

1 **Appendix A** Hosts, origins and accession numbers of ASPV isolates used in this study

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Isolate	Host	Origin	Accession no.
CYD	Quince (<i>Cydonia oblonga</i>)	Italy	KT835289.1
Aurora-1	Apple (<i>Malus domestica</i>)	Canada	HE963831.1
PA66		Germany	D21829.2
PB66		Germany	KF321966.1
Hannover		Germany	KF321967.1
PM8		Germany	KF319056.1
IF38		Japan	AB045371.1
Palampur		India	FR694186.1
YT		China	KF915809.1
YL		China	KJ522472.1
GA2		China	KY702580.1
GA4		China	KY702581.1
AKS		China	KY242757.1
XC		China	KY490039.1
KL1	Pear (<i>Pyrus sinkiangensis</i>)	China	JF946775.1
KL9		China	JF946772.1
HB-HN1	Pear (<i>P. pyrifolia</i>)	China	KU308398.1
YLX	Pear (<i>P. sinkiangensis</i> × <i>P. bretschneideri</i>)	China	KY798310.1

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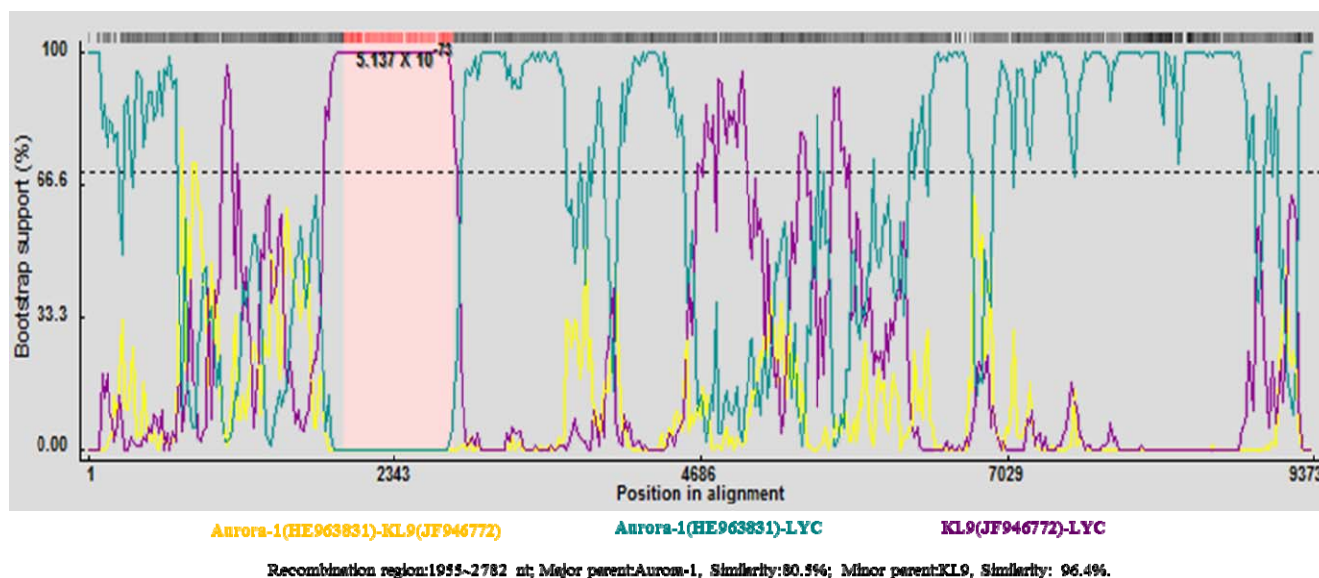
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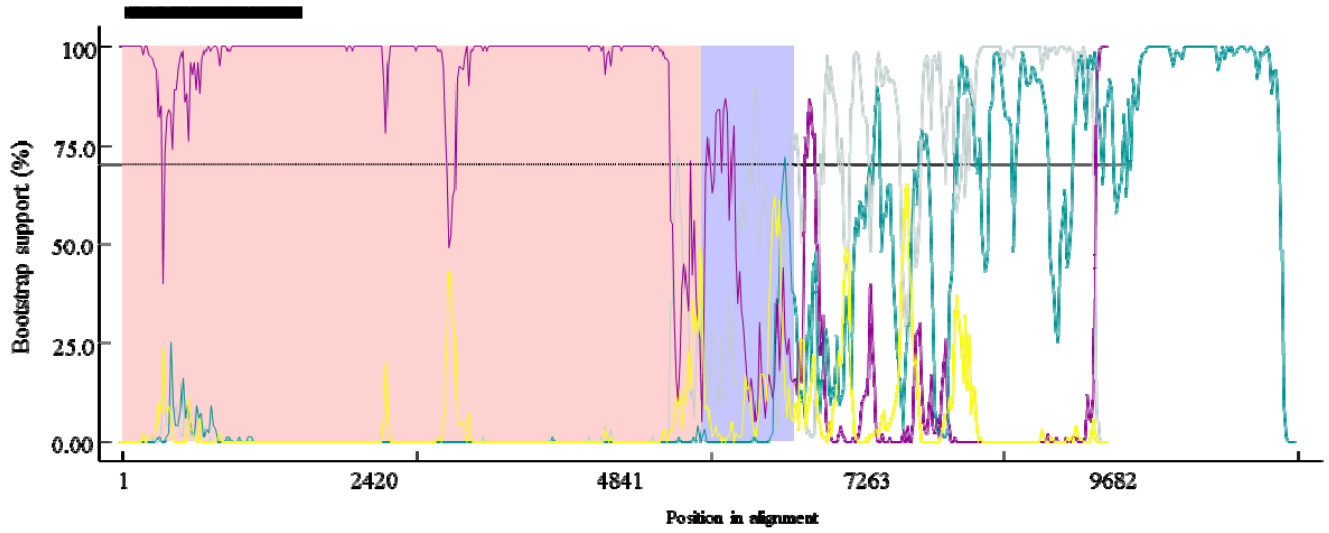
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Appendix B The putative recombinant event in ASPV-LYC genome as detected by seven methods in the software RDP3.

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XC(KY490039)–LYC(MG763895) XC(KY490039)–HB-HN1(KU308398) LYC(MG763895)–HB-HN1(KU308398)

Recombination region:40~5696 nt; Major parent: XC, Similarity: 79.9%; Minor parent: LYC, Similarity: 87.2%.

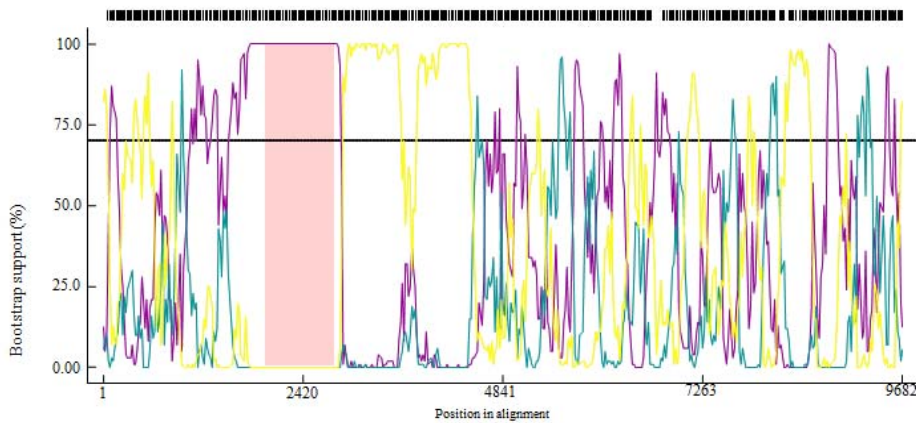
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30 **Appendix C** The putative recombinant event in ASPV isolate HB-HN1 genome as detected by seven methods in
 31 the software RDP3.

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PMB(KF319086)–LYC(MG763895) PMB(KF319086)–KL9(JF946772) LYC(MG763895)–KL9(JF946772)

Recombination region:1928~2764 nt; Major parent: Unknown; Minor parent: LYC, Similarity: 96.2%.

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35 **Appendix D** The putative recombinant event in ASPV isolate KL9 genome as detected by seven methods in
 36 the software RDP3.

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      *      20      *      40      *      60      *      80      *      100
LYC      : MASNDSSPSSAPMVSAKETSLVTSAPNPSVVASLFTSSPVATSATP--EGTRATQTEAVVSQVQSVAPLLSGFDPNLHGRLSSEQYRAAQERAAERGFLEG-- : 100
HB-HN6   : ...V...CT...S.V...AL...PV...AF... : 104
HB-HN9   : ...VE...VP...T.V.DA...L.V...LS.VN.VS...VG.S...F...S...G... : 105
YX-MRS   : .T...D.Q...V...L...D......S.TS----- : 82

      *      120     *      140     *      160     *      180     *      200     *
LYC      : ---LSRRNQTPTSAYALTSNPFETGNAYGSAFQASMGAYPSLQSQGQPSEPSAQRLLFPLPHGVSPSVHDSNLRPQVEQSQNAFLVFFTLGNRAPRTASSLSGGM : 202
HB-HN6   : .R...S.A.V...L...L.HVG...FPEG.N...SH...Q...TTVA...V...A... : 209
HB-HN9   : S.R...L...AN...S...F...T...S.PFW...AS...Q...S...S.DA...AT...AS.-G... : 209
YX-MRS   : -----S...H... : 173

      220     *      240     *      260     *      280     *      300     *
LYC      : RRRIDSVGLKSLLYEPCAGVVANDCKLRALGVALLGMLGEGHOLTEVGVYLARHCADVGSASEKSTLLGTFPGSNLTLEEVGTRKLNKOTEGCTLRCYCAFYAKHVWN : 307
HB-HN6   : ..... : 314
HB-HN9   : ..... : 314
YX-MRS   : .....L...S... : 278

      320     *      340     *      360     *      380     *      400     *
LYC      : LMLQIQSPPANWVGKEFKFETRYAAFDFFFGVESSASLEPADGLVRLPTCAERVANATSKELQMYRLRSMEGTQAVNFGEVIGGKVGPKPVLSLRK : 403
HB-HN6   : ..... : 410
HB-HN9   : ..... : 410
YX-MRS   : ..... : 374

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40 **Appendix E** Prediction of antigenic determinants of the coat proteins of four *Apple stem pitting virus* (ASPV)
41 isolates characterized by western blot analyses. Epitope regions predicted by the Kolaskar and Tongaonkar
42 method (1990) were underlined. Dots indicated the identical aa residues.

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