



Article

Supplementary Tables S1

Solanum tuberosum Microtuber development under darkness unveiled through RNAseq Transcriptomic analysis.

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Tables S1. Upregulated Genes with Response to cytokinins and Associated function,

Response to Osmotic stress and Associated function, Response to One Carbon Metabolism and Associated function, Response to Carbon Metabolism and Associated function, Related to Citrate Cycle and Associated function, to Acyl Carrier Proteins and Associated function, to Fatty acid biosynthesis and metabolism and Associated function, to Thylakoids and Associated function, to Redoxins and Associated function, to Response to oxidative stress and Associated function, to Ribosomal proteins, Mutants and Associated function, to Immunophylins and Associated function, to Mitotic cell cycle and Associated function, to E2F activation and Associated function, to Cytoskeleton and Associated function, to Motor proteins and Associated function, to Methylation and Associated function, to Histone binding and Associated function, to Sterol biosynthetic process and terpenoid backbone biosynthesis and Associated function, to Amino sugar and nucleotide sugar metabolism and Associated function, to Sulfur metabolism and Associated function, to Disulfide isomerase activity and Associated function, Related to DNA replication and Associated function. Primer design of DEG used to validate the genome-wide analysis of MTs development of potato *S. tuberosum* cv. Alpha.

Upregulated Genes with Response to cytokinins and Associated function.

N°	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	<i>ARR8</i>	PGSC0003DMT400076758	Two-component response regulator arr-a family.
2	<i>ARR1</i>	PGSC0003DMT400060506	Two-component response regulator arr-b family.
3	<i>ARR2</i>	PGSC0003DMT400065835	Two-component response regulator arr-b family.
4	<i>RR3</i>	PGSC0003DMT400076758	Functions as response regulator involved in His-to-Asp phosphorelay signal transduction.
5	<i>ARR4</i>	PGSC0003DMT400058306	Two-component response regulator arr-a family.
6	<i>ARR5</i>	PGSC0003DMT400063187	Two-component response regulator ARR5.
7	<i>ARR9</i>	PGSC0003DMT400076726	Two-component response regulator ARR9.
8	<i>ARR11</i>	PGSC0003DMT400031260	Two-component response regulator ARR11.
9	<i>FBA6</i>	PGSC0003DMT400006894	Fructose-bisphosphate aldolase, class I.

10	<i>ENO1</i>	PGSC0003DMT400062986	Enolase 1, chloroplastic.
11	<i>EBP</i>	PGSC0003DMT400043311	Ethylene-responsive transcription factor RAP2-3.
12	<i>GAPCP-1</i>	PGSC0003DMT400029242	Glyceraldehyde-3-phosphate dehydrogenase GAPCP1, chloroplastic.
13	<i>DAP</i>	PGSC0003DMT400069487	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein.
14	<i>ACC1</i>	PGSC0003DMT400022054	Acetyl-CoA carboxylase/ biotin carboxylase 1.
15	<i>TIL</i>	PGSC0003DMT400020425	Apolipoprotein d and lipocalin family protein.
16	<i>TPI</i>	PGSC0003DMT400071330	Triosephosphate isomerase, cytosolic.
17	<i>MDH</i>	PGSC0003DMT400050235	Plastidic nad-dependent malate dehydrogenase.
18	<i>APX3</i>	PGSC0003DMT400015799	L-ascorbate peroxidase 3.
19	<i>APS1</i>	PGSC0003DMT400034962	3'-phosphoadenosine 5'-phosphosulfate synthase.
20	<i>CSP41A</i>	PGSC0003DMT400033560	Chloroplast stem-loop binding protein of 41 kDa a, chloroplastic.
21	<i>ZFP5</i>	PGSC0003DMT400040327	Zinc finger protein 5.
22	<i>AT5G19370</i>	PGSC0003DMT400012014	Rhodanese-like domain-containing protein.
23	<i>AT1G68360</i>	-	Diaminopimelate epimerase, chloroplastic.
24	<i>LOG10</i>	PGSC0003DMT400057413	Riboside 5'-monophosphate phosphoribohydrolase log10.
25	<i>LOG3</i>	PGSC0003DMT400027157	Cytokinin riboside 5'-monophosphate phosphoribohydrolase.
26	<i>HXK1</i>	PGSC0003DMT400006474	Hexokinase-1.

Upregulated Genes with Response to Osmotic stress and Associated function.

N°	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	<i>FBA6</i>	PGSC0003DMT400006894	Fructose-bisphosphate aldolase, class I.
2	<i>CRT1b</i>	Calreticulin	Calreticulin 1b.
3	<i>TUB8</i>	PGSC0003DMT400028800	Tubulin beta-8 chain.
4	<i>LOS2</i>	Enolase-like	Bifunctional enolase 2/ transcriptional activator.
5	<i>LOS2</i>	PGSC0003DMT400028690	Bifunctional enolase 2/ transcriptional activator.
6	<i>ENO1</i>	PGSC0003DMT400062986	Enolase 1, chloroplastic.
7	<i>TPI</i>	PGSC0003DMT400071330	Triosephosphate isomerase, cytosolic.
8	<i>mMDH1</i>	MMDH	Lactate/malate dehydrogenase family protein.
9	<i>MDH</i>	PGSC0003DMT400050235	Plastidic nad-dependent malate dehydrogenase.
10	<i>FSD2</i>	PGSC0003DMT400013447	Superoxide dismutase [Fe] 2, chloroplastic.
11	<i>FSD2</i>	PGSC0003DMT400070920	Superoxide dismutase [Fe] 2, chloroplastic.
12	<i>MSD1</i>	PGSC0003DMT400042937	Superoxide dismutase [Mn] 1, mitochondrial.
13	<i>AT3G52960</i>	Peroxioredoxin-2E-2	Peroxioredoxin-2E, chloroplastic.
14	<i>At5g06290</i>	PGSC0003DMT400042222	2-Cys peroxiredoxin BAS1-like, chloroplastic.
15	<i>GPX7</i>	PGSC0003DMT400067601	Putative glutathione peroxidase 7, chloroplastic.
16	<i>AT3G52960</i>	PGSC0003DMT400072641	Peroxioredoxin-2E.
17	<i>At5g06290</i>	PGSC0003DMT400072569	2-Cys peroxiredoxin BAS1-like, chloroplastic.
18	<i>GSTF8</i>	PGSC0003DMT400029561	Glutathione S-transferase F8, chloroplastic.

19	CNX1	PGSC0003DMT400036920	Calnexin homolog 1.
20	ATARCA	PGSC0003DMT400014419	Transducin/WD40 repeat-like superfamily protein.
21	RACK1B_AT	PGSC0003DMT400074094	Receptor for activated C kinase 1B.

Upregulated Genes with Response to One Carbon Metabolism and Associated function.

N°	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	SHM1	PGSC0003DMT400016362	Serine hydroxymethyltransferase 1, mitochondrial.
2	THY-1	PGSC0003DMT400001937	Bifunctional dihydrofolate reductase-thymidylate synthase 1.
3	MAT3	PGSC0003DMT400072701	Methionine adenosyltransferase 3.
4	SMT2	PGSC0003DMT400047969	24-methylenesterol C-methyltransferase 2.
5	SHM4	PGSC0003DMT400040717	Glycine hydroxymethyltransferase.

Upregulated Genes with Response to Carbon Metabolism and Associated function.

N°	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	CAC2	PGSC0003DMT400042238	Acetyl Co-enzyme a carboxylase biotin carboxylase subunit.
2	CAC1	PGSC0003DMT400083101	Biotin carboxyl carrier protein of acetyl-CoA carboxylase 1.
3	ACAT2	PGSC0003DMT400028289	Acetyl-CoA acetyltransferase, cytosolic 1.
4	EMB3003	PGSC0003DMT400023831	Pyruvate dehydrogenase e2 component.
5	AT2G35120	PGSC0003DMT400027015	Glycine cleavage system H protein 2, mitochondrial.

6	<i>At1g01090</i>	PGSC0003DMT400007571	Pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic.
7	<i>SHM4</i>	PGSC0003DMT400040717	Glycine hydroxymethyltransferase.
8	<i>SHM1</i>	PGSC0003DMT400016362	Serine hydroxymethyltransferase 1.
9	<i>MTHFR2</i>	PGSC0003DMT400041701	Methylenetetrahydrofolate reductase (nadph).
10	<i>ASP1</i>	PGSC0003DMT400017112	Aspartate aminotransferase, mitochondrial.
11	<i>PPC3</i>	PGSC0003DMT400054791	Phosphoenolpyruvate carboxylase (PEPC).
12	<i>FDH</i>	PGSC0003DMT400001303	Formate dehydrogenase, chloroplastic/mitochondrial.
13	<i>AT2G34590</i>	PGSC0003DMT400019358	Pyruvate dehydrogenase E1 component subunit beta-3, chloroplastic.
14	<i>PPC3</i>	PGSC0003DMT400039809	Phosphoenolpyruvate carboxylase (PEPC).
15	<i>mMDH1</i>	PGSC0003DMT400032266	Lactate/malate dehydrogenase family protein.
16	<i>PPC4</i>	PGSC0003DMT400019322	Phosphoenolpyruvate carboxylase 4.
17	<i>MDH</i>	PGSC0003DMT400050235	Plastidic nad-dependent malate dehydrogenase.
18	<i>PKP-ALPHA</i>	PGSC0003DMT400066112	Plastidial pyruvate kinase 1.
19	<i>PKp3</i>	PGSC0003DMT400062238	Plastidial pyruvate kinase 3, chloroplastic.
20	<i>AT3G52990</i>	PGSC0003DMT400072411	Pyruvate kinase family protein.
21	<i>AT3G02360</i>	PGSC0003DMT400064670	6-phosphogluconate dehydrogenase, decarboxylating 3.
22	<i>EMB2024</i>	PGSC0003DMT400047627	Probable 6-phosphogluconolactonase 5, chloroplastic.
23	<i>AT3G52990</i>	PGSC0003DMT400006945	Pyruvate kinase family protein.
24	<i>GAPCP-2</i>	PGSC0003DMT400029242	Glyceraldehyde-3-phosphate dehydrogenase GAPCP2.

25	<i>GAPC2</i>	PGSC0003DMT400044944	Glyceraldehyde-3-phosphate dehydrogenase GAPC2.
26	<i>PGK</i>	PGSC0003DMT400056871	Encodes cytosolic phosphoglycerate kinase (PGK)
27	<i>AT1G12230</i>	PGSC0003DMT400012218	Aldolase superfamily protein.
28	<i>FBA6</i>	PGSC0003DMT400006894	Fructose-bisphosphate aldolase, class I.
29	<i>LOS2</i>	PGSC0003DMT400007048	Bifunctional enolase 2/ transcriptional activator.
30	<i>ENO1</i>	PGSC0003DMT400062986	Enolase 1, chloroplastic.
31	<i>TPI</i>	PGSC0003DMT400071330	Triosephosphate isomerase, cytosolic.
32	<i>OASA1</i>	PGSC0003DMT400082113	O-acetylserine (thiol) lyase (oas-tl) isoform a1.
33	<i>SERAT2;2</i>	PGSC0003DMT400037270	Serine acetyltransferase 3, mitochondrial.
34	<i>AT1G22170</i>	PGSC0003DMT400024493	Phosphoglycerate mutase family protein.
35	<i>LOS2</i>	PGSC0003DMT400028690	Bifunctional enolase 2/ transcriptional activator.
36	<i>CYSC1</i>	PGSC0003DMT400000156	Bifunctional L-3-cyanoalanine synthase/cysteine synthase C1, mitochondrial.
37	<i>PGDH</i>	PGSC0003DMT400023675	D-3-phosphoglycerate dehydrogenase / 2-oxoglutarate reductase.
38	<i>EDA9</i>	PGSC0003DMT400059818	D-3-phosphoglycerate dehydrogenase / 2-oxoglutarate reductase.

Upregulated Genes Related to Citrate Cycle and Associated function.

N°	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	<i>ACLB-1</i>	PGSC0003DMT400061710	ATP-citrate synthase beta chain protein 1.
2	<i>PPC3</i>	PGSC0003DMT400054791	Cytosolic phosphoenolpyruvate carboxylase (PEPC).

3	<i>PPC3</i>	PGSC0003DMT400039809	Cytosolic phosphoenolpyruvate carboxylase (PEPC).
4	<i>ACLB-2</i>	PGSC0003DMT400011963	ATP-citrate synthase beta chain protein 2.
5	<i>FDH</i>	PGSC0003DMT400001303	Formate dehydrogenase.
6	<i>mMDH1</i>	PGSC0003DMT400032266	Lactate/malate dehydrogenase family protein.
7	<i>PPC4</i>	PGSC0003DMT400019322	Phosphoenolpyruvate carboxylase 4.
8	<i>ACLA-2</i>	PGSC0003DMT400035064	ATP-citrate synthase alpha chain protein 2.
9	<i>At1g01090</i>	PGSC0003DMT400007571	Pyruvate dehydrogenase E1 component subunit alpha 3.
10	<i>MDH</i>	PGSC0003DMT400050235	Plastidic nad-dependent malate dehydrogenase.
11	<i>PKP-ALPHA</i>	PGSC0003DMT400066112	Plastidial pyruvate kinase 1.
12	<i>AT2G34590</i>	PGSC0003DMT400019358	Pyruvate dehydrogenase E1 component subunit beta-3.
13	<i>AT3G52990</i>	PGSC0003DMT400006945	Pyruvate kinase family protein.
14	<i>AT3G52990</i>	PGSC0003DMT400072411	Pyruvate kinase family protein.
15	<i>AT4G17260</i>	PGSC0003DMT400012233	Lactate/malate dehydrogenase family protein.
16	<i>EMB3003</i>	PGSC0003DMT400023831	Pyruvate dehydrogenase e2 component.

Upregulated Genes Related to Acyl Carrier Proteins and Associated function.

N°	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	<i>ACP4</i>	PGSC0003DMT400036981	Acyl carrier protein 4.
2	<i>ACP2</i>	PGSC0003DMT400079040	Acyl carrier protein 2.
3	<i>ACP5</i>	PGSC0003DMT400027652	Acyl carrier protein 5.

4	<i>AT5G10160</i>	PGSC0003DMT400032718	Thioesterase superfamily protein.
5	<i>EMB3147</i>	PGSC0003DMT400055055	Catalytic transferases acyl-carrier-protein S-malonyltransferases.
6	<i>AT1G24360</i>	PGSC0003DMT400069374	3-oxoacyl-[acyl-carrier-protein] reductase.

Upregulated Genes Related to Fatty acid biosynthesis and metabolism and Associated function.

N°	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	<i>AT5G59770</i>	PGSC0003DMT400040154	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase.
2	<i>KCR1</i>	PGSC0003DMT400032914	Very-long-chain 3-oxoacyl-CoA reductase 1.
3	<i>CER10</i>	PGSC0003DMT400060224	3-oxo-5- α -steroid 4-dehydrogenase family protein.
4	<i>PAS2</i>	PGSC0003DMT400060612	Very-long-chain (3r)-3-hydroxyacyl-coa dehydratase.
5	<i>AT5G10160</i>	PGSC0003DMT400032718	Thioesterase superfamily protein.
6	<i>AT1G24360</i>	PGSC0003DMT400045027	3-oxoacyl-[acyl-carrier-protein] reductase, chloroplastic.
7	<i>FAB1</i>	PGSC0003DMT400035344	3-oxoacyl-[acyl-carrier-protein] synthase II, chloroplastic.
8	<i>T3P18.20</i>	PGSC0003DMT400067652	3-oxoacyl-[acyl-carrier-protein] synthase III, chloroplastic.
9	<i>KASI</i>	PGSC0003DMT400077561	3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplastic.
10	<i>AT1G24360</i>	PGSC0003DMT400069374	3-oxoacyl-[acyl-carrier-protein] reductase, chloroplastic.
11	<i>CAC1</i>	PGSC0003DMT400083101	Biotin carboxyl carrier protein of acetyl-CoA carboxylase 1, chloroplastic.

12	<i>EMB3147</i>	PGSC0003DMT400055055	Catalytic transferases [acyl-carrier-protein] S-malonyltransferases binding.
13	<i>CAC2</i>	PGSC0003DMT400042238	Acetyl Co-enzyme A carboxylase biotin carboxylase subunit.
14	<i>ACAT2</i>	PGSC0003DMT400028289	Acetyl-CoA acetyltransferase, cytosolic 1.

Upregulated Genes Related to Thylakoids and Associated function.

Nº	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	<i>FDH</i>	PGSC0003DMT400001303	Formate dehydrogenase, chloroplastic/mitochondrial.
2	<i>AT2G34460</i>	PGSC0003DMT400021415	NAD(P)-binding Rossmann-fold superfamily protein.
3	<i>AOR</i>	PGSC0003DMT400079606	Oxidoreductase, zinc-binding dehydrogenase family protein.
4	<i>PnsB5</i>	PGSC0003DMT400015589	Photosynthetic ndh subcomplex b5.
5	<i>PSI-P</i>	PGSC0003DMT400029398	Thylakoid membrane phosphoprotein of 14 kDa.
6	<i>CSP41A</i>	PGSC0003DMT400033560	Chloroplast stem-loop binding protein of 41 kDa, chloroplastic.
7	<i>ATHM2</i>	PGSC0003DMT400055831	Thioredoxin superfamily protein.
8	<i>AT3G52960</i>	PGSC0003DMT400072641	Peroxisoredoxin-2E, chloroplastic.
9	<i>AT3G52960</i>	PGSC0003DMT400007049	Peroxisoredoxin-2E-2, chloroplastic-like.
10	<i>FSD2</i>	PGSC0003DMT400013447	Superoxide dismutase [Fe] 2, chloroplastic.
11	<i>FSD2</i>	PGSC0003DMT400070920	Superoxide dismutase [Fe].
12	<i>TROL</i>	PGSC0003DMT400000605	Rhodanese-like domain-containing protein 4.

13	<i>Pnsl5</i>	PGSC0003DMT400013412	Peptidyl-prolyl cis-trans isomerase b (cyclophilin b).
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Upregulated Genes Related to Redoxins and Associated function.

N°	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	<i>GPX7</i>	PGSC0003DMT400067601	Putative glutathione peroxidase 7, chloroplastic.
2	<i>MSD1</i>	PGSC0003DMT400042937	Superoxide dismutase [Mn] 1, mitochondrial.
3	<i>At5g06290</i>	PGSC0003DMT400072569	2-Cys peroxiredoxin BAS1-like.
4	<i>ATHM2</i>	PGSC0003DMT400055831	Thioredoxin superfamily protein.
5	<i>AT3G52960</i>	PGSC0003DMT400072641	Peroxiredoxin-2E, chloroplastic.
6	<i>AT3G52960</i>	PGSC0003DMT400007049	Peroxiredoxin-2E-2, chloroplastic-like.
7	<i>FSD2</i>	PGSC0003DMT400013447	Superoxide dismutase [Fe] 2, chloroplastic.
8	<i>FSD2</i>	PGSC0003DMT400070920	Superoxide dismutase [fe], chloroplastic.
9	<i>At5g06290</i>	PGSC0003DMT400042222	2-Cys peroxiredoxin BAS1-like, chloroplastic.

Upregulated Genes Related to Response to oxidative stress and Associated function.

N°	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	<i>GPX7</i>	PGSC0003DMT400067601	Putative glutathione peroxidase 7, chloroplastic.
2	<i>MSD1</i>	PGSC0003DMT400042937	Superoxide dismutase [Mn] 1, mitochondrial.
3	<i>At5g06290</i>	PGSC0003DMT400072569	2-Cys peroxiredoxin BAS1-like, chloroplastic.
4	<i>AT3G52960</i>	PGSC0003DMT400072641	Peroxiredoxin-2E, chloroplastic.

5	<i>AT3G52960</i>	PGSC0003DMT400007049	Peroxioredoxin-2E-2, chloroplastic-like.
6	<i>FSD2</i>	PGSC0003DMT400013447	Superoxide dismutase [Fe] 2, chloroplastic.
7	<i>FSD2</i>	PGSC0003DMT400070920	Superoxide dismutase [fe], chloroplastic.
8	<i>At5g06290</i>	PGSC0003DMT400042222	2-Cys peroxiredoxin BAS1-like, chloroplastic.



Upregulated Genes Related to Ribosomal proteins, Mutants and Associated function.

1

N°	ID <i>A. thaliana</i>	ID <i>S. tuberosum</i>	Annotated function	Extrarribosomal function	Mutant phenotype
1	<i>RPSA</i>	PGSC0003DMT400039497	Ribosomal protein SA	-	Cases of isolated congenital asplenia.
2	<i>RPS2e</i>	PGSC0003DMT400063904	Ribosomal protein S2e	-	-
3	<i>RPS3a</i>	PGSC0003DMT400083968	Ribosomal protein S3a	-	-
4	<i>RPS6a</i>	RPS6a	Ribosomal protein S6a	Key downstream effector of the TOR signaling pathway (Chen et al., 2018 [1]). Free RPS6 binds directly to the rRNA gene promoter in Arabidopsis (Kim et al., 2014 [2])	Embryo lethal (Tzafrir et al., 2003 [3]); Reduced leaf area and enhanced var2-mediated leaf variegation (Wang et al., 2018 [4]), slow growth (haplodeficiency) in paralog A-B double mutant (Creff et al., 2010 [5]). Low temperature albino phenotype (Wang et al., 2018 [4]), pale leaves and defective thylakoid architecture (Sun et al., 2016 [6]).
5	<i>RPS13</i>	PGSC0003DMT400070434	Ribosomal protein S2e	Induced by low temperature treatment (Kim et al., 2004 [7]).	Narrow pointed leaves; change of shape of trichomes; delayed root growth (Ito et al., 2000 [8]); late flowering, Embryo lethal (Romani et al., 2012 [9]).
6	<i>RPS15a-1</i>	PGSC0003DMT400065156	Ribosomal protein S15a	-	Type II uS8, evolutionarily divergent and plant-specific paralogue, larger leaf, root and cell area (Szick-Miranda et al., 2010 [10])
7	<i>RPS16</i>	PGSC0003DMT400077257	Ribosomal protein S9	-	Abnormal pollen development and impaired pollen tube growth (Lu et al., 2020 [11]). Embryo lethal (Ma and Dooner, 2004 [12]), albino in three-leaf stage in rice (Qiu et al., 2018 [13]).

8	<i>RPS17</i>	PGSC0003DMT400060127	Ribosomal protein S17	-	Embryo lethal (Tzafrir et al., 2004 [14]); Reductions in growth, leaf pigments and photosynthesis (Romani et al., 2012 [9]), embryo lethality in maize (Schultes et al., 2000 [15]).
9	<i>RPS25e</i>	PGSC0003DMT400054605	Ribosomal protein S25e	-	-
10	<i>RPS29</i>	PGSC0003DMT400069470	Ribosomal protein S29	Contain the conserved zinc finger motif that could take on a wide variety of cellular functions by providing stable structural scaffolds (Chan et al., 1993 [16]).	-
11	<i>RPS30</i>	PGSC0003DMT400006164	Ribosomal protein S30	-	Indole-3-carbinol tolerance (Finkelshtein et al., 2021 [17]).
12	<i>RPL4</i>	PGSC0003DMT400071725	Ribosomal protein L1	-	Embryo lethal. Abnormal basal ribosome activity, abnormal transition from globular to heart stage of embryogenesis (Romani et al., 2012 [9]).
13	<i>RPL8</i>	PGSC0003DMT400064385	Ribosomal protein L8	-	Embryo lethal (Tzafrir et al., 2004 [14]).
14	<i>RPL11</i>	PGSC0003DMT400031869	Ribosomal protein L11	-	Mutant has decreased the effective quantum yield of photosystem II; Pale green plants; Reduced growth rate.
15	<i>RPL12</i>	PGSC0003DMT400008687	Ribosomal protein L12	-	Decreased non-host disease resistance against bacterial pathogens (Nagaraj et al., 2016 [18]); Albino lethal phenotype at seedling stage (Zhao et al., 2016 [19]).
16	<i>RPL13a</i>	PGSC0003DMT400040760	Ribosomal protein L13a	Overexpression of a brinjal RPL13a in potato has been observed to enhance resistance to <i>Verticillium dahliae</i> (Yang et al., 2013 [20]).	Single base substitution affects chloroplast development in rice grown under low temperature conditions (Song et al., 2014 [21]),

					lethal albino seedlings of T-DNA insertion mutants (Lee et al., 2019 [22]).
17	<i>RPL18</i>	PGSC0003DMT400011931	Ribosomal protein L18	-	Non-cellularized endosperm and arrested embryos (Zhang et al., 2015 [23]); Reduced leaf area (Wang et al., 2018 [4]); Required for both male gametophyte function and embryo development (Yan et al., 2016 [24]).
18	<i>RPL24</i>	PGSC0003DMT400085766	Ribosomal protein L24	Essential for translation initiation of several proteins, including ETTIN (ETT) and MONOPTEROS (MP) (auxin response factors) (Nishimura et al., 2005 [25]); Plays an indirect role in promoting MIR gene transcription (Li et al., 2017 [26]).	Suppresses proline accumulation of the parental mutant zinc ring finger 1 (<i>atrzf1</i>) of <i>Arabidopsis thaliana</i> (Park et al., 2017 [27]); Reductions in growth, leaf pigments and photosynthesis (Romani et al., 2012 [9]).
19	<i>RPL24e</i>	PGSC0003DMT400072655	Ribosomal protein L24e	-	Narrow pointed leaves; cotyledon and leaf vascular pattern defects; defects of the apical-basal pattern of the gynoecium; reduced plant size; reduced fertility (Nishimura et al., 2005 [25]).
20	<i>RPL25</i>	PGSC0003DMT400040794	Ribosomal protein L25	-	-
21	<i>RPL27</i>	RPL27	Structural constituent of the ribosome; involved in translation	-	Abnormal basal ribosome activity, abnormal transition from globular to heart stage of embryogenesis.
22	<i>RPL27</i>	PGSC0003DMT400061374	Ribosomal protein L27	-	Abnormal basal ribosome activity, abnormal transition from globular to heart stage of embryogenesis.
23	<i>RPL27a</i>	PGSC0003DMT400046820	Ribosomal protein L27a	-	Affected plant shoot development, including leaf pattern, inflorescence and floral meristem function, and seed development (Szakonyi et al., 2011 [28]). Affection of the development of the female gametophyte (Zsögön et al., 2014 [29]).

24	<i>RPL29e</i>	PGSC0003DMT400069847	Ribosomal protein L29e	-	Osteogenesis delayed and fragility of adult bone increased (Oristian et al., 2009 [30]).
25	<i>RPL31</i>	PGSC0003DMT400009481	Ribosomal protein L31	-	Slow growth phenotype (Aseev et al., 2011 [31]).
26	<i>RPL34e</i>	PGSC0003DMT400080291	Ribosomal protein L34e	-	-
27	<i>RPL35</i>	PGSC0003DMT400060449	Ribosomal protein L35	-	Affectation of the development of the female gametophyte (Zsögön et al., 2014 [29]). Abnormal basal ribosome activity, abnormal transition from globular to heart stage of embryogenesis (Romani et al., 2012 [9]).
28	<i>RPL35</i>	PGSC0003DMT400069913	Ribosomal protein L35	-	-
29	<i>RPL40</i>	PGSC0003DMT400047686	Ribosomal protein L40	Formation of a special cellular structure to facilitate prerRNA processing and ribosome assembly (Finley et al., 1989 [32]).	Embryo lethal (Tzafrir et al., 2004 [14]).
30	<i>RPL40</i>	PGSC0003DMT400000364	Ribosomal protein L40	The covalent association of these RPs to ubiquitin could promote the formation of a special cellular structure to facilitate prerRNA processing and ribosome assembly (Finley et al., 1989 [32]).	Embryo lethal (Tzafrir et al., 2004 [14]).
31	<i>ATARCA</i>	PGSC0003DMT400014419	Transducin/WD40 repeat-like superfamily protein; Major component of the RACK1.	Key integrator and mediator of hormonal control of translation (Chen et al., 2006 [33]; Guo and Chen, 2008 [34]); connects heterotrimeric G protein with a MAPK cascade to form a unique signaling pathway in plant immunity (Cheng et al., 2015 [35])	Pointed leaf phenotype and partial genetic redundancy of paralogs by complementation studies (Guo and Chen, 2008 [34]), AtRPL4D restored by sac52-d (AtRPL10A), sac53-d (AtRACK1A), sac56-d, and thermospermine (Takehi et al., 2015 [36]).

32	<i>RACK1</i>	PGSC0003DMT400074094	Receptor for activated C kinase 1B	Key integrator and mediator of hormonal control of translation (Chen et al., 2006 [33]; Guo and Chen, 2008 [34]); connects heterotrimeric G protein with a MAPK cascade to form a unique signaling pathway in plant immunity (Cheng et al., 2015 [35])	Pointed leaf phenotype and partial genetic redundancy of paralogs by complementation studies (Guo and Chen, 2008 [34]), AtRPL4D restored by sac52-d (AtRPL10A), sac53-d (AtRACK1A), sac56-d, and thermospermine (Takehi et al., 2015 [36]).
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Upregulated Genes Related to Immunophylins and Associated function.

N°	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	<i>XYL1</i>	PGSC0003DMT400037696	Thermoinhibition resistant germination 1.
2	<i>PDIL2-2</i>	PGSC0003DMT400001769	Arabidopsis thaliana protein disulfide isomerase 10.
3	<i>XYL1</i>	PGSC0003DMT400041054	Thermoinhibition resistant germination 1.
4	<i>CNX1</i>	PGSC0003DMT400036920	Calnexin homolog 1.
5	<i>PDIL1-1</i>	PGSC0003DMT400045299	Arabidopsis thaliana protein disulfide isomerase 5.
6	<i>Pnsl5</i>	PGSC0003DMT400013412	Peptidyl-prolyl cis-trans isomerase b (cyclophilin b).
7	<i>PDIL1-2</i>	PGSC0003DMT400036388	Encodes a protein disulfide isomerase-like (PDIL) protein.
8	<i>CRT1b</i>	PGSC0003DMT400007177	Calreticulin 1b.
9	<i>ROC3</i>	PGSC0003DMT400004125	Peptidyl-prolyl cis-trans isomerase CYP19-1.
10	<i>FKBP12</i>	PGSC0003DMT400083778	Arabidopsis thaliana fk506-binding protein 12.
11	<i>SOS3</i>	PGSC0003DMT400023568	Calcium-binding EF-hand family protein.
12	<i>ROC3</i>	PGSC0003DMT400011344	Peptidyl-prolyl cis-trans isomerase CYP19-1.

Upregulated Genes Related to Mitotic cell cycle and Associated function.

N°	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	<i>AT3G42660</i>	PGSC0003DMT400063296	Transducin family protein / WD-40 repeat family protein.
2	<i>EMB2656</i>	PGSC0003DMT400034628	ARM repeat superfamily protein; EMBRYO DEFECTIVE 2656 (EMB2656).

3	<i>AT3G57060</i>	PGSC0003DMT400076712	Condensin complex subunit 1.
4	<i>CYCA2;4</i>	PGSC0003DMT400067117	Cyclin A2;4 (CYCA2;4).
5	<i>CYCA3;1</i>	PGSC0003DMT400030222	Putative cyclin-A3-1; Cyclin A3;1 (CYCA3;1).
6	<i>SYN3</i>	PGSC0003DMT400065014	Sister chromatid cohesion 1 protein 3.
7	<i>CYCA3;1</i>	PGSC0003DMT400030176	Putative cyclin-A3-1.
8	<i>POLA2</i>	PGSC0003DMT400044958	DNA polymerase alpha subunit B.
9	<i>AT5G52220</i>	PGSC0003DMT400040416	Conserved gene of unknown function.
10	<i>SMC3</i>	PGSC0003DMT400003351	Structural maintenance of chromosomes protein 4.
11	<i>AT4G16970</i>	PGSC0003DMT400067513	Protein kinase superfamily protein.
12	<i>CYCB2;3</i>	PGSC0003DMT400003868	Cyclin B2;3 (CYCB2;3).
13	<i>CYC1BAT</i>	PGSC0003DMT400015245	G2/mitotic-specific cyclin-B.
14	<i>CYCB2;4</i>	PGSC0003DMT400025854	G2/mitotic-specific cyclin-B.
15	<i>MCM3</i>	PGSC0003DMT400021420	Minichromosome maintenance (MCM2/3/5) family protein.
16	<i>AT1G07270</i>	PGSC0003DMT400078033	Cell division control protein 6.
17	<i>MCM6</i>	PGSC0003DMT400035464	Minichromosome maintenance (MCM2/3/5) family protein.
18	<i>CDC45</i>	PGSC0003DMT400071831	CDC45 (Cell division cycle 45)-like protein.
19	<i>AT2G20635</i>	PGSC0003DMT400082809	ATP binding protein kinases protein serine/threonine kinases.
20	<i>AUR1</i>	PGSC0003DMT400065470	Serine/threonine-protein kinase Aurora-1.
21	<i>PPK1</i>	PGSC0003DMT400074667	Serine/threonine-protein kinase ttk/mps1.
22	<i>At1g03780</i>	PGSC0003DMT400056261	Targeting protein for XKLP2.

23	<i>AT3G60660</i>	PGSC0003DMT400018071	Spindle and kinetochore-associated protein 1 homolog.
24	<i>TUB8</i>	PGSC0003DMT400053750	Tubulin beta-8 chain.
25	<i>TUB8</i>	PGSC0003DMT400037093	Tubulin beta-8 chain.
26	<i>TUB8</i>	PGSC0003DMT400078206	Tubulin beta-8 chain.
27	<i>AT5G60930</i>	PGSC0003DMT400024240	P-loop containing nucleoside triphosphate hydrolases superfamily protein.
28	<i>TUB8</i>	PGSC0003DMT400028800	Tubulin beta-8 chain.
29	<i>SGA2</i>	PGSC0003DMT400078369	Probable histone chaperone ASF1A.
30	<i>CDT1A</i>	PGSC0003DMT400028257	Chromatin licensing and DNA replication factor 1.
31	<i>BUBR1</i>	PGSC0003DMT400025922	BUB1-related.
32	<i>Haspin</i>	PGSC0003DMT400047135	Serine/threonine-protein kinase haspin.
33	<i>MAD2</i>	PGSC0003DMT400045025	Mitotic spindle checkpoint protein MAD2.
34	<i>CYCA3;2</i>	PGSC0003DMT400055428	Cyclin-dependent protein kinase 3;2 (CYCA3;2).
35	<i>AT3G02820</i>	PGSC0003DMT400080556	Zinc knuckle (CCHC-type) family protein.
36	<i>AT4G15890</i>	PGSC0003DMT400011993	Uncharacterized protein AT4g15890; Its function is described as binding.

Upregulated Genes Related to E2F activation and Associated function.

Nº	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	<i>ORC6</i>	PGSC0003DMT400008733	Origin of replication complex subunit 6.
2	<i>ORC4</i>	PGSC0003DMT400078378	Origin recognition complex subunit 4.

3	<i>ORC5</i>	PGSC0003DMT400000500	Origin recognition complex protein 5.
4	<i>CDT1a</i>	PGSC0003DMT400028257	Chromatin licensing and DNA replication factor 1.
5	<i>SPT16</i>	PGSC0003DMT400046987	Global transcription factor C.
6	<i>TSO2</i>	PGSC0003DMT400052217	Ferritin/ribonucleotide reductase-like family protein.
7	<i>MCM6</i>	PGSC0003DMT400035464	Minichromosome maintenance (MCM/3/5) family protein.
8	<i>SMC3</i>	PGSC0003DMT400003351	Structural maintenance of chromosomes protein 4.
9	<i>MCM2</i>	PGSC0003DMT400005594	Minichromosome maintenance (MCM/3/5) family protein.
10	<i>RNR1</i>	PGSC0003DMT400060658	Ribonucleoside-diphosphate reductase large subunit.
11	<i>CHR11</i>	PGSC0003DMT400040011	ISWI chromatin-remodeling complex ATPase CHR11.
12	<i>POLA2</i>	PGSC0003DMT400044958	DNA polymerase alpha subunit B.
13	<i>PSF2</i>	PGSC0003DMT400060503	DNA replication complex GINS protein PSF2.
14	<i>CHR1</i>	PGSC0003DMT400038561	ATP-dependent DNA helicase DDM1.
15	<i>TOPII</i>	PGSC0003DMT400017488	DNA topoisomerase 2.
16	<i>RPA2</i>	PGSC0003DMT400035809	Replication protein A 32 kDa subunit A.
17	<i>RPA70B</i>	PGSC0003DMT400063329	Replication protein A 70 kDa DNA-binding subunit B.
18	<i>MCM5</i>	PGSC0003DMT400030898	Minichromosome maintenance (MCM2/3/5) family protein.
19	<i>RECQL1</i>	PGSC0003DMT400007294	ATP-dependent DNA helicase Q-like 1.
20	<i>ATIM</i>	PGSC0003DMT400016842	Timeless family protein.
21	<i>MCM4</i>	PGSC0003DMT400079535	Minichromosome maintenance (MCM/3/5) family protein.
22	<i>THY-1</i>	PGSC0003DMT400001937	Bifunctional dihydrofolate reductase-thymidylate synthase 1.

23	<i>PHR2</i>	PGSC0003DMT400081378	Photolyase/blue-light receptor 2.
24	<i>TIM</i>	PGSC0003DMT400080556	Triosephosphate isomerase, chloroplastic.
25	<i>SYN3</i>	PGSC0003DMT400065014	Sister chromatid cohesion 1 protein 3.
26	<i>BRCA1</i>	PGSC0003DMT400023253	Arabidopsis thaliana breast cancer susceptibility1.
27	<i>PCNA2</i>	PGSC0003DMT400078207	Proliferating cell nuclear antigen 2.
28	<i>MCM3</i>	PGSC0003DMT400021420	Minichromosome maintenance (MCM2/3/5) family protein.
29	<i>CDC6</i>	PGSC0003DMT400078033	Cell division control protein 6.
30	<i>CDC45</i>	PGSC0003DMT400071831	CDC45 (Cell division cycle 45)-like protein.
31	<i>POLA3</i>	PGSC0003DMT400032030	DNA primases; POLA3.

Upregulated Genes Related to Cytoskeleton and Associated function.

N°	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	<i>AIR9</i>	PGSC0003DMT400054558	Outer arm dynein light chain 1 protein.
2	<i>AT3G27640</i>	PGSC0003DMT400032878	Transducin/WD40 repeat-like superfamily protein.
3	<i>AT4G02110</i>	PGSC0003DMT400023253	BRCT domain-containing protein At4g02110.
4	<i>AT4G16970</i>	PGSC0003DMT400067513	Protein kinase superfamily protein.
5	<i>BUBR1</i>	PGSC0003DMT400025922	BUB1-related (BUB1: budding uninhibited by benzimidazol 1).
6	<i>TUB8</i>	PGSC0003DMT400053750	Tubulin beta-8 chain.
7	<i>Haspin</i>	PGSC0003DMT400047135	Serine/threonine-protein kinase haspin.
8	<i>TUB8</i>	PGSC0003DMT400078206	Tubulin beta-8 chain.

9	<i>TUB8</i>	PGSC0003DMT400037093	Tubulin beta-8 chain.
10	<i>EB1C</i>	PGSC0003DMT400064236	Microtubule-associated protein RP/EB family member 1C.
11	<i>TUB8</i>	PGSC0003DMT400028800	Tubulin beta-8 chain.
12	<i>AT3G60660</i>	PGSC0003DMT400018071	Spindle and kinetochore-associated protein 1 homolog.
13	<i>AUR1</i>	PGSC0003DMT400065470	Serine/threonine-protein kinase Aurora-1.
14	<i>AT5G60930</i>	PGSC0003DMT400024240	P-loop containing nucleoside triphosphate hydrolases superfamily protein.
15	<i>AT2G36200</i>	PGSC0003DMT400023094	P-loop containing nucleoside triphosphate hydrolases superfamily protein.
16	<i>AT4G21820</i>	PGSC0003DMT400042507	Its function is described as calmodulin binding. Located in chloroplast.
17	<i>PPK1</i>	PGSC0003DMT400074667	Serine/threonine-protein kinase ttk/mps1.
18	<i>AT3G45850</i>	PGSC0003DMT400040181	P-loop containing nucleoside triphosphate hydrolases superfamily protein.
19	<i>MAP65-1</i>	PGSC0003DMT400033471	65-kDa microtubule-associated protein 1.
20	<i>PLE</i>	PGSC0003DMT400070431	Microtubule associated protein (MAP65/ASE1) family protein.
21	<i>AT3G45850</i>	PGSC0003DMT400005133	P-loop containing nucleoside triphosphate hydrolases superfamily protein.
22	<i>MAP65-5</i>	PGSC0003DMT400008510	Microtubule-associated protein 65-5.
23	<i>At1g03780</i>	PGSC0003DMT400056261	Targeting protein for XKLP2.
24	<i>MAP65-5</i>	PGSC0003DMT400057428	Microtubule-associated protein 65-5.
25	<i>AT3G45850</i>	PGSC0003DMT400078142	P-loop containing nucleoside triphosphate hydrolases superfamily protein.

Upregulated Genes Related to Motor proteins and Associated function.

N°	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	AT3G45850	PGSC0003DMT400078142	P-loop containing nucleoside triphosphate hydrolases superfamily protein.
2	AT5G60930	PGSC0003DMT400024240	P-loop containing nucleoside triphosphate hydrolases superfamily protein.
3	AT2G36200	PGSC0003DMT400023094	P-loop containing nucleoside triphosphate hydrolases superfamily protein.
4	AT3G45850	PGSC0003DMT400040181	P-loop containing nucleoside triphosphate hydrolases superfamily protein.
5	AT3G45850	PGSC0003DMT400005133	P-loop containing nucleoside triphosphate hydrolases superfamily protein.

Upregulated Genes Related to Methylation and Associated function.

N°	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	UPM1	PGSC0003DMT400065013	Uroporphyrin-iii c-methyltransferase.
2	AT4G03130	PGSC0003DMT400056558	BRCT domain-containing DNA repair protein.
3	AT2G41450	PGSC0003DMT400033151	N-acetyltransferases; Its function is described as N-acetyltransferase activity.
4	VIM1	PGSC0003DMT400084297	Zinc finger (C3HC4-type RING finger) family protein.
5	MET1	PGSC0003DMT400079464	DNA (cytosine-5)-methyltransferase 1.
6	CMT3	PGSC0003DMT400010941	DNA (cytosine-5)-methyltransferase CMT3.
7	CYP51G1	PGSC0003DMT400042257	Sterol 14alpha-demethylase. Involved in sterol biosynthesis.
8	SMT1	PGSC0003DMT400017668	Cycloartenol-C-24-methyltransferase.

9	<i>APG1</i>	PGSC0003DMT400049690	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein.
10	<i>G-TMT</i>	PGSC0003DMT400006168	Tocopherol O-methyltransferase, chloroplastic.
11	<i>SMT2</i>	PGSC0003DMT400047969	24-methylenesterol C-methyltransferase 2.
12	<i>PMEAMT</i>	PGSC0003DMT400014749	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein.
13	<i>THY-1</i>	PGSC0003DMT400001937	Bifunctional dihydrofolate reductase-thymidylate synthase 1.

Upregulated Genes Related to Histone binding and Associated function.

N°	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	<i>AT3G57060</i>	PGSC0003DMT400056558	Condensin complex subunit 1.
2	<i>SGA2</i>	PGSC0003DMT400078369	Probable histone chaperone ASF1A.
3	<i>SPT16</i>	PGSC0003DMT400046987	Global transcription factor C; Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes.
4	<i>VIM1</i>	PGSC0003DMT400084297	Zinc finger (C3HC4-type RING finger) family protein.
5	<i>AT4G15890</i>	PGSC0003DMT400011993	Uncharacterized protein AT4g15890.

Upregulated Genes Related to Sterol biosynthetic process and terpenoid backbone biosynthesis and Associated function.

N°	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	<i>APG1</i>	PGSC0003DMT400049690	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein.

2	<i>G-TMT</i>	PGSC0003DMT400006168	Tocopherol O-methyltransferase, chloroplastic.
3	<i>VTE5</i>	PGSC0003DMT400043567	Phytol kinase 1, chloroplastic.
4	<i>BAS</i>	PGSC0003DMT400048796	Terpenoid cyclases family protein; Converts oxidosqualene to beta-amyrin.
5	<i>RTNLB19</i>	PGSC0003DMT400018853	Plant 3beta-hydroxysteroid-4alpha-carboxylate 3-dehydrogenase.
6	<i>CYP51G1</i>	PGSC0003DMT400042257	Sterol 14alpha-demethylase.
7	<i>SMT1</i>	PGSC0003DMT400017668	Cycloartenol-C-24-methyltransferase.
8	<i>DWF1</i>	PGSC0003DMT400054476	Cell elongation protein / DWARF1 / DIMINUTO (DIM).
9	<i>HYD1</i>	PGSC0003DMT400071184	Probable 3-beta-hydroxysteroid-Delta(8), Delta(7)-isomerase.
10	<i>FK</i>	PGSC0003DMT400007043	Ergosterol biosynthesis ERG4/ERG24 family.
11	<i>SMT2</i>	PGSC0003DMT400047969	24-methylenesterol C-methyltransferase 2.
12	<i>CPI1</i>	PGSC0003DMT400011907	Cycloeucalenol cycloisomerase.
13	<i>SMO1-1</i>	PGSC0003DMT400033236	Plant 4,4-dimethylsterol c-4alpha-methyl-monooxygenase.
14	<i>STE1</i>	PGSC0003DMT400067881	Delta(7)-sterol-C5(6)-desaturase 1.
15	<i>AT4G00560</i>	PGSC0003DMT400000064	NAD(P)-binding Rossmann-fold superfamily protein.
16	<i>SMO2-1</i>	PGSC0003DMT400005519	Sterol 4-alpha-methyl oxidase 1

Upregulated Genes Related to Amino sugar and nucleotide sugar metabolism and Associated function.

N°	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	<i>CYT1</i>	PGSC0003DMT400022961	Glucose-1-phosphate adenylyltransferase family protein.
2	<i>GME</i>	PGSC0003DMT400050094	GDP-D-mannose 3',5'-epimerase.
3	<i>UGD2</i>	PGSC0003DMT400087395	UDP-glucose 6-dehydrogenase family protein.
4	<i>RHM1</i>	PGSC0003DMT400018192	Rhamnose biosynthesis 1.
5	<i>NRS/ER</i>	PGSC0003DMT400058533	UDP-4-KETO-6-DEOXY-D-GLUCOSE-3,5-EPIMERASE-4-REDUCTASE 1.
6	<i>UGP2</i>	PGSC0003DMT400034699	UTP-glucose-1-phosphate uridylyltransferase 1.
7	<i>UGD2</i>	PGSC0003DMT400003666	UDP-glucose 6-dehydrogenase family protein.

Upregulated Genes Related to Sulfur metabolism and Associated function.

N°	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	<i>APS1</i>	PGSC0003DMT400048741	3'-phosphoadenosine 5'-phosphosulfate synthase.
2	<i>APK</i>	PGSC0003DMT400055243	ADENOSINE-5'-PHOSPHOSULFATE (APS) KINASE 1.
3	<i>HL</i>	PGSC0003DMT400022081	3'(2'), 5'-bisphosphate nucleotidase.
4	<i>APR1</i>	PGSC0003DMT400042488	5'-adenylylsulfate reductase 1, chloroplastic.
5	<i>APR3</i>	PGSC0003DMT400051168	5'-adenylylsulfate reductase 3, chloroplastic.
6	<i>CYSC1</i>	PGSC0003DMT400000156	Bifunctional L-3-cyanoalanine synthase/ cysteine synthase C1.

7	<i>SERAT2;2</i>	PGSC0003DMT400037270	Serine acetyltransferase 3, mitochondrial.
8	<i>OASA1</i>	PGSC0003DMT400082113	O-acetylserine (thiol) lyase (oas-tl) isoform a1.

Upregulated Genes Related to Disulfide isomerase activity and Associated function.

N°	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	<i>AT3G42660</i>	PGSC0003DMT400063296	Transducin family protein / WD-40 repeat family protein.
2	<i>CNX1</i>	PGSC0003DMT400036920	Calnexin homolog 1.
3	<i>PDIL1-1</i>	PGSC0003DMT400045299	Arabidopsis thaliana protein disulfide isomerase 5.
4	<i>CRT1b</i>	PGSC0003DMT400007177	Calreticulin 1b.
5	<i>PDIL1-2</i>	PGSC0003DMT400036388	Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily.

Upregulated Genes Related to DNA replication and Associated function

N°	ID <i>A. thaliana</i>	ID <i>Solanum tuberosum</i>	Associated function
1	<i>PDIL2-2</i>	PGSC0003DMT400001769	Arabidopsis thaliana protein disulfide isomerase 10.
2	<i>RNR1</i>	PGSC0003DMT400060658	Ribonucleoside-diphosphate reductase large subunit.
3	<i>RECQL1</i>	PGSC0003DMT400007294	ATP-dependent DNA helicase Q-like 1.
4	<i>ETG1</i>	PGSC0003DMT400062461	Mini-chromosome maintenance complex-binding protein.
5	<i>PCNA2</i>	PGSC0003DMT400078207	Proliferating cell nuclear antigen 2.

6	<i>AT4G18590</i>	PGSC0003DMT400022900	Nucleic acid-binding, OB-fold-like protein.
7	<i>TSO2</i>	PGSC0003DMT400052217	Ferritin/ribonucleotide reductase-like family protein.
8	<i>RPA2</i>	PGSC0003DMT400035809	Replication protein A 32 kDa subunit A.
9	<i>AT3G02820</i>	PGSC0003DMT400080556	Zinc knuckle (CCHC-type) family protein.
10	<i>AT4G16970</i>	PGSC0003DMT400067513	Protein kinase superfamily protein.
11	<i>AT1G07270</i>	PGSC0003DMT400078033	Cell division control protein 6.
12	<i>POLA2</i>	PGSC0003DMT400044958	DNA polymerase alpha subunit B.
13	<i>MCM3</i>	PGSC0003DMT400021420	Minichromosome maintenance (MCM2/3/5) family protein.
14	<i>DPB2</i>	PGSC0003DMT400079711	Dna polymerase epsilon subunit 2.
15	<i>MCM10</i>	PGSC0003DMT400015838	Minichromosome maintenance protein 10.
16	<i>POLA3</i>	PGSC0003DMT400032030	DNA primases.
17	<i>MCM6</i>	PGSC0003DMT400035464	Minichromosome maintenance (mcm2/3/5) family protein.
18	<i>RPA70B</i>	PGSC0003DMT400063329	Replication protein A 70 kDa DNA-binding subunit B.
19	<i>CDC45</i>	PGSC0003DMT400071831	CDC45 (Cell division cycle 45)-like protein.
20	<i>MCM4</i>	PGSC0003DMT400079535	Minichromosome maintenance (mcm2/3/5) family protein.
21	<i>SPT16</i>	PGSC0003DMT400046987	Global transcription factor C.
22	<i>AT3G27640</i>	PGSC0003DMT400032878	Transducin/WD40 repeat-like superfamily protein.
23	<i>ORC5</i>	PGSC0003DMT400000500	Origin recognition complex protein 5.
24	<i>ORC6</i>	PGSC0003DMT400008733	Origin of replication complex subunit 6.
25	<i>CDT1A</i>	PGSC0003DMT400028257	Chromatin licensing and DNA replication factor 1.

26	<i>ORC4</i>	PGSC0003DMT400078378	Origin recognition complex subunit 4.
27	<i>MCM5</i>	PGSC0003DMT400030898	Minichromosome maintenance (MCM2/3/5) family protein.
28	<i>MCM2</i>	PGSC0003DMT400005594	Minichromosome maintenance (mcm2/3/5) family protein.
29	<i>PSF2</i>	PGSC0003DMT400060503	DNA replication complex GINS protein PSF2.
30	<i>PRL</i>	PGSC0003DMT400023333	Minichromosome maintenance (MCM2/3/5) family protein.
31	<i>AT3G55490</i>	PGSC0003DMT400078521	Dna replication complex gins protein psf3-like.
32	<i>DEL1</i>	PGSC0003DMT400062857	E2F transcription factor-like E2FE.

Primer design of DEG used to validate the genome-wide analysis of MTs development of potato *S. tuberosum* cv. Alpha.

Gen ID	Sequences	ID NCBI
<i>UBQ1</i>	L: GCTTCGTGGAGGGATTATTGA	XM_006339693.1
	R: GAGGATGTAGGCGAGCATAAC	
<i>FKBP12</i>	L: GGGAGTGGAGAAGGAAGTTATC	XM_006351679.2
	R: GGTCTCTATCTTTCCCGTAACC	
<i>RPL29</i>	L: AATCAGTCGTACAAGGCTCAC	XM_015312492.1
	R: GCATACCTCTGGTTCCTCAAG	
<i>RPL11</i>	L: GAGAAGCTGCCGATCTTAAT	XM_006343698.2
	R: TCGGAGGGTCAATGTCAATTC	
<i>PRXQ</i>	L: ATGGCTTCTCTATCCGTCTCT	XM_006353712.2
	R: CTGGAGACAATGGTGAGGTTT	
<i>PCNA2</i>	L: CTACGTCTTGTTCAAGGAAGTC	XM_006350753.2
	R: ATGGCTTGCAAGAGAGAATCC	
<i>SWI/SNF</i>	L: GTGTTGCTGCACCTGTAAATC	XM_006356044.2
	R: CACCGAGTGGTGAATGTAGAA	
<i>TSO2</i>	L: ACCTAACATCCGGTGAAAGAC	XM_006338637.2
	R: GGCGATTGGAACCCATAGA	
<i>BRCA1</i>	L: CGGTGTGCAAAGTTCCATTTC	XM_006354922.2
	R: TTGACTCCTGAAGCGATTTC	
<i>RNR1</i>	L: GAGTAACCGTGACGAGTGTATG	XM_006346669.2
	R: CAGCAGGCATGGAGAGATAAA	
<i>THY-1</i>	L: GTGCTAAGGTCCTACAAGAGAAG	XM_006365063.2
	R: CCAAATCACCTCTTCCCTATC	
<i>E2F3</i>	L: CCTGAGGATTACCACCGATTT	XM_006348424.2
	R: ATAGCCTGTCTTCCGCTTTAG	
<i>LOG10</i>	L: GGCGGGTTCAAGATAGGTAAG	XM_006346105.2
	R: CTACATCTCACAACAGCATCCA	

<i>EFα1</i>	L: TTTGGCCCTACTGGTTTGAC	NM_001288491.1
	R: GCACTGGAGCATATCCGTTT	
<i>SEC3</i>	L: GCTTGCACACGCCATATCAAT	XM_006342542.2
	R: TGGATTTTACCACCTTCCGCA	

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