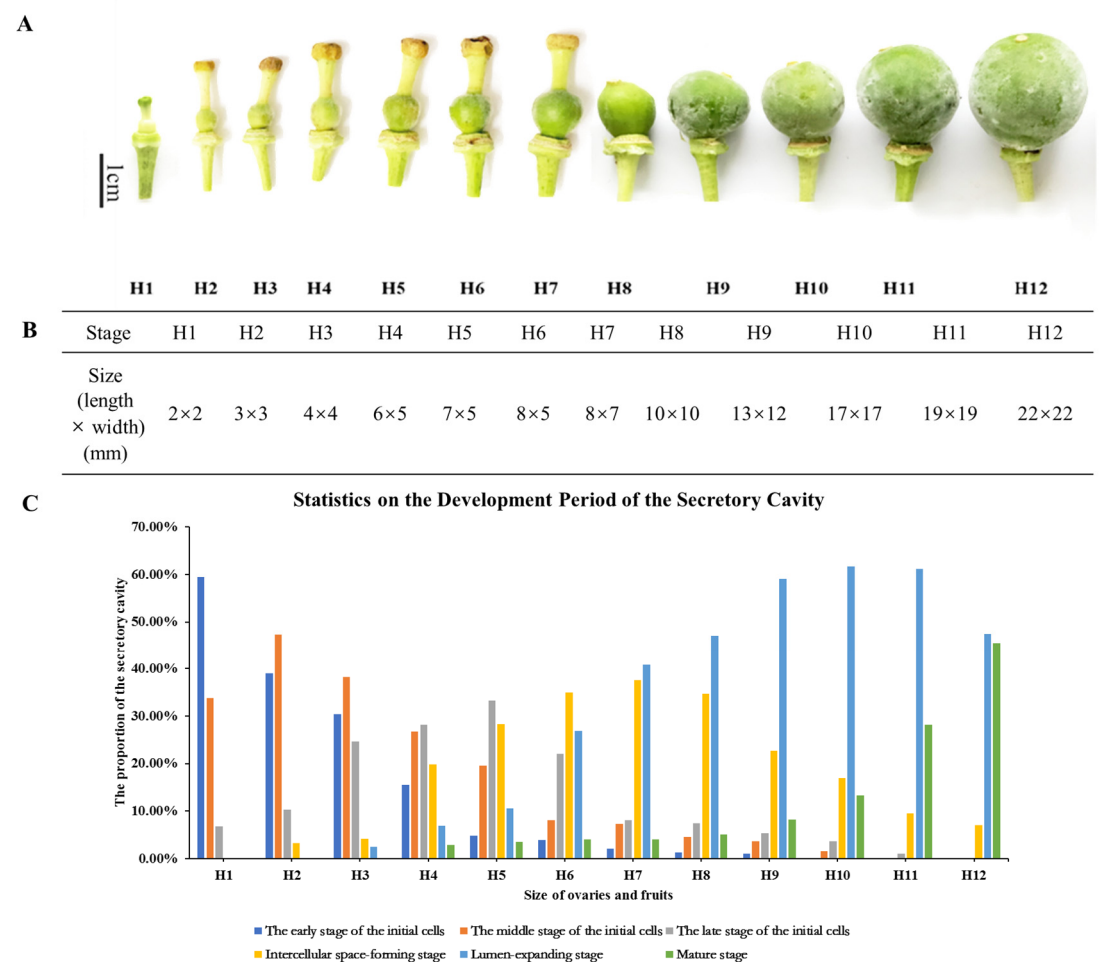


**Table S1. The sequence of gene specific primers.**

Gene	Forward(5'-3')	Reserve(5'-3')
<i>CgENDO1(RT)</i>	GAAGCTCTGATCGCCGACAT	GATTTGTGCCTGAACCAGCG
<i>β-Actin</i>	CACACTGGAGTGATGGTTGG	ATTGGCCTTGGGGTTAAGAG
<i>CgENDO1(Clone)</i>	ATGGGGGGATTGTGCCCTTTA	TCATGTAGCTGCTGCAAATTC TTC
<i>CgENDO1(PGEX)</i>	TGGATCCCCGGAATTCATGGG GGGATTGTGCCCTTTA	CTCGAGTCGACCCGGTCATGT AGCTGCTGCAAATTCTTC

Note:  $\beta$ -Actin is the internal control for quantitative real-time PCR. *CgENDO1(RT)* is for quantitative real-time PCR. *CgENDO1(Clone)* is for gene clone; *CgENDO1(PGEX)* is for expression of *CgENDO1* in the *in vitro* Escherichia coli.

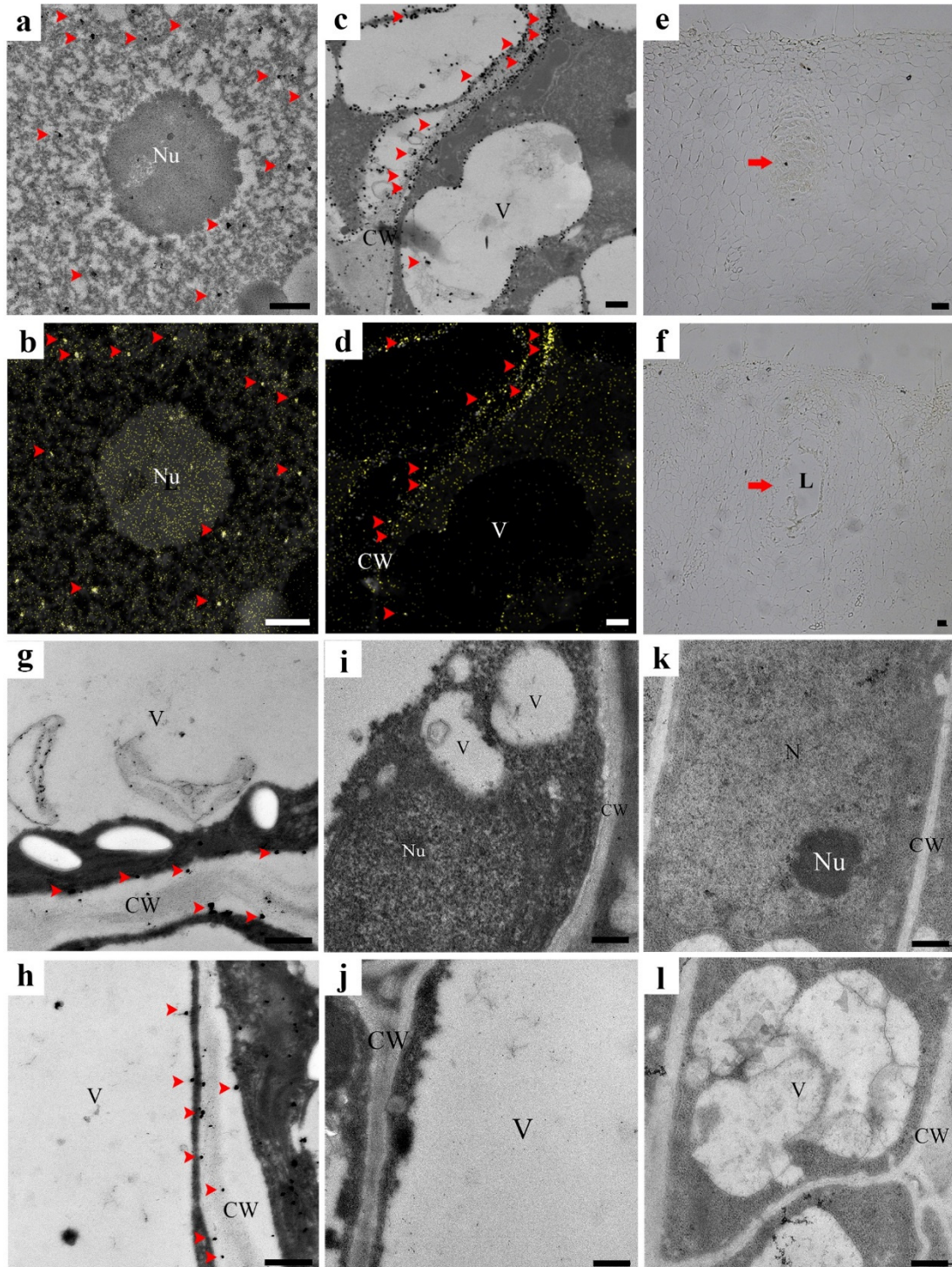


**Figure S1. Statistics of sampling standards at different developmental stages of the secretory cavity of *Citrus grandis* ‘Tomentosa’ fruits.**

**A. Morphology of *Citrus grandis* ‘Tomentosa’ fruits.**

**B. Sampling standard of different developmental stages of secretory cavity of *Citrus grandis* ‘Tomentosa’ fruits.**

**C. Proportion statistics of secretory cavity development stages in different fruit sizes. Sample form: diameter (size, 1mm×1mm); Sample quantity: 20.**



**Figure S2. Control.**

**(a)-(d)  $\text{Zn}^{2+}$  subcellular localization methodology validation, which display EDS spectrum analysis of secretory cavity cells of *Citrus grandis* 'Tomentosa' fruits.** (a) shows the black precipitations in the nucleus (arrowhead), (b) shows the black precipitations in the cell walls (arrowhead), (c) shows black precipitation in the nucleus

contains Ag elements (arrowhead), (d) shows black precipitation in the cell walls contains Ag elements (arrowhead).

**(e)-(f) *in situ* hybridization control.**

**(g)-(h)  $\text{Zn}^{2+}$  subcellular localization control.** (g), (h) shows non-secretory cavity cells of *Citrus grandis* 'Tomentosa' fruits. There are little  $\text{Zn}^{2+}$  in the cell wall (arrowhead).

**(i)-(l) Immunogold particles control.** (i), (j) shows non-secretory cavity cells. There are no immunogold particles in the nucleus, vacuole and cell wall. (k), (l) shows the globular region. (k) shows control in which the antibody replaced with pre-immune serum. (l) shows control which is used PBST instead of the antibody.

**N: Nucleus; Nu: Nucleolus; V: Vacuole; CW: Cell Wall.**

**Bar = 500 nm.**



S1.seq WGNLGHETVAYTAQSFSVASTESFCQNTLGEDSTS..YIAN 39  
P1.seq WGAIGHATVAYVAQHYVSFEAASWAQGLGSSSS..YIAS 39  
ZEN1.seq WSKEGHVMTCTAQELLSEDAAHAVCMILPLYVKG..NISA 39  
BEN1.seq WGKEGHYMTCKTADGFLTSEALTGVKALLPSWANG..EIAE 39  
AtENDO1.seq WSKEGHILTCRTAQNLLEAGFAHVVENILPLYVKG..DISA 39  
AtENDO2.seq WGKEGHEIICKTAOTRLDETAAKAVKEILPESAE..DSS 39  
AtENDO3.seq WGIAGHYAVCKTAQSYFEEDTVAVKKILPESANG..EIAA 39  
AtENDO4.seq WGKEGHYTVCKTAEQSYFEEDTVAAVKKILPKSALG..DIAA 39  
AtENDO5.seq WGNKGHYTVCKTAEQFFELDTIAAVKKILPESVDGGGLAD 40  
CgENDO1.seq WSKEGHIMTCRTAQSLLEFLAAHAVENILPCHVNG..DISA 39  
Consensus w gh a l l

S1.seq VATPRTTY..KYTLAGEFSKPYEFI..LAQDNPPCSGCVLY 76  
P1.seq IASWAEY..RLISAGKWSASLEFI..LAEDNPPTNCNVDY 76  
ZEN1.seq LCWVETQIRHWYRYRW..TSPIEFIDTFDD....ACSFYD 73  
BEN1.seq VCSWAL....SQFRFYRWRSSTIEFA..DTP....GDCKFSY 70  
AtENDO1.seq LCWVETQIRHWYRYRW..TSHIEYIDTFDQ....ACSYEY 73  
AtENDO2.seq LCIPATRV..KFRYHW..SSPIEYI..NTPD....ACSYQY 70  
AtENDO3.seq VCSWDEI..KKLPQKRWISALIEFA..DTPD....YKCNVEY 73  
AtENDO4.seq VCSWDEI..KHHWQKRWISPIEYV..DTPD....YKCNVEY 73  
AtENDO5.seq FCSWDEI..KKLSQKQWTSPIEYV..NTPE....YKCNVEY 74  
CgENDO1.seq LCWVETQIRHWYRYRW..TSPIEFIDTFDD....ACTEYV 73  
Consensus w d h c y

S1.seq DRCC....GSAGCSISATCNYNILLESPNGS.....E. 105  
P1.seq ERCC....GSSGCSISATANYTQPVLSISS.....EN 106  
ZEN1.seq TRDCHISNMGVIMOVACATKNFESQLSHY..CHGTSDRRYN 112  
BEN1.seq ARDCHITKGNKNVQVCAINNYTAALQCSS.....SPFN 104  
AtENDO1.seq SRDCHLQHGKLTMOVCAIGNFTSCLQHY..GEGTSDRRYN 112  
AtENDO2.seq NRDCKLESSEKGRQVACATNNYTCLLSYKTAASSQSQYN 110  
AtENDO3.seq SRCC....PKDQCVTGAITNNYIMSTSENSSQIVHYN 108  
AtENDO4.seq CRDCHETHKNQDRCVTCAITNNYIMCIMSASENSTIVHYN 113  
AtENDO5.seq CRDCHETHKHKDRCVTCAITNNYIMCIMSASENSQIVHYN 114  
CgENDO1.seq SRDCHETHGKKNVCIVCAITNFTSCLLHY..REGSSDRPHN 112  
Consensus rdc c al n t

S1.seq ALNAPKRVVHFGIDTHQPIH..LENLEAGGNGIDVTYIGET 144  
P1.seq HAAAPKRVVHFGIDTHQPIH..LEAYAVGGNKINVTYIGYH 145  
ZEN1.seq MTEALFLSHFMGLIHQHMVGFTEDEGGNIDLRWFRHK 152  
BEN1.seq PTESMFLAEFVGVHQMCGHVIDLGGNITKRWYRRK 144  
AtENDO1.seq MTEALFLSHFMGLIHQHMVGFTEDEGGNIDLRWYRRK 152  
AtENDO2.seq LTEALFLSHFMGLIHQELVSVASDKGGNITVHVWYTRK 150  
AtENDO3.seq LTEALFLSHFMGLIHQELHGFICDLGGNITKVHWYRQE 148  
AtENDO4.seq LTEALFLSHFMGLIHQELHVGFLGDEGGNITVVRWYRRK 153  
AtENDO5.seq LTEALFLSHFMGLVHQLHTGFLGLGGNITLVNWHYHNK 154  
CgENDO1.seq MTEALFLSHFMGLVHQMVGFTSDEGGNITLRWFRHK 152  
Consensus l f h gd qp h ggn i

S1.seq TNLHHIWDITNMPEEAAGGYSLSVAKTYADLITERIK.TGT 183  
P1.seq DNIHSDWITYMPCKLIGGFALSASWAKTIVQNIIE.SGN 184  
ZEN1.seq SNLHHVWREIITAAEALYDKMESLQKAIQANFTHGL. 191  
BEN1.seq SNLHHVWSDVITQTMKDFDKDQIAMIESIQRNIT..DD. 182  
AtENDO1.seq SNLHHVWREIITALKENYDKNLLLEDCELEKNITNGL. 191  
AtENDO2.seq ANLHHIWDITNLIEADLYNSALEGMVLAKKNIT..TE. 188  
AtENDO3.seq TNLHHVWDMITIEALETYYNSSLFRMIHELQAKLK..NG. 186  
AtENDO4.seq TNLHHVWDMITIEALKTYYNSSLFIMIEALQANLT..ND. 191  
AtENDO5.seq SNLHHVWDMITIEALETYYNSSLFHMICQALQAKLK..NG. 192  
CgENDO1.seq SNLHHVWREIITAIADYYDKTELLIQDIVANFTDEV. 191  
Consensus nlh wd

S1.seq YSSKKLSWIDGILIKLPVSTSMIWAALANTY..VCSIVLDD 222  
P1.seq YTAQAIGWIRGDNISEPITTATRWASLANAL.VCTVVMPPH 223  
ZEN1.seq .....WSDEVNSWKDC..EDISNCVNKYAKESIALAC 221  
BEN1.seq .....WSSEKQWETCRSKTTTCAEKYACESAVLAC 213  
AtENDO1.seq .....WHDELSSWTEC..NDLIACEHKYASESIKILAC 221  
AtENDO2.seq .....WADCVKRWETC..TKKTACFDIYASEGICAAC 218  
AtENDO3.seq .....WSNEVPSWESQINQIACFNPIYASESIDILAC 217  
AtENDO4.seq .....WSNEVPSWESQINQIACFNPIYASESINILAC 222  
AtENDO5.seq .....WSNEVPSWKSCHFHQACENLYASESIDILAC 223  
CgENDO1.seq .....WHDEVSSWKDC..DNLKCKENKYATESINMAC 221  
Consensus

S1.seq GLAYINST...DISGEYKKSQPVFEELIAKACVRIAPAWL 259  
P1.seq GAALALCTG...DIYPTYDSDVIDTIELCIAKGCYRIANWI 260  
ZEN1.seq KWGYEGVEAGETISDLYFLSRPIVMKRIACCGVRIAMIL 261  
BEN1.seq .LAYEGVECDITGDEYFKALPVVQKRLACCGVRIAMIL 252  
AtENDO1.seq KWGYKGVKSGETISEEYFNTRIPIVMKRIACCGVRIAMIL 261  
AtENDO2.seq DWAYKGVTEGDTIEDEYFYSRIPIVYQRIACCGVRIATL 258  
AtENDO3.seq KYAYRNATAGTTIGDYFVSRIPIVVEKRIACCGVRIAGTL 257  
AtENDO4.seq KYAYRNATFGTTIGDLYFLSRPIPIVEKRIACCGVRIATL 262  
AtENDO5.seq KYAYRNATFGTTIGDEYFLSRPIVVEKRIACCGVRIATL 263  
CgENDO1.seq KWGYKGVTFGETIADLYFNSRPIPIVMKRIACCGVRIAMFL 261  
Consensus l y g rl

S1.seq DLIASCPSS..... 267  
P1.seq NEIHGSEIAK..... 270  
ZEN1.seq NRVEGSSSSLELALVP 277  
BEN1.seq NRIFSGNGFLQSI... 265  
AtENDO1.seq NRVESIDHAIAGVAAT 277  
AtENDO2.seq NRIFG..... 263  
AtENDO3.seq NRIFSAKRKLARA... 270  
AtENDO4.seq NRIFSSKPKHAGS... 275  
AtENDO5.seq NRIFSAKPKIAGL... 276  
CgENDO1.seq NRIFSCSDEEFAAAT. 276  
Consensus

**Figure S3. Comparison of the functional domains of CgENDO1 and different Zn<sup>2+</sup> dependent nucleases and zinc ion binding sites involved in PCD.**

S1 = *Aspergillus oryzae* 3.042 (EIT80979.1); P1 = *Penicillium citrinum* (P24289.1); ZEN1 = *Zinnia elegans* (BAA28948.1); BEN1 = *Hordeum vulgare* subsp. Vulgare (BAA28942.1); AtENDO1 (BFN1) = *Arabidopsis thaliana* (AAD00693.1); AtENDO2 = *Arabidopsis thaliana* (NP\_176996.1); AtENDO3 = *Arabidopsis thaliana* (OAO99578.1); AtENDO4 = *Arabidopsis thaliana* (NP\_001328107.1); AtENDO5 = *Arabidopsis thaliana* (OAO96613.1) (Arrow indicates conserved sequence to bind three Zn<sup>2+</sup> when enzymes work.)