A. ECL1^{FtsX}

```
Lla_Il1403         --ILNTSKISNGIENNVRIVAYMKLDVHDQETKIQDPKDNKKTINNPDHLKIYDSIKKVP 58
Spy_MGAS10394      ----NIQRVASGVENNVHINTYLQVDSTDAAKVIQNTAG--EPVNNDNYHSVYDKIAQIK 54
Spn_D39            SVIFNTAKLATDIENNVRVVVYIRKDVEDNSQTIEKE-G--QTVTNNDYHKVYDSLKNMS 57
Smi_B6             -------KLATDIENNVRVMVYIRKDVADNSETIEKE-G--QTVTNNDYHKVYNALKGMS 50
Sth_LMD-9          -VILNTQKLASDIEKNIQVNVYLDPDSTDASETVKELSG--QIVANKDYHKIYNALTKIK 57
Efa_TX1330         ----NATKLAQDIEGNVDVSVFVDIGTKD-----------------EEMKKLEKELNDLD 39
Ban_Ames           -AIMNMNHFATKVEQDVEIRVHIDPAAKEADQ-----------------KKLEDDMSKIA 42
Bsu_168            --MLNLNNMATNAEKQVEIKVLIDLTADQKAQ-----------------DKLQNDIKELK 41
                          ..:   * :: : . :     :                     .: . :  :

                          ▬▬▬                        ▬▬▬                ●
Lla_Il1403         NVKTVEFSSKEAQLKELTKALGNNWNLFKG--DANPLYDAYIVEADKPANVKSVTSKISK 116
Spy_MGAS10394      GVKKITFSSKDEQLKKLQETLGDVWNMYDQ--DTNPLQDIYLIETQTPKQVKAITKKIRT 112
Spn_D39            TVKSVTFSSKEEQYEKLTEIMGDNWKIFEG--DANPLYDAYIVEANTPNDVKTIAEDAKK 115
Smi_B6             TVKSVTFSSKEEQYEKLTETMGDNWKIFEG--DANPLYDAYIVDTNTPSDVKTVAEEAKK 108
Sth_LMD-9          GVDKVTFSSKEEQKKQLIETMGSSFETATG--DANPLSDVYIVQTKSPDDVSRVAKEAKA 115
Efa_TX1330         HVKKVEFSSKEQELKKIQNEMGDSWKLFEG--DNNPLYDVYVVSATDPSYTKQVAEKAAD 97
Ban_Ames           KVESIKYSSKEEELKRLIKSLGDSGKTFELFEQDNPLKNVFVVKAKEPTDTATIAKKIEK 102
Bsu_168            GIQSVTFSSKEKELDQLVDSFGDSGKSLTMKDQENPLNDAFVVKTTDPHDTPNVAKKIEK 101
                    :..: :***: : ..: . :*.  :      : *** : :::.:  *  .  ::..

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Lla_Il1403         LSGIEKATYGGANTAKLFQIAQGIRTWGT 145
Spy_MGAS10394      IEGVEAADYGGINSDKLFKFS-------- 133
Spn_D39            IEGVSEVQDGGANTERLFKLASFIRV--- 141
Smi_B6             IEGVSEVQDGGANTERLFKLAS------- 130
Sth_LMD-9          IQGVDNANFGGSDTEILMATMKRVQFWGI 144
Efa_TX1330         LKNVSRSDYGGASSDRIFQIAGAVRTWG- 125
Ban_Ames           MQFVSNVQYGKGQVERLFDTVKTGRNIGI 131
Bsu_168            MDHVYKVTYGKEEVSRLFKVVGVSRN--- 127
                   :. :     *  .   ::
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● Changes (A177V, F179S, W183L, and S264L) that suppress either *pcsB*$^{L78S\ L219P}$ or *pcsB*$^{(A160P}$ Ts mutation

● Changes (V266A and Q268E) that that are allele specific and only suppress the *pcsB*$^{L78S\ L219P}$ Ts mutation

● *ftsX*^{I150K} Ts mutation

▬ Consecutive identical amino acids

B. ECL2^{FtsX}

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                                ●●●
                                 ● ● ●
Spy_MGAS10394      ---YDLVYKHFAQELQRNNLSMYPLDP- 24
Spn_D39            FIVYQIVYQSVNKSLVGQNLSMISPDLF 28
Smi_B6             ---YKMVYQSVNKSLVGQNLSMISPEV- 24
Efa_TX1330         --------QLINPSLLRSHYSLIHPEN- 19
Lla_Il1403         --------VSLTPSLQSQKLAMFAPKE- 19
Ban_Ames           -VTYNSLQGMFNEKLGGTIFELLPYSP- 26
Bsu_168            --------GWVVPKVQGSFVSLLPYNP- 19
Sth_LMD-9          -------YSTLNPDFVKGGISMYDAD-- 19
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