Figure 2 - figure supplement 1

```
PfPMV      ------------------------------------------------------------
TgASP5     MEAGAMGGSSFLSFSSGPSAETSPSSLSPPTSSSPSPSPQLVSDSVESLHAKRPLAQSSR

PfPMV      ------------------------------------------------------------
TgASP5     SSSRTAASTCFCWQGEGQENEAAPTISQEERRGGSMTAASAGHLETAREEAARCLGCSYT

PfPMV      ------------------------------------------------------------
TgASP5     GEERRGASSATSVLSLGGERGRPPSRSSSLWTFSGLLSPLAFRSRRCCPQFSSSSSPLSP

PfPMV      ------------------------------------------------------------
TgASP5     LPHPRGAPASACGSAVITDRAGRPASPLSFSRLASPVSDPSGVCPPRVVAARVWRLLSSV

PfPMV      -------------------------------------MNNYFLRKENFFILFCFVFVSIFF
TgASP5     LFSLVNCARLFPRRLSRRPDPLRKPRAQVWSASSRSLQALLLATVALFA-ACSSLHGSSL
                                                ::  :* .  :*   *  : .  :

PfPMV      V---------------SNVTIIKCNNVENKIDNVGKKIENVGKKIGDMENKNDNVENKN-
TgASP5     LGAQAASPTPPFLSLSSSPRSLASDSAKKGSNAPEQSREQRGEREGERQRPDKGEENGET
           :               *.   : .:..::  :   :. *: *:: *: :. :.  ** :

PfPMV      -----------DNVGNKNDN-----------VKNASSDLYKYKLYGDIDEYAYYFLDIDI
TgASP5     EETFPAASGVVPAPGLKVADLPRTGPPVDLLGLPIRKKVFRARLYGSMFSYAYYFLDILV
                             * *  :                  ..::: :***.: .******** :

                                                                NAP1 insert
PfPMV      GKPSQRISLILDTGSSSLSFPCNGCKDCGIHMEKPYNLNYSKTSSILYCNKSNCPYGLK-
TgASP5     GTPPQRASVILDTGSSLLAFPCAGCSECGQHLDPAMDTSRSATGEWIDCKEQERCFGSCS
           *.* ** *:******* *:*** **.:** *::   : . * *.. : *::.:  :*

                                          flap
PfPMV      -------------CVGNKCEYLQSYCEGSQIYGFYFSDIVTLPSYNNKNKISFEKLMGCH
TgASP5     GGTPLGGLGGGGVSSMRRCMYTQTYSEGSAIRGIYFSDVVALGEVEQKNPPVRYDFVGCH
                         .  .:* * *:*.*** * *:****:*:* . ::**     .::***

PfPMV      MHEESLFLHQQATGVLGFSLTKPNGVPTFVDLLFKHTPSL-KPIYSICVSEHGGELIIGG
TgASP5     TQETNLFVTQKAAGIFGISFPKGHRQPTLLDVMFGHTNLVDKKMFSVCISEDGGLLTVGG
            :* .**: *:*:*::*:*: * .  **::*::* **  : * ::*:*:**.** * :**

PfPMV      YEPDYFLSNQKEKQKMDKSDNNSSNKGNVSIKLKNNDKNDDEENNSKDVIVSNNVEDIVW
TgASP5     YEPTLLVAPPESESTPATEALRP-VAGES------------ASRRISEKTSPHHAALLTW
           ***  :::  :.:..  ..  .    *:             ... .:    ...  :.*

PfPMV      QAITRKYYYYIKIYGLDLYGTNIMDK--KELDMLVDSGSTFTHIPENIYNQINYYLDILC
TgASP5     TSIISHSTYRVPLSGMEVEGLVLGSGVDDFGNTMVDSGTTYSYFPPAVFSRWRSFLSR--
            :*  :  * : : *::: *  : .   .  : :****:*:::*  ::.: . :*.

                                 helix-turn-helix
PfPMV      IHDMTNIYEINKRLKLTNESLNKPLVYFEDFKTALKNIIQNENLCIKIVDGVQCWKSLEN
TgASP5     -----------------------------------FCTPELFCERERDGRPCWRVSPG
                                              :   * :* :  **  **:

PfPMV      L------PNLY--ITLSNNYKMIWKPSSYLYKK-ESFWCKGLEKQVNNKPILGLTFFKNK
TgASP5     TDLSSIFPPIKVSFGDEKNSQVWWWPEGYLYRRTGGYFCDGLDDNKVSASVLGLSFFKNK
                  * :   :  .:* :: * *..***::  .::*.**:.:  .  :***:*****

PfPMV      QVIFDLQQNQIAFIESKCPSNLTSSRPRTFNEYREKENI---FLK---------------
TgASP5     QVLFDREQDRVGFAAAKCPSFFLDQRPRGPDSGDGPKGRPTAPFTVPPLRVPVPMDGGGV
           **:** :*:::.*  :**** : ..***  :.    :      :.

                          transmembrane domain
PfPMV      --------VSYINLYCLWLLLALTILLSLILYVRKMFY--------MDYFPLSDQNKSPI
TgASP5     PGDAKQPEGLPLSPQQLWVAAALVVVAILIAVTVILLHTIKRPSRSSAVVPAPSAPRLPF
                     :.   **:  **.::  **  .  :::          .*  .  : *:

PfPMV      QEST-------------------------------------------------------
TgASP5     AQNSKSAGRFARGLGHGALGVGNPVYVQRTQRYREVQEAQPHTADAYYDVEEDRFTGEDD
            :.:

PfPMV      ---------------------------------------------
TgASP5     GDFFGDDSVPSAEEQETAPSLSLREESSPFSASQSTLLDLPLGGE
```

14.4% Identity (153/1065), 32.6% Similarity (347/1065)

$\Delta asp5_{CRISPR}$

LKVADLCPEQDPQ.

ASP5MUT-HA$_3$

ASP5-Mut GTPPQRASVILATGSSL

ASP5-Mut SGVDDFGNTMVASGTTY