(A)

```
gi|22652868|        MGLTEIMLVL-VSLAFVATAAAHDCQNGTRPASEEKREGCDYYCWNTETKSWDKFFFGNGERCFYNNGDEGLCQNGECHLTTDSGVPNDTDAKIEETEEELEA----------------------------------
gi|22164158|        MGLTEIMLVL-VSLAFVATAAAHDCQNGTRPASEEKREGYDYYCWNTETKSWDKFFFGNGERCFYNNGDEGLCQNGECHLTTDSGVPNDTDAKIEETEEELEA----------------------------------
gi|22164164|        MGLTGTTLVL-VSLVFFGSAAAHNCKNGTRPASEENREGCDYYCWNDGTNSWDQFFFGNGEICFYNSGEKGICQNGECHLTNNSGGPNETDENTPATTEKPKQKKKKTKKPKKPKRKSKKDQ----------------
gi|22164176|        MGLTGTTLVL-VSLAFFGSAAAHNCKNGTRPASEENREGCDYYCWNDGTNSWDQFFFGNGEICFYNSGEKGICQNGECHLTNNSGGPNETDDNTPAPTEKPKQKKKKPKKPKKPKRKSKKDH----------------
gi|15428308|        MGLTGTMLVL-VSLAFFGSAAAHNCQNGTRPASEQDREGCDYYCWNAETKSWDQFFFGNGEKCFYNSGDHGTCQNGECHLTNNSGGPNETDDYTPAPTEKPKQKKKKTKKTKKPKRKSKKDQEKNL-------------
gi|22164190|        MGLTGTTLML-VCVAFFGTAAAHNCKNGTRPASEENREGCDYYCWNEVTNSWDQFFFGNGERCFYNTGENGKCQNGECHLTTNSDGPNETDDNTPPPTEKPK----------------------------------
gi|22164156|        MGLTGTTLVL-VCVAFFGSAAAHNCQNGTRPASEENREGCDYYCWNEVTNSWDQFFFGNGERCFYNTGENGKCQNGECHLTTNSDGPNETDDNTPPPTEKPKQKKKKPKKPKKPKRKSKKDQ----------------
gi|22164184|        MGLTGTTLVL-VCVAFFGTAAAHNCKNGTRPASEENREGCDYYCWNEVTNSWDQFFFGNGERCFYNTGENGKCQNGECHLTTNSGGPDDTDDNTPPPTEKPKQKKKKPKKPKKPKRKSKKDQ----------------
gi|22164186|        MGLTGTTLVL-VCVAFFGSAAAHNCQNGTRPASEKNREGCDYYCWNAETKSWDQFFFGDGERCFYNTGENGTCRNGECHLTTSSGGPNETDDNTPPPTEKPKQKKKKPKKTKKPKRKSRKDQ----------------
gi|22164174|        MGLTGTTLVL-VSLAFFGSAAAHNCQNGTRPTSEKNREGCDFYCWNADTNLWDKFFFGNGEKCFYNTGEKGTCLNGECHLTTSSGGPDDTGDNTPPPTEKPKQKKKKPKKTKKPKRKSKKDQKENF------------
gi|22164194|        MGLTGTALVL-VSLAFFGSAAAHNCQNGTRPASEENREGCDYYCWNSETQSWDQYFFGDGERCFYNSGDRGICQNGECHLTTSSGGPDDTDENTPPPTEKPKQKKKKPKKTKEPKRKSKKD----------------
IP_5_100_90_1_CLU   MGLTGATLVL-VSLAFFGSAAAHNCKNGTRPASEENREGCDFYCWSTDTNSWEIFFFGNGEECFYNNGDRGTCQDGACHLTTHSGGPNETDDYTPAPTEKPKQKKKKPKKTKKPKRNSKKD----------------
IP_clu3             MGLTGATLVQGVSLAFFGSAAAHNCKNGTRPASEENREGCDFYCWSTDTNSWEIFFFGNGEECFYNNGDRGTCQDGACHLTTHSGGPNETDDYTPAPTEKPEQKKKKPKKTKKPKRNTKKKKKKKKKKNFLGPPGPH
IP_5_100_90_1_CLU1  MGLTGATLVL-VSLAFFGSAAAHNCQNGTRPASEENREGCDFYCWNTDTNSWDIFFFGNGEKCFYNNGDRGTCQDGACHLTTHSGGPNETDDYTPAPTEKPKQKKKKPKKTKKPKRKSKKD----------------
IP_5_100_90_2A_CLU  MGLTGITLVL-VSLAFFGSAAAHNCQNGTRPASEENREGCDFYCWNAGTNSWDIFFFGNGEKCFYNNGDRGTCQDGACHLTTHSGGPNETDDYTPAPTEKPKQKKKKPKKTKKPKRKSKKDKEG-----NF-------
IP_5_100_90_2_CLU   MGLTGATLVL-VSLAFFGSAAAHNCKNGTRPASEETREGCDFYCWNTDTSSWDIFFFGNGEKCFYNNGDRGTCRDGACHLTTLSGGPNETDDYTSAPTEKPKQKKKKLKKTKKPKRKSKKD----------------
gi|45593710|        MGLTGTTLVL-ASLAFFGSAAAHNCKNGTRPASEEKREGCDFYCWNSDTSRCDQFFFRDGETCFYNNGDRGSCQNGECHLNTNSGVPTHNDDYTPSPTEKPKQKKKKPKKTKKPKRQSNKD----------------
IP-7-60-92-2-CLU    MGLTGITLVL-VSFAFFGSVAAHNCQNGTRPTSEQNREGCDYYCWNTDTKSWDQFFFGNGERCFYSNGDTGVCTNGECHLNTESSVPTETDVETPAPTKKPKQKKKKQKKTKKPKR----------------------
IP_5_100_90_25_CLU  MGLTGITLVL-VSFAFFGSVAAHNCQNGTRPASEQNREGCDYYCWNTDTKSWDQFFFGNGERCFYSNGDTGVCTNGECHLNTESGVPTETDVETPAPTKKPKHKKKKQKKSKKPKG----------------------
IP_5_100_90_6_CLU   MGLTGTTLVL-VSFAFFGSVAAHNCQNGTRPASEENREGCDYYCWNTDTRSWEQFFFGNGERCFYNTGEKGECKNGECHLTTESGVPTDTDVDTPAPTKKPKQKKKKQKKTKKPKR----------------------
gi|22164182|        MEFTGITLVL-VSLTFFGSAAAETCRNGTRPGSQTQREGCDYYCWNSQTSSWDKYFFGDNEPCFYNTGLRGTCQNGECHLTSEGGVPTDPNQYPSEPTEKPKKNKKKSKKTKKPKKTKKPKDN---------------
gi|22164160|        MEFTGITLLL-VSLAFFGSAAAETCRNGTRPASQTQREGCDYYCWNLQTSSWDKYFFGDNEPCFYNTGLRGTCQNGECHLTSEGGVPTDPNQYPSEPTEKPKKNKKKSKKTKKPKKTKKPKDN---------------
gi|22164178|        MEFTGITLVL-VSVAFFGSAAAETCRNGTRPASQTDREGCDYYCWNTLTSSWDKYFFGDEEPCFYNTGLRGTCKNGGCHLTSEGNVPTDPDQYPSEPTEKPKKSKKKSKKTKKPKKTKKPKDN---------------
gi|22164180|        MEFTGITLVL-VSVAFFGSAAAETCRNGTRPASQTDREGCDYYCWNTLTSSWDKYFFGDEEPCFYNTGLRGTCKNGECHLTSEGGVPTDPNQYPSEPTEKPKKNKKKSKKTKKPKKSKKPKDN---------------
gi|22164168|        MELTGITLVL-VSLALFGSAAAETCRNGTRPASQTDREGCDYYCWNTLTSSWDKYFFGDEEPCFYNTGLKGTCKNGECHLTSEGGVPTDPHQYPSEPTEKPKKNKKKSKKTKKPKKSKKPKNN---------------
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Poly K (lysine) tail

(B)

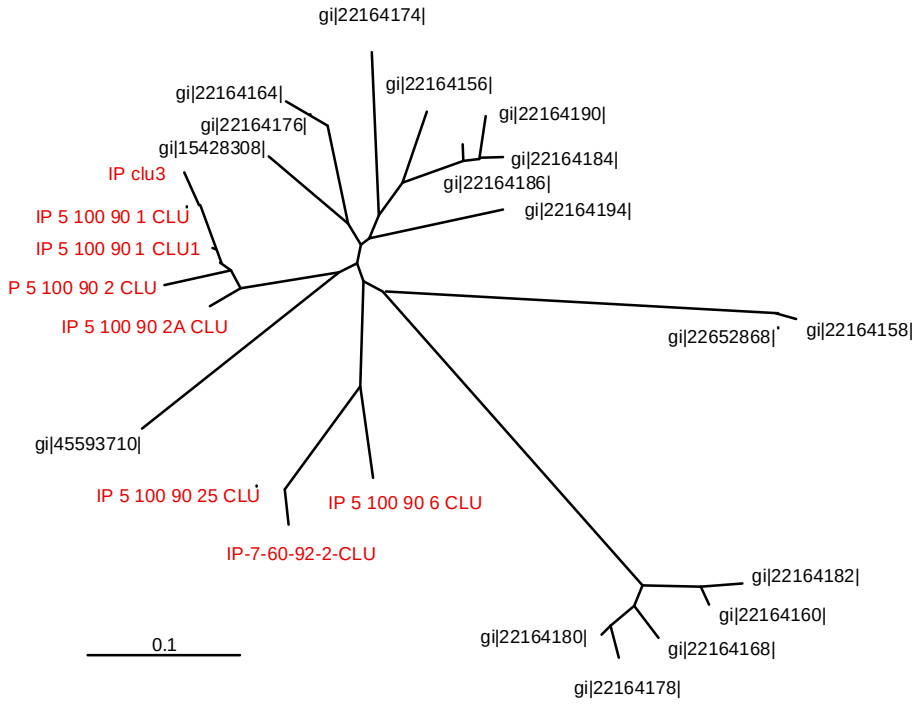

Figure 2