFIAGLSIG  
 olc17\_jandaei\_4 LSYFVLFLISVIF---DGSSFSQLDRPSRALMAALVIPTL---ARHKVKLEVLLCGFACG  
 olc18\_sp\_EERV15 LSYFVLFLVISVIV---DGSSFSQLDRPSRALMAALVIPTL---AKHKVKLEVLLCGFACG  
 olc26\_enceheleia FLYFLVLVSTML---DSRELSQLDRPSRALMAMTLPLL---ARHKVKLDVLLFGFVG  
 olc8\_bv\_sobria VFYFVMSISVWL---DGGRISEIDRASRALMAAAMLPLL---ARVPVRLPMLLSGIGIG  
 olc10\_caviae\_83 SLYFLVMVISVWF---DGGKISQIDRASRALMAVILPLL---ACVPVRLPILLSGCGVG  
 olc28\_caviae\_42 LLYFLVMSLSVWL---DGGKFSEIDRASKALMAAAILPLV---ACMPVRLNILLSGCGIG  
 olc3\_caviae\_A23 VVQSLSWVASRQFVPDYALKYPSVKSMAYLFFFLGLAYWL---KGDPRRIVITLLTFLCLG  
 olc27\_simiae LVQCIPWVIGHFTSLPTAEGNPGLDRLLKLYLFLLGSTLL---EGRERRVFWLWGCAALG  
 olc16\_diversa IVVFIVGLFSRLL---SPGDIRDVGYFFYKGLFLVFPILLTFRDKENRQLAFVLSMAG  
 olc29\_veronii\_1 IAVFLFGVFAKII---SPSSFVDIGHFFYKGMFFLVFPALVISLREKTNRQLAFSISMLG

\*

olc1\_piscicola\_ GMGL-----GMLSIWQYQ-H-----GMVRVEG-FTNAILFSQAALTILAILN-WF-----V  
 olc2\_salmonici GIGL-----GIMSLWQYQ-S-----GIVRVEG-FTNAILFSQAALTILAILN-WF-----V  
 olc22\_tecta GIGL-----GLLSLWQYE-N-----GIVRVEG-FTNAILFSQSALTILAILN-WC-----L  
 olc4\_veronii\_Hm GFGL-----GVISIWQYN-H-----GVARVEG-FTNAIFSQALTILAILN-SF-----F  
 olc5\_popoffi GIAI-----GLLAIWQYH-N-----GMLRVEG-FTNAILFAQGALILAILN-FW-----F  
 olc6\_enteropelo GISI-----GLLAIWQH-Q-N-----GMFRVEG-FTNAILFAQGALILAILN-GF-----F  
 olc21\_taiwanens GISI-----GGLSVWQYY-H-----GLDRVEG-YTNAILFSQAALVMFILN-MM-----F  
 olc20\_veronii\_A GWIV-----GFLAIKEVS-E-----GISRVGG-YTNAILFAQGALVLFILN-LH-----V  
 olc11\_veronii\_A GCVA-----GAVGLYEYAVL-----DIRRVGG-VINQIPFALYVAITLLIA-----IY  
 olc25\_sp\_ZOR000 GVAA-----GILGVYEYAIL-----DISRIGG-VVNQIPFTLYVAITCVIS-----IA  
 olc7\_veronii\_B5 AVIS-----GFIAIYDKIYI-----GMERAFG-DGMPIQSGNISMTLGLFC-LCA---YF  
 olc12\_caviae\_42 ACIA-----GSAIYDKFYL-----GMERAFG-DIMPIQAGNISMTLGLLC-LCG---YF  
 olc13\_media\_423 ACIA-----GAIAIYDKFYL-----GMERAFG-DIMPIQAGNISMTLGLLC-LCG---YF  
 olc14\_media\_ws ACIA-----GAIAIYDKFYL-----GMERAFG-DIMPIQAGNISMTLGLLC-LCG---YF  
 olc15\_allosacch AFIA-----GIVSSYEKFYL-----GVDRAFE-NMMPIQGGDISMTLGVLS-LCS---YF  
 olc9\_allosaccha AVSS-----GLIAIYEKFYL-----GMPRAFD-ESMPIQSGNISMTLALLC-LCA---FF  
 olc19\_sobria\_42 AISS-----GLIAIYEKVYL-----RMPRAFD-DSMPIQSGNISMTLALLC-LCA---FF  
 olc24\_salmonici AISS-----GLIAIYERFYL-----GMPRAFY-ASMPIQSGNISMTLALLC-LCA---FF  
 olc23\_145 AISS-----GLIAIYEKVYL-----RMPRAFD-DSMPIQSGNISMTLALLC-LCA---FF  
 olc17\_jandaei\_4 ALIA-----ACIAIYDKFYL-----GYERAFEFYSIPIQSGNISMSLGLFC-LCG---YF  
 olc18\_sp\_EERV15 ALIA-----AGIAIYDKFYL-----GYERAFEFYSMPIQSGNISMSLGLFC-LCG---YF  
 olc26\_enceheleia AIIS-----ACIAIYDKFYL-----GYERAFDFYSMPIQSGNISMSLGVFC-LCG---FL  
 olc8\_bv\_sobria SILA-----FGIAVYDKFVL-----GYERAFS-DMMPIQSGNIAMSLGLFC-LCG---MF  
 olc10\_caviae\_83 ALLA-----CGIAIHDKFIL-----GYERAFN-DMMPLQSGNIAMSLGLFC-LCG---LL  
 olc28\_caviae\_42 AILA-----FAIAIHDKFFL-----AYERAFG-DVMPIQSGNIAMSLGLFC-LCG---LL  
 olc3\_caviae\_A23 VIFTFAYHSSFFSIVETGLD-----GARVDFN-YRNAQHGS LIAGACFLFFVLLL---LT  
 olc27\_simiae LLAVVL---VQLPEWQRGLK-----GMRVDFG-IRNAQHTAMFFGILLGC-VCFAGRWL  
 olc16\_diversa FSIS-----VFMSFIQAFILPDAGWNGERVSG-LWDILRWAEITTFVFVFL-----LA  
 olc29\_veronii\_1 FLLS-----VLWSFVQAFVLLPHTWGGGERFGG-FWDIGRWAEITTFVFVAFM-----LP

:

olc1\_piscicola\_ FQQRWLPRWFRRGALIGLIAALFALYLSQSRGVWLALGVILAYVIC-YKAYFKPWKYVAV  
olc2\_salmonici FQQRQLLRWIRYGALVALVAALFALYLSQSRGGWLALGGIVGYVIC-YKALFKPWKYIAI  
olc22\_tecta FIRARKVCWVKTGSLSVITASLLALYLSQSRGVWLALGAVIGLLII-YKSLYKPLKYAFI  
olc4\_veronii\_Hm SVSFSENRLKWFHIIISALFSLGALYLSQSRGVWLAFMVVITCFLL-FKIKTKPLKYISI  
olc5\_popoffi FAQESSLLARCLYIISIFAISAIYLSQSRGAWLALVVVTVFLF-VKAIKEPIKYFSW  
olc6\_enteropelo FGQDESNNKFVKCGYLIGAGAAVIAIYLSQSRGVWLALLMLAMLALS-IKATKKPVKYMAL  
olc21\_taiwanens VVFSCQRIYVSFLASVAVLGSYALYQSQRGVWIAAVFIIMIVSF-VKLKHKPIKLSLL  
olc20\_veronii\_A LFHESQAITKKLITIIGVGLSLVAIYLSQSRGVWLSLIIVMVVYFT-VN-RHILIKNIRI  
olc11\_veronii\_A TVLNNQNRNVNLLVWLSIIGSVFAIVMSEVRGVWLALIFTAILVC-YQLKKWTVRRMAS  
olc25\_sp\_ZOR000 TYLQCDNKYLKVLVSIVLSGVSFAIMTEVRGVWLSIILTIISLVL-FQLKRFGARRISL  
olc7\_veronii\_B5 WHRENNEYVFSKIMLAACLMLGSLSGTRGGWVLLPVIITTIMHYQRSGRRYFLWVF  
olc12\_caviae\_42 WYKSKGNIKTAMFMLFACAMGMLGSLSGTRGGWVLLPIIILTIIVNHFRGNLCRIDKIVS  
olc13\_media\_423 WYKSKGNVKTAMFMLFACAMGMLGSLSGTRGGWVLLPLIILTIISHFRGNLCRIDKIVA  
olc14\_media\_ws WYKSKGNVKTAMFMLFACAMGMLGSLSGTRGGWVLLPLIILTIISHFRGNLCRIDKIVA  
olc15\_allosacch WFKKNGSFIIAMFMLASCAMGMLGSLSGTRGGWVLLPIILFTIVFHFKETLCKVDKMFV  
olc9\_allosaccha WFRHLGKKSIAAFMLLSFLMGGIGSFLSGTRGGWVLLPIILFTIVFYFRKQLSLKDGLYA  
olc19\_sobria\_42 WFRNIGRKGIAAFMLLSFLMGGIGSFLSGTRGGWVLLPIVLLTIVFYFRKQLSLKDGLYA  
olc24\_salmonici WFRYRGKKGIAAFLLLSFLMGGIGSFLSGTRGGWVLLPIVLLTIIIFYFRKQLCLKDGIYA  
olc23\_145 WFRSIGRNKISAFMLFSFLMGGMGSLSGTRGGWVLLPIILVTIVFYFRKQLCLKDGLYA  
olc17\_jandaei\_4 WSRANKFYNYSSFFYMIGAISGLIGSFLSGSRGGWVLLPVVIFSILMLYRNLIASNERKGL  
olc18\_sp\_EERV15 WYRAKNAKYFSYLYMLGAISGFTGSFLSGARGGWVLLPVVVISILMLYRKIITNNEKKGL  
olc26\_encheleia WCRAKEKRRRSYFYLLSTLAGLTGSFLSGTRGGWVLLPVVVSILFFYRGAISKDRKWL  
olc8\_bv\_sobria WAQKKERLAFSLFMLLGACGGMGASFLSGTRGGWVLLPVILLTIGMVFEYLYRKGSIAL  
olc10\_caviae\_83 WAQKKGKLAFSFFMLLGACGAGMGASFLSGTRGGWVLLPVILFTIAVLFEKCLYRKTTLMV  
olc28\_caviae\_42 WAQKKGKLAFALFMLVGTACGAGMGASFLSGSRGGWVMLPVILITIAMLFKECLYRKGTLM  
olc3\_caviae\_A23 SKFRKLSLGNAGILLGILLFGVFSVIL-QSRQSWLAISASLAILPLLGGGEHWPRRKVV  
olc27\_simiae SARRRQWLWRLPLLLAVLAVAVLGIVVTQTRAVFLAVGAAAILGVVLWGLMQRPHWNLL  
olc16\_diversa KLFDENALHKKYVIFLCMCFVAVSLILSGGRAGWVAVIVTSTLYML-FLNKKYLIVSALL  
olc29\_veronii\_1 KLSDDMTASKKVALGLFLFVTFLSLIISGGRAGWIAASFVVMYI-FMNRKMLYVFTPV

\* ::

olc1\_piscicola\_ AI-LCT--ATTGAIY-HTNQLVQVRVAEA---VSDINS-AEKGSYD----SSWGLRVIAW  
olc2\_salmonici AM-LCI--ASIGITY-HTNQLVQLRVADA---VSDLNF-AEKGSYN----SSWGLRVVAV  
olc22\_tecta TL-LLV--ALAGGLY-QTNTIVQGRMAEA---VSDIKG-IEGGTY--SSWGLRVVAV  
olc4\_veronii\_Hm TL-GLL--LVLGMLC-LNSSIVKNRIDSG---LSDVVN-MENGNY--TSGLRLVAV  
olc5\_popoffi FL-ILS--CVLVITF-YESDMLKIRIQUES---LSELSM-MESNNY--TSWGLRMAW  
olc6\_enteropelo FL-IVF--ILLTIVF-SETEVFKIRIQUES---LSELSM-MESNNY--TSWGLRMAW  
olc21\_taiwanens IL-AFI--ISMILLY-QYSPVVQQRILDA---TSDLDK-MQGNYS--TSWGLRLMAW  
olc20\_veronii\_A IL-PGL--IIILVAFNYSNIFIQRMNAV---KNNFIQ-MDKGNYQ---TSIGLRFVW  
olc11\_veronii\_A MA-VVA--LAMLVLL-SLIPAIEQVDET---RQETIQ-ISAGNKD---TSIGIRLQLW  
olc25\_sp\_ZOR000 IT-AAT--LIVLFSF-YTIPELSQRVNV---KQEFVQ-ISKGNMD---TSIGLRFQLW  
olc7\_veronii\_B5 TC-IVI--GGFGIIS-TPQTGVLDRIKTA---KSDIVQFIDGENPD---TSIGIRFQLW  
olc12\_caviae\_42 AV-FGL--GLLAIVA-IPQTGVAERIHVA---RSDIVQFMDGKNK---TSIGIRFQLW  
olc13\_media\_423 AV-FGL--GLLAIVA-IPQTGVAERIQVA---RSDIVQFVDGKNK---TSIGIRFQLW  
olc14\_media\_ws AV-FGL--GLLAIVA-IPQTGVAERIQVA---RSDIVQFVDGKNK---TSIGIRFQLW  
olc15\_allosacch AI-LML--GMIGVVS-IPQTNVLVRIDAA---RSDVVHFVIGDKNK---TSIGIRFQLW  
olc9\_allosaccha ST-VCA--LLLFLAM-LPQSGVMDRIYNA---KADVHYFDGVNPD---TSIGIRLQLW  
olc19\_sobria\_42 ST-VCA--LLIFLAM-LPQSGVMDRIYNA---KADVHYFDGVNPD---TSIGIRLQLW  
olc24\_salmonici ST-VCA--LLLFLAT-LPQSGVMDRIYTA---KEDVVHYLDGVNPD---TSIGIRLQLW  
olc23\_145 GS-VCV--LLLFLAL-LPQSGVMDRIYAA---KEDIVHYIDGLNPD---TSIGIRLQLW  
olc17\_jandaei\_4 LC-LLF--IIIAMVL-APQTGMLKRFDA---KTDIEQYVDGTNLD---TSIGIRFQLW  
olc18\_sp\_EERV15 LF-LFA--IVIAMVL-TPQTGMLKRFDA---KTDIEQYIDGTNLD---TSIGIRFQLW  
olc26\_encheleia LL-ILV--TVSSIVF-TPQSGVIKRVYEA---HSDIVRYIDGSERN---TSIGIRFQLW  
olc8\_bv\_sobria ITCILL--CGGILVL-QPQSGVEARIEQA---QHDISQYLDKTNLN---TSIGIRLQLW  
olc10\_caviae\_83 LVGGLL--CGGFLIV-QPQSGVEARIELA---QNDISQYLDKTNLN---TSIGIRLQLW  
olc28\_caviae\_42 VISVLL--CGVFFV--QPESGVEKRIELA---QRDISQYMDKTNLN---TSIGIRLQLW  
olc3\_caviae\_A23 TY-AIL--LMTMLAL-YQVSFIRERLLAGFVHQGDVHA-ILTNWNEVRDFSIGVRLKTW  
olc27\_simiae LV-LALGGVLIGTTLHYFKSQTIGRSGAE---ANVIEM-VWEGKLDRIPTYSVGTRVNTW  
olc16\_diversa LG-AGT--FIIGKWEPEKIEFVMGRALSV-----TE-TKED---YSNYSRLLMW  
olc29\_veronii\_1 AC-VLI--FSLYLAMPSQFNAVAGRATSV-----TETTSKD---YSNFSRLLMW

\*

\*

\*

\*

olc1\_piscicola\_ QSAWLGFLD-----SPVAGVGTGDFDALKQTQINNHHQVSPLIF-----HPALVHSHNQ  
 olc2\_salmoniciid QSAWLGFLD-----APLTGVGTNGFDALKQEQQVARGLVPLAL-----NAALAHASHQ  
 olc22\_tecta ESAWLGFLD-----SPLIGVGTGFTAVKEQQISQGLVSPVM-----DPALAHASHQ  
 olc4\_veronii\_Hm ESAWLGFLD-----SPLIGVGTGFDALKQEQQVKGGLVLPQALL-----NPALAHAHNQ  
 olc5\_popoffi RSAWAGFVD-----NPLLGVLGDGFKTMQQQQLLDGIIVNKFYV-----DYGMYHAHNQ  
 olc6\_enteropelo KSAWFGFIE-----HPLLGVLGDGFKNIQHQQLLDGIIVDNFYV-----NYGMYHAHNQ  
 olc21\_taiwanens KSAWFGFIE-----YPIFGIGYHGLDGLRLDQLKLGIVDQFYI-----NNGVYHAHNQ  
 olc20\_veronii\_A KSAWLGFLD-----YPFIGVGKDGIDELKKQQVSEHKINPVLLV-GDAGLGMPHAHNQ  
 olc11\_veronii\_A HSAIEI IKA-----HPLMGVGTGKYQNIMEQQYQQGVITS AVL-----SFKNAHYHNQ  
 olc25\_sp\_ZOR000 HSAIEI IKD-----HPLMGVGTGKYPDLMVRQYQQGMISELAL-----SFKDAHFNHQ  
 olc7\_veronii\_B5 SSAWDAFQK-----KPIFGWGNNGIRQIHKQQLEQKISEFIY-----NFN-YHAHNQ  
 olc12\_caviae\_42 YSAFDAFQK-----KPLFGWGNNGLQQAHTVQLAAGEISEFLY-----KFN-FHAHNQ  
 olc13\_media\_423 YSALDAFQK-----KPLFGWGNNGLQQAHAQLAAGEISDFLY-----DFN-FHAHNQ  
 olc14\_media\_ws YSALDAFQK-----KPLFGWGNNGLQQAHAQLAAGEISDFLY-----DFN-FHAHNQ  
 olc15\_allosacch YSALDSYLH-----KPFIFGWGNNGIRQSQLEQLKSGKITQFIY-----DFD-SHAHNQ  
 olc9\_allosaccha ESAYNSFLE-----KPIFGWGNNGIRLSQLNQYNNNGSISEFIY-----NFN-SHAHNQ  
 olc19\_sobria\_42 ESAYNSFLE-----KPIFGWGNNGIRLSQLNQYNNNGSISEFIY-----NFN-SHAHNQ  
 olc24\_salmonici ESAYNSFLE-----KPIFGWGNNGVRLSQLNQNNNGAMSEFIY-----NFN-SHAHNQ  
 olc23\_145 DSAYHSFLE-----KPIFGWGNNGVRLSQLNQYNNNGSISEFIY-----NFN-SHAHNQ  
 olc17\_jandaei\_4 RSAWDSFKE-----KPFIFGWGQDGLRESQKQQLKENKITNFIY-----NFN-YHAHNQ  
 olc18\_sp\_EERV15 GSAWDSFKE-----RPFIFGWGQDGLRESQKQQLKNEITNFIY-----NFN-YHAHNQ  
 olc26\_enceheleia RSAWDSFIE-----KPIFGWGHDLGRISQKQQLDAGKITEFIY-----NFN-YHAHNQ  
 olc8\_bv\_sobria QSAWQSFTQ-----KPLFGWGNHGIRISQQEQLGQGEISQFIY-----DFN-YHAHNQ  
 olc10\_caviae\_83 QSAWQSFTQ-----KPLFGWGNHGIRQSQAQLARGEISQFIY-----DFN-SHAHNQ  
 olc28\_caviae\_42 KSAWQSFTQ-----KPLFGWGNHGIRQSQAQLARGEISQFIY-----DFN-SHAHNQ  
 olc3\_caviae\_A23 LEAIQWFLA-----HPFFGTGYGS-----QSLVITLSKTLDPDI-----TREFRHLHNS  
 olc27\_simiae LVWEKIKE-----RPLFGWGREA-----RSWVIEQSPTLPWV-----KQEFGLHLHNY  
 olc16\_diversa GNGLKWLEANMVDNPRQFMFGIGFKRFEKEYTEYLDSDSRELINITHGNYSMRDLHNA  
 olc29\_veronii\_1 GNGVSLLENHLSHYPRKFLFGIGFNKFQTEYSAYLNKISNTEDLIKLTQGNYSLNDLHNS

. \* \* . \* .

olc1\_piscicola\_ YMQLNVVRGGIGFVALVIFLGLPL-----YFAAKNINRI-----SAGVLVPLAF  
 olc2\_salmoniciid YMQLNVIRGGIGFVVLVAFLLFLPL-----WLSMKKMGGD-----AACVLIPLSF  
 olc22\_tecta YMQLNIIRGAVGILALAIFLFYPM-----KLLVERAGWG-----SPYTMIPLSF  
 olc4\_veronii\_Hm YLQTLVIRGGIGFIFLLGILILPA-----IFFAKEMGFV-----SAGVFIPISF  
 olc5\_popoffi FIQNMVIRGILGLLAAALILVYPM-----WLFWQQSKLV-----SAGFIITLST  
 olc6\_enteropelo FMQNMVVRGILGLLVAIAVLVYPM-----IFFYHRTKVL-----SAGFMVSFGV  
 olc21\_taiwanens FMQNILIRGMLGGVVAILVLIYPI-----VIARRSFGVF-----SASTLVPIGI  
 olc20\_veronii\_A FLNQLVMRGLVGFIPT-----GFLCISISSVC  
 olc11\_veronii\_A YLDSYVRYGVPGLLIVFVIFMSPY-----LLYGLQCTPQ-----GFLCISISSVC  
 olc25\_sp\_ZOR000 YLDSYVRYGLIGLVAIAIFLSPL-----FLYGLKDVGW-----KNICLAIALIC  
 olc7\_veronii\_B5 FLDEMAKRGIIGLFALCLVIFYPI-----SVFYKYKKSLSMKY-----ILMAVASLTL  
 olc12\_caviae\_42 FLDEMAKRGIIGLLVLLIMYLYPL-----YLFYKHRGDSLLP-----IMLAVTSLTL  
 olc13\_media\_423 FFDEMAKRGVIGLLALLSMYLYPL-----YLFYKHRGDSLLP-----IMLAVTSLTL  
 olc14\_media\_ws FFDEMAKRGVIGLLALLSMYLYPL-----YLFYKHRGDSLLP-----IMLAVTSLTL  
 olc15\_allosacch FLDEMSKRGTGLVILMMFLYPV-----LIYRRLTKINLITP-----IMLGVSVLCT  
 olc9\_allosaccha FLDELAKRGIIGFLMLALLYFYPL-----WVASKNRNLLVS-----SMLAVSSLTL  
 olc19\_sobria\_42 FLDELAKRGA VGFLMLVMLYLYPL-----WVASKNKNLLVS-----SMLAVSSLTL  
 olc24\_salmonici FLDELAKRGIIGLLMLTLLIFYPI-----WVASKNKNLLVS-----SMLAVSSLTL  
 olc23\_145 FLDELAKRGIIGLLMLTLLIFYPI-----WVASKNRNLLVS-----SMLAVSSLTL  
 olc17\_jandaei\_4 YLEEMAKRGIIGLLVLIAMLCVPI-----ILVKKRFSIMAQESLAYSGGVLVIVTCLTT  
 olc18\_sp\_EERV15 YLEEMAKRGMGLFVLLAMLSLPV-----VLVKSMSMCMREQSAAYGASVIVIVTCLTT  
 olc26\_enceheleia YLEMAKRGIIGLSSLLGILFIPM-----VIAKSRMVGASITSSVFGGLTIVMATCLTT  
 olc8\_bv\_sobria FLDEMAKRGIIGLVAFLLILLTLP-----FLVKRRLRAPHDID-VHCGAALVIVTVFSC  
 olc10\_caviae\_83 FLDEMAKRGIIGLGLSLLFMLIAPV-----LIVRRKL RQPHNID-VHCGATLLIVTTFSS  
 olc28\_caviae\_42 FLDEMAKRGIIGLGLSLLFMLIAPV-----LIVRRKL RQPHNID-VHCGATLLIVTTFSS  
 olc3\_caviae\_A23 NMETLVCWGVAGFLVLYGTLSVLRQVLCPPVSSRF-----IKMLAISF  
 olc27\_simiae FIEIQLSYGLAGSLWLLGMVVATL---WGCWAAWRRGDMP-----LDVCLFGFCF  
 olc16\_diversa YIDSSNKMGVLYTVLFYAFLVFVA-----YSFIRNGIAH-----QGVGLILSFV  
 olc29\_veronii\_1 YLDSANKMGFLYTLFFYGS LIFIV-----YLFYKKE SLI-----KGCILIA PFL

:: \*

olc1\_piscicola AINSL----SDVPFEHQGVLYLYTLVFIWFAHE-----FEKDTCTS-----  
 olc2\_salmonici AISAFA----SDVPFEHQDILYLYVLSMIFIWYSSE-----LRENKSAL-----  
 olc22\_tecta AVSAL----SDVPFEHQNTLYLYALSIVFCWCAIE-----FNMEKKAS-----  
 olc4\_veronii\_Hm AVGAV----FDVPFEHQSMYLYSFLIFILFCHE-----LKQD-----L---L  
 olc5\_popoffi FVCAL----TDVPIEHQNTLYIYLISLFFIFFKNE-----GRFNEKVVL-----  
 olc6\_enteropelo FVCAL----SDVPMEHQNTLYIYMITLFSLCLSYE-----IEKNKEAMS-----  
 olc21\_taiwanens LICSL----SDVPLEHQNTLYIYTLVLCWFYENAH--LLEGVNSEEGISEK-----  
 olc20\_veronii\_A -----  
 olc11\_veronii\_A LIAGL----TDVPLIHTGIIYVIIILYSAVIYLTSC-----DYKKTQL-----  
 olc25\_sp\_ZOR000 IFAAL----TDVPLIHTGIIYIILYPAIIFLSCS-----NNASGEVLNY-----T  
 olc7\_veronii\_B5 IDYSL----SQAFISHNSGIVFFVFCFSLITSLN-----ETNKEEV-----  
 olc12\_caviae\_42 IDYSL----SQAFISHNSGITFVSFLFLVEITMLN-----NSAEIRKNE-----K  
 olc13\_media\_423 VDYSL----SQAFISHNSGITFVSFLLLVKITMLN-----NSAEIRKNN-----E  
 olc14\_media\_ws VDYSL----SQAFISHNSGITFVSFLLLVKITMLN-----NSAEIRKNN-----E  
 olc15\_allosacch IDYSL----SQAFLNHNSGIIFFSMLTAILVTSV-----SEQMMMDR-----  
 olc9\_allosaccha VDYSL----SQAFISHNSGMIFFMFLFSALITTIK-----VSPLEGRK-----  
 olc19\_sobria\_42 IDYSL----SQAFINHNSGIIFFMFLFSVLISMFS-----TNSTSEALND-----  
 olc24\_salmonici IDYSL----SQAFINHNSGIIFFMFLFSVLITALP-----TVPTNSKEINVEAKSD  
 olc23\_145 VDYSL----SQAFINHNSGMIFFMFLFSALITTIK-----ASPLEERK-----  
 olc17\_jandaei\_4 ADYHL----SQAYFHNHNSGISFFVFLVLALSVSM-----DDGNH-----  
 olc18\_sp\_EERV15 ADYHI----SQSYFAHNHNSGITFFIFSMVFGFSATF-----KDAEVLL-----  
 olc26\_encheleia IDYNL----SQAYFAHNHNSGITFFIFSLVLSLSASL-----EGKTQS-----  
 olc8\_bv\_sobria IDYSL----SQAFLGHNHNSGSTFVFSVLVIFMSIVF-----GGPNGIK-----  
 olc10\_caviae\_83 IDYCL----SQAFFGHNSGITFFVSSLVIAASIVF-----KESDTE-----  
 olc28\_caviae\_42 IDYCL----SQAFFGHNSGISFFVASLVMTASIVF-----GSQNEDSRH-----  
 olc3\_caviae\_A23 ILYWLIINNFEFFYMRSGQWVFSVFMGAIYSTALHWELNRLGKEGHENLRH-----  
 olc27\_simiae VFYFLIVNNFESYFSEWTGGLAFNLIMAGLVSLAWR---RSFPVNAHQ-----  
 olc16\_diversa ILGVF----YANYLEFQTSVFFFLALSHSSV-----AMRRRD-----  
 olc29\_veronii\_1 ILGVF----YTNYLEFQTYIFFFVVALAYSEV-----EQYNVDNHKVRA-----

**Supplementary Figure 1(b).** Predicted transmembrane regions plots for O-Antigen ligase domain-containing predicted proteins for each of the types assigned for *wa* Region 1

















