Table 1 Suppl. Identification of SNP responsive clones isolated by SSH in litchi primordia.

Clone	Accession No. of matching sequence	Matching sequence in public database	Source of matching sequence	Best e-value (*BLASTx*)
Transport facilitation				
12	HQ425639.1	lipid transfer protein (LTP)	*Dimocarpus longan*	6.00E-52
86	JN572691.1	aquaporin PIP1 (PIP1）	*Dimocarpus longan*	2.00E-21
126	NM_126423.3	flavonol sulfotransferase-like protein (SOT12)	*Arabidopsis thaliana*	2.00E-18
279	JF720322.1	tubulin β-6	*Brassica oleracea var.*	1.40E-01
810	XM_002879581.1	putative tonoplast intrinsic protein	*Arabidopsis lyrata*	1.00E-17
579	NM_117145.2	oligopeptide transporter 7 (OPT7)	*Arabidopsis thaliana*	3.00E-03
664	NM_102495.4	Ribosome associated membrane protein RAMP4 (AT1G27330)	*Arabidopsis thaliana*	2.00E-10
1190	XM_002519892.1	electron carrier	*Ricinus communis*	8.00E-102
1377	AJ272202.1	mitochondrial half-ABC transporter (STA1 gene)	*Arabidopsis thaliana*	1.00E-16
176	NM_127375.1	phosphatidylinositol transfer-like protein	*Arabidopsis thaliana*	5.00E-110
Transcription regulation				
566	NM_121600.3	S-adenosylmethionine decarboxylase-like protein	*Arabidopsis thaliana*	2.00E-19
196	EU961518.1	metallothionein-like protein	*Zea mays*	2.00E-17
435	NM_127399.3	Gibberellin-regulated family protein (AT2G18420)	*Arabidopsis thaliana*	2.00E-09
566	NM_121600.3	S-adenosylmethionine decarboxylase-like protein	*Arabidopsis thaliana*	4.00E-22
948	EU961518.1	metallothionein-like protein	*Zea mays*	3.00E-20
Stress response				
2	DQ659678.1	vegetative storage protein (VSP1)	*Litchi chinensis*	3E-176
4	JF920723.1	mannose/glucose-specific lectin	*Litchi chinensis*	2E-84
350	AJ237984.1	putative proline-rich cell wall protein	*Vitis vinifera*	3.20E-01
461	HQ667571.1	oxygen evolving enhancer protein 1 (OEE1)	*Litchi chinensis*	2.00E-84
591	AF319165.1	dehydration-responsive protein	*Prunus persica*	1.00E-37
1014	EU627185.1	antimicrobial peptide snakin	*Capsicum annuum*	2.00E-09
Sugar metabolism				
80	NM_001124981.1	fructose-bisphosphate aldolase, class I (AT2G36460)	*Arabidopsis thaliana*	3E-58
232	AY054466.1	carbonic anhydrase	*Arabidopsis thaliana*	1.00E-10
368	HQ589339.1	chloroplast ribulose-1,5-bisphosphate carboxylase/oxygenase	*Litchi chinensis*	3.00E-174
428	EF694978.1	chloroplast protein	*Arnebia euchroma*	2.00E-05
489	NM_118058.3	Long-chain-alcohol oxidase	*Arabidopsis thaliana*	2.00E-52
Secondary metabolism				
21	XM_002271975.1	similar to anthocyanidin reductase	*Vitis vinifera*	2.00E-60
74	AB009350.1	chalcone synthase CHS3	*Citrus sinensis*	7.00E-41
105	FJ473421.1	peroxidase 4	*Litchi chinensis*	2.00E-119
154	AK227165.1	monodehydroascorbate reductase (NADH) - like protein	*Arabidopsis thaliana*	2.00E-48
482	EU527187.1	laccase	*Litchi chinensis*	1.00E-107
48	BT000029.1	putative copper amine oxidase (At2g42490)	*Arabidopsis thaliana*	7.00E-20
Intracellular signalling				
67	AY311484.1	ethylene receptor (ERS)	*Litchi chinensis*	1.00E-58
76	NM_001198137.1	gibberellin-regulated protein 14-like (LOC100265557),	*Vitis vinifera*	5.00E-37
695	XM_002279196.2	SKP1-like protein 1A (LOC100267502),	*Vitis vinifera*	8.00E-62
260	AB293942.1	G protein beta-subunit-like protein	*Nicotiana tabacum*	4.00E-35
503	AY082522.1	Aux/IAA protein	*Vitis vinifera*	4.00E-71
1360	D63787.1	diacylglycerol kinase	*Arabidopsis thaliana*	1.80E-01
163	AJ277744.1	ABA and calcium induced protein phosphatase 2C (PP2C)	*Fagus sylvatica*	8.00E-17
Others				
14	FJ628090.1	Chanthaburi ribosomal protein L9 gene	*Sonneratia ovata*	8.00E-99
10	NM_120231.3	chlorophyll *a-b* binding protein CP29.1 (LHCB4.1)	*Arabidopsis thaliana*	5.00E-71
47	NM_116771.5	polyubiquitin 10 (UBQ10)	*Arabidopsis thaliana*	3.00E-65
81	AB263748.2	self-incompatibility (S-) locus region	*Ipomoea trifida*	1.60E+00
696	XM_002285001.1	ripening-induced protein 1-like (MRIP1)	*Vitis vinifera*	2.90E-01
107	NM_122036.4	40S ribosomal protein S8-1 (AT5G20290)	*Arabidopsis thaliana*	4.00E-58
470	XM_002517981.1	ATP binding protein	*Ricinus communis*	2.00E-70
144	BT000835.1	nodulin-like protein	*Arabidopsis thaliana*	3.00E-37
179	EU081898.1	polyubiquitin (WubiG)	*Triticum aestivum*	2.00E-45
1087	NM_102497.1	Ribosome associated membrane protein RAMP4	*Arabidopsis thaliana*	3.00E-34
228	AF180758.1	60S ribosomal protein L10	*Vitis riparia*	9.00E-80
583	NM_115123.2	Nucleic acid-binding, OB-fold-like protein	*Arabidopsis thaliana*	9.00E-33
265	XM_002277367.2	ubiquitin-conjugating enzyme E2	*Vitis vinifera*	8.00E-92
479	XM_002520718.1	small nuclear ribonucleoprotein	*Ricinus communis*	2.00E-10
107	XM_002275058.2	40S ribosomal protein S8-like (LOC100257178)	*Vitis vinifera*	4.00E-64
1000	EF489507.1	ESR3 ubiquitin ligase-like protein	*Oryza sativa Japonica*	7.00E-73
1417	GQ497217.1	transgenic GMO cassette	*Glycine max*	8.00E-34
1309	HM627638.1	miraculin-like protein 1	*Citrus limonia*	2.00E-18
Unknown protein				
6	AY072318.1	unknown protein	*Arabidopsis thaliana*	1.00E-18
30	XM_002517751.1	conserved hypothetical protein	*Ricinus communis*	5.00E-49
96	XM_002515252.1	conserved hypothetical protein	*Ricinus communis*	2.00E-04
148	AY072318.1	unknown protein (At3g08030)	*Arabidopsis thaliana*	1.00E-17
573	XM_002876941.1	hypothetical protein	*Arabidopsis lyrata*	4.00E-12
815	AY080594.1	unknown protein (At1g32460)	*Arabidopsis thaliana*	8.00E-06
1061	AY063045.1	unknown protein (At5g64400)	*Arabidopsis thaliana*	1.00E-32
158	EU976925.1	hypothetical protein	*Zea mays*	1.40E-01

No matching sequences were found in the NCBI database: 817, 891, 923, 1036, 1410