Supplemental data 1: Sequence alignment of the members of the two monophyletic lineages within the AtMIKC* subgroup.

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AGL30           MGRVKLKIKKLENTNGRQSTFAKRKNGILKKANELSILCDIDIVLLMFSPTGKAAICCGT 60
AGL94           MGRVKLKIKKLQNMNGRRCTYTKRRHGIMKKAKELSILCDIDVVLLMFSPMGKASICIG- 59
AGL65           MGRVKLKIKRLESTSNRQVTYTKRKNGILKKAKELSILCDIDIVLLMFSPTGRATAFHGE 60
                *********:*:. ..*: *::**::**:***:*********:******* *:*:   *

AGL30           RSSMEEVIAKFSQVTPQERTKRKFESLENLKKTFQKLDHDVNIREFIASSNS-TVEDLST 119
AGL94           KHSIGEVIAKFAQLSPQERAKRKLENLEALRKTFMKANHDIDISKFLDRISTPTVEVLSE 119
AGL65           HSCIEEVISKFAQLTPQERTKRKLESLEALKKTFKKLDHDVNIHDFLG-ARNQTIEGLSN 119
                : .: ***:**:*::****:***:*.** *:*** * :**::* .*:    . *:* **

AGL30           QARILQARISEIHGRLSYWTEPDKINNVEHLGQLEISIRQSLDQLRAHKEHFGQQQQAMQ 179
AGL94           KIRFLQTQLSDIHTRLSYWTDVDNIDSVDVLQQLEHSLRQSLAQIYGRKASMPQRQQQQL 179
AGL65           QVAIYQAQLMECHRRLSCWTNIDRIENTEHLDLLEESLRKSIERIQIHKEHYRKNQLLPI 179
                :  : *::: : * *** **: *.*:..: *  ** *:*:*: ::  :*    :.*

AGL30           IENANFVKDWSTCSMQDGIQIPLEQQLQSMSWILNSNTTNIVTEEHNSIPQ-----REVE 234
AGL94           MS--SQCKNQLQTEIDIDFGMEMEQQLENFSWVRTDENMNVPIEEEDPNLQLHHMYKDIT 237
AGL65           ECATTQFHSGIQLPMAMGGNSSMQEAHS-MSWLPDNDHQQTILPGDSSFLP--------H 230
                    .  :.     :  .    :::  . :**:  .:  :     ...

AGL30           CSASSSFGSYPGYFGTGKSPEMTIPGQETSFLDELNTG-------QLKQDTSS-QQQFTN 286
AGL94           CSASSALGNYSGLFSKS-----------SDILQKLETG-------SIPGTSADPNQQFSN 279
AGL65           REMDGSIPVYSSCFFESTKPEDQICSNPGQQFEQLEQQGNGCLGLQQLGEEYSYPTPFGT 290
                 . ..::  *.. *  .            . :::*:         .      .    * .

AGL30           NNNITAYNPNLHNDMNHHQTLPPPPLPLTLPHAQVYIPMNQREYHMNGFFEAPPPDSSAY 346
AGL94           ---LSFLNDQKLKQLAEWSLLGSP-----------------ADYYVSQILEAS------Y 313
AGL65           TLGMEEDQEKKIKSEMELNNLQQQQQQQQQQQQQDPSMYDPMANNNGGCFQIPHDQSMFV 350
                   :   : :  :.  . . *                         .  :: .

AGL30           NDNTNQTRFGSSSSSLPCSISMFDEYLFSQMQQPN---- 381
AGL94           KPQIGGKNNGASSETLPY-VAVFDDPLYFWVNNGCSS-- 349
AGL65           NDHHHHHHHHHQNWVPDSMFGQTSYNQVCVFTPPLELSR 389
                : :    .   ..      ..  .      .



AGL66           MGRVKLEIKRIENTTNRQVTFSKRRNGLIKKAYELSILCDIDIALLMFSPSDRLSLFSGK 60
AGL104          MGRVKLEIKRIENTTNRQVTFSKRRNGLIKKAYELSILCDIDIALIMFSPSDRLSLFSGK 60
AGL67           MGRVKLELKRIEKSTNRQITFSKRKKGLIKKAYELSTLCDIDLALLMFSPSDRLCLFSGQ 60
                *******:****::****:*****::********** *****:**:********.****:

AGL66           TRIEDVFSRYINLSDQERENALVFPDQSRRPDFQSKEYLLRTLQQLKAENDIALQLTN-- 118
AGL104          TRIEDVFSRFINLPKQERESALYFPDQNRRPDIQNKECLLRILQQLKTENDIALQVTN-- 118
AGL67           TRIEDVLARYINLPDQERENAIVFPDQSKRQGIQNKEYLLRTLEKLKIEDDMALQINEPR 120
                ******::*:***..****.*: ****.:* .:*.** *** *::** *:*:***:.:

AGL66           PTAINSDVE-ELEHEVYKLQQQLLMAEEELRKYEPDPIRFTTMEEYETCEKQLMDTLTRV 177
AGL104          PAAINSDVE-ELEHEVCRLQQQLQMAEEELRRYEPDPIRFTTMEEYEVSEKQLLDTLTHV 177
AGL67           PEATNSNVEVELEQEVCRLQQQLQISEEELRKFEPDPMRLTSMEEIEACEANLINTLTRV 180
                * * **:** ***:** :***** ::*****::****:*:*:*** *..* :*::***:*

AGL66           NQRREHILSQDQLSSYEASALQQQQSMGGPFGNDVVGGWLTENGPNEAHLFDASAHS--- 234
AGL104          VQRRDHLMS-NHLSSYEASTMQPN--IGGPFVNDVVEGWLPENGTNQTHLFDASAHSNQL 234
AGL67           VQRREHLLR----KSCEAQSNQQS--MDGILLNDIVEDWGPEPEPKQAHMIANSAHHS-- 232
                 ***:*::     .* **.: * .  :.* : **:* .* .*  .:::*::  ***

AGL66           -----AMYETLLQGSSSSSNQNNIMGESNVSNHNGDMFQEWAQAYNSTTAHNPSTLFPPM 289
AGL104          RELSSAMYEPLLQGSSSSSNQNN-MSECHVTNHNGEMFPEWAQAYSS------SALFASM 287
AGL67           ---NQPSYDLLLRRSNSSSNQNPK------------------------------------ 253
                     . *: **: *.******

AGL66           QHQHGLVVDPNIEEIE------IPVMKKDAQADHEVSDYDIRMPQLSSQ 332
AGL104          QQQH-EGVGPSIEEMMPAQQSDIPGVTAETQVDHEVSDYETKVPQLSSQ 335
AGL67           -------------------------------------------------
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