

**Supplementary Figure S3.** Multiple alignment of the partial deduced aa sequences (~ 315 aa) of putative RdRps of the AstVs detected in mongooses (designated as Mon-AstVs) with those of other AstVs. The Mon-AstVs retained the putative RdRp catalytic core domain (shown with underline) and the polymerase motif A, -B and -C (highlighted with yellow, blue, and green, respectively) that are conserved among RdRps within the family *Astroviridae*. The conserved catalytic residues ('D' within polymerase motif A, and 'GDD' within polymerase motif C) are shown with the '#' symbol. A '-' indicates absence of an 'aa' residue at that position. The 'group/name of the virus/detected in animal' have been shown for the Mon-AstVs, whilst the 'name of the virus/host/GenBank accession number' have been mentioned for the other AstVs. Positions of aa residues correspond to those of the putative ORF1ab product of MaAstV-8/Human/GQ415660. Abbreviations: aa, amino acid; AstV, astrovirus; AvAstV, avastrovirus; MaAstV, mamastrovirus; RdRp, RNA-dependent RNA polymerase; UCAstV, unclassified AstV.

960

MaAstV-8/Human/GQ415660	KFTYKEPMSNIKDKYKREWNFAMRVLRRREFDYLVDVMTDITATSKNSDSTPSYPKCLWW
AvAstV-2/Chicken/AB033998	KFDYGDVAVD-FVQDYPELTAFADAVALAEVGYMEGTHVPIQETSKNMDSTPAFPKMLDF
UCAstV/Agama/MZ375145	KFTYREPCEDIKNKYREEWDFATYCVLMEYSYMQDTKLTPIWYTTKNEDSIPGYPKFLYW
UCAstV/Gecko/MG599919	KFVYREPLDDIKNKYRPEWDFATYCVLIEFSYMTDSRLVPIGSTSKNQDSIPGYPKFFWF
Group-I/Mon-14/Mongoose	KFIYREPMDNIAQKFPLEWAFATEVVLREYSYMQDTDLDMAYTTKNPNSTPGYPKFYYW
Group-I/Mon-21/Mongoose	KFIYREPMDNIAQKFPLEWAFATEVVLREYSYMQDTDLDMAYTTKNPNSTPGYPKFYYW
Group-I/Mon-32/Mongoose	KFIYREPMDNIAQKFPLEWAFATEVVLREYSYMQDTDLDMAYTTKNPNSTPGYPKFYYW
Group-I/Mon-38/Mongoose	KFIYREPMDNIAQKFPLEWAFATEVVLREYSYMQDTDLDMAYTTKNPNSTPGYPKFYYW
Group-I/Mon-52/Mongoose	KFIYREPMDNIAQKFPLEWAFATEVVLREYSYMQDTDLDMAYTTKNPNSTPGYPKFYYW
Group-II/Mon-43/Mongoose	-FIYREPKHGIRHLYPEEWDFADEVVLTEYSYMQDTHIIPISSTTKNVDSTPGYPKFEYW
Group-II/Mon-59/Mongoose	KFIYREPKHGIRHLYPEEWDFADEVVLTEYSYMQDTHIIPISSTTKNVDSTPGYPKFEYW
Group-II/Mon-61/Mongoose	--IYREPKHGIRHLYPEEWDFADEVVLTEYSYMQDTHIIPISSTTKNVDSTPGYPKFEYW
Group-II/Mon-63/Mongoose	-FIYREPKHGIRHLYPEEWDFADEVVLTEYSYMQDTHIIPISSTTKNVDSTPGYPKFEYW
Group-II/Mon-66/Mongoose	KFIYREPKHAIRHLYPEEWDFADEVVLTEYSYMQDTHIIPISSTTKNVDSTPGYPKFEYW
Group-II/Mon-78/Mongoose	-FIYREPKHGIRHLYPEEWDFADEVVLTEYSYMQDTHIIPISSTTKNVDSTPGYPKFEYW
Group-II/Mon-79/Mongoose	KFIYREPKHGIRHLYPEEWDFADEVVLTEYSYMQDTHIIPISSTTKNVDSTPGYPKFEYW
Group-II/Mon-81/Mongoose	KFIYREPKHGIRHLYPEEWDFADEVVLTEYSYMQDTHIIPISSTTKNVDSTPGYPKFEYW
MaAstV-8/Human/GQ415660	KTEAEYLKDRGYQDYITQLESIKKGE-RPRVLWYFLKKEILKLSKIEDGDIRQIVCSDP
AvAstV-2/Chicken/AB033998	DSERDYLEAHGMKEYIDTQLGVQ---SGKPLWWCFLKNEILKEKKVSEDDIRIITCSDP
UCAstV/Agama/MZ375145	QTERDYIQDCGRSEYMSVWQISDKTFDLSPVWYSFLKLEPTTFEIEAEYRMIMCTDP
UCAstV/Gecko/MG599919	STEKEYLDKCGQREYFQLWDKIKDPEFTESPVWYSFLKMEPTTLDKIESDYRMIMCTDP
Group-I/Mon-14/Mongoose	NDEEEYVRDCGMDEYYEVWRQISKPC-KKVPVWWSFLKLEPTLEEKIREENYRMIMCTDP
Group-I/Mon-21/Mongoose	NDEEEYVRDCGMDEYYEVWRQISKPC-KKVPVWWSFLKLEPTLEEKIREENYRMIMCTDP
Group-I/Mon-32/Mongoose	NDEEEYVRDCGMDEYYEVWRQISKPC-KKVPVWWSFLKLEPTLEEKIREENYRMIMCTDP
Group-I/Mon-38/Mongoose	NDEEEYVRDCGMDEYYEVWRQISKPC-KKVPVWWSFLKLEPTLEEKIREENYRMIMCTDP
Group-I/Mon-52/Mongoose	NDEEEYVRDCGMDEYYEVWRQISKPC-KKVPVWWSFLKLEPTLEEKIREENYRMIMCTDP
Group-II/Mon-43/Mongoose	DSEYSYLEECGFREYYETWDQIKDKDFDENPLWWSFLKMETTQKEIKQQDYRMIMCTDP
Group-II/Mon-59/Mongoose	DSEYSYLEECGFREYYETWDQIKDKDFDENPLWWSFLKMETTQKEIKQQDYRMIMCTDP
Group-II/Mon-61/Mongoose	DSEYSYLEECGFREYYETWDQIKDKDFDENPLWWSFLKMETTQKEIKQQDYRMIMCTDP
Group-II/Mon-63/Mongoose	DSEYSYLEECGFREYYETWDQIKDKDFDENPLWWSFLKMETTQKEIKQQDYRMIMCTDP
Group-II/Mon-66/Mongoose	DSEYSYLEECGFREYYETWDQIKDKDFDENPLWWSFLKMETTQKEIKQQDYRMIMCTDP
Group-II/Mon-78/Mongoose	DSEYSYLEECGFREYYETWDQIKDKDFDENPLWWSFLKMETTQKEIKQQDYRMIMCTDP
Group-II/Mon-79/Mongoose	DSEYSYLEECGFREYYETWDQIKDKDFDENPLWWSFLKMETTQKEIKQQDYRMIMCTDP
Group-II/Mon-81/Mongoose	DSEYSYLEECGFREYYETWDQIKDKDFDENPLWWSFLKMETTQKEIKQQDYRMIMCTDP
MaAstV-8/Human/GQ415660	IFARIGCVFEEHQNNLMKMRTKTRMGQCGWSPFCGGFNDRVKRLVDKGNN#LFVEFDWTRY
AvAstV-2/Chicken/AB033998	VITRLGASFDSEQNRMKERTETHHAQVGWTPFFGGLDKRVRRITSCGRTQVLELDWTRF
UCAstV/Agama/MZ375145	VYTRVGSVFQHQNELMKOHTYQRAGQMGWTPFKGGLDMTLRR-ISEGAEYIMELDWTRF
UCAstV/Gecko/MG599919	CYTRIGAVFEQHQNELMKEHTHQRAGQMGWCPFKGGLDRTLRR-ISSGMTKFLELDWTRF
Group-I/Mon-14/Mongoose	VFTRIGACFEQHQNELMKAHTRTHAGQVGWTPFKGGLDLTLRR-IAKDSECFLELDWTRF
Group-I/Mon-21/Mongoose	VFTRIGACFEQHQNELMKAHTRTHAGQVGWTPFKGGLDLTLRR-IAKDSECFLELDWTRF
Group-I/Mon-32/Mongoose	VFTRIGACFEQHQNELMKAHTRTHAGQVGWTPFKGGLDLTLRR-IAKDSECFLELDWTRF
Group-I/Mon-38/Mongoose	VFTRIGACFEQHQNELMKAHTRTHAGQVGWTPFKGGLDLTLRR-IAKDSECFLELDWTRF
Group-I/Mon-52/Mongoose	VFTRIGACFEQHQNELMKAHTRTHAGQVGWTPFKGGLDLTLRR-IAKDSECFLELDWTRF
Group-II/Mon-43/Mongoose	VFTRIGACFEQHQNELMKSHTLOKAGQMGWTPFKGGIDYTLRR-IAKNSQYFLELDWTRF
Group-II/Mon-59/Mongoose	VFTRIGACFEQHQNELMKSHTLOKAGQMGWTPFKGGIDYTLRR-IAKNSQYFLELDWTRF
Group-II/Mon-61/Mongoose	VFTRIGACFEQHQNELMKSHTLOKAGQMGWTPFKGGIDYTLRR-IAKNSQYFLELDWTRF
Group-II/Mon-63/Mongoose	VFTRIGACFEQHQNELMKSHTLOKAGQMGWTPFKGGIDYTLRR-IAKNSQYFLELDWTRF
Group-II/Mon-66/Mongoose	VFTRIGACFEQHQNELMKSHTLOKAGQMGWTPFKGGIDYTLRR-IAKNSQYFLELDWTRF
Group-II/Mon-78/Mongoose	VFTRIGACFEQHQNELMKSHTLOKAGQMGWTPFKGGIDYTLRR-IAKNSQYFLELDWTRF
Group-II/Mon-79/Mongoose	VFTRIGACFEQHQNELMKSHTLOKAGQMGWTPFKGGIDYTLRR-IAKNSQYFLELDWTRF
Group-II/Mon-81/Mongoose	VFTRIGACFEQHQNELMKSHTLOKAGQMGWTPFKGGIDYTLRR-IAKNSQYFLELDWTRF

[illegible][illegible]

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PEDYDVRVVDMYATVFGMW  
VNYDPQVTIDMYKNIFGMW  
VP-DVDMIVDMYEKVFWMW  
EP-NIDMIVKMYADIFGMW  
VP-DRNLLISMYENIYGMW  
VP-DRNLLISMYENIFGMW  
VP-DRNLLISMYENIFGMW  
VP-DRNLLISMYENIFGM-  
TP-DRNLLISMYESIFGMW  
LP-NKELIIDMYEQIFGM-  
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