

## Differential expression of genes identified by suppression subtractive hybridization in petals of opening carnation flowers

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**Table S2.** List of primers used for real-time RT-PCR

Accession number	Forward primer	Reverse primer
AB517644	5'-GGT AGA ATC CAT GTA GAG TCG G-3'	5'-GTC TGA TGT TCA CTA CAG TG-3'
AB517645	5'-CCA CCT TGG GAG CAA TTG TA-3'	5'-CTC TCC ACT ATC TCC TTT CAA GCT-3'
AB517646	5'-GCA ATC AAT TGT ACC TTT TGT TG-3'	5'-GTC ATT TCA TAT GGG CTG AA-3'
AB517647	5'-GGG CTG AGA TTG GCT CAT AA-3'	5'-CTC CTA GAG AGT TTC CGC A-3'
AB517648	5'-GGC ATC CTA GGG TAA GCA AA-3'	5'-ACC TAA CGA ATC CTA CGG AA-3'
AB517649	5'-CTG TCG GTT TGA GAG AAG C-3'	5'-CGA GCA TCA CGG TCT TTC TA-3'
AB517650	5'-GTT TGA TGA ACA ACT CAA GCA T-3'	5'-GGC CAA AGT ATT AAA TAA TAC AGG-3'
AB517651	5'-GGG TTC GAT TAT AGC CTT TT-3'	5'-ACA TCT GCA CTT GTG TAC TCT-3'
AB517652	5'-GGG CAA CAT ACA CTG CAC GT-3'	5'-AGT ACT ACC AAG CTG CAT GCA TGC-3'
AB517653	5'-GTG GCT ACA CAT ACG TTT G-3'	5'-CCA TAC AAG TCT CAA TAT CAA C-3'
AB517654	5'-ACC CAT GAA GAT GAG AGG CG-3'	5'-ATC ATC TGT GAT ATG CCC AC-3'
AB517655	5'-GAC ATA TTC TCC CCA TTC ATA TAT-3'	5'-CAC CTT AAC ATG TGT CAT AAG G-3'
AB517656	5'-GGG AGC TTC CTA TGT TTT AA-3'	5'-CAC TTG GAA ATT TAC ACT CAA TTT T-3'
AB517657	5'-CTC TGA CTG ACC TGT GAT TG-3'	5'-TCC TAA ATA CTT GAC CCG TC-3'
AB517658	5'-GCG TCA ACC AGT GTC GGT GAA-3'	5'-CAT AAC TCT GTC GAT CCC TA-3'
AY007315 ( <i>DcACT1</i> )	5'-CGT CAC CAA CTG GGA TGA CA-3'	5'-GAG AGA ACG GCC TGG ATG GC-3'

## A

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DcLTP1 1  MASSAMKKVACAVILICIVMTAPY--ATAAMTCGQVSGNLGFCITLYLKGAPGPSALCCAG 58
DcLTP2 1  MASSSAMRKVACAMILICIVMTAPY--ATEALTTCGQVSGSLASCISYLKGPGPSGACCEG 58
DcLTP3 1  MWNT--KNIICALIMCMIMISAQNVVVFAVTCGQVASNLSGCIPEYLKGPGPSGCCCEG 57

DcLTP1 59  IKRLNGMACTEPDRKTACGCLKSAAAIISGINYGLASCLPKCGVSTPYEISPSIDCSKV 118
DcLTP2 59  IKRLNGMACTEPDRKTACGCLKSAAAIISGINYGLANALPKCGVSTPYEISPNIDCSKV 118
DcLTP3 58  IKRLNGMACTEPDRKTACNCLKSESASISGINYGLASCLPKCGVSTPYEISPSIDCSKV 117

DcLTP1 119 N 119
DcLTP2 119 H 119
DcLTP3 118 R 118

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## B

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AB517657 1  MLTSKLLITTTITFIILLITTTATVSAATRTTFAAVAVEDGGYIRLPSVKSYAVTTTRLMSS- 59
At1g53210 1  MRFRSLIS--LIFLIFFTSSAYARFVSLNPSSTSLISDGDGGSNLAGSGSVIKSVVAP 58
|.....
AB517657 59  -SNGTEECEQTYGFIPCTITWAGNMFLLICVYGLMYLAATLSDGSELLLEILGPGIVGG 118
At1g53210 59  AEEKTEACEQTYGFIPCTITWAGNMFLLICVYGLMYLAATLSDGSELLLEILGPGIVGG 118
|.....
AB517657 119  LFLFLGALPDAMLILVSGISGSTSEPAQSQVSVGMGLLAGSTVMLLTVIWTGTCILIGKCD 178
At1g53210 119  LFLFLGALPDAMLILVSGISGDAATAQSQVSVGMGLLAGSTVMLLTVIWTGTCIVVVKCD 178
|.....
AB517657 179  MDGTEAIDLIDTKGFSLLCGVSSTDIWTSYAARIMVLSVLPFLVQLPQLHSLSGRELA 238
At1g53210 179  LRDSIAVNNQDTRGFSLKISGVSTDIWTSYAARIMVLSVLPFLVQLPQLHSLSGRELA 238
|.....
AB517657 239  VLFGLISVLMMLISYCVYQVFPWAQDRRLDYVKKRIMIGELRHLLOKHEVDRLEFNSIG 298
At1g53210 239  VLTALISVLMMLISYCVYQVFPWIQRRRLAFKHKHVISGILRHKKQHALGRLLDDEG 297
|.....
AB517657 299  TENHEVMEQIEKALIDQGDHLSKGELEAFVIGMRIESVSLSEEDLAEKTLKAFDTERHD 358
At1g53210 298  QDEHWIRKIFLITIDANNDSHLSAAELKALLIGISFEDIDFDKDDAVGKVLQDFDKT-ID 356
|.....
AB517657 359  DRIDLDEFIRGTSKLFFTVVRGDRSMHNG--DALEHLDRYDEESKREHLLG----EANE 412
At1g53210 357  EQVDQREFFVRGKQWLIQAMGGAPSGPEAGPRTMKELDNFHVQIKREHLLGDNENGBND 416
|.....
AB517657 413  EGGEEIENPKRTIKAVIEIVIGELIAAAAFADPLVDVVDNFSIATSIPSEFFISFIALPLA 472
At1g53210 417  EGGSEVADPKNITIKAAIILLIGAAIAAAAFADPLVDVVDNFSIATSIPSEFFISFIALPLA 476
|.....
AB517657 473  TNSSEAVSAIIFASRKKIRASLTFSELYGAATMNNVLCLSVFLAVVYVRGLIWNFSSEV 532
At1g53210 477  TNSSEAVSAIIFASRKKIRASLTFSELYGAVTMMNNVLCLSVFLAVVYVRGLIWNFSSEV 536
|.....
AB517657 533  LVIEFLVCTIMGALGSEFRTSEFPLWTSIAFFFLYFFSLVLYVYLDYVFCWS 581
At1g53210 537  LVILIVCLVMGSEFRTTYPLWTCFIAYLLYFFSLGLVYVLDYVFCWS 585
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Fig. S1. ClustalW alignment of deduced amino acid sequences of putative lipid transfer protein (LTP) genes and putative sodium/calcium exchanger (NCX) genes. Identical and similar amino acid residues are shaded by black and gray, respectively, and dashes indicate gaps. (A) Deduced amino acid sequences of three putative LTP genes (AB517652, AB517653, AB517654) are compared. The eight-cysteine motif characteristic to plant LTPs (Yeats and Rose, 2008) is indicated by circles. Identity of deduced amino acid sequence was 85.7% between DcLTP1 and DcLTP2, 61.2% between DcLTP1 and DcLTP3 and 59.5% between DcLTP2 and DcLTP3, respectively. (B) Deduced amino acid sequences of a putative NCX gene (AB517657) and its homologous gene from *Arabidopsis* (At1g53210) are compared. Putative calcium binding domains are indicated by solid underlines and transmembrane domains predicted by the TMpred program are indicated by dotted underlines. Identity of deduced amino acid sequence was 58.8% between the two proteins.