

Identification of a molecular marker associated with lignotuber in *Eucalyptus ssp.*

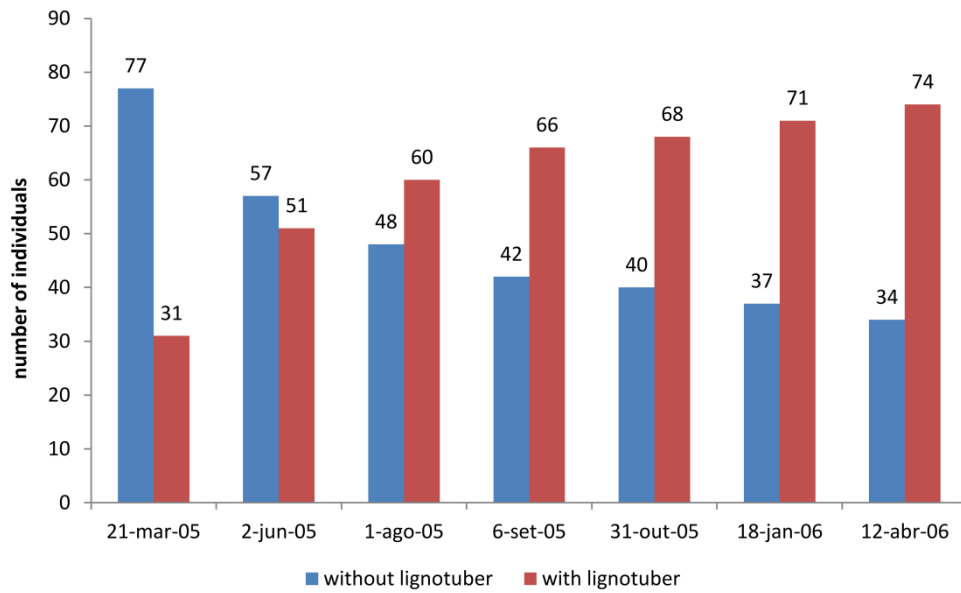
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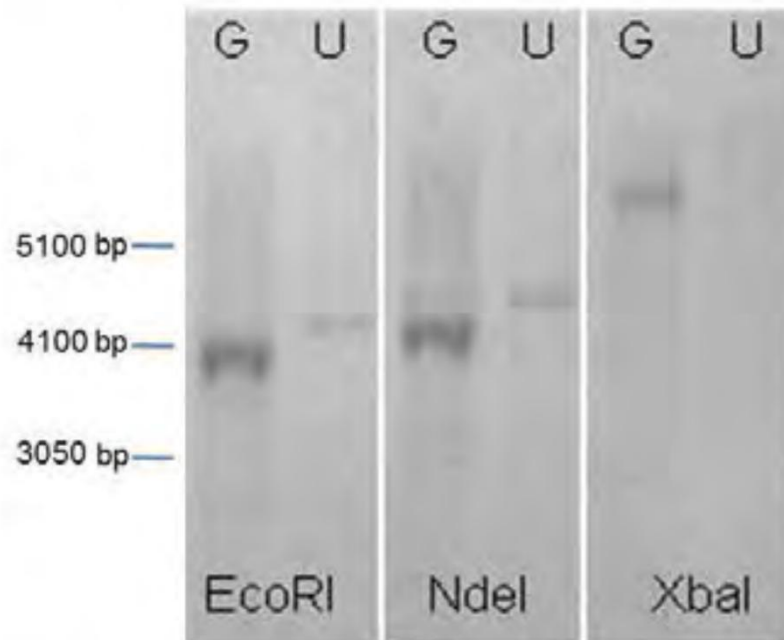
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Supplementary Figure 1. F2 cross individuals (hybrids of *Eucalyptus grandis* x *E. urophylla*) submitted to hydric and nutrient stress in greenhouse. The evaluation after 12 months showed a 3:1 ratio (with lignotuber ; without lignotuber) as showed by qui-square test.



Supplementary Figure 3. Southern blot technique with DNA of *E. grandis* (G) and *E. urophylla* (U) digested with restriction enzymes *EcoRI*, *NdeI*, and *XbaI*, showing a single copy of the *ELig* marker in the species.



Eucgr_D00282	K03538 - ribonuclease P protein subunit POP4 (POP4, RPP29) (1 of 1) OS=Egrandis	F:GO:0003723; F:GO:0004526; C:GO:0005730; P:GO:0008033; C:GO:0030677; P:GO:0090502	F:RNA binding; F:ribonuclease P activity; C:nucleolus; P:RNA processing; C:ribonuclease P complex; P:RNA phosphodiester bond hydrolysis, endonucleolytic	EC:3.1.30; EC:3.1.26; EC:3.1.26.5	Acting on ester bonds; Acting on ester bonds; Ribonuclease P	no IPS match	no IPS match	no IPS match
Eucgr_D00284 Eucgr_D00285	PF12937 - F-box-like (F-box-like) (1 of 50) OS=Egrandis uncharacterized protein OS=Egrandis	F:GO:0005515	F:protein binding			IPR001810 (PFAM); G3DSA:1.20.1280.50 (GENE3D); mobdb-lite (MOBIDB_LITE); mobdb-lite (MOBIDB_LITE); mobdb-lite (MOBIDB_LITE); PTHR1215 (PANTHER); PTHR1215-SF2 (PANTHER); IPR001810 (PROSITE_PROFILES); IPR036047 (SUPERFAMILY)	F:GO:0005515	F:protein binding
Eucgr_D00286	PF12937 - F-box-like (F-box-like) (1 of 50) OS=Egrandis	F:GO:0005515	F:protein binding			no IPS match	no IPS match	no IPS match
Eucgr_D00287	2.6.1.13 - Ornithine aminotransferase / Ornithine-oxo-acid transaminase (1 of 1) OS=Egrandis	F:GO:0004587; F:GO:0030170; P:GO:005129	F:ornithine-oxo-acid transaminase activity; P:pyridoxal phosphate binding; P:L-proline biosynthetic process	EC:2.6.1.13	Ornithine aminotransferase	no IPS match	no IPS match	no IPS match
Eucgr_D00288	K11517 - (S)-2-hydroxy-acid oxidase (HAO) (1 of 5) OS=Egrandis	F:GO:0010181; F:GO:0016491; P:GO:0055114	F:FMN binding; F:oxidoreductase activity; P:oxidation-reduction process			no IPS match	no IPS match	no IPS match
Eucgr_D00289 Eucgr_D00290	PTHR3077-SF17 - PROTEIN TIFY 5A-RELATED (1 of 2) OS=Egrandis uncharacterized protein OS=Egrandis					mobdb-lite (MOBIDB_LITE); mobdb-lite (MOBIDB_LITE)	no GO terms	no GO terms
Eucgr_D00291	PTHR10543-SF42 - 9-CIS-EPOXYCAROTENOID DIOXYGENASE NCE22, CHLOROPLASTIC-RELATED (1 of 2) OS=Egrandis	F:GO:0016702; F:GO:0046872; P:GO:0055114	F:oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen; F:metal ion binding; P:oxidation-reduction process	EC:1.13.11	Acting on single donors with incorporation of molecular oxygen (oxygenases). The oxygen incorporated need not be derived from O2	IPR004294 (PFAM); mobdb-lite (MOBIDB_LITE); mobdb-lite (MOBIDB_LITE); IPR004294 (PANTHER); PTHR10543-SF42 (PANTHER)	F:GO:0016702; P:GO:0055114	F:oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen; P:oxidation-reduction process
Eucgr_D00292	2.7.49 - RNA-directed DNA polymerase / Revertase (1 of 28) OS=Egrandis					PTHR34676 (PANTHER); PTHR34676-SF2 (PANTHER)	no GO terms	no GO terms
Eucgr_D00293	PTHR32227-SF85 - GLYCOSYL HYDROLASES FAMILY PROTEIN (1 of 1) OS=Egrandis	F:GO:0004553; P:GO:0005975; C:GO:0016021	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carbohydrate metabolic process; C:integral component of membrane			IPR000490 (PFAM); G3DSA:3.20.20.80 (GENE3D); PTHR32227-SF85 (PANTHER); PTHR32227 (PANTHER); IPR017853 (SUPERFAMILY)	F:GO:0004553; P:GO:0005975	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carbohydrate metabolic process
Eucgr_D00295	K04507 - calycyclin binding protein (CACYBP, SIP) (1 of 1) OS=Egrandis	F:GO:0008171; P:GO:0032259; F:GO:0046983; F:GO:0005524; C:GO:0005737; C:GO:0005874; F:GO:0008017; F:GO:0008568; P:GO:0016853; P:GO:0051013	F:O-methyltransferase activity; P:methylation; F:protein dimerization activity			mobdb-lite (MOBIDB_LITE)	no GO terms	no GO terms
Eucgr_D00296	PTHR23074/PTHR23074-SF92 - AAA ATPase // SUBFAMILY NOT NAMED (1 of 1) OS=Egrandis	F:GO:0008171; P:GO:0032259; F:GO:0046983; F:GO:0005524; C:GO:0005737; C:GO:0005874; F:GO:0008017; F:GO:0008568; P:GO:0016853; P:GO:0051013	F:ATP binding; C:cytosol; C:microtubule; F:microtubule binding; F:microtubule-severing ATPase activity; F:isomerase activity; P:microtubule severing	EC:3.6.1.3; EC:3.6.1.15; EC:3.6.4.3	Adenosinetriphosphatase; Nucleoside-triphosphate phosphatase; Microtubule-severing ATPase	no IPS match	no IPS match	no IPS match
Eucgr_D00297	PTHR10209-SF171 - GIBBERELLIN 2-BETA-DIOXYGENASE 2-RELATED (1 of 1) OS=Egrandis	F:GO:0016491; F:GO:0046872; P:GO:0055114	F:oxidoreductase activity; F:metal ion binding; P:oxidation-reduction process			IPR027443 (G3DSA:2.60.120.GENE3D); IPR026992 (PFAM); mobdb-lite (MOBIDB_LITE); PTHR10209 (PANTHER); PTHR10209-SF387 (PANTHER); SSF51197 (SUPERFAMILY)	no GO terms	no GO terms
Eucgr_D00298	PTHR11742-SF7 - ENDOPLASMIC RETICULUM MANNOSYL-OLIGOSACCHARIDE 1,2-ALPHA-MANNOSIDASE (1 of 1) OS=Egrandis	F:GO:0004571; F:GO:0005509; P:GO:0008152; C:GO:0016021	F:mannosyl-oligosaccharide 1,2-alpha-mannosidase activity; F:calcium ion binding; P:metabolic process; C:integral component of membrane	EC:3.2.1.113; EC:3.2.1.24	Mannosyl-oligosaccharide 1,2-alpha-mannosidase; Alpha-mannosidase	IPR001382 (PRINTS); IPR001382 (PFAM); IPR012341 (G3DSA:1.50.10.GENE3D); mobdb-lite (MOBIDB_LITE); mobdb-lite (MOBIDB_LITE); PTHR11742-SF55 (PANTHER); PTHR11742 (PANTHER); IPR036026 (SUPERFAMILY)	F:GO:0003824; F:GO:0004571; F:GO:0005509; C:GO:0016020	F:catalytic activity; F:mannosyl-oligosaccharide 1,2-alpha-mannosidase activity; F:calcium ion binding; C:membrane
Eucgr_D00299	PTHR22792-SF58 - LA-RELATED PROTEIN 6A (1 of 1) OS=Egrandis	F:GO:0003723; C:GO:0005634; P:GO:0006396; C:GO:1990994	F:RNA binding; C:nucleus; P:RNA processing; C:ribonucleoprotein complex			mobdb-lite (MOBIDB_LITE); mobdb-lite (MOBIDB_LITE); mobdb-lite (MOBIDB_LITE)	no GO terms	no GO terms
Eucgr_D00300	2.7.8.13 - Phospho-N-acetylmuramoyl-pentapeptide-transferase / UDP-MurNAc-pentapeptide phosphotransferase (1 of 1) OS=Egrandis	F:GO:0008963; C:GO:0016021	F:phospho-N-acetylmuramoyl-pentapeptide-transferase activity; C:integral component of membrane	EC:2.7.8.13	Phospho-N-acetylmuramoyl-pentapeptide-transferase	IPR000715 (PANTHER); PTHR22926-SF8 (PANTHER)	F:GO:0008963; C:GO:0016021	F:phospho-N-acetylmuramoyl-pentapeptide-transferase activity; C:integral component of membrane
Eucgr_D00301	K02955 - small subunit ribosomal protein S14e (RP-S14e, RPS14) (1 of 3) OS=Egrandis	F:GO:0003735; C:GO:0005840; P:GO:0006412; F:GO:0004497; F:GO:0005506; C:GO:0016021; F:GO:0016705; F:GO:0020037; P:GO:0055114	F:structural constituent of ribosome; C:ribosome; P:translation			no IPS match	no IPS match	no IPS match
Eucgr_D00302	K09832 - cytochrome P450, family 710, subfamily A (CYP710A) (1 of 1) OS=Egrandis	F:GO:0003723; C:GO:0005634; P:GO:0006396; C:GO:1990994	F:monoxygenase activity; F:iron ion binding; C:integral component of membrane; F:oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen; F:heme binding; P:oxidation-reduction process			IPR036396 (G3DSA:1.10.630.GENE3D); PTHR24286 (PANTHER); PTHR24286-SF0 (PANTHER); IPR036396 (SUPERFAMILY)	F:GO:0005506; F:GO:0016705; F:GO:0020037; P:GO:0055114	F:oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen; F:heme binding; P:oxidation-reduction process
Eucgr_D00303	PTHR10052/PTHR10052-SF9 - 60S RIBOSOMAL PROTEIN L18A // SUBFAMILY NOT NAMED (1 of 6) OS=Egrandis	C:GO:0016021	C:integral component of membrane			mobdb-lite (MOBIDB_LITE)	no GO terms	no GO terms
Eucgr_D00304	K02882 - large subunit ribosomal protein L18Ac (RP-L18Ac, RPL18A) (1 of 2) OS=Egrandis	F:GO:0003735; C:GO:0005840; P:GO:0006412	F:structural constituent of ribosome; C:ribosome; P:translation			IPR023573 (PFAM); G3DSA:3.10.20.10 (GENE3D); IPR028877 (PANTHER); PTHR10052-SF19 (PANTHER); IPR028877 (HAMARY); SSF160374 (SUPERFAMILY)	F:GO:0003735; C:GO:0005840; P:GO:0006412	F:structural constituent of ribosome; C:ribosome; P:translation
Eucgr_D00305	PTHR11712-SF226 - 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I, CHLOROPLASTIC (1 of 1) OS=Egrandis	P:GO:0006633; F:GO:0016747; F:GO:0003677; C:GO:0005634	P:fatty acid biosynthetic process; F:transferase activity, transferring acyl groups other than amino-acyl groups			IPR014030 (PFAM); IPR016039 (G3DSA:3.40.47.GENE3D); PTHR11712-SF226 (PANTHER); PTHR11712 (PANTHER); IPR016039 (SUPERFAMILY)	F:GO:0003824	F:catalytic activity
Eucgr_D00306	PTHR13711-SF200 - HIGH MOBILITY GROUP B PROTEIN 14 (1 of 1) OS=Egrandis	F:GO:0003824; C:GO:0016021	F:DNA binding; C:nucleus			no IPS match	no IPS match	no IPS match
Eucgr_D00307 Eucgr_D00308	5.3.1.27 - 6-phospho-3-hexuloisomerase / Phospho-3-hexuloisomerase (1 of 2) OS=Egrandis uncharacterized protein OS=Egrandis	F:GO:0003824; C:GO:0016021	F:catalytic activity; C:integral component of membrane			no IPS match no IPS match	no IPS match no IPS match	no IPS match no IPS match
Eucgr_D00309	PTHR32468-SF17 - CATION/H(+) ANTIporter 10-RELATED (1 of 2) OS=Egrandis	F:GO:0015299; C:GO:0016021; P:GO:1902600	F:solute/proton antiporter activity; C:integral component of membrane; P:proton transmembrane transport			IPR006153 (PFAM); IPR038770 (G3DSA:1.20.1530.GENE3D); PTHR32468-SF17 (PANTHER); PTHR32468 (PANTHER)	P:GO:0006812; F:GO:0015299; C:GO:0016021; P:GO:0055085	P:cation transport; F:solute/proton antiporter activity; C:integral component of membrane; P:transmembrane transport
Eucgr_D00310	K00654 - serine palmitoyltransferase (SPT) (1 of 1) OS=Egrandis	F:GO:0005506; F:GO:0009055; P:GO:0009058; C:GO:0009535; C:GO:0009539; P:GO:0009767; C:GO:0016021; F:GO:0020037; F:GO:0030170	F:iron ion binding; F:electron transfer activity; P:biosynthetic process; C:chloroplast thylakoid membrane; C:photosystem II reaction center; P:photosynthetic electron transport chain; C:integral component of membrane; F:heme binding; F:pyridoxal phosphate binding			no IPS match	no IPS match	no IPS match
Eucgr_D00311	PTHR11945-SF229 - F23H11.23 PROTEIN-RELATED (1 of 4) OS=Egrandis	F:GO:0000977; C:GO:0005634; P:GO:0045944; F:GO:0046983	F:RNA polymerase II regulatory region sequence-specific DNA binding; C:nucleus; P:positive regulation of transcription by RNA polymerase II; F:protein dimerization activity			IPR002100 (PRINTS); IPR002100 (SMART); IPR021000 (PFAM); IPR036879 (G3DSA:3.40.1810.GENE3D); mobdb-lite (MOBIDB_LITE); PTHR11945 (PANTHER); PTHR11945-SF229 (PANTHER); IPR002100 (PROSITE_PROFILES); IPR033896 (CDD); IPR036879 (SUPERFAMILY)	F:GO:0000977; F:GO:0003677; P:GO:0045944; F:GO:0046983	F:RNA polymerase II regulatory region sequence-specific DNA binding; F:DNA binding; P:positive regulation of transcription by RNA polymerase II; F:protein dimerization activity
Eucgr_D00312	PTHR11945-SF229 - F23H11.23 PROTEIN-RELATED (1 of 4) OS=Egrandis	F:GO:0000977; C:GO:0005634; P:GO:0045944; F:GO:0046983	F:RNA polymerase II regulatory region sequence-specific DNA binding; C:nucleus; P:positive regulation of transcription by RNA polymerase II; F:protein dimerization activity			IPR002100 (PRINTS); IPR002100 (SMART); IPR021000 (PFAM); IPR036879 (G3DSA:3.40.1810.GENE3D); mobdb-lite (MOBIDB_LITE); PTHR11945 (PANTHER); PTHR11945-SF229 (PANTHER); IPR002100 (PROSITE_PROFILES); IPR033896 (CDD); IPR036879 (SUPERFAMILY)	F:GO:0000977; F:GO:0003677; P:GO:0045944; F:GO:0046983	F:RNA polymerase II regulatory region sequence-specific DNA binding; F:DNA binding; P:positive regulation of transcription by RNA polymerase II; F:protein dimerization activity
Eucgr_D00313	PTHR11945-SF229 - F23H11.23 PROTEIN-RELATED (1 of 4) OS=Egrandis	F:GO:0000977; C:GO:0005634; P:GO:0045944; F:GO:0046983	F:RNA polymerase II regulatory region sequence-specific DNA binding; C:nucleus; P:positive regulation of transcription by RNA polymerase II; F:protein dimerization activity			IPR002100 (PRINTS); IPR002100 (SMART); IPR021000 (PFAM); IPR036879 (G3DSA:3.40.1810.GENE3D); mobdb-lite (MOBIDB_LITE); PTHR11945 (PANTHER); PTHR11945-SF229 (PANTHER); IPR002100 (PROSITE_PROFILES); IPR033896 (CDD); IPR036879 (SUPERFAMILY)	F:GO:0000977; F:GO:0003677; P:GO:0045944; F:GO:0046983	F:RNA polymerase II regulatory region sequence-specific DNA binding; F:DNA binding; P:positive regulation of transcription by RNA polymerase II; F:protein dimerization activity
Eucgr_D00314	K10735 - GINS complex subunit 4 (GINS4, SLD5) (1 of 1) OS=Egrandis	P:GO:0006261	C:nucleus; P:DNA-dependent DNA replication			G3DSA:1.20.58.1030 (GENE3D); IPR036224 (SUPERFAMILY)	no GO terms	no GO terms

Eucgr_D00315	K09647 - mitochondrial inner membrane protease subunit 1 (IMP1) (1 of 3) OS=Egrandis	P:GO:0006508; F:GO:0008236; C:GO:0016021	P:proteolysis; F:serine-type peptidase activity; C:integral component of membrane			G3DSA:2.10.109.10 (GENE3D); IPR015927 (PFAM); PTHR12383 (PANTHER); PTHR12383-SF29 (PANTHER); cd06539 (CDD); IPR036286 (SUPERFAMILY)	no GO terms	no GO terms
Eucgr_D00316	PTHR30620/PTHR30620-SF30 - PERIPLASMIC BETA-GLUCOSIDASE-RELATED // SUBFAMILY NOT NAMED (1 of 2) OS=Egrandis	F:GO:0004553; P:GO:0005975	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carbohydrate metabolic process			IPR026891 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR026891 (PFAM); IPR036881 (G3DSA:3.40.50.GENE3D); PTHR42721 (PANTHER); PTHR42721-SF11 (PANTHER); IPR036881 (SUPERFAMILY)	F:GO:0004553; P:GO:0005975	F:hydrolase activity, hydrolyzing O- glycosyl compounds; P:carbohydrate metabolic process
Eucgr_D00317	PTHR12565-SF155 - TRANSCRIPTION FACTOR BHLH144 (1 of 1) OS=Egrandis	P:GO:0006355; F:GO:0046983	P:regulation of transcription, DNA-templated; F:protein dimerization activity			mobdb-lite (MOBIDB_LITE); mobdb- lite (MOBIDB_LITE); IPR024097 (PANTHER); PTHR12565-SF155 (PANTHER); IPR011598 (PROSITE_PROFILES); IPR036638 (SUPERFAMILY)	P:GO:0006355; F:GO:0046983	P:regulation of transcription, DNA- templated; F:protein dimerization activity
Eucgr_D00318	PTHR27000-SF16 - LRR RECEPTOR-LIKE SERINE/THREONINE-PROTEIN KINASE FLS2 (1 of 3) OS=Egrandis	F:GO:0004672; F:GO:0005515; F:GO:0005524; P:GO:000468; C:GO:0016021	F:protein kinase activity; F:protein binding; F:ATP binding; P:protein phosphorylation; C:integral component of membrane			PR00019 (PRINTS); SM00365 (SMART); IPR003591 (SMART); IPR000719 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR001611 (PFAM); IPR000719 (PFAM); IPR013210 (PFAM); G3DSA:3.30.200.20 (GENE3D); IPR032675 (G3DSA:3.80.10.GENE3D); IPR032675 (G3DSA:3.80.10.GENE3D); IPR032675 (G3DSA:3.80.10.GENE3D); IPR032675 (G3DSA:3.80.10.GENE3D); IPR001611 (PFAM); IPR032675 (G3DSA:3.80.10.GENE3D); PTHR43887 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); SSF52047 (SUPERFAMILY); SSF52058 (SUPERFAMILY); SSF52058 (SUPERFAMILY)	F:GO:0004672; F:GO:0005515; F:GO:0005524; P:GO:000468	F:protein kinase activity; F:protein binding; F:ATP binding; P:protein phosphorylation
Eucgr_D00319	K08912 - light-harvesting complex II chlorophyll a/b binding protein 1 (LHCB1) (1 of 5) OS=Egrandis	C:GO:0009522; C:GO:0009523; C:GO:0009535; P:GO:0009765; C:GO:0016021; F:GO:0016168; P:GO:0018298	C:photosystem I; C:photosystem II; C:chloroplast thylakoid membrane; P:photosynthesis, light harvesting; C:integral component of membrane; F:chlorophyll binding; P:protein-chromophore linkage			IPR023329 (G3DSA:1.10.3460.GENE3D); IPR022796 (PFAM); mobdb-lite (MOBIDB_LITE); IPR001344 (PANTHER); PTHR21649-SF55 (PANTHER); SSF103511 (SUPERFAMILY)	P:GO:0009765; C:GO:0016020	P:photosynthesis, light harvesting; C:membrane
Eucgr_D00320	K08912 - light-harvesting complex II chlorophyll a/b binding protein 1 (LHCB1) (1 of 5) OS=Egrandis	C:GO:0009522; C:GO:0009523; C:GO:0009535; P:GO:0009765; C:GO:0016021; F:GO:0016168; P:GO:0018298	C:photosystem I; C:photosystem II; C:chloroplast thylakoid membrane; P:photosynthesis, light harvesting; C:integral component of membrane; F:chlorophyll binding; P:protein-chromophore linkage			IPR023329 (G3DSA:1.10.3460.GENE3D); IPR022796 (PFAM); mobdb-lite (MOBIDB_LITE); PTHR21649-SF55 (PANTHER); IPR001344 (PANTHER); SSF103511 (SUPERFAMILY)	P:GO:0009765; C:GO:0016020	P:photosynthesis, light harvesting; C:membrane
Eucgr_D00321	K08912 - light-harvesting complex II chlorophyll a/b binding protein 1 (LHCB1) (1 of 5) OS=Egrandis	C:GO:0009522; C:GO:0009523; C:GO:0009535; P:GO:0009765; C:GO:0016021; F:GO:0016168; P:GO:0018298	C:photosystem I; C:photosystem II; C:chloroplast thylakoid membrane; P:photosynthesis, light harvesting; C:integral component of membrane; F:chlorophyll binding; P:protein-chromophore linkage			IPR023329 (G3DSA:1.10.3460.GENE3D); IPR022796 (PFAM); IPR001344 (PANTHER); PTHR21649-SF55 (PANTHER); SSF103511 (SUPERFAMILY)	P:GO:0009765; C:GO:0016020	P:photosynthesis, light harvesting; C:membrane
Eucgr_D00322	K08912 - light-harvesting complex II chlorophyll a/b binding protein 1 (LHCB1) (1 of 5) OS=Egrandis	C:GO:0009522; C:GO:0009523; C:GO:0009535; P:GO:0009765; C:GO:0016021; F:GO:0016168; P:GO:0018298	C:photosystem I; C:photosystem II; C:chloroplast thylakoid membrane; P:photosynthesis, light harvesting; C:integral component of membrane; F:chlorophyll binding; P:protein-chromophore linkage			IPR023329 (G3DSA:1.10.3460.GENE3D); IPR022796 (PFAM); mobdb-lite (MOBIDB_LITE); IPR001344 (PANTHER); PTHR21649-SF55 (PANTHER); SSF103511 (SUPERFAMILY)	P:GO:0009765; C:GO:0016020	P:photosynthesis, light harvesting; C:membrane
Eucgr_D00323	PTHR12526-SF304 - STARCH SYNTHASE 4, CHLOROPLASTIC/AMYLOPLASTIC-RELATED (1 of 1) OS=Egrandis	F:GO:0004373	F:glycogen (starch) synthase activity	EC:2.4.1.11	Glycogen(starch) synthase	no IPS match	no IPS match	no IPS match
Eucgr_D00324	PTHR31376-SF17 - PURINE PERMEASE 10-RELATED (1 of 8) OS=Egrandis	F:GO:0005215; C:GO:0016021	F:transporter activity; C:integral component of membrane			PF16913 (PFAM); PTHR31376-SF17 (PANTHER); IPR030182 (PANTHER); SSF103481 (SUPERFAMILY)	F:GO:0005215; C:GO:0016021	F:transporter activity; C:integral component of membrane
Eucgr_D00325	PTHR31376-SF17 - PURINE PERMEASE 10-RELATED (1 of 8) OS=Egrandis	F:GO:0005215; C:GO:0016021	F:transporter activity; C:integral component of membrane			PF16913 (PFAM); IPR030182 (PANTHER); PTHR31376-SF17 (PANTHER)	F:GO:0005215; C:GO:0016021	F:transporter activity; C:integral component of membrane
Eucgr_D00326	PTHR31376-SF17 - PURINE PERMEASE 10-RELATED (1 of 8) OS=Egrandis	F:GO:0005215; C:GO:0016021	F:transporter activity; C:integral component of membrane			PF16913 (PFAM); IPR030182 (PANTHER); PTHR31376-SF17 (PANTHER); SSF103481 (SUPERFAMILY)	F:GO:0005215; C:GO:0016021	F:transporter activity; C:integral component of membrane
Eucgr_D00327	PTHR31376-SF17 - PURINE PERMEASE 10-RELATED (1 of 8) OS=Egrandis	F:GO:0005215; C:GO:0016021	F:transporter activity; C:integral component of membrane			PF16913 (PFAM); mobdb-lite (MOBIDB_LITE); PTHR31376-SF17 (PANTHER); IPR030182 (PANTHER)	F:GO:0005215; C:GO:0016021	F:transporter activity; C:integral component of membrane
Eucgr_D00328	PTHR31376-SF17 - PURINE PERMEASE 10-RELATED (1 of 8) OS=Egrandis	F:GO:0005215; C:GO:0016021	F:transporter activity; C:integral component of membrane			PF16913 (PFAM); IPR030182 (PANTHER); PTHR31376-SF17 (PANTHER); SSF103481 (SUPERFAMILY)	F:GO:0005215; C:GO:0016021	F:transporter activity; C:integral component of membrane
Eucgr_D00330	PTHR31376-SF17 - PURINE PERMEASE 10-RELATED (1 of 8) OS=Egrandis	F:GO:0005215; C:GO:0016021	F:transporter activity; C:integral component of membrane			PF16913 (PFAM); IPR030182 (PANTHER); PTHR31376-SF17 (PANTHER)	F:GO:0005215; C:GO:0016021	F:transporter activity; C:integral component of membrane
Eucgr_D00331	PTHR31376-SF17 - PURINE PERMEASE 10-RELATED (1 of 8) OS=Egrandis	F:GO:0005215; C:GO:0016021	F:transporter activity; C:integral component of membrane			PF16913 (PFAM); IPR030182 (PANTHER); PTHR31376-SF17 (PANTHER); SSF103481 (SUPERFAMILY)	F:GO:0005215; C:GO:0016021	F:transporter activity; C:integral component of membrane
Eucgr_D00332	PTHR31376-SF17 - PURINE PERMEASE 10-RELATED (1 of 8) OS=Egrandis	F:GO:0005215; C:GO:0016021	F:transporter activity; C:integral component of membrane			PF16913 (PFAM); IPR030182 (PANTHER); PTHR31376-SF17 (PANTHER)	F:GO:0005215; C:GO:0016021	F:transporter activity; C:integral component of membrane
Eucgr_D00333	uncharacterized protein OS=Egrandis	C:GO:0016021	C:integral component of membrane			mobdb-lite (MOBIDB_LITE); mobdb- lite (MOBIDB_LITE); PTHR36715 (PANTHER)	no GO terms	no GO terms
Eucgr_D00334	uncharacterized protein OS=Egrandis	C:GO:0016021	C:integral component of membrane			no IPS match	no IPS match	no IPS match
Eucgr_D00335	2.3.1.45 - N-acetylneuraminate 7-O(or 9-O)-acetyltransferase (1 of 2) OS=Egrandis	C:GO:0016021	C:integral component of membrane			IPR012419 (PFAM); PTHR13533-SF22 (PANTHER); PTHR13533 (PANTHER) IPR003657 (SMART); IPR003657 (PFAM); IPR036576 (G3DSA:2.20.25.GENE3D); PTHR31221 (PANTHER); PTHR31221-SF56 (PANTHER); IPR003657 (PROSITE_PROFILES); IPR036576 (SUPERFAMILY)	no GO terms	no GO terms
Eucgr_D00336	PTHR31221-SF19 - WRKY TRANSCRIPTION FACTOR 28-RELATED (1 of 1) OS=Egrandis	F:GO:0003700; C:GO:0005634; P:GO:0006355; F:GO:0043565	F:DNA-binding transcription factor activity; C:nucleus; P:regulation of transcription, DNA-templated; F:sequence-specific DNA binding			IPR003280 (PRINTS); IPR013099 (PFAM); G3DSA:1.10.287.70 (GENE3D); G3DSA:1.10.287.70 (GENE3D); mobdb-lite (MOBIDB_LITE); PTHR1003-SF126 (PANTHER); PTHR1003 (PANTHER); SSF81324 (SUPERFAMILY); SSF81324 (SUPERFAMILY)	F:GO:0003700; P:GO:0006355; F:GO:0043565	F:DNA-binding transcription factor activity; P:regulation of transcription, DNA-templated; F:sequence-specific DNA binding
Eucgr_D00337	PTHR11003-SF126 - POTASSIUM INWARD RECTIFIER (KIR)-LIKE CHANNEL 3-RELATED (1 of 2) OS=Egrandis	F:GO:0005267; F:GO:0005509; C:GO:0016021; P:GO:0071805	F:potassium channel activity; F:calcium ion binding; C:integral component of membrane; P:potassium ion transmembrane transport			mobdb-lite (MOBIDB_LITE); mobdb- lite (MOBIDB_LITE)	F:GO:0005267; C:GO:0016020; P:GO:0071805	F:potassium channel activity; C:membrane; P:potassium ion transmembrane transport
Eucgr_D00338	K14801 - pre-rRNA-processing protein TSR4 (TSR4) (1 of 3) OS=Egrandis	C:GO:005737; F:GO:0046872	C:cytoplasm; F:metal ion binding			mobdb-lite (MOBIDB_LITE); mobdb- lite (MOBIDB_LITE)	no GO terms	no GO terms
Eucgr_D00339	PTHR21535-SF49 - MAGNESIUM TRANSPORTER CORA-LIKE FAMILY PROTEIN (1 of 3) OS=Egrandis	C:GO:0016021; P:GO:0030001; F:GO:0046873; P:GO:0055085	C:integral component of membrane; P:metal ion transport; F:metal ion transmembrane transporter activity; P:transmembrane transport			mobdb-lite (MOBIDB_LITE); mobdb- lite (MOBIDB_LITE); mobdb-lite (MOBIDB_LITE); PTHR21535-SF50 (PANTHER); PTHR21535 (PANTHER)	no GO terms	no GO terms