

GO categories of genes commonly down-regulated in 3n *peg* mutants

Molecular Function

GO term	p-value	Number	Definition
GO:0004553	3,86E-05	7	hydrolase activity, hydrolyzing O-glycosyl compounds
GO:0016798	9,38E-05	7	hydrolase activity, acting on glycosyl bonds
GO:0004650	8,03E-04	3	polygalacturonase activity
GO:0015491	9,68E-03	2	cation:cation antiporter activity
GO:0046910	1,17E-02	2	pectinesterase inhibitor activity
GO:0005507	3,55E-02	2	Copper ion binding
GO:0015297	4,13E-02	2	antiporter activity
GO:0004857	4,31E-02	2	enzyme inhibitor activity
GO:0004674	4,53E-02	3	protein serine/threonine kinase activity

Biological Process

GO term	p-value	Number	Definition
GO:0005975	4,53E-04	8	carbohydrate metabolism
GO:0007169	4,52E-03	3	transmembrane receptor protein tyrosine kinase signaling pathway
GO:0007167	4,52E-03	3	enzyme linked receptor protein signaling pathway
GO:0007166	7,34E-03	3	cell surface receptor linked signal transduction
GO:0042545	2,81E-02	2	cell wall modification

GO categories of genes commonly up-regulated in 3n *peg* mutants

Molecular Function

GO term	p-value	Number	Definition
GO:0008289	1,96E-05	5	lipid binding
GO:0045735	1,01E-02	2	nutrient reservoir activity
GO:0016684	2,16E-02	2	oxidoreductase activity, acting on peroxide as acceptor
GO:0004601	2,16E-02	2	peroxidase activity
GO:0016209	2,84E-02	2	antioxidant activity
GO:0016789	2,95E-02	3	carboxylic ester hydrolase activity
GO:0004091	3,17E-02	2	carboxylesterase activity
GO:0016298	3,26E-02	2	lipase activity

Biological Process

GO term	p-value	Number	Definition
GO:0006869	4,06E-06	5	lipid transport
GO:0042538	2,39E-03	2	hyperosmotic salinity response
GO:0006972	2,69E-03	2	hyperosmotic response
GO:0016053	3,80E-02	2	organic acid biosynthesis
GO:0046394	3,80E-02	2	carboxylic acid biosynthesis