

Supplementary Table 2

NAC TFs showing the presence of novel functional domain along with NAC domains.

NAC TFs	Species	Active site
Pavir.Ha00781	<i>Panicum virgatum</i>	<i>Aldehyde dehydrogenases cysteine active site</i>
Carubv10005139m	<i>Capsella rubella</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
491912	<i>Arabidopsis lyrata</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
GSBRNA2T00058100001	<i>Brassica napus</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
GSBRNA2T00078811001	<i>Brassica napus</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
XP_013638893.1	<i>Brassica oleracea</i>	<i>Antenna complexes beta subunits signature</i>
Prupe.2G196600.1.p	<i>Prunus persica</i>	<i>ATP synthase alpha and beta subunits signature</i>
Pavir.J01198	<i>Panicum virgatum</i>	<i>Cysteine proteases inhibitors signature</i>
GSMUA_Achr9P20400_001	<i>Musa acuminata</i>	<i>Endopeptidase Clp serine active site</i>
ACHN289231	<i>Actinidia chinensis</i>	<i>Heavy-metal-associated domain</i>
LOC_Os01g47670	<i>Oryza sativa</i>	<i>Inorganic pyrophosphatase signature</i>
Thhalv10009374m	<i>Eutrema salsugineum</i>	<i>Inorganic pyrophosphatase signature</i>
Niben101Scf07168g02012.1	<i>Nicotiana benthamiana</i>	<i>Lipocalin signature</i>
XP_011088938.1	<i>Sesamum indicum</i>	<i>Pancreatic trypsin inhibitor (Kunitz) family signature</i>
KHN08560.1	<i>Glycine soja</i>	<i>Putative AMP-binding domain signature</i>
MLOC_75795.1	<i>Hordeum vulgare</i>	<i>Zinc carboxypeptidases, zinc-binding region 2 signature</i>
Vradi01g03390.1	<i>Vigna radiata</i>	<i>2Fe-2S ferredoxin-type iron-sulfur binding region signature</i>
FANhyb_rscf00000665.1.g00005.1	<i>Fragaria ananassa</i>	<i>2-oxo acid dehydrogenases acyltransferase component lipoyl binding site</i>
XP_010916182.1	<i>Elaeis guineensi</i>	<i>4Fe-4S ferredoxin-type iron-sulfur binding domain profile</i>
XP_010916183.1	<i>Elaeis guineensi</i>	<i>4Fe-4S ferredoxin-type iron-sulfur binding domain profile</i>
GSMUA_Achr11P03780_001	<i>Musa acuminata</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
GSMUA_Achr11P17510_001	<i>Musa acuminata</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
GSMUA_Achr6P36840_001	<i>Musa acuminata</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
GSMUA_Achr7P06640_001	<i>Musa acuminata</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>

GSMUA_Achr8P11590_001	<i>Musa acuminata</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
NNU_008894-RA	<i>Nelumbo nucifera</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
NNU_012069-RA	<i>Nelumbo nucifera</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
Phvu1.011G005700	<i>Phaseolus vulgaris</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
PDK_30s1016001g009	<i>Phoenix dactylifera</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
Spipo1G0086600	<i>Spirodela polyrhiza</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
Zosma265g00020	<i>Zostera marina</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
ACHN002691	<i>Actinidia chinensis</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
ACHN093311	<i>Actinidia chinensis</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
ACHN157011	<i>Actinidia chinensis</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
ACHN317511	<i>Actinidia chinensis</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
ACO007609.1	<i>Ananus comosus</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
Aqcoe7G078200.1.p	<i>Aquilegiacoerulea</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
Bv5_097990_fpf.t1	<i>Beta vulgaris</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
Brast07G026300.1.p	<i>Brachypodium stacei</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
XP_004514529.1	<i>Cicer arietinum</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
XP_010933718.1	<i>Elaeis guineensi</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
Glyma-09G231700.1.p	<i>Glycine max</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
KHN11660.1	<i>Glycine soja</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
Medtr4g036030.1	<i>Medicago truncatula</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
XP_010108028.1	<i>Morus notabilis</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
PDK_30s1016001g009	<i>Phoenix dactylifera</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
Tp57577_TGAC_v2_mRNA3761	<i>Trifolium pratense</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
Vang05g07280	<i>Vigna angularis</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
C.cajan_20892	<i>Cajanus cajan</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
GSVIVT01001264001	<i>Vitis vinifera</i>	<i>7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase signature</i>
Aradu.Y1DM8	<i>Arachis duranensis</i>	<i>ABC transporters family signature</i>
Araip.HYM8C	<i>Arachis ipaensis</i>	<i>ABC transporters family signature</i>

mrna03833-1-v1-0-hybrid	<i>Fragaria vesca</i>	<i>Adenosine and AMP deaminase signature</i>
PSME_00042313-RA	<i>Pseudotsuga menziesii</i>	<i>Adenosine and AMP deaminase signature</i>
Zosma69g00740	<i>Zostera marina</i>	<i>Adipokinetic hormone family signature</i>
Pavir.8NG107600.1.p	<i>Panicum virgatum</i>	<i>Aldehyde dehydrogenases cysteine active site</i>
Pavir.8NG113600.1.p	<i>Panicum virgatum</i>	<i>Aldehyde dehydrogenases cysteine active site</i>
RrC2674_p3	<i>Raphanus raphanistrum</i>	<i>Aldehyde dehydrogenases cysteine active site</i>
Rsa1.0_00285.1_g00018.1	<i>Raphanus sativus</i>	<i>Aldehyde dehydrogenases cysteine active site</i>
Araha-3365s0007	<i>Arabidopsis halleri</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
AT4G28530	<i>Arabidopsis thaliana</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
Bra010362	<i>Brassica rapa</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
Bra011037	<i>Brassica rapa</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
Cagra-1225s0038	<i>Capsella grandiflora</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
evm.model.supercontig_80.94	<i>Carica papaya</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
Kalax.0013s0167	<i>Kalanchoe laxiflora</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
Kalax.0154s0005	<i>Kalanchoe laxiflora</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
Thhalv10025606m	<i>Thellungiella halophila</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
Araha.3365s0007.1.p	<i>Arabidopsis halleri</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
KFK29397.1	<i>Arabis alpina</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
XP_013603495.1	<i>Brassica oleracea</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
XP_009109087.1	<i>Brassica rapa</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
XP_009129548.1	<i>Brassica rapa</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
Csa10g014090.1	<i>Camelina sativa</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
Csa11g015230.1	<i>Camelina sativa</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
Csa12g021980.1	<i>Camelina sativa</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
Carubv10005139m	<i>Capsella rubella</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
Thhalv10025606m	<i>Eutrema salsugineum</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
Kalax-0013s0167.1.p	<i>Kalanchoe marnieriana</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
Kalax-0154s0005.1.p	<i>Kalanchoe marnieriana</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>

RrC20539_p1	<i>Raphanus raphanistrum</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
Rsa1.0_13977.1_g00001.1	<i>Raphanus sativus</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
GSBRNA2T00104607001	<i>Brassica napus</i>	<i>Aldehyde dehydrogenases glutamic acid active site</i>
Bv3_050780_usim.t1	<i>Beta vulgaris</i>	<i>Aldo/keto reductase family putative active site signature</i>
FANhyb_rscf00000207.1.g00009.1	<i>Fragaria ananassa</i>	<i>Aldo/keto reductase family putative active site signature</i>
Zmw_sc01138.1.g00130.1	<i>Zoysia matrella</i>	<i>Aldo/keto reductase family putative active site signature</i>
Zpz_sc00095.1.g00090.1.am.mk	<i>Zoysia pacifica</i>	<i>Aldo/keto reductase family putative active site signature</i>
LOC_Os12g22940	<i>Oryza sativa</i>	<i>Alkaline phosphatase active site</i>
OMERI12G11070.1	<i>Oryza meridionalis</i>	<i>Alkaline phosphatase active site</i>
ORUFI12G10910.1	<i>Oryza rufipogon</i>	<i>Alkaline phosphatase active site</i>
BGIOGA037293.1	<i>Oryza sativa Indica</i>	<i>Alkaline phosphatase active site</i>
LOC_Os12g22940.1	<i>Oryza sativa japonica</i>	<i>Alkaline phosphatase active site</i>
Carubv10012206m	<i>Capsella rubella</i>	<i>Aminoacyl-transfer RNA synthetases class-I signature</i>
Oropetium_20150105_22096	<i>Oropetium thomaeum</i>	<i>Aminotransferases class-II pyridoxal-phosphate attachment site</i>
ObartAA03S_FGP10288	<i>Oryza barthii</i>	<i>Aminotransferases class-II pyridoxal-phosphate attachment site</i>
ORGLA12G0169600.1	<i>Oryza glaberrima</i>	<i>Aminotransferases class-II pyridoxal-phosphate attachment site</i>
OpuncBB_FGP10000	<i>Oryza punctata</i>	<i>Aminotransferases class-II pyridoxal-phosphate attachment site</i>
LOC_Os12g43530	<i>Oryza sativa</i>	<i>Aminotransferases class-II pyridoxal-phosphate attachment site</i>
Oropetium_20150105_22096A	<i>Oropetium thomaeum</i>	<i>Aminotransferases class-II pyridoxal-phosphate attachment site</i>
ORGLA12G0169600.1	<i>Oryza glaberrima</i>	<i>Aminotransferases class-II pyridoxal-phosphate attachment site</i>
OGLUM12G21360.1	<i>Oryza glumaepatula</i>	<i>Aminotransferases class-II pyridoxal-phosphate attachment site</i>
KN539001.1	<i>Oryza longistaminata</i>	<i>Aminotransferases class-II pyridoxal-phosphate attachment site</i>
OMERI12G14510	<i>Oryza meridionalis</i>	<i>Aminotransferases class-II pyridoxal-phosphate attachment site</i>
ONIVA12G18630.1	<i>Oryza nivara</i>	<i>Aminotransferases class-II pyridoxal-phosphate attachment site</i>
OPUNC12G17870.1	<i>Oryza punctata</i>	<i>Aminotransferases class-II pyridoxal-phosphate attachment site</i>
ORUFI12G21970.1	<i>Oryza rufipogon</i>	<i>Aminotransferases class-II pyridoxal-phosphate attachment site</i>
BGIOGA035784.1	<i>Oryza sativa Indica</i>	<i>Aminotransferases class-II pyridoxal-phosphate attachment site</i>
LOC_Os12g43530.1	<i>Oryza sativa japonica</i>	<i>Aminotransferases class-II pyridoxal-phosphate attachment site</i>

XP_009146239.1	<i>Brassica rapa</i>	<i>Antenna complexes beta subunits signature</i>
Zmw_sc05821.1.g00010.1	<i>Zoysia matrella</i>	<i>ArgE / dapE / ACY1 / CPG2 / yscS family signature 1</i>
Zpz_sc00055.1.g00240.1.am.mkhc	<i>Zoysia pacifica</i>	<i>ArgE / dapE / ACY1 / CPG2 / yscS family signature 1</i>
Medtr4g134460.1	<i>Medicago truncatula</i>	<i>Aspartate and glutamate racemases signature 1</i>
XP_010545324.1	<i>Tarenaya hassleriana</i>	<i>Aspartate and glutamate racemases signature 1</i>
XP_010545325.1	<i>Tarenaya hassleriana</i>	<i>Aspartate and glutamate racemases signature 1</i>
Brast02G382000.1.p	<i>Brachypodium stacei</i>	<i>Aspartokinase signature</i>
Brast02G383700.1.p	<i>Brachypodium stacei</i>	<i>Aspartokinase signature</i>
EMT33859	<i>Aegilops tauschii</i>	<i>ATP Binding site and proton acceptor</i>
Gorai.008G130300.1	<i>Gossypium raimondii</i>	<i>ATP synthase alpha and beta subunits signature</i>
PH01000820G0540	<i>Phyllostachys heterocycla</i>	<i>ATP synthase alpha and beta subunits signature</i>
Pta007882	<i>Pinus taeda</i>	<i>ATP synthase alpha and beta subunits signature</i>
ppa020746m	<i>Prunus persica</i>	<i>ATP synthase alpha and beta subunits signature</i>
Solyc08g008660.2.1	<i>Solanum lycopersicum</i>	<i>ATP synthase alpha and beta subunits signature</i>
PGSC0003DMP400010296	<i>Solanum tuberosum</i>	<i>ATP synthase alpha and beta subunits signature</i>
PGSC0003DMP400010297	<i>Solanum tuberosum</i>	<i>ATP synthase alpha and beta subunits signature</i>
CA11g08290	<i>Capsicum annuum</i>	<i>ATP synthase alpha and beta subunits signature</i>
Cotton_A_26426_BGI-A2_v1.0	<i>Gossypium arboreum</i>	<i>ATP synthase alpha and beta subunits signature</i>
XP_010100656.1	<i>Morus notabilis</i>	<i>ATP synthase alpha and beta subunits signature</i>
PH01000820G0540	<i>Phyllostachys heterocycla</i>	<i>ATP synthase alpha and beta subunits signature</i>
XP_008233055.1	<i>Prunus mume</i>	<i>ATP synthase alpha and beta subunits signature</i>
Sme2.5_02517.1_g00007.1	<i>Solanum melongena</i>	<i>ATP synthase alpha and beta subunits signature</i>
Sopen08g004490.1	<i>Solanum pennellii</i>	<i>ATP synthase alpha and beta subunits signature</i>
Zmw_sc04326.1.g00020.1	<i>Zoysia matrella</i>	<i>ATP synthase alpha and beta subunits signature</i>
Ciclev10019282m	<i>Citrus clementina</i>	<i>ATP synthase alpha and beta subunits signature</i>
Gh_A12G1049	<i>Gossypium hirsutum</i>	<i>ATP synthase alpha and beta subunits signature</i>
Sopim08g008660.0.1	<i>Solanum pimpinellifolium</i>	<i>ATP synthase alpha and beta subunits signature</i>
Pbr032225.1	<i>Pyrus bretschneideri</i>	<i>ATP-dependent DNA ligase AMP-binding site</i>

Pbr032225.1	<i>Pyrus bretschneideri</i>	<i>ATP-dependent DNA ligase AMP-binding site</i>
Spipo1G0084400	<i>Spirodela polyrhiza</i>	<i>Bacterial regulatory proteins, araC family signature</i>
MLOC_19933.1	<i>Hordeum vulgare</i>	<i>Beta-ketoacyl synthases active site</i>
MLOC_19933.1	<i>Hordeum vulgare</i>	<i>Beta-ketoacyl synthases active site</i>
Thecc1EG018508t	<i>Theobroma cacao</i>	<i>C-5 cytosine-specific DNA methylases active site</i>
Aqcoe1G058100.1.p	<i>Aquilegiacoerulea</i>	<i>Cadherin domain signature</i>
KFK30695.1	<i>Arabis alpina</i>	<i>Carbamoyl-phosphate synthase subdomain signature 2</i>
ObartAA03S_FGP25558	<i>Oryza barthii</i>	<i>Cysteine proteases inhibitors signature</i>
ORGLA06G0236900.1	<i>Oryza glaberrima</i>	<i>Cysteine proteases inhibitors signature</i>
OpuncBB_FGP25111	<i>Oryza punctata</i>	<i>Cysteine proteases inhibitors signature</i>
LOC_Os06g51070	<i>Oryza sativa</i>	<i>Cysteine proteases inhibitors signature</i>
462845378	<i>Eragrostis tef</i>	<i>Cysteine proteases inhibitors signature</i>
ORGLA06G0236900.1	<i>Oryza glaberrima</i>	<i>Cysteine proteases inhibitors signature</i>
OGLUM06G29360.1	<i>Oryza glumaepatula</i>	<i>Cysteine proteases inhibitors signature</i>
OMERI06G27920.1	<i>Oryza meridionalis</i>	<i>Cysteine proteases inhibitors signature</i>
ONIVA06G30950.1	<i>Oryza nivara</i>	<i>Cysteine proteases inhibitors signature</i>
OPUNC06G25510.1	<i>Oryza punctata</i>	<i>Cysteine proteases inhibitors signature</i>
ORUFI06G29930.1	<i>Oryza rufipogon</i>	<i>Cysteine proteases inhibitors signature</i>
BGIOSGA020507.1	<i>Oryza sativa Indica</i>	<i>Cysteine proteases inhibitors signature</i>
LOC_Os06g51070.1	<i>Oryza sativa japonica</i>	<i>Cysteine proteases inhibitors signature</i>
Pavir.4NG342400.1.p	<i>Panicum virgatum</i>	<i>Cysteine proteases inhibitors signature</i>
Pavir.7KG085500.1.p	<i>Panicum virgatum</i>	<i>Cysteine proteases inhibitors signature</i>
Zmw_sc02823.1.g00180.1	<i>Zoysia matrella</i>	<i>Cysteine proteases inhibitors signature</i>
Zpz_sc01253.1.g00030.1.sm.mk	<i>Zoysia pacifica</i>	<i>Cysteine proteases inhibitors signature</i>
Zjn_sc00068.1.g03510.1.sm.mk	<i>Zoysia japonica</i>	<i>Cysteine proteases inhibitors signature</i>
OGLUM01G06950.1	<i>Oryza glumaepatula</i>	<i>Cytochrome P450 cysteine heme-iron ligand signature</i>
KN539290.1	<i>Oryza longistaminata</i>	<i>Cytochrome P450 cysteine heme-iron ligand signature</i>
KN539290.1	<i>Oryza longistaminata</i>	<i>Cytochrome P450 cysteine heme-iron ligand signature</i>

OMERI07G10400	<i>Oryza meridionalis</i>	<i>Cytochrome P450 cysteine heme-iron ligand signature</i>
Zmw_sc00276.1.g00230.1	<i>Zoysia matrella</i>	<i>Cytochrome P450 cysteine heme-iron ligand signature</i>
Zmw_sc02343.1.g00060.1	<i>Zoysia matrella</i>	<i>Cytochrome P450 cysteine heme-iron ligand signature</i>
Zpz_sc03671.1.g00030.1.am.mk	<i>Zoysia pacifica</i>	<i>Cytochrome P450 cysteine heme-iron ligand signature</i>
Sobic.003G105800.1.p	<i>Sorghum bicolor</i>	<i>Endopeptidase Clp serine active site</i>
GRMZM2G123246_P01	<i>Vzea mays</i>	<i>Endopeptidase Clp serine active site</i>
EMT14807	<i>Aegilops tauschii</i>	<i>Eukaryotic and viral aspartyl proteases active site</i>
Tae025010	<i>Triticum aestivum</i>	<i>Eukaryotic and viral aspartyl proteases active site</i>
Tae030617	<i>Triticum aestivum</i>	<i>Eukaryotic and viral aspartyl proteases active site</i>
Tae045052	<i>Triticum aestivum</i>	<i>Eukaryotic and viral aspartyl proteases active site</i>
EMS63374	<i>Triticum urartu</i>	<i>Eukaryotic and viral aspartyl proteases active site</i>
Itr_sc004419.1.g00003.1	<i>Ipomea trifida</i>	<i>Eukaryotic and viral aspartyl proteases active site</i>
Traes_7DL_BDD45DB24.2	<i>Triticum aestivum</i>	<i>Eukaryotic and viral aspartyl proteases active site</i>
Zjn_sc00092.1.g00060.1.am.mk	<i>Zoysia japonica</i>	<i>Eukaryotic and viral aspartyl proteases active site</i>
Zmw_sc03455.1.g00010.1	<i>Zoysia matrella</i>	<i>Eukaryotic and viral aspartyl proteases active site</i>
Zpz_sc03692.1.g00060.1.sm.mk	<i>Zoysia pacifica</i>	<i>Eukaryotic and viral aspartyl proteases active site</i>
Niben101Scf07508g02004.1	<i>Nicotiana benthamiana</i>	<i>FGGY family of carbohydrate kinases signature 2</i>
MA_18939g0010	<i>Picea abies</i>	<i>Fumarate lyases signature</i>
Rsa1.0_01603.1.g00007.1	<i>Raphanus sativus</i>	<i>Fumarate lyases signature</i>
GSMUA_Achr10P10790_001	<i>Musa acuminata</i>	<i>GHMP kinases putative ATP-binding domain</i>
Peinf101Scf00337g03028.1	<i>Petunia inflata</i>	<i>Glucoamylase active site region signature</i>
Cucsa.083540.1	<i>Cucumis sativus</i>	<i>Glyceraldehyde 3-phosphate dehydrogenase active</i>
ONIVA05G06750.1	<i>Oryza nivara</i>	<i>Glycoprotease family signature</i>
Cc08_g16900	<i>Coffea canephora</i>	<i>Glycosyl hydrolases family 5 signature</i>
30147.m014211	<i>Ricinus communis</i>	<i>Glycosyl hydrolases family 9 active sites signature 2</i>
Kalax-0686s0005.1.p	<i>Kalanchoe marnieriana</i>	<i>Hemopexin domain signature</i>
Kalax-0609s0006.1.p	<i>Kalanchoe marnieriana</i>	<i>Hemopexin domain signature</i>
Scf00060.g6196.t1	<i>Utricularia gibba</i>	<i>Histone H4 signature</i>

XP_016648489.1	<i>Prunus mume</i>	<i>Histone H4 signature</i>
Prupe.4G138500.1.p	<i>Prunus persica</i>	<i>Histone H4 signature</i>
Zmw_sc06792.1.g00040.1	<i>Zoysia matrella</i>	<i>Histone H4 signature</i>
ObartAA03S_FGP17273	<i>Oryza barthii</i>	<i>HMG-I and HMG-Y DNA-binding domain (A+T-hook)</i>
LOC_Os03g59730	<i>Oryza sativa</i>	<i>HMG-I and HMG-Y DNA-binding domain (A+T-hook)</i>
Bradi1g04229.1.p	<i>Brachypodium distachyon</i>	<i>HMG-I and HMG-Y DNA-binding domain (A+T-hook)</i>
Brast02G355100.1.p	<i>Brachypodium stacei</i>	<i>HMG-I and HMG-Y DNA-binding domain (A+T-hook)</i>
OGLUM03G38320.1	<i>Oryza glumaepatula</i>	<i>HMG-I and HMG-Y DNA-binding domain (A+T-hook)</i>
OMERI03G35410.1	<i>Oryza meridionalis</i>	<i>HMG-I and HMG-Y DNA-binding domain (A+T-hook)</i>
ORUFI03G40160.1	<i>Oryza rufipogon</i>	<i>HMG-I and HMG-Y DNA-binding domain (A+T-hook)</i>
BGIOGA009581.1	<i>Oryza sativa Indica</i>	<i>HMG-I and HMG-Y DNA-binding domain (A+T-hook)</i>
LOC_Os03g59730.1	<i>Oryza sativa japonica</i>	<i>HMG-I and HMG-Y DNA-binding domain (A+T-hook)</i>
Pbr020079.1	<i>Pyrus bretschneideri</i>	<i>Immunoglobulins and major histocompatibility complex proteins signature</i>
EcC046909.20	<i>Eucalyptus camaldulensis</i>	<i>Immunoglobulins and major histocompatibility complex proteins signature</i>
EcS504758.10	<i>Eucalyptus camaldulensis</i>	<i>Immunoglobulins and major histocompatibility complex proteins signature</i>
Pbr020079.1	<i>Pyrus bretschneideri</i>	<i>Immunoglobulins and major histocompatibility complex proteins signature</i>
ORGLA01G0211000.1	<i>Oryza glaberrima</i>	<i>Inorganic pyrophosphatase signature</i>
Pbr026815.1	<i>Pyrus bretschneideri</i>	<i>Inorganic pyrophosphatase signature</i>
Thhalv10009374m	<i>Thellungiella halophila</i>	<i>Inorganic pyrophosphatase signature</i>
XP_010108843.1	<i>Morus notabilis</i>	<i>Inorganic pyrophosphatase signature</i>
ORGLA01G0211000.1	<i>Oryza glaberrima</i>	<i>Inorganic pyrophosphatase signature</i>
OGLUM01G29620.1	<i>Oryza glumaepatula</i>	<i>Inorganic pyrophosphatase signature</i>
OMERI01G23440.1	<i>Oryza meridionalis</i>	<i>Inorganic pyrophosphatase signature</i>
ONIVA01G29020.1	<i>Oryza nivara</i>	<i>Inorganic pyrophosphatase signature</i>
ORUFI01G28690.1	<i>Oryza rufipogon</i>	<i>Inorganic pyrophosphatase signature</i>

LOC_Os01g47670.1	<i>Oryza sativa japonica</i>	<i>Inorganic pyrophosphatase signature</i>
Pbr026815.1	<i>Pyrus bretschneideri</i>	<i>Inorganic pyrophosphatase signature</i>
GSVIVT01026495001	<i>Vitis vinifera</i>	<i>Iron-containing alcohol dehydrogenases signature 1</i>
OB07G24770.1	<i>Oryza brachyantha</i>	<i>Legume lectins beta-chain signature</i>
ORGLA03G0364100.1	<i>Oryza glaberrima</i>	<i>Legume lectins beta-chain signature</i>
OGLUM03G39450.1	<i>Oryza glumaepatula</i>	<i>Legume lectins beta-chain signature</i>
OGLUM03G39510.1	<i>Oryza glumaepatula</i>	<i>Legume lectins beta-chain signature</i>
KN538833.1	<i>Oryza longistaminata</i>	<i>Legume lectins beta-chain signature</i>
OMERI03G36390.1	<i>Oryza meridionalis</i>	<i>Legume lectins beta-chain signature</i>
OMERI03G36430.1	<i>Oryza meridionalis</i>	<i>Legume lectins beta-chain signature</i>
ONIVA03G41430.1	<i>Oryza nivara</i>	<i>Legume lectins beta-chain signature</i>
ONIVA03G41480.1	<i>Oryza nivara</i>	<i>Legume lectins beta-chain signature</i>
OPUNC03G36710.1	<i>Oryza punctata</i>	<i>Legume lectins beta-chain signature</i>
OPUNC03G36760.1	<i>Oryza punctata</i>	<i>Legume lectins beta-chain signature</i>
BGIOGA013858.1	<i>Oryza sativa Indica</i>	<i>Legume lectins beta-chain signature</i>
BGIOGA013866.1	<i>Oryza sativa Indica</i>	<i>Legume lectins beta-chain signature</i>
LOC_Os03g61249.1	<i>Oryza sativa japonica</i>	<i>Legume lectins beta-chain signature</i>
LOC_Os03g61319.1	<i>Oryza sativa japonica</i>	<i>Legume lectins beta-chain signature</i>
Nta011914	<i>Nicotiana tabacum</i>	<i>Lipocalin signature</i>
Niben101Ctg05879g00002.1	<i>Nicotiana benthamiana</i>	<i>Lipocalin signature</i>
Niben101Scf01337g00001.1	<i>Nicotiana benthamiana</i>	<i>Lipocalin signature</i>
Niben101Scf08665g00007.1	<i>Nicotiana benthamiana</i>	<i>Lipocalin signature</i>
Niben101Scf13438g00001.1	<i>Nicotiana benthamiana</i>	<i>Lipocalin signature</i>
Niben101Scf15279g00002.1	<i>Nicotiana benthamiana</i>	<i>Lipocalin signature</i>
XP_009762991.1	<i>Nicotiana sylvestris</i>	<i>Lipocalin signature</i>
XP_009763090.1	<i>Nicotiana sylvestris</i>	<i>Lipocalin signature</i>
XP_009782335.1	<i>Nicotiana sylvestris</i>	<i>Lipocalin signature</i>
XP_009792222.1	<i>Nicotiana sylvestris</i>	<i>Lipocalin signature</i>

XP_009794230.1	<i>Nicotiana glauca</i>	<i>Lipocalin signature</i>
XP_016449500.1	<i>Nicotiana tabacum</i>	<i>Lipocalin signature</i>
XP_016469037.1	<i>Nicotiana tabacum</i>	<i>Lipocalin signature</i>
XP_016474545.1	<i>Nicotiana tabacum</i>	<i>Lipocalin signature</i>
XP_016477162.1	<i>Nicotiana tabacum</i>	<i>Lipocalin signature</i>
XP_016490755.1	<i>Nicotiana tabacum</i>	<i>Lipocalin signature</i>
XP_016504577.1	<i>Nicotiana tabacum</i>	<i>Lipocalin signature</i>
XP_016510726.1	<i>Nicotiana tabacum</i>	<i>Lipocalin signature</i>
XP_009598748.1	<i>Nicotiana tomentosiformis</i>	<i>Lipocalin signature</i>
XP_009601217.1	<i>Nicotiana tomentosiformis</i>	<i>Lipocalin signature</i>
XP_009602879.1	<i>Nicotiana tomentosiformis</i>	<i>Lipocalin signature</i>
XP_009628837.1	<i>Nicotiana tomentosiformis</i>	<i>Lipocalin signature</i>
KFK42489.1	<i>Arabis alpina</i>	<i>Mannitol dehydrogenases signature</i>
OB09G21580.1	<i>Oryza brachyanta</i>	<i>N-6 Adenine-specific DNA methylases signature</i>
Sobic.003G110900.1.p	<i>Sorghum bicolor</i>	<i>N-6 Adenine-specific DNA methylases signature</i>
Zosma53g00110	<i>Zostera marina</i>	<i>N-6 Adenine-specific DNA methylases signature</i>
Aqcoe2G375500.1.p	<i>Aquilegiacoerulea</i>	<i>N-6 Adenine-specific DNA methylases signature</i>
scaffold07459-snap-gene-0.9	<i>Castanea mollissima</i>	<i>N-6 Adenine-specific DNA methylases signature</i>
OB04G27030.1	<i>Oryza brachyantha</i>	<i>N-6 Adenine-specific DNA methylases signature</i>
OB09G21580.1	<i>Oryza brachyantha</i>	<i>N-6 Adenine-specific DNA methylases signature</i>
Csa16g023250.1	<i>Camelina sativa</i>	<i>Neutral zinc metalloproteinases, zinc-binding region signature</i>
Ote100091280041	<i>Ocimum tenuiflorum</i>	<i>Neutral zinc metalloproteinases, zinc-binding region signature</i>
Neem_8133_f_4	<i>Azadirachta indica</i>	<i>Nt-dnaJ domain signature</i>
FANhyb_rscf00000018.1.g00013.1	<i>Fragaria ananassa</i>	<i>Nt-dnaJ domain signature</i>
EPS67213.1	<i>Genlisea aurea</i>	<i>Peroxidases active site signature</i>
Ciclev10008619m	<i>Citrus clementina</i>	<i>pfkB family of carbohydrate kinases signature 1</i>
Pavir.J21162	<i>Panicum virgatum</i>	<i>pfkB family of carbohydrate kinases signature 2</i>
Thhalv10006408m	<i>Thellungiella halophila</i>	<i>pfkB family of carbohydrate kinases signature 2</i>

Thhalv10006408m	<i>Eutrema salsugineum</i>	<i>pfkB</i> family of carbohydrate kinases signature 2
Zpz_sc00266.1.g00320.1.am.mk	<i>Zoysia pacifica</i>	Phospholipase A2 histidine active site
GSMUA_Achr11P08970_001	<i>Musa acuminata</i>	Phosphopantetheine attachment site
ObartAA03S_FGP27339	<i>Oryza barthii</i>	Phosphopantetheine attachment site
ORGLA07G0243600.1	<i>Oryza glaberrima</i>	Phosphopantetheine attachment site
OpuncBB_FGP26901	<i>Oryza punctata</i>	Phosphopantetheine attachment site
LOC_Os07g37920	<i>Oryza sativa</i>	Phosphopantetheine attachment site
Sobic.002G342100.1.p	<i>Sorghum bicolor</i>	Phosphopantetheine attachment site
Sobic.002G342100.1.p	<i>Sorghum bicolor</i>	Phosphopantetheine attachment site
GRMZM2G179885_P01	<i>Zea mays</i>	Phosphopantetheine attachment site
scaffold07067-augustus-gene-0.6	<i>Castanea mollissima</i>	Phosphopantetheine attachment site
Glyma-13G174700.1.p	<i>Glycine max</i>	Phosphopantetheine attachment site
KHN09961.1	<i>Glycine soja</i>	Phosphopantetheine attachment site
LPERR07G16320.1	<i>Leersia perrieri</i>	Phosphopantetheine attachment site
ORGLA07G0243600.1	<i>Oryza glaberrima</i>	Phosphopantetheine attachment site
OGLUM07G18780.1	<i>Oryza glumaepatula</i>	Phosphopantetheine attachment site
KN538693.1	<i>Oryza longistaminata</i>	Phosphopantetheine attachment site
OMERI07G15720.1	<i>Oryza meridionalis</i>	Phosphopantetheine attachment site
ONIVA07G17340.1	<i>Oryza nivara</i>	Phosphopantetheine attachment site
OPUNC07G17890.1	<i>Oryza punctata</i>	Phosphopantetheine attachment site
ORUFI07G19770.1	<i>Oryza rufipogon</i>	Phosphopantetheine attachment site
BGIOSGA024071.1	<i>Oryza sativa Indica</i>	Phosphopantetheine attachment site
LOC_Os07g37920.1	<i>Oryza sativa japonica</i>	Phosphopantetheine attachment site
KFK41460.1	<i>Arabis alpina</i>	Polygalacturonase active site
Rsa1.0_00061.1_g00015.1	<i>Raphanus sativus</i>	Polygalacturonase active site
Sobic.005G041000.1.p	<i>Sorghum bicolor</i>	Polyprenyl synthases signature 1
.XP_010536267.1	<i>Tarenaya hassleriana</i>	PPM-type phosphatase domain signature
Solyc04g079940.2.1	<i>Solanum lycopersicum</i>	Prokaryotic membrane lipoprotein lipid attachment site profile

Scf00187.g11893.t1	<i>Utricularia gibba</i>	<i>Prokaryotic membrane lipoprotein lipid attachment site profile</i>
Niben101Scf01153g00009.1	<i>Nicotiana benthamiana</i>	<i>Prokaryotic membrane lipoprotein lipid attachment site profile</i>
Niben101Scf01153g00009.1	<i>Nicotiana benthamiana</i>	<i>Prokaryotic membrane lipoprotein lipid attachment site profile</i>
XP_009789698.1	<i>Nicotiana glauca</i>	<i>Prokaryotic membrane lipoprotein lipid attachment site profile</i>
XP_009789699.1	<i>Nicotiana glauca</i>	<i>Prokaryotic membrane lipoprotein lipid attachment site profile</i>
XP_016453035.1	<i>Nicotiana glauca</i>	<i>Prokaryotic membrane lipoprotein lipid attachment site profile</i>
XP_016471015.1	<i>Nicotiana glauca</i>	<i>Prokaryotic membrane lipoprotein lipid attachment site profile</i>
XP_016487616.1	<i>Nicotiana glauca</i>	<i>Prokaryotic membrane lipoprotein lipid attachment site profile</i>
XP_016487617.1	<i>Nicotiana glauca</i>	<i>Prokaryotic membrane lipoprotein lipid attachment site profile</i>
XP_009603640.1	<i>Nicotiana glauca</i>	<i>Prokaryotic membrane lipoprotein lipid attachment site profile</i>
Sopim04g079940.0.1	<i>Solanum pimpinellifolium</i>	<i>Prokaryotic membrane lipoprotein lipid attachment site profile</i>
Glyma-13G243200.1.p	<i>Glycine max</i>	<i>Putative AMP-binding domain signature</i>
Si039061m	<i>Setaria italica</i>	<i>Regulator of chromosome condensation (RCC1) signature 2</i>
Seita.9G169600.1.p	<i>Setaria italica</i>	<i>Regulator of chromosome condensation (RCC1) signature 2</i>
GRMZM2G156977_P01	<i>Zea mays</i>	<i>Ribosomal protein L24e signature</i>
Cotton_A_00183_BGI-A2_v1.0	<i>Gossypium arboreum</i>	<i>Ribosomal protein L31 signature</i>
Gh_A01G0250	<i>Gossypium hirsutum</i>	<i>Ribosomal protein L31 signature</i>
KN539025.1	<i>Oryza longistaminata</i>	<i>Ribosomal protein L36 signature</i>
RrC831_p3	<i>Raphanus raphanistrum</i>	<i>Ribosomal protein S10 signature</i>
Cotton_A_09649_BGI-A2_v1.0	<i>Gossypium arboreum</i>	<i>Ribosomal protein S19e signature</i>
Zjn_sc00034.1.g02530.1.am.mk	<i>Zoysia japonica</i>	<i>Ribosomal protein S8 signature</i>
Spipo0G0093000	<i>Spirodela polyrhiza</i>	<i>Ribosome-binding factor A signature</i>
PH01000491G0390	<i>Phyllostachys heterocycla</i>	<i>Rubredoxin signature</i>
PH01000491G0390	<i>Phyllostachys heterocycla</i>	<i>Rubredoxin signature</i>
Bradi3g12470.1	<i>Brachypodium distachyon</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>
Pahal.F00337	<i>Panicum hallii</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>
Pavir.Fa00048	<i>Panicum virgatum</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>
Si013361m	<i>Setaria italica</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>

Si013378m	<i>Setaria italica</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>
Si013524m	<i>Setaria italica</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>
Sevir.6G256500	<i>Setaria viridis</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>
GRMZM2G125777_P01	<i>Zea mays</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>
Bradi3g12470.1.p	<i>Brachypodium distachyon</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>
Brast03G309200.1.p	<i>Brachypodium stacei</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>
Do003945.1	<i>Dichantheium oligosanthes</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>
Itr_sc000194.1_g00003.1	<i>Ipomea trifida</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>
Pahal.F00337.1	<i>Panicum hallii</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>
Pavir.6KG413300.1.p	<i>Panicum virgatum</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>
Pavir.6NG362800.1.p	<i>Panicum virgatum</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>
Seita.6G251900.1.p	<i>Setaria italica</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>
Sme2.5_05012.1_g00010.1	<i>Solanum melongena</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>
XP_010543143.1	<i>Tarenaya hassleriana</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>
XP_010543151.1	<i>Tarenaya hassleriana</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>
XP_010543159.1	<i>Tarenaya hassleriana</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>
Traes_5BL_3BA7EA9A3	<i>Triticum aestivum</i>	<i>Serine proteases, subtilase family, aspartic acid active site</i>
cassava4-1_025821m	<i>Manihot esculenta</i>	<i>Serine proteases, trypsin family, serine active site</i>
KZV46422.1	<i>Dorcoceras hygrometricum</i>	<i>Serine/Threonine protein kinases active-site signature</i>
Gh_D11G0701	<i>Gossypium hirsutum</i>	<i>Serine/Threonine protein kinases active-site signature</i>
XP_010551540.1	<i>Tarenaya hassleriana</i>	<i>Serine/threonine specific protein phosphatases signature</i>
OMERI04G25580.2	<i>Oryza meridionalis</i>	<i>Sigma-54 interaction domain ATP-binding region A signature</i>
RrC3821_p1	<i>Raphanus raphanistrum</i>	<i>Sigma-54 interaction domain ATP-binding region A signature</i>
AUR62000898	<i>Chenopodium quinoa</i>	<i>Signal peptidases I serine active site</i>
Cucsa.284890.1	<i>Cucumis sativus</i>	<i>Signal peptidases I serine active site</i>
scaffold02306-augustus-gene-0.21	<i>Castanea mollissima</i>	<i>Signal peptidases I serine active site</i>
OB07G32110.1	<i>Oryza brachyanta</i>	<i>Signal peptidases I signature 3</i>
GSBRNA2T00106219001	<i>Brassica napus</i>	<i>Signal peptidases I signature 3</i>

OB07G32110.1	<i>Oryza brachyantha</i>	<i>Signal peptidases I signature 3</i>
XP_013583708.1	<i>Brassica oleracea</i>	<i>Signal peptidases I signature 3</i>
Tp57577_TGAC_v2_mRNA33521	<i>Trifolium pratense</i>	<i>Soybean trypsin inhibitor (Kunitz) protease inhibitors family signature</i>
Aqcoe3G142100.1.p	<i>Aquilegiacoerulea</i>	<i>SRP54-type proteins GTP-binding domain signature</i>
EcC047434.20	<i>Eucalyptus camaldulensis</i>	<i>Sugar transport proteins signature 2</i>
Eucgr-I01940.1.p	<i>Eucalyptus grandis</i>	<i>Sugar transport proteins signature 2</i>
KHN21163.1	<i>Glycine soja</i>	<i>Synaptobrevin signature</i>
TRAES3BF073600100CFD_t1	<i>Triticum aestivum</i>	<i>Syntaxin / epimorphin family signature</i>
PH01002656G0020	<i>Phyllostachys heterocycla</i>	<i>TonB-dependent receptor proteins signature 1</i>
AA11G00017	<i>Aethionema arabicum</i>	<i>TonB-dependent receptor proteins signature 1</i>
AA32G01100	<i>Aethionema arabicum</i>	<i>TonB-dependent receptor proteins signature 1</i>
PH01002656G0020	<i>Phyllostachys heterocycla</i>	<i>TonB-dependent receptor proteins signature 1</i>
XP_010520901.1	<i>Tarenaya hassleriana</i>	<i>TonB-dependent receptor proteins signature 1</i>
XP_010539252.1	<i>Tarenaya hassleriana</i>	<i>TonB-dependent receptor proteins signature 1</i>
C.cajan_41044	<i>Cajanus cajan</i>	<i>TonB-dependent receptor proteins signature 1</i>
Zosma1g02650	<i>Zostera marina</i>	<i>Translationally controlled tumor protein (TCTP) domain signature 2</i>
Spipo0G0093000	<i>Spirodela polyrhiza</i>	<i>Trp-Asp (WD) repeats signature</i>
Tp4g25130	<i>Thellungiella parvula</i>	<i>Trp-Asp (WD) repeats signature</i>
483400	<i>Arabidopsis lyrata</i>	<i>Trp-Asp (WD) repeats signature</i>
Bostr.25993s0479.1.p	<i>Boechera stricta</i>	<i>Trp-Asp (WD) repeats signature</i>
GSBRNA2T00045062001	<i>Brassica napus</i>	<i>Trp-Asp (WD) repeats signature</i>
GSBRNA2T00084755001	<i>Brassica napus</i>	<i>Trp-Asp (WD) repeats signature</i>
XP_013634618.1	<i>Brassica oleracea</i>	<i>Trp-Asp (WD) repeats signature</i>
XP_013634619.1	<i>Brassica oleracea</i>	<i>Trp-Asp (WD) repeats signature</i>
.XP_013634620.1	<i>Brassica oleracea</i>	<i>Trp-Asp (WD) repeats signature</i>
XP_009142151.1	<i>Brassica rapa</i>	<i>Trp-Asp (WD) repeats signature</i>
XP_008221120.1	<i>Prunus mume</i>	<i>Trp-Asp (WD) repeats signature</i>
KFK37142.1	<i>Arabis alpina</i>	<i>Trp-Asp (WD) repeats signature</i>

Kalax-0139s0008.1.p	<i>Kalanchoe marnieriana</i>	<i>Tubulin subunits alpha, beta, and gamma signature</i>
Kalax-0355s0005.1.p	<i>Kalanchoe marnieriana</i>	<i>Tubulin subunits alpha, beta, and gamma signature</i>
XP_016502907.1	<i>Nicotiana tabacum</i>	<i>Tubulin-beta mRNA autoregulation signal</i>
Zmw_sc03169.1.g00010.1	<i>Zoysia matrella</i>	<i>Tubulin-beta mRNA autoregulation signal</i>
GSMUA_Achr7P09510_001	<i>Musa acuminata</i>	<i>Zinc carboxypeptidases, zinc-binding region 2 signature</i>
Pavir.Ab01115	<i>Panicum virgatum</i>	<i>Zinc carboxypeptidases, zinc-binding region 2 signature</i>
Pavir.J12496	<i>Panicum virgatum</i>	<i>Zinc carboxypeptidases, zinc-binding region 2 signature</i>
PDK_30s745071g005	<i>Phoenix dactylifera</i>	<i>Zinc carboxypeptidases, zinc-binding region 2 signature</i>
MLOC_75795.1	<i>Hordeum vulgare</i>	<i>Zinc carboxypeptidases, zinc-binding region 2 signature</i>
Pavir-1KG158700.1.p	<i>Panicum virgatum</i>	<i>Zinc carboxypeptidases, zinc-binding region 2 signature</i>
Pavir-1KG168100.1.p	<i>Panicum virgatum</i>	<i>Zinc carboxypeptidases, zinc-binding region 2 signature</i>
PDK_30s745071g005	<i>Phoenix dactylifera</i>	<i>Zinc carboxypeptidases, zinc-binding region 2 signature</i>
Traes_3AS_74E386CE7.1	<i>Triticum aestivum</i>	<i>Zinc carboxypeptidases, zinc-binding region 2 signature</i>
TRAES3BF096900070CFD_t1	<i>Triticum aestivum</i>	<i>Zinc carboxypeptidases, zinc-binding region 2 signature</i>
Do016529.1	<i>Dichanthelium oligosanthes</i>	<i>Zinc finger BED-type profile</i>
Araip.9MG9F	<i>Arachis ipaensis</i>	<i>Zinc finger C2H2 type domain signature</i>
PDK_30s663981g010	<i>Phoenix dactylifera</i>	<i>Zinc-containing alcohol dehydrogenases signature</i>
PDK_30s663981g010	<i>Phoenix dactylifera</i>	<i>Zinc-containing alcohol dehydrogenases signature</i>
Araha.61839s0001.1.p	<i>Arabidopsis halleri</i>	
OB11G21460.1	<i>Oryza brachyantha</i>	
