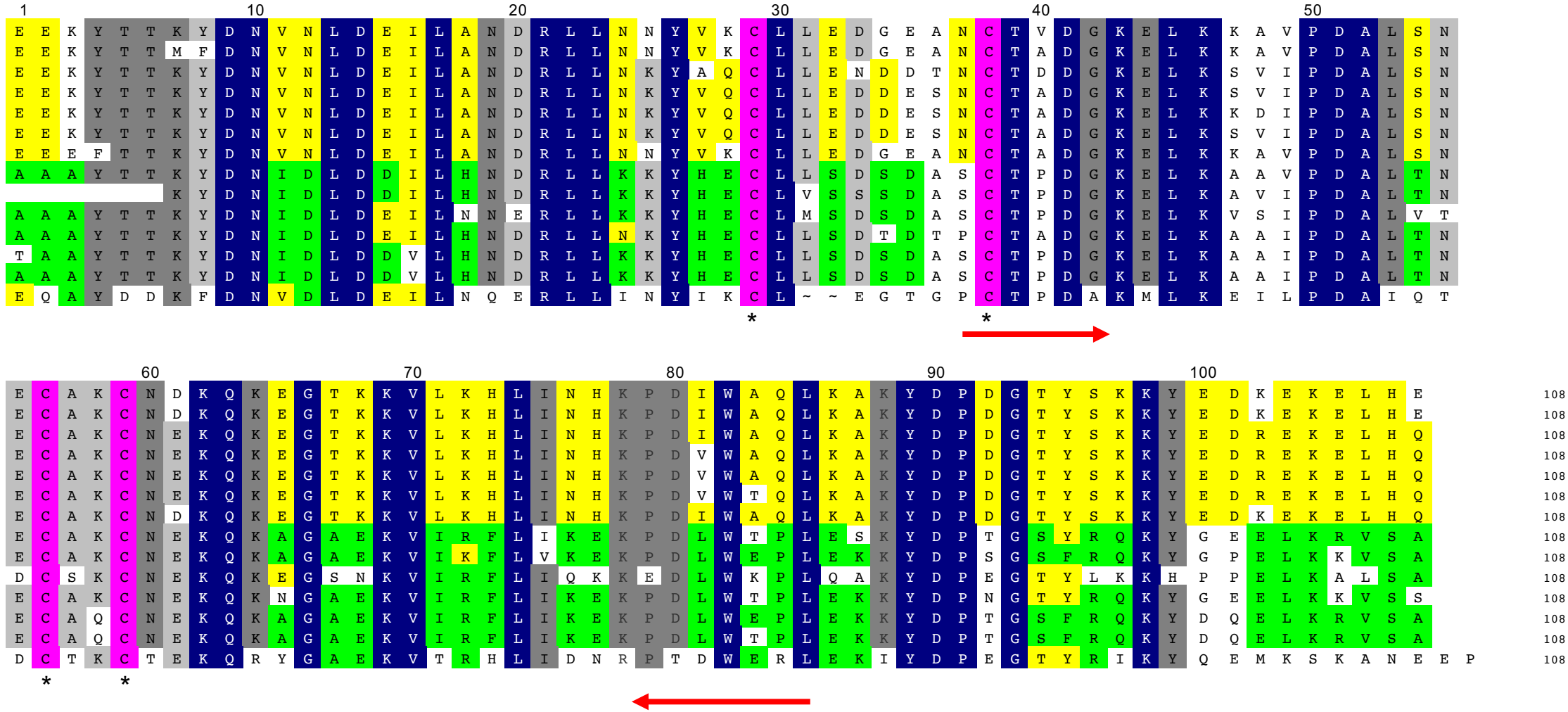
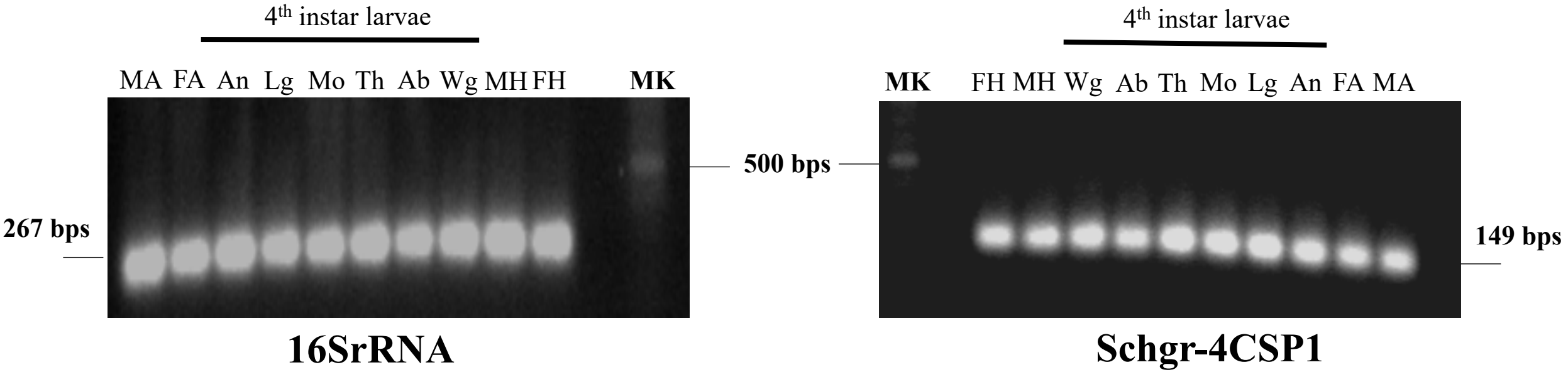
A.


1 10 20 30 40 50
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CSP-sg6 EEKYTTKYDNVNLDEILANDRLLNKYVQCLLEDDESNCTADGKELKSVIPDALSN
CSP-sg7 EEEFTTKYDNVNLDEILANDRLLNNYVKCLLEDGEANCTADGKELKKAVPDALSN
Schgr-4CSP1 AAAYTTKYDNIDLDDILHNDRLLKKYHECLLSDSDASCTPDGKELKAAVPDALTN
LmigOS-D1 KYDNIDLDDILHNDRLLKKYHECLVSSSDASCTPDGKELKAVIPDALTN
LmigOS-D2 AAAYTTKYDNIDLDEILNNERLLKKYHECLMSDSDASCTPDGKELKVSIPDALVT
LmigOS-D3 AAAYTTKYDNIDLDEILHNDRLLNKYHECLLSDTDTPCTADGKELKAAIPDALTN
LmigOS-D4 TAAYTTKYDNIDLDDVLHNDRLLKKYHECLLSDSDASCTPDGKELKAAIPDALTN
LmigOS-D5 AAAYTTKYDNIDLDDVLHNDRLLKKYHECLLSDSDASCTPDGKELKAAIPDALTN
DmelOS-D EQAYDDKFDNVDLDEILNQERLLINYIKCL~~EGTGPCTPDAKMLKEILPDAIQT
60 70 80 90 100
CSP-sg1 ECAKCNDKQKEGTKKVLKHLINHKPDIWAQLKAKYDPDGTYSKKYEDKEKELHE 108
CSP-sg2 ECAKCNDKQKEGTKKVLKHLINHKPDIWAQLKAKYDPDGTYSKKYEDKEKELHE 108
CSP-sg3 ECAKCNEKQKEGTKKVLKHLINHKPDIWAQLKAKYDPDGTYSKKYEDREKELHQ 108
CSP-sg4 ECAKCNEKQKEGTKKVLKHLINHKPDVWAQLKAKYDPDGTYSKKYEDREKELHQ 108
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CSP-sg7 ECAKCNDKQKEGTKKVLKHLINHKPDIWAQLKAKYDPDGTYSKKYEDKEKELHQ 108
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LmigOS-D1 ECAKCNEKQKAGAEKVIKFLVKEKPDLWEPLEKKYDPSGSFRQKYGPELKKVSA 108
LmigOS-D2 DCSKCNEKQKEGSNKVIRFLIQKKEDLWKPLQAKYDPEGTYLKKHPPELKALSA 108
LmigOS-D3 ECAKCNEKQKNGAEKVIRFLIKEKPDLWTPLEKKYDPNGTYRQKYGEELKKVSS 108
LmigOS-D4 ECAQCNEKQKAGAEKVIRFLIKEKPDLWEPLEKKYDPTGSFRQKYDQELKRVSA 108
LmigOS-D5 ECAQCNEKQKAGAEKVIRFLIKEKPDLWTPLEKKYDPTGSFRQKYDQELKRVSA 108
DmelOS-D DCTKCTEKQRYGAEKVTRHLIDNRPTDWERLEKIYDPEGTYRIKYQEMKSKANEEP 108

B.


4th instar larvae
MA FA An Lg Mo Th Ab Wg MH FH
MK
267 bps
500 bps
4th instar larvae
MK
FH MH Wg Ab Th Mo Lg An FA MA
149 bps
16SrRNA
Schgr-4CSP1

