

Supplementary table: Details of best promising Hits of ESTs having SSR were obtained through Fastannotator.

Serial No	Entry	Biological Process	Cellular Component	Molecular Function
1	gi 17519141 gb BM188183.1 BM188183	GO:0009813 flavonoid biosynthetic process GO:0042398 cellular modified amino acid biosynthetic process GO:0080167 response to karrikin		GO:0045430 chalcone isomerase activity
2	gi 54682355 gb CV656076.1 CV656076	GO:0009813 flavonoid biosynthetic process		GO:0016210 naringenin-chalcone synthase activity
3	gi 71820633 gb DR998024.1 DR998024	GO:0055114 oxidation-reduction process GO:0006558 L-phenylalanine metabolic process GO:0009805 coumarin biosynthetic process GO:0009809 lignin biosynthetic process GO:0009811 stilbene biosynthetic process GO:0006118 electron transport		GO:0020037 heme binding GO:0016710 trans-cinnamate 4-monooxygenase activity GO:0009055 electron carrier activity
4	gi 25799294 gb CA755255.1 CA755255	GO:0009809 lignin biosynthetic process GO:0055114 oxidation-reduction process GO:0009805 coumarin biosynthetic process GO:0009811 stilbene biosynthetic process		GO:0045551 cinnamyl-alcohol dehydrogenase activity GO:0000166 nucleotide binding GO:0008270 zinc ion binding GO:0052747 sinapyl alcohol dehydrogenase activity
5	gi 56431124 gb CX023192.1 CX023192	GO:0051555 flavonol biosynthetic process GO:0055114 oxidation-reduction process	GO:0005737 cytoplasm	GO:0045486 naringenin 3-dioxygenase activity GO:0045431 flavonol synthase activity GO:0031418 L-ascorbic acid binding GO:0005506 iron ion binding GO:0016702 oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen
6	gi 226808327 gb GO563021.1 GO563021	GO:0009414 response to water deprivation GO:0006073 cellular glucan metabolic process	GO:0005618 cell wall GO:0048046 apoplast	GO:0016762 xyloglucan:xyloglucosyl transferase activity GO:0033946 xyloglucan-specific endo-beta-1,4-glucanase activity
7	gi 209724892 gb BW669581.1 BW669581	GO:0006073 cellular glucan metabolic process GO:0007047 cellular cell wall organization	GO:0005618 cell wall GO:0048046 apoplast	GO:0016762 xyloglucan:xyloglucosyl transferase activity GO:0004553 hydrolase activity, hydrolyzing O-

				glycosyl compounds
8	gi 209724609 gb BW677716.1 BW677716	GO:0009651 response to salt stress GO:0018279 protein N-linked glycosylation via asparagine	GO:0005886 plasma membrane GO:0008250 oligosaccharyltransferase complex	GO:0004579 dolichyl-diphosphooligosaccharide-protein glycotransferase activity
9	gi 55857142 gb CV881934.1 CV881934	GO:0009414 response to water deprivation GO:0006073 cellular glucan metabolic process	GO:0005618 cell wall GO:0048046 apoplast	GO:0016762 xyloglucan:xyloglucosyl transferase activity GO:0033946 xyloglucan-specific endo-beta-1,4-glucanase activity
10	gi 27387337 gb CA900345.1 CA900345	GO:0009399 nitrogen fixation GO:0006542 glutamine biosynthetic process GO:0009252 peptidoglycan biosynthetic process	GO:0005737 cytoplasm	GO:0004356 glutamate-ammonia ligase activity GO:0005524 ATP binding
11	gi 56162853 gb CV986979.1 CV986979	GO:0055114 oxidation-reduction process		GO:0033788 leucoanthocyanidin reductase activity GO:0000166 nucleotide binding
12	gi 254066103 gb GR726006.1 GR726006	GO:0009240 isopentenyl diphosphate biosynthetic process GO:0015995 chlorophyll biosynthetic process GO:0009908 flower development GO:0016114 terpenoid biosynthetic process GO:0009060 aerobic respiration GO:0006096 glycolysis GO:0046686 response to cadmium ion GO:0006694 steroid biosynthetic process	GO:0005829 cytosol GO:0005739 mitochondrion GO:0009507 chloroplast	GO:0004452 isopentenyl-diphosphate delta-isomerase activity GO:0016787 hydrolase activity
13	gi 182974060 gb FF599768.1 FF599768	GO:0035634 response to stilbenoid GO:0006695 cholesterol biosynthetic process GO:0016114 terpenoid biosynthetic process	GO:0005777 peroxisome GO:0005829 cytosol GO:0005739 mitochondrion	GO:0030145 manganese ion binding GO:0016787 hydrolase activity GO:0000287 magnesium ion binding GO:0004452 isopentenyl-diphosphate delta-isomerase activity
14	gi 209712696 gb BW684626.1 BW684626	GO:0015995 chlorophyll biosynthetic process GO:0009908 flower development GO:0015979 photosynthesis GO:0006694 steroid biosynthetic process GO:0016114 terpenoid biosynthetic process	GO:0009507 chloroplast GO:0005829 cytosol GO:0005739 mitochondrion	GO:0046872 metal ion binding GO:0016787 hydrolase activity GO:0004452 isopentenyl-diphosphate delta-isomerase activity
15	gi 209728353 gb BW659990.1 BW659990	GO:0009240 isopentenyl diphosphate biosynthetic process GO:0015995 chlorophyll biosynthetic process	GO:0005829 cytosol GO:0005739 mitochondrion	GO:0004452 isopentenyl-diphosphate delta-isomerase activity GO:0016787 hydrolase activity

		GO:0009908 flower development GO:0050992 dimethylallyl diphosphate biosynthetic process GO:0009060 aerobic respiration GO:0006096 glycolysis GO:0015979 photosynthesis GO:0046686 response to cadmium ion GO:0006694 steroid biosynthetic process GO:0016114 terpenoid biosynthetic process	GO:0009536 plastid	
16	gi 209727623 gb BW663783.1 BW663783	GO:0009240 isopentenyl diphosphate biosynthetic process GO:0015995 chlorophyll biosynthetic process GO:0009908 flower development GO:0050992 dimethylallyl diphosphate biosynthetic process GO:0016114 terpenoid biosynthetic process GO:0015979 photosynthesis GO:0006694 steroid biosynthetic process	GO:0005829 cytosol GO:0005739 mitochondrion GO:0009507 chloroplast	GO:0004452 isopentenyl-diphosphate delta-isomerase activity GO:0016787 hydrolase activity
17	gi 209712023 gb BW668424.1 BW668424	GO:0009240 isopentenyl diphosphate biosynthetic process GO:0015995 chlorophyll biosynthetic process GO:0009908 flower development GO:0050992 dimethylallyl diphosphate biosynthetic process GO:0009060 aerobic respiration GO:0006096 glycolysis GO:0015979 photosynthesis GO:0046686 response to cadmium ion GO:0006694 steroid biosynthetic process GO:0016114 terpenoid biosynthetic process	GO:0005829 cytosol GO:0005739 mitochondrion GO:0009536 plastid	GO:0004452 isopentenyl-diphosphate delta-isomerase activity GO:0016787 hydrolase activity
18	gi 71824350 gb DT001742.1 DT001742	GO:0034265 isopentenyl adenine biosynthetic process GO:0008033 tRNA processing	GO:0005634 nucleus GO:0009536 plastid	GO:0052622 ATP dimethylallyltransferase activity GO:0005524 ATP binding GO:0009824 AMP dimethylallyltransferase activity GO:0052623 ADP dimethylallyltransferase activity
19	gi 226770420 gb GO523629.1 GO523629	GO:0006633 fatty acid biosynthetic process GO:0055114 oxidation-reduction process GO:0042967 acyl-carrier-protein biosynthetic process	GO:0005835 fatty acid synthase complex GO:0009941 chloroplast envelope GO:0009570 chloroplast stroma GO:0009579 thylakoid	GO:0016631 enoyl-[acyl-carrier-protein] reductase activity GO:0005507 copper ion binding GO:0004318 enoyl-[acyl-carrier-protein] reductase (NADH) activity GO:0000166 nucleotide binding

20	gi 5442510 gb AI822237.1 AI822237	GO:0006979 response to oxidative stress GO:0006952 defense response GO:0010224 response to UV-B GO:0009611 response to wounding GO:0006559 L-phenylalanine catabolic process GO:0009699 phenylpropanoid biosynthetic process GO:0009555 pollen development GO:0046274 lignin catabolic process GO:0009819 drought recovery GO:0046244 salicylic acid catabolic process GO:0080167 response to karrikin GO:0006570 tyrosine metabolic process GO:0009821 alkaloid biosynthetic process	GO:0005737 cytoplasm	GO:0045548 phenylalanine ammonia-lyase activity
21	gi 25802852 gb CA758813.1 CA758813	GO:0009788 negative regulation of abscisic acid mediated signaling pathway GO:0008360 regulation of cell shape GO:0009414 response to water deprivation GO:0048509 regulation of meristem development GO:0018344 protein geranylgeranylation GO:0018343 protein farnesylation GO:0006694 steroid biosynthetic process GO:0016114 terpenoid biosynthetic process	GO:0005965 protein farnesyltransferase complex GO:0005953 CAAX-protein geranylgeranyltransferase complex	GO:0004662 CAAX-protein geranylgeranyltransferase activity GO:0004660 protein farnesyltransferase activity GO:0004311 farnesyltransferase activity GO:0046982 protein heterodimerization activity
22	gi 209717502 gb BW654405.1 BW654405	GO:0042218 1-aminocyclopropane-1-carboxylate biosynthetic process		GO:0030170 pyridoxal phosphate binding GO:0008483 transaminase activity GO:0016847 1-aminocyclopropane-1-carboxylate synthase activity
23	gi 209725557 gb BW677859.1 BW677859	GO:0042218 1-aminocyclopropane-1-carboxylate biosynthetic process GO:0006522 alanine metabolic process GO:0006531 aspartate metabolic process GO:0015976 carbon utilization		GO:0030170 pyridoxal phosphate binding GO:0004021 L-alanine:2-oxoglutarate aminotransferase activity GO:0016847 1-aminocyclopropane-1-carboxylate synthase activity
24	gi 56433440 gb CX024350.1 CX024350	GO:0009098 leucine biosynthetic process GO:0009651 response to salt stress GO:0009097 isoleucine biosynthetic process GO:0009099 valine biosynthetic process	GO:0009316 3-isopropylmalate dehydratase complex GO:0009570 chloroplast stroma	GO:0003861 3-isopropylmalate dehydratase activity
25	gi 25799399 gb CA755360.1 CA755360	GO:0009094 L-phenylalanine biosynthetic process		GO:0004664 prephenate dehydratase activity

		GO:0000162 tryptophan biosynthetic process GO:0006571 tyrosine biosynthetic process		
26	gi 313127819 gb HS106796.1 HS106796	GO:0006468 protein phosphorylation GO:0007165 signal transduction GO:0009069 serine family amino acid metabolic process		GO:0004697 protein kinase C activity GO:0004713 protein tyrosine kinase activity GO:0005524 ATP binding
27	gi 25799833 gb CA755794.1 CA755794	GO:0009789 positive regulation of abscisic acid mediated signaling pathway GO:0010111 glyoxysome organization GO:0009611 response to wounding GO:0009695 jasmonic acid biosynthetic process GO:0006635 fatty acid beta-oxidation GO:0006550 isoleucine catabolic process GO:0006552 leucine catabolic process GO:0006574 valine catabolic process GO:0006699 bile acid biosynthetic process GO:0018874 benzoate metabolic process GO:0042967 acyl-carrier-protein biosynthetic process	GO:0005829 cytosol GO:0005777 peroxisome GO:0005739 mitochondrion GO:0005730 nucleolus GO:0005774 vacuolar membrane GO:0009507 chloroplast	GO:0003988 acetyl-CoA C-acyltransferase activity
28	gi 21620941 gb BQ618947.1 BQ618947	GO:0006550 isoleucine catabolic process GO:0006552 leucine catabolic process GO:0006574 valine catabolic process GO:0006633 fatty acid biosynthetic process GO:0006699 bile acid biosynthetic process GO:0018874 benzoate metabolic process GO:0042967 acyl-carrier-protein biosynthetic process	GO:0005777 peroxisome GO:0005773 vacuole	GO:0003988 acetyl-CoA C-acyltransferase activity
29	gi 25798095 gb CA754056.1 CA754056	GO:0042218 1-aminocyclopropane-1-carboxylate biosynthetic process GO:0009853 photorespiration GO:0006522 alanine metabolic process GO:0006531 aspartate metabolic process GO:0006544 glycine metabolic process GO:0006563 L-serine metabolic process GO:0006566 threonine metabolic process GO:0015976 carbon utilization	GO:0005777 peroxisome GO:0009570 chloroplast stroma GO:0005829 cytosol	GO:0008453 alanine-glyoxylate transaminase activity GO:0030170 pyridoxal phosphate binding GO:0004021 L-alanine:2-oxoglutarate aminotransferase activity GO:0047958 glycine:2-oxoglutarate aminotransferase activity GO:0016847 1-aminocyclopropane-1-carboxylate synthase activity
30	gi 226763339 gb GO519325.1 GO519325	GO:0009813 flavonoid biosynthetic process GO:0009733 response to auxin stimulus GO:0055114 oxidation-reduction process	GO:0005789 endoplasmic reticulum membrane GO:0016021 integral to	GO:0016711 flavonoid 3'-monooxygenase activity GO:0009055 electron carrier activity GO:0020037 heme binding

		GO:0009411 response to UV GO:0006118 electron transport	membrane	GO:0019825 oxygen binding
31	gi 49633098 gb CO416850.1 CO416850	GO:0006412 translation GO:0042254 ribosome biogenesis	GO:0005730 nucleolus GO:0009506 plasmodesma GO:0005886 plasma membrane GO:0022625 cytosolic large ribosomal subunit GO:0009507 chloroplast GO:0005783 endoplasmic reticulum	GO:0003735 structural constituent of ribosome
32	gi 8334112 gb BE039096.1 BE039096	GO:0009759 indole glucosinolate biosynthetic process GO:0000162 tryptophan biosynthetic process GO:0010114 response to red light GO:0052544 defense response by callose deposition in cell wall GO:0048830 adventitious root development GO:0009411 response to UV GO:0009684 indoleacetic acid biosynthetic process GO:0009641 shade avoidance GO:0055114 oxidation-reduction process GO:0009682 induced systemic resistance GO:0006118 electron transport	GO:0005783 endoplasmic reticulum GO:0005886 plasma membrane GO:0005739 mitochondrion	GO:0020037 heme binding GO:0009055 electron carrier activity GO:0033771 licodione synthase activity GO:0019825 oxygen binding
33	gi 203711834 gb GD250318.1 GD250318	GO:0006555 methionine metabolic process GO:0055114 oxidation-reduction process GO:0046653 tetrahydrofolate metabolic process		GO:0004489 methylenetetrahydrofolate reductase (NADPH) activity
34	gi 25802318 gb CA758279.1 CA758279	GO:0006694 steroid biosynthetic process GO:0016114 terpenoid biosynthetic process	GO:0016021 integral to membrane	GO:0004310 farnesyl-diphosphate farnesyltransferase activity
35	gi 219524684 gb GH456542.1 GH456542	GO:0000162 tryptophan biosynthetic process GO:0006571 tyrosine biosynthetic process GO:0009094 L-phenylalanine biosynthetic process	GO:0009536 plastid	GO:0004834 tryptophan synthase activity