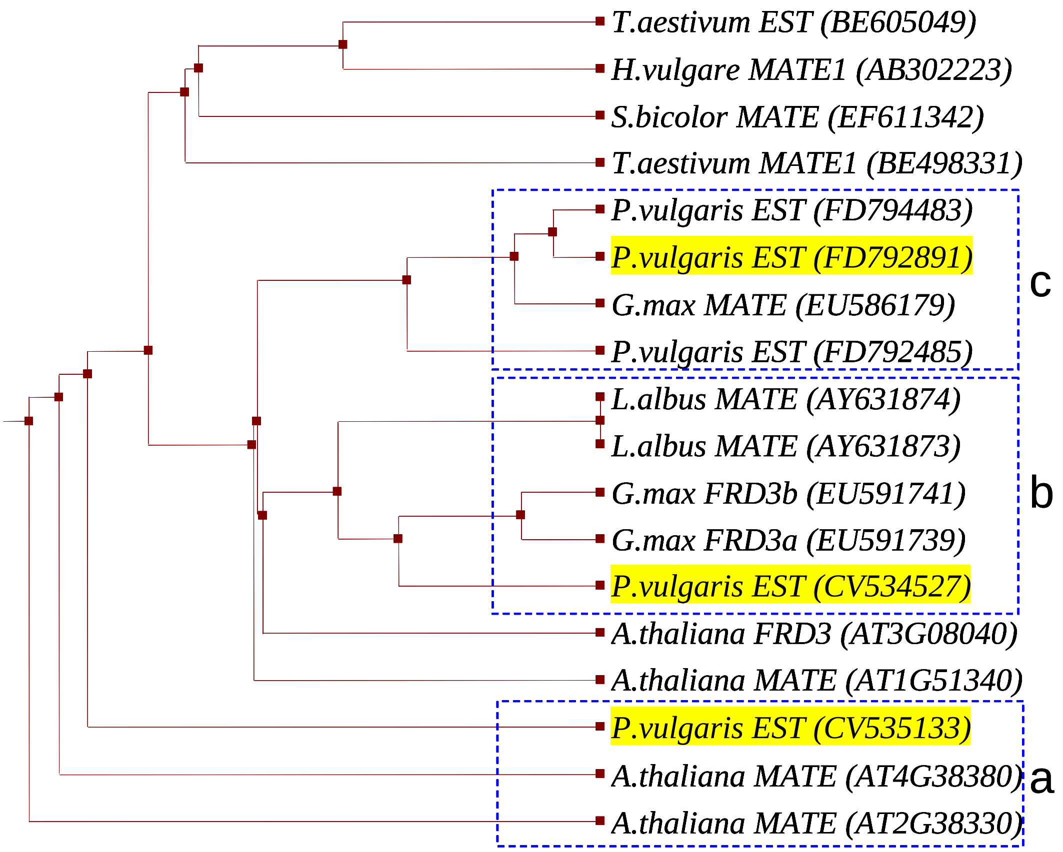
SUPPLEMENTARY DATA

FIG. S1. Sequence alignment tree of *MATE* genes along with *Phaseolus vulgaris* ESTs having high similarity to the known *MATE* genes. The alignment was done using the online MAFFT software (Katoh *et al.* 2009. *Methods in Molecular Biology* **537**: 39–64).



SUPPLEMENTARY DATA

TABLE S1. Up-regulated genes induced by 4 h of Al treatment in the Al-resistant common bean genotype ‘Quimbaya’. The SSH method was used to identify differentially expressed genes. Sequences that did not have significant similarity in the NCBI database (no hits) are excluded from this list.

Clone ID.	**GeneBank Acc. #**	**Gene product**	**Sequence identity**	**E_value**	**GO: Biological Process / putative function**
Primary metabolism					
0_21	NM_106704.3	3-isopropylmalate dehydrogenase	79%	6.E-120	leucine biosynthetic process, metabolic process
0_77	AY063233.1	succinoaminoimidazolecarboximide ribonucleotide synthetase (pur7)	97%	1.E-179	purine nucleotides biosynthesis
0_156	M64246.1	adenosine triphosphatase (atpa)	99%	0.E+00	ATP synthesis coupled proton transport
Stress response/ Plant defence					
0_175	DQ118114.1	trehalose-6-phosphate phosphatase	85%	3.E-123	trehalose biosynthetic process, desiccation tolerance
0_178	DQ340249.1	cytochrome P450 monooxygenase (CYP51G1)	92%	0.E+00	plant defense
0_23	U54703.1	dehydrin	99%	0.E+00	response drought/osmotic stress
0_27	AF149279.2	peroxidase 4 precursor (FBP4)	99%	0.E+00	H_2O_2 catabolic process, response to oxidative stress
0_164	AF149277.1	peroxidase 1 precursor (FBP1)	79%	1.E-104	H_2O_2 catabolic process, response to oxidative stress
0_181	X06411.1	chalcone synthase	94%	6.E-70	flavonoid biosynthesis, response to oxidative stress, wounding
0_79	M99431.1	heat shock protein 83 (Hsp83)	82%	1.E-154	stress response, protein folding (stabilize proteins)
0_84	BI497821.1	heat shock protein DnaJ	75%	6.E-48	stress response, protein folding (stabilize proteins)
0_16	AF192758.1	indole-3-acetic acid induced protein ARG-2 homolog	85%	8.E-43	response to stress
0_148	AB073552.1	t-complex polypeptide 1	80%	7.E-88	protein folding, chaperonin for tubulin and actin
0_182	AB002667.1	1-aminocyclopropane-1-carboxylic acid oxidase (ACC-oxidase)	92%	0.E+00	ethylene biosynthesis, stress response
Signal transduction					
0_38	NM_115950.3	guanine nucleotide exchange family protein	71%	4.E-91	regulation of ARF protein signal transduction
0_137	AJ299064.1	GTP-binding protein	88%	0.E+00	signal transduction, intracellular protein transport
0_64	U64917.1	farnesylated protein GMFP7	70%	1.E-15	signal transduction, metal ion transport
0_71	DQ531849.1	ADP-ribosylation factor 1 (ARF1)	86%	8.E-157	small GTPase mediated signal transduction
0_28	EU019557.1	WRKY9	85%	7.E-132	transcription regulation, DNA-dependent
0_183	EU418733.1	STOP1 (C2-H2 zinc finger protein)	84%	0.E+00	transcription regulation, response to acidity, response to Al^{3+} ion
Transcription factor					
0_180	AY091454.1	methionyl-tRNA synthetase	74%	1.E-49	methionyl-tRNA aminoacylation, response to cadmium ion,
0_57	NM_104171.2	brix domain-containing protein	77%	2.E-163	ribosome biogenesis and rRNA binding
0_7	NM_111591.3	60S ribosomal protein L13A (RPL13aA)	78%	2.E-100	translation

Clone ID.	**GeneBank Acc. #**	**Gene product**	**Sequence identity**	**E_value**	**GO: Biological Process / putative function**
0_17	AY935814.1	26S ribosomal RNA	98%	4.E-148	translation
0_20	X17535.1	ribosomal RNA (5.8S, 18S & 25S)	96%	8.E-163	translation
0_22	AF074398.1	ribosomal RNA gene (5.8S, ITS1 & ITS2)	99%	0.E+00	translation
0_25	DQ826356.1	ribosomal protein S8	81%	2.E-76	translation
0_36	M31024.1	ribosomal protein S11	90%	2.E-88	translation
0_47	NM_115247.3	40S ribosomal protein S3	82%	1.E-135	translation
0_56	AF115165.1	ribosomal RNA (small subunit, 5.8S)	100%	0.E+00	translation
0_155	X17535.1	ribosomal RNA gene (5.8S, 18S, 25S & ITS)	96%	8.E-163	translation
0_179	DQ008820.1	ribosomal RNA (large subunit, mitochondrial)	98%	0.E+00	translation
Transport					
0_153	DQ072165.1	mitochrondrial voltage-dependent anion-selective channel	97%	1.E-154	anion transport
0_163	U36430.1	dynamin-like protein SDL5A	87%	2.E-30	vesicle trafficking, endocytosis, cell cycle, cytokinesis
0_9	U97023.1	putative aquaporin-1 (Mip-1)	97%	0.E+00	transport
0_81	AF275315.1	water-selective transport intrinsic membrane protein 1	82%	2.E-163	transport
0_139	DQ450071.1	putative major intrinsic protein	82%	8.E-100	transport
Cytoskeleton/Cell wall associated					
0_45	NM_100817.3	glucan endo-1,3-beta-glucosidase-related	69%	3.E-31	cell wall biogenesis/degradation, plant defense
Protein degradation					
0_6	NM_119786.3	serine carboxypeptidase S28 family protein	72%	6.E-89	proteolysis
0_80	NM_128670.4	peptidase (serine-type peptidase)	66%	1.E-33	proteolysis
0_76	AF527442.1	polyubiquitin 2	91%	5.E-90	protein modification
0_157	D28123.1	ubiquitin	85%	0.E+00	protein modification
unclassified					
0_172	NM_203086.2	phospholipase/carboxylesterase family protein	81%	2.E-88	unknown
unknown					
0_1	DQ306838.1	unknown	78%	2.E-32	unknown
0_39	AP004949.1	unknown	73%	2.E-49	unknown
0_69	CR962130.3	unknown	74%	4.E-34	unknown
0_72	NM_118838.4	unknown	75%	1.E-129	unknown
0_177	AC153643.25	unknown	70%	3.E-55	unknown

TABLE S2. Down-regulated genes induced by 4 h of Al treatment in the Al-resistant common bean genotype 'Quimbaya'. The SSH method was used to identify differentially expressed genes. Sequences that did not have a significant similarity in the NCBI database (no hits) are excluded from this list.

Clone ID.	**GeneBank Acc. #**	**Gene product**	**Sequence identity**	**E-value**	**GO: Biological Process / Putative function**
Primary metabolism					
4_38	XM_002529320.1	putative acyltransferase	86%	6.E-22	fatty acid biosynthetic process, lipid metabolism
4_73	AF452451.1	cysteine synthase	89%	3.E-97	cysteine biosynthetic process from serine
4_81	AY496909.1	enolase	95%	2.E-163	glycolysis
4_86	L12157.1	NADP-specific isocitrate dehydrogenase (idh1)	88%	2.E-138	tricarboxylic acid cycle, glyoxylate cycle
4_26	AF191098.1	nucleoside diphosphate kinase (ndpk)	78%	4.E-76	nucleosides triphosphate (CTP, GTP & UTP) biosynthesis
4_76	F575931.1	adenosine kinase 2	77%	3.E-46	purine ribonucleoside salvage
4_6	NM_100850.2	putative phosphoglyceromutase	79%	7.E-92	glycolysis, response to cadmium ion, response to cold
Stress response/ Plant defence					
4_57	U20502.1	calnexin	80%	5.E-119	protein folding, response to salt stress
4_3	DQ340238.1	cytochrome P450 monooxygenase (CYP81E11)	78%	4.E-95	plant defense
4_111	DQ340234.1	cytochrome P450 monooxygenase (CYP83E8)	73%	3.E-34	plant defense
4_131	XM_002526702.1	chaperone protein dnaJ	81%	4.E-91	stress response, protein folding
4_37	AJ011939.1	peroxidase	70%	2.E-24	response to oxidative stress
Transcription factor					
4_137	J03919.1	auxin-regulated protein (Aux28)	94%	0.E+00	auxin mediated signaling pathway, regulation of transcription
4_65	DQ787051.1	transcription factor bZIP110	75%	2.E-80	regulation of transcription, DNA-dependent
Translation					
4_17	AK226319.1	putative ribophorin I	73%	1.E-38	protein amino acid glycosylation
4_130	XM_002534101.1	ribophorin	78%	1.E-57	protein amino acid glycosylation
4_12	AF528526.1	40S ribosomal S4 protein	88%	1.E-172	translation
4_112	M31024.1	ribosomal protein S11	89%	1.E-83	translation
4_52	X56856.1	elongation factor EF-1a	90%	0.E+00	translational elongation
Transport					
4_136	AJ003197.1	adenine nucleotide translocator	80%	3.E-27	ADP/ATP transport
4_117	U97023.1	putative aquaporin-1 (Mip-1)	97%	0.E+00	Water transport
4_135	DQ087218.1	aquaporin (Aqp1)	100%	2.E-149	Water transport
4_32	AB107919.1	AUX1-like auxin influx carrier protein	90%	6.E-74	auxin polar transport, auxin mediated signaling pathway
4_45	AK226470.1	oxoglutarate/malate translocator-like protein	81%	3.E-46	transport
4_55	U34333.1	proline-rich 14 kDa protein	99%	0.E+00	lipid transport
4_75	XM_002510718.1	organic anion transporter	79%	1.E-93	organic anion transport
4_22	AY220098.1	vacuolar ATPase subunit E	98%	0.E+00	ATP hydrolysis coupled proton transport
Cytoskeleton/Cell wall associated					
4_100	U60500.1	actin (Soy57)	96%	3.E-116	major component of the cytoskeleton, cell motility
4_49	DQ340400.1	endo-1,4-beta-glucanase precursor (Cel7)	93%	2.E-175	cell wall modification, plant cell elongation

Clone ID.	GeneBank Acc. #	Gene product	Sequence identity	E-value	GO: Biological Process / Putative function
4_133	NM_102471.4	glycine-rich protein	71%	5.E-43	cell wall organization
4_19	NM_180089.1	dynamin-related protein (ADL1D)	76%	4.E-76	microtubule-associated force-producing protein
4_2	AJ520103.1	65kD microtubule associated protein	82%	3.E-156	building of cortical microtubules, cell expansion
4_53	X81982.1	profilin	99%	5.E-125	actin cytoskeleton organization
Protein degradation					
4_15	AJ006095.1	26S protease regulatory subunit 6	90%	5.E-164	protein catabolic process
4_11	AP009544.1	subtilase	89%	4.E-32	proteolysis, negative regulation of catalytic activity
unclassified					
4_64	NM_119879.2	copper ion binding (SKS15)	68%	8.E-60	oxidation reduction
4_5	AM503587.1	parvulin-type peptidyl-prolyl cis/trans isomerase	84%	4.E-51	protein folding
4_24	NM_100673.3	SIT4 phosphatase-associated family protein	85%	5.E-50	unknown
Unknown					
4_8	EU196765.1	unknown	98%	0.E+00	unknown
4_16	AC175047.3	unknown	81%	2.E-49	unknown
4_20	AC155881.2	unknown	77%	4.E-32	unknown
4_28	AC157349.7	unknown	77%	3.E-53	unknown
4_58	NM_202364.2	unknown	70%	6.E-74	unknown
4_62	AP004577.1	unknown	81%	2.E-67	unknown
4_67	NM_121313.4	unknown	75%	8.E-41	unknown
4_69	AP006699.1	unknown	84%	2.E-87	unknown
4_84	NM_001071150.1	unknown	70%	4.E-38	unknown
4_87	DQ181626.1	unknown	78%	2.E-66	unknown
4_113	AK246332.1	unknown	83%	5.E-50	unknown
4_115	NM_001084815.1	unknown	68%	1.E-38	unknown
4_119	AC140026.11	unknown	81%	2.E-66	unknown
4_121	NM_001054328.1	unknown	86%	2.E-41	unknown
4_122	DQ306777.1	unknown	83%	6.E-55	unknown
4_127	AC199697.2	unknown	83%	5.E-50	unknown