

Table S1. *In silico* analysis of off-target activity of sgRNAs used in this study

	Target	Chromosome	Position	Direction	Mismatches	Bulge Size
AeAPN1	crRNA: GGATTGGAGCTAGCGGTAACNGG	3	9134967	+	0	0
	DNA: GGATTGGAGCTAGCGGTAACCGG					
	crRNA: GTGCGTCGAGACTACAAGACNGG	3	9135072	+	0	0
	DNA: GTGCGTCGAGACTACAAGACAGG					
	crRNA: GGTCTACAGTCGGCCATCCANGG	1	2906250 78	+	0	0
	DNA: GGTCTACAGTCGGCCATCCAGGG					
AeAPN2	crRNA: GGTTCGTCGCACACTCAGCANGG	1	2906251 72	-	0	0
	DNA: GGTTCGTCGCACACTCAGCACGG					

	1	10	20	30	40	50
WT	MIVLKWSVVLWGGLTLATYGTVAERPLSDVSDSDVDPQIAPAFAVEESEIIPLOQEVDES					
AeAPN1-KO	MIVLKWSVVLWGGLTLATYGTVAERPLSDVSDSDVDPQIAPAFAVEESEIIPLOQEVDES					
	60	70	80	90	100	110
WT	YRLPKTSYPTHYELRLRTEVHTGNRQFDGTVAIHLNVVEATNAIVVHRRSLTIQKANL					
AeAPN1-KO	YRLPKTSYPTHYELRLRTEVHTGNRQFDGTVAIHLNVVEATNAIVVHRRSLTIQKANL					
	120	130	140	150	160	170
WT	AFIPTPEADPQQQLNDPTWTYDANVEQLSFNSETLLNPGSYILTVEYNGRLSDSEDGFY					
AeAPN1-KO	AFIPTPEADPQQQLNDPTWTYDANVEQLSFNSETLLNPGSYILTVEYNGRLSDSEDGFY					
	180	190	200	210	220	230
WT	ISSYVNKDGVTKYLATTOFESTSARMAFFPCYDEPGLKATFALWITHDVLTYTANSNMPY					
AeAPN1-KO	ISSYVNKDGVTKYLATTOFESTSARMAFFPCYDEPGLKATFALWITHDVLTYTANSNMPY					
	240	250	260	270	280	290
WT	TTTIDGDIRVTQFEVTPKMSTYLLAFVVSDFQRLGTLHSVYARPNAIDEVVFAVEAG					
AeAPN1-KO	TTTIDGDIRVTQFEVTPKMSTYLLAFVVSDFQRLGTLHSVYARPNAIDEVVFAVEAG					
	300	310	320	330	340	
WT	QKILEKLD AHLGIGYDHPQMKQFAIPDFAAGAMENWGLVITYREQYLLFNPELSTYR					
AeAPN1-KO	QKILEKLD AHLGIGYDHPQMKQFAIPDFAAGAMENWGLVITYREQYLLFNPELSTYR					
	350	360	370	380	390	400
WT	TKTNIA TVIAHE YAHQWF GNLVSP EWWEYIWLNEGFATLYEYYATHLAYPEVGWELF					
AeAPN1-KO	TKTNIA TVIAHE YAHQWF GNLVSP EWWEYIWLNEGFATLYEYYATHLAYPEVGWELF					
	410	420	430	440	450	460
WT	NTQVIQAAMVPDGLTTRPMTWNADTPRSIASLFD RVAYPKSGSVLNMMRNVLGEINW					
AeAPN1-KO	NTQVIQAAMVPDGLTTRPMTWNADTPRSIASLFD RVAYPKSGSVLNMMRNVLGEINW					
	470	480	490	500	510	520
WT	TAGLKAYLTARQFDGANADHLYVGLQSAIGKNVLP EGVTVKAIQMDTAN EKGYPVLS					
AeAPN1-KO	TAGLKAYLTARQFDGANADH PDSGLV CDEPTKPEILLSSRKSGSSRIIVREPIRTYG....					
	530	540	550	560	570	580
WT	VRRTYETGDIIISQERFISDRKVPNTNVMIPYNYVHQSKADFDDLSF SWLSTKAAR					
AeAPN1-KO						
	590	600	610	620	630	
WT	INTEVPANEWIIFNKQQVGYRVNYDANNWELITNALINNLSIDRLNRAQLIDDAYW					
AeAPN1-KO						
	640	650	660	670	680	690
WT	LARSGRLDIEVLMLKLLTYLKDETEYAPWTAANNVLSYFNGKLRGTPAYKDFTTMVDHL					
AeAPN1-KO						
	700	710	720	730	740	750
WT	IKKVYKTLDTVAVSDTEPLLHKYLYKQISTWACLIGNEDCLKRTKEALQKEVTEGIPV					
AeAPN1-KO						
	760	770	780	790	800	810
WT	HPDVATVVYCNGLRTADVAEYQYLYKRIYPTQNWAFRSMIISALGCSENKQFLKDFLQ					
AeAPN1-KO						
	820	830	840	850	860	870
WT	TAIGSGSGVEIN YKTAERTQIVQAVYSGGRAGVDALIEFLRDPNMLREFVAILDVNT					
AeAPN1-KO						
	880	890	900	910	920	
WT	LNSALSNIASRTNTQEELDMLNDLIVDLGTYITPQTAEAAARATVQANFAWQQSAEAIL					
AeAPN1-KO						
	930	940	950	960	970	980
WT	TMNEVGFVDSIEPEPTTIVSPDSTTVSPASSTTAGSTTVAGSSTTEDDGGAAATIAVS					
AeAPN1-KO						
	990	1000				
WT	VTLLIGAVAVALEN					
AeAPN1-KO						

Figure S1. Amino acid sequence alignment of AeAPN1 isoform from WT and AeAPN1-KO strains.

	1	10	20	30	40	50
WT	MLLKEVFLCALVLSVSADRPSSWRKVEGDLADEPEVELLQEVNGAYRLPTVTVPTHYNL					
AeAPN2-KO	MLLKEVFLCALVLSVSADRPSSWRKVEGDLADEPEVELLQEVNGAYRLPTVTVPTHYNL					
	60	70	80	90	100	110
WT	HLKTAIHENEREFQGTVEIFFNVLESTDTVTVHNRRLLVIWKVTLYSVTGEGQTELGSP					
AeAPN2-KO	HLKTAIHENEREFQGTVEIFFNVLESTDTVTVHNRRLLVIWKVTLYSVTGEGQTELGSP					
	120	130	140	150	160	170
WT	EFETDADTEHLAIKHSAMAPGSYMVKVEFNGILQNNNNQGGFFASSYVDDTGKRHYLA					
AeAPN2-KO	EFETDADTEHLAIKHSAMAPGSYMVKVEFNGILQNNNNQGGFFASSYVDDTGKRHYLA					
	180	190	200	210	220	230
WT	SSKFEPHTHARSAPPCFDEPKLKATFTLSITHSKDYNANMMPRDGALVPDVEDDASFT					
AeAPN2-KO	SSKFEPHTHARSAPPCFDEPKLKATFTLSITHSKDYNANMMPRDGALVPDVEDDASFT					
	240	250	260	270	280	290
WT	TKFLKSTKMSTYLLAFVSNFAIRTSQYQTVYARPNVYGETEFPDQAGVDILNALSAY					
AeAPN2-KO	TKFLKSTKMSTYLLAFVSNFAIRTSQYQTVYARPNVYGETEFPDQAGVDILNALSAY					
	300	310	320	330	340	
WT	TGVEYTKYMPKMTQIAIPDRGSGAMENWGLVTYCEPVLLFNPTINSYRTRKKNVITIIA					
AeAPN2-KO	TGVEYTKYMPKMTQIAIPDRGSGAMENWGLVTYCEPVLLFNPTINSYRTRKKNVITIIA					
	350	360	370	380	390	400
WT	HEFAHQWFGNLVSPDWWDYIWLNEGFAIVYEEYAAQLAYPETRYMDLWGVVEVIQNAFA					
AeAPN2-KO	HEFAHQWFGNLVSPDWWDYIWLNEGFAIVYEEYAAQLAYPETRYMDLWGVVEVIQNAFA					
	410	420	430	440	450	460
WT	ADARESVRPMTWNAATPSEIAGLFDTVAYDKSGSVLNMFRVAFQDDNWREGLVSYFNN					
AeAPN2-KO	ADARESVRPMTWNAATPSEIAGLFDTVAYDKSGSVLNMFRVAFQDDNWREGLVSYFNN					
	470	480	490	500	510	520
WT	RELDGAIADHLYQCLELAVTGKGLLPSEFNVKDVMSWTTVAGFPLLTVRDYKTGDI					
AeAPN2-KO	RELDGAIADHLYQCNREGSVAKIFQRQRCDGFVDNRGRIPCSIQLRNEVVA.....					
	530	540	550	560	570	580
WT	FVSQERFYSDRQLPNAHVYHPYNYATKSTPSFDTLNFEWLSTKAAKLTITIPAEWDI					
AeAPN2-KO						
	590	600	610	620	630	
WT	IFNKQQTGYRVNYDTKNWKLIIAALQENPSTIHVQNRAQLINDAYNLARAERLDLTV					
AeAPN2-KO						
	640	650	660	670	680	690
WT	PLELMTYLLKQETAYPPWAAASSVLTYFNNKLRGTSQYPHFLNYVTELIQPIYSTQYVN					
AeAPN2-KO						
	700	710	720	730	740	750
WT	SVLASETAMDKYLLKQTIISTWACRIDHQNCLAVTGNALRIAVAANIPVHPDIATVVYCY					
AeAPN2-KO						
	760	770	780	790	800	810
WT	GLHGTEETEFVWLYERLLASKNQAEAVLIDSLGCSQNKEFLKSFLLMTSIGSGATFNF					
AeAPN2-KO						
	820	830	840	850	860	870
WT	LETERTIVSSVYSASRAGVDALIEFLGDVKKLIDEFISRLGSSTLNNAVANIASRTNN					
AeAPN2-KO						
	880	890	900	910	920	
WT	EQELEQLAALLTLGDKVVSANTASSARATVRNNFAWFQSLGLVAEEFFAAYKQ					
AeAPN2-KO						

Figure S2. Amino acid sequence alignment of AeAPN2 isoform from WT and AeAPN1-KO strains.

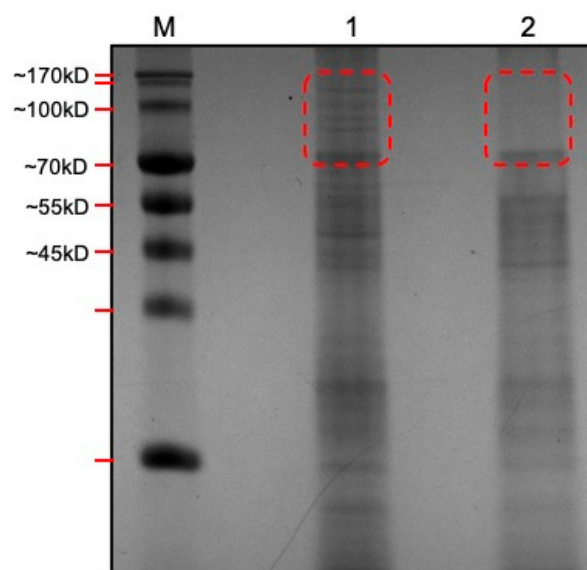


Figure S3. SDS-PAGE profile of midgut BBMV protein from the WT strain and the *AeAPN1/AeAPN2*-KO strain, and the target regions of Coomassie blue stained gels were framed by red dashed boxes. Lane M: Prestained Color Protein Ladder (Beyotime, China), Lane 1: the midgut BBMV proteins from the WT strain, Lane 2: the midgut BBMV proteins from the *AeAPN1/AeAPN2*-KO strain.

Table S2. *AeAPN1* and *AeAPN2* peptides identified from midgut BBMV of the WT strain

<i>AeAPN1</i> peptides		<i>AeAPN2</i> peptides	
IYPTQNWAFR	TLDVTAVSDTEPL LHK	MTQIAIPDR	EGLVSYFNRR
MAFPCYDEPGLK	DFLQTAIGGSGSG VEINYK	IVSSVYSASR	DVMDSWTTVAGFPLLT VR
QFAIPDFAAGAM ENWGLVTYR	DFTTMVDHLIK	QLPNAHVYHVPYNYAT K	DYNAVANMPR
QFDGANADHLYV GLQSAIQGK	DETEYAPWTAAN NVLSYFNGK	LIHAALQENPSTIHVQNR	ESVRPMTWNAATPSEI AGLFDTVAYDK
RIYPTQNWAFR	EFVAILDVNTLNS ALSNIASR	LGSSTLNNAVANIASR	IDHQNCLAVTGNALR
QTISTWACLIGNE DCLK	EQYLLFNPELSTY R	LIDEFISR	LDLTVPLELMTYLK
NVLGEINWTAGL K	AGVDALIEFLR	LTTTIPAEWDWIFNK	GSGAMENWGLVITYGE PVLLFNPTINSYR

NVLPEGVTVK	AGVDALIEFLRDP NMLR	LPTVTVPHTHYNLHLK	HSSAMAPGSYMK
INTEVPANEWIIF NK	KVPNTNVWMIPY NYVHQSK	VSANTASSAR	AQLINDAYNLAR
LSDSEDGFYISSYV NK	ADFDDLSTFSWLS TK	VTLYSVTGEGQTELGSP FETDADTEHLAIK	MTQIAIPDR
VPNTNVWMIPYN YVHQSK	LDIEVLMK	VEFNGILQNNNNQGFFA SSYVDDTGKR	QETAYPPWAAASSVLT YFNNK
VTQFEVTPK	LDAHLGIGYYDH MPQMK	TAIHENER	FEPTHAR
YLATTQFESTSAR	AIMDTWANER	STPSFDTLNFEWLSTK	QQTGYR (AAEL018249-PB; AAEL019828-PA; AAEL012783-PA)
SMIISALGCSENK	GTPAYKDFTTMV DHLK	SAFPCFDEPK	VNYDTK
TADVAEYQYLYK	AQLIDDAYWLAR	SGSVLNMFR (AAEL019828-PA; AAEL008163-PA)	
RTYETGDIISQER	AGVDALIEFLRDP NMLR	VAFQDDNWR	
SIASLFDR	LDAHLGIGYYDH MPQMK	TNNEQELEQLEALLTTL GDK	
SGSVLNMFR	MSTYLLAFVVSDF QR	TGDIFVSQER	
TQIVQAVYSGGR	GYPVLSVR	DGALVPDVDDASFVTTK	
TYETGDIISQER	QQVGYYR	ATFTLSITHSK	
TSYPHTYELR	LLTYLK	AVLIDSLGCSQNK	
DPNMLR		ELDGAIAADHLYQGLELA VTGK	