

Supplementary Material

Table S1 – Functional annotations off SSRs containing similarity with proteins in GenBank.

SSR identification	Functional annotation	First Hit - BlastX -NR	E-Value	Gene Ontology / AmiGO annotation	PFAM DOMAIN
SSR-IAC20	Conserved hypothetical protein	ref[XP_002326779.1 predicted protein [<i>Populus trichocarpa</i>]	7.41E-15		
SSR-IAC22	Gdsl-motif lipase hydrolase	emb[CAO24082.1 unnamed protein product [<i>Vitis vinifera</i>]	7.40E-19	Lipid catabolic process (P); hydrolase activity, acting on ester bonds (F); extracellular region (C)	SGNH_plant_lipase_like
SSR-IAC24	Gag-protease poly protein	emb[CAN81436.1 hypothetical protein [<i>Vitis vinifera</i>]	1.43E-09	F:peptidase activity	Reverse transcriptase (RNA-dependent DNA polymerase) retrovirus
SSR-IAC27	Adenosine nucleotide translocator	gb[EEF44404.1 ADP,ATP carrier protein, putative [<i>Ricinus communis</i>]	5.33E-06	F:transporter activity; F: ATP:ADP transporter; C:integral to membrane; C:membrane; C:mitochondrial inner membrane; C:mitochondrion; P:transport; C:plasma membrane; C:chloroplast; F:binding	Mitochondrial carrier protein
SSR-IAC29	MADS box protein/ SEPALLATA1	gb[ABD17386.1 MADS-box protein SEP3-1 [<i>Taihangia rupestris</i>]	4.00E-13	F:sequence-specific DNA binding; F:transcription factor activity; P:regulation of transcription, DNA-dependent P: flower development	MADS BOX
SSR-IAC52	Conserved hypothetical protein	gb[ACJ85266.1 unknown [<i>Medicago truncatula</i>]	5.04E-23		
SSR-IAC53	Zinc finger protein	emb[CAN74885.1 hypothetical protein [<i>Vitis vinifera</i>]	3.00E-34	P:regulation of transcription; F:zinc ion binding; F:transcription factor activity	ZnF_C2H2 domain
SSR-IAC58	Leucine aminopeptidase	gb[ACJ85545.1 unknown [<i>Medicago truncatula</i>]	8.82E-17	F:manganese ion binding; F:metalloexopeptidase activity; P:response to stress; F:aminopeptidase activity; C:chloroplast; P:proteolysis; F:zinc ion binding	Cytosol aminopeptidase family
SSR-IAC59	RING finger protein	gb[ACF79111.1 unknown [<i>Zea mays</i>]	4.53E-11		RING-finger (Really Interesting New Gene) domain
SSR-IAC77	Mads-box protein	gb[EES15309.1 hypothetical protein SORBIDRAFT_07g026200 [<i>Sorghum bicolor</i>]	5.20E-22	F:sequence-specific DNA binding; F:transcription factor activity; P:regulation of transcription, DNA-dependent P: flower development	MADS BOX
SSR-IAC83	Arginine N-methyltransferase 6	gb[ACU21309.1 unknown [<i>Glycine max</i>]	3.00E-16	F : protein methyltransferase activity, F: protein amino acid methylation;	Methyltransferase domain

SSR-IAC87	Retrotransposon ty3-gypsy subclass	gb AAF13073.1 putative retroelement pol polyprotein [<i>Arabidopsis thaliana</i>]	4.44E-09	C:chromatin; F:chromatin binding; F:DNA binding; C:nucleus; F:nucleic acid binding; F:RNA binding; F:RNA-directed DNA polymerase activity; P:chromatin assembly or disassembly; P:DNA integration; F:aspartic-type endopeptidase activity; P:RNA-dependent DNA replication; P:proteolysis; C:plastid	RT_LTR: Reverse transcriptases (RTs) from retrotransposons
SSR-IAC91	Conserved hypothetical protein	emb CAN64580.1 hypothetical protein [<i>Vitis vinifera</i>]	6.39E-04		
SSR-IAC127	Photosystem I subunit b	gb ABW22789.1 photosystem I P700 apoprotein A2 [<i>Phaseolus vulgaris</i>]	2.03E-48	F:electron carrier activity; F:iron ion binding; P:transport; F:magnesium ion binding; P:protein-chromophore linkage; F:chlorophyll binding; F:4 iron, 4 sulfur cluster binding; C:integral to membrane; C:chloroplast; C:thylakoid; C:photosystem I; P:photosynthesis; P:electron transport chain	Photosystem I psaA/psaB protein
SSR-IAC129	Putative athila transposon protein	pir S66306 hypothetical protein 1 - <i>Arabidopsis thaliana</i> retrotransposon	2.00E-04		
SSR-IAC179	Retrotransposon ty3-gypsy subclass	gb AAD19359.1 polyprotein [<i>Sorghum bicolor</i>]	1.16E-11	F:RNA binding; F:nucleic acid binding; C:mitochondrion; P:DNA integration; P:RNA-dependent DNA replication; F:ribonuclease H activity; F:RNA-directed DNA polymerase activity; F:DNA binding	RT_LTR: Reverse transcriptases (RTs) from retrotransposons
SSR-IAC180	Hypothetical protein	gb EDL79735.1 similar to FLJ46154 protein (predicted) [<i>Rattus norvegicus</i>]	5.90E-11		
FJUNA245	Clathrin assembly protein	ref XP_002324864.1 predicted protein [<i>Populus trichocarpa</i>]	8.00E-16	F: phosphatidylinositol binding; F: clathrin binding; F: clathrin coat assembly; P: clathrin coat assembly	ANTH domain family
FJUNA390	ADP,ATP carrier protein	gb ACU21147.1 unknown [<i>Glycine max</i>]	2.00E-08	F:transporter activity; F: ATP:ADP transporter; C:integral to membrane; C:membrane; C:mitochondrial inner membrane; C:mitochondrion; P:transport; C:plasma membrane; C:chloroplast; F:binding	Mitochondrial carrier protein