A

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KU056477.1_                       ................GGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGG   102
KU360259.1_DL14/08                ................GGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGG   102
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KJ789182.1_TJ                     ................GGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGG   102
MT468550.1_hSD-1/2019             ................GGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGG   102
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MT949536.1_SD18                   ................GGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGG   102
MT468549.1_HuBXY/2018             ...........................GGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGG    91
KP098534.1_HeN1                   GGGGTCTCTAAGGGCGTCTACTAAGGGGTCATGCTAATGGGGTGCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGG..........   109
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KM189914.3_HNB                    ......................................GGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGG.....    70
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KX423960.1_Ea__Hubei_             ..................................................GGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGG.....    59
MT949537.1_HuB17                  ......................................GGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGG.....................    59
KU315430.1_Ea                     ......................................GGGGTCTCTAAGGGGTCTGTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTTTAAGGGG.....................    59
KJ717942.1_Kaplan                 ......................................GGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGG    69
JQ809330.1_DUL34Pass              ......................................GGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGG    80
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JF797218.1_Kaplan                 ..................................................GGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGG    69
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MK080279.1_HLJ-2013               ..................................................GGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGG.....................    59
AP018925.1_MY-1                   ............................GGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGG.....................    70
KU198433.1_ADV32751/Italy2014     ......................................GGGGTCTCTAGTGGGTCTCTAGGGGTCTCTAGGGGTCTCTAGGGGTCTCTAGGGGTCTCTAAGGGGTCTCTAGG    80
KU552118.1_LA                     ............................GGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGG.    90
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LC342744.1_RC1                    ......................................GGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGGTCTCTAAGGGG.....................    59
Consensus                                                                                  gggtct ta ggggtctcta ggggtctcta ggggtct ta gggg
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KP722022.1_HN1201         GGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGGGG................    88
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KU056477.1_               GGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG..................    86
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KT824771.1_HLJ8           GGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG..................    86
KJ789182.1_TJ             GGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG..................    86
MT468550.1_hSD-1/2019     GGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG..................    86
KM189912.1_HNX            GGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGG............AGGAGAGAGGGCTGTGGGAGAGAGGG...    89
MT949536.1_SD18           GGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG..................    86
MT468549.1_HuBXY/2018     GGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG..................    86
KP098534.1_HeN1           GGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGG...................    85
MG551316.1_JS-2012_F50    GGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG..................    86
MT150583.1_JSY7           GGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG..................    86
MG589642.1_JS-2012_F120   GGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG..................    86
KM189914.3_HNB            GGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG..................    86
KU057086.1_HB1201         ...............GGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGGCGTGTGGGAGAGAGGGCGTGTGGGAGAGAGGGCTGTGGGAGAGAGGGG    90
JQ809329.1_DUL34gfp       ...............GGGAGAGAGGGCGGTGGGAGAGAGGG.CGGTGGGAGAGAGGGCGGTGGGAGAGAGGGCGGTGGGAGAGAGGGCGGTGGGAGAGAGGG...    86
MH582511.1_GD0304         GGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG..................    86
KX423960.1_Ea__Hubei_     GGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG..................    86
MT949537.1_HuB17          GGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG..................    86
KU315430.1_Ea             GGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG..................    86
KJ717942.1_Kaplan         ...............GGGAGAGAGGGCGGTGGGAGAGAGGG.CGGTGGGAGAGAGGGCGGTGGGAGAGAGGGCGGTGGGAGAGAGGGCGGTGGGAGAGAGGG...    86
JQ809330.1_DUL34Pass      ...............GGGAGAGAGGGCGGTGGGAGAGAGGG.CGGTGGGAGAGAGGGCGGTGGGAGAGAGGGCGGTGGGAGAGAGGGC..................    72
JQ809328.1_Kaplan         ...............GGGAGAGAGGGCGGTGGGAGAGAGGG.CGGTGGGAGAGAGGGCGGTGGGAGAGAGGGCGGTGGGAGAGAGGGCGGTGGGAGAGAGGG...    86
JF797218.1_Kaplan         ...............GGGAGAGAGGGCGGTGGGAGAGAGGG.CGGTGGGAGAGAGGGCGGTGGGAGAGAGGGCGGTGGGAGAGAGGGCGGTGGGAGAGAGGG...    86
BK001744.1_               ...............GGGAGAGAGGGCGGTGGGAGAGAGGG.CGGTGGGAGAGAGGGCGGTGGGAGAGAGGGCGGTGGGAGAGAGGGCGGTGGGAGAGAGGG...    86
MK618718.1_AnH1/CHN2015   ...............GGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGGAGAGAGGG.....................................    56
MK080279.1_HLJ-2013       ...............GGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG..................    71
AP018925.1_MY-1           GGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG..................    86
KU552118.1_LA             ...............GGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGGCTGTGGGAGAGAGGGCTGTGGGAGAGAGGG..................    71
KM189913.1_Fa             ...............................GGGAGAGAGGG.CTGTGGGAGAGAGGG.............................................    26
LC342744.1_RC1            ...............GGGAGAGAGGGCTGTGGGAGAGAGGG.CTGTGGGAGAGAGGG.............................................    41
Consensus                                                            gggagagaggg c gtgggagagggg
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Figure S1. The conserved G-core sequence of OriL-S (A) and OriL-A (B), these sequences were derived from NCBI (www.ncbi.nlm.nih.gov), and MEGA6 software was used for multiple sequences alignment. The consensus G-core sequence was labeled with red.