

Physiological and molecular analysis of the interaction between aluminium toxicity and drought stress in common bean (*Phaseolus vulgaris*)

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Supplementary material

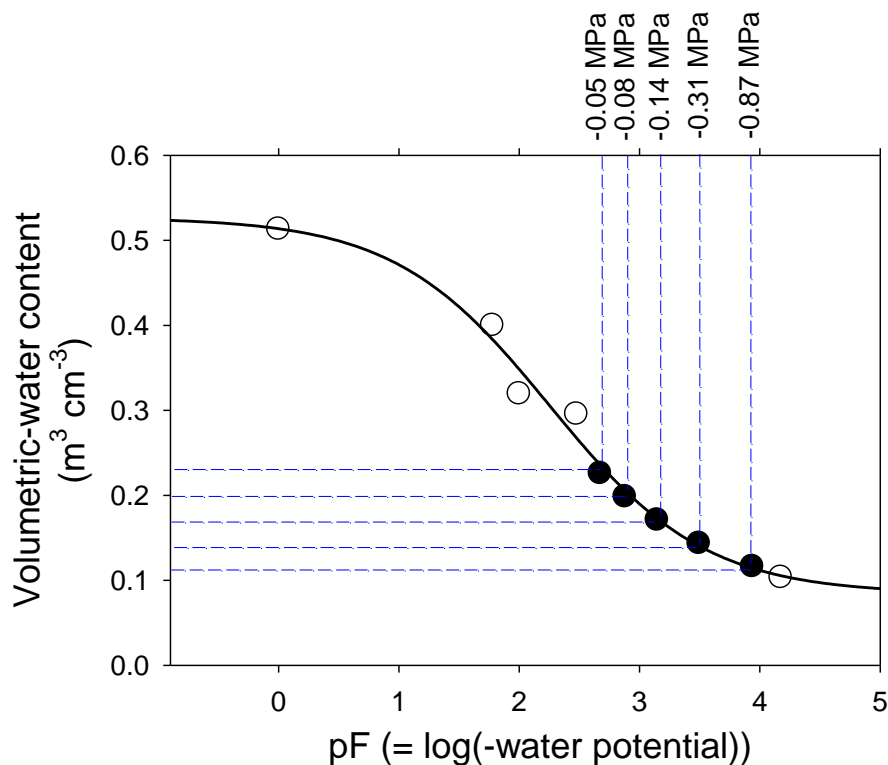


Fig. S1. The soil water retention curve of an Oxisol from the Llanos region of Colombia. The filled dots indicate the soil-moisture treatments used in the present study; the corresponding soil-water potentials in MPa are presented on the top of the graph.

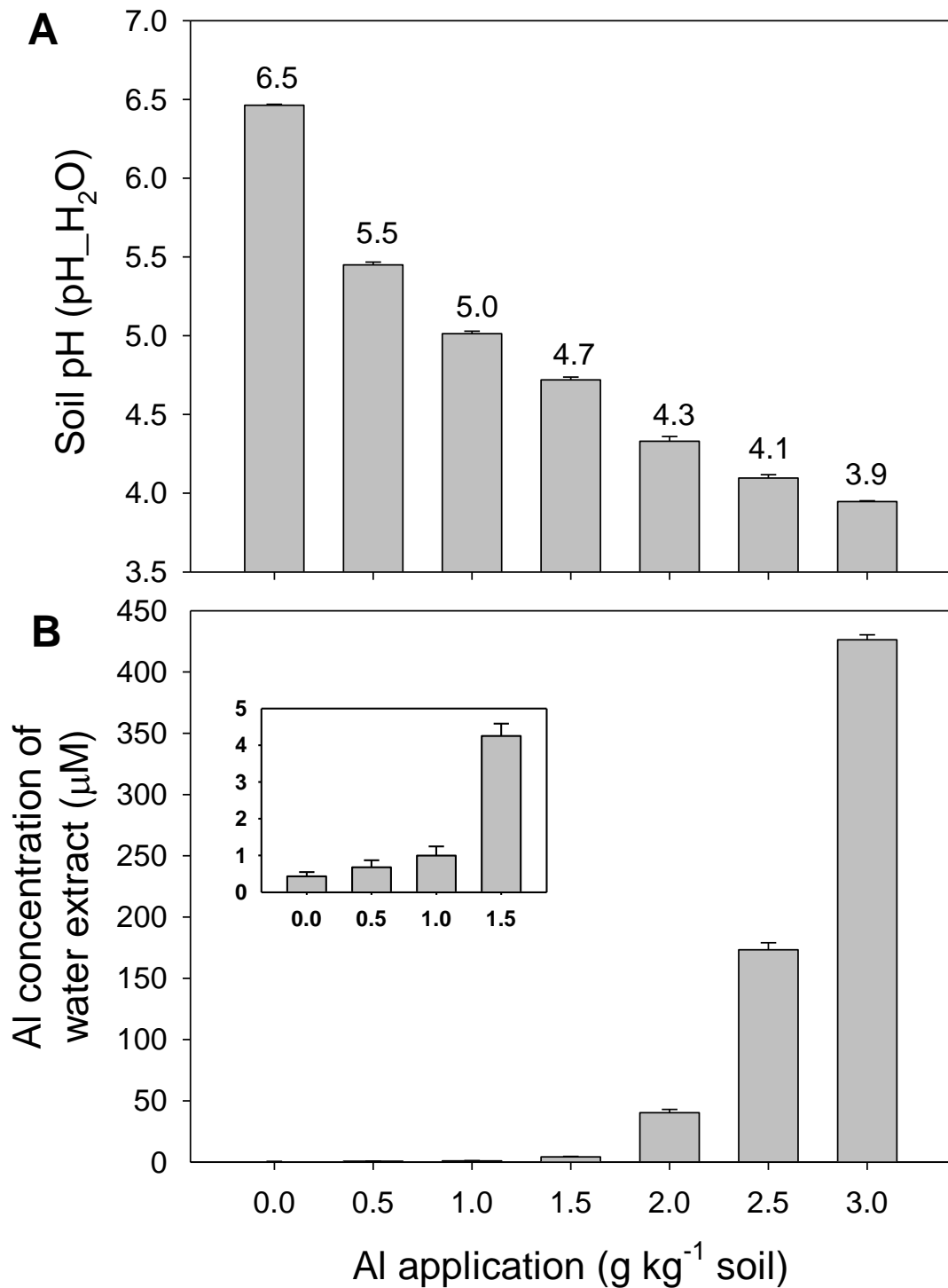


Fig. S2. Soil pH (pH_{H₂O}) (A) and the corresponding Al concentrations in the water extracts (B) at different levels of Al application (0 to 3.0 g kg⁻¹ soil). 10 mg air dried soil was incubated in 20 ml distilled water (pH_{H₂O}), and shaken for 1 h, then the soil pH and Al concentrations were determined. In B, the inserted graph shows the downscaled data for the Al supplies from 0 to 1.5 g kg⁻¹ soil.

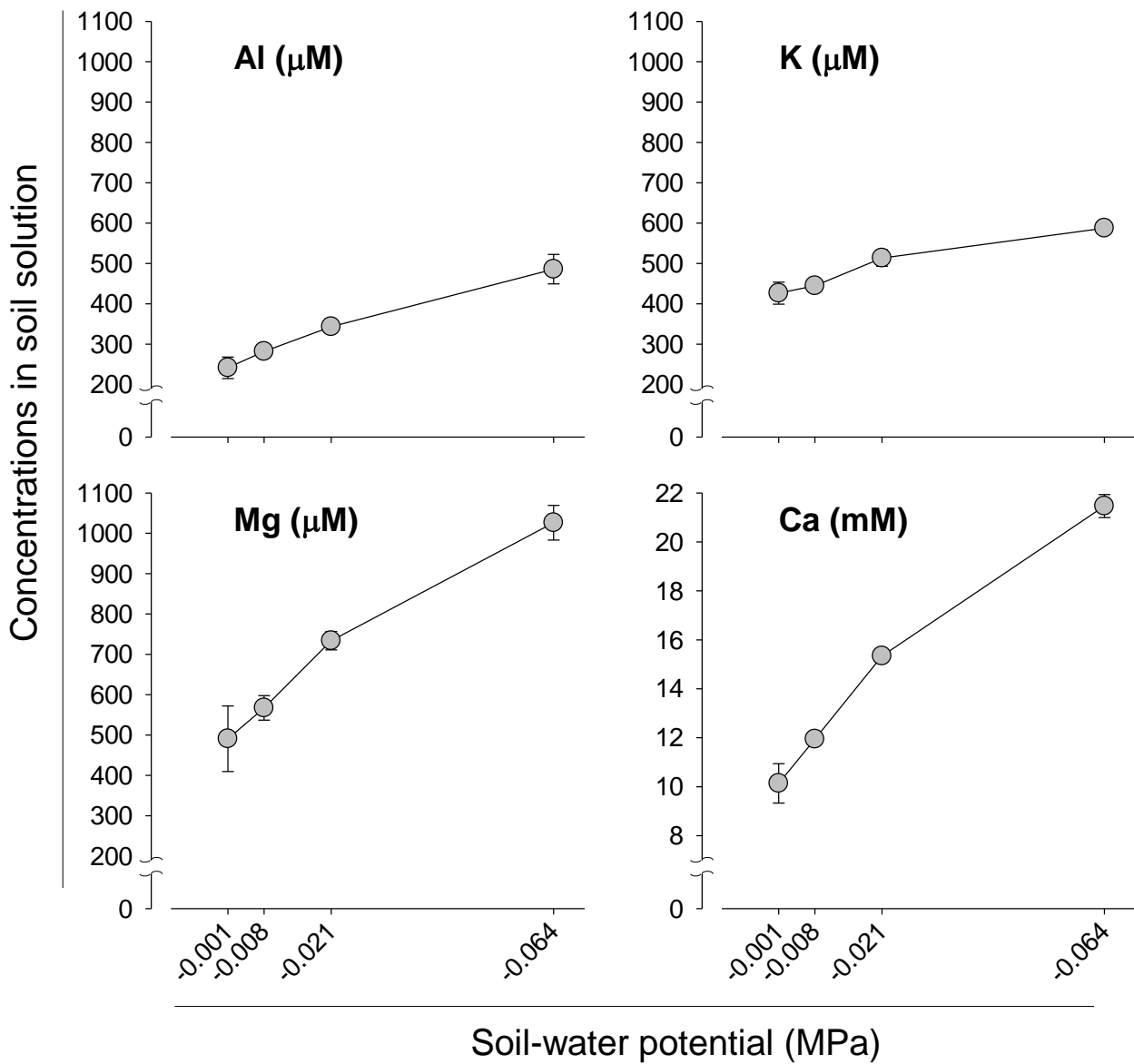


Fig. S3. The concentrations of Al, Ca, Mg and K in the soil solution under different levels of soil moisture. The soil solution from the incubated soil treated with 2 g Al was obtained by centrifugation (see Materials and Methods). Bars represent means \pm SD, n = 3.

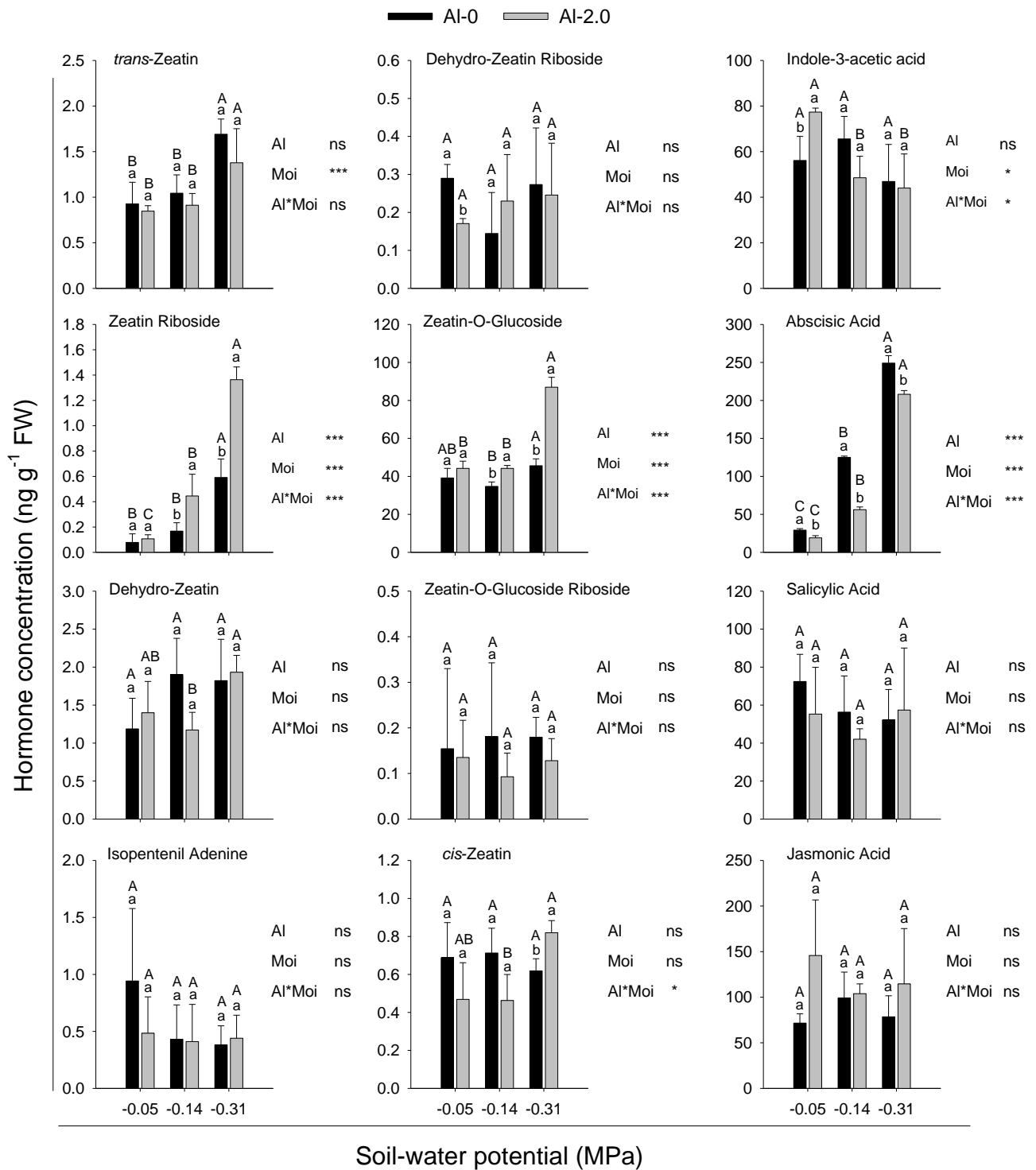


Fig. S4. Phytohormone concentrations in the 1-cm root tips of the common bean genotype VAX 1 as affected by soil moisture and Al supply (g kg^{-1} soil). Two-day-old seedlings were grown in soil for 24 h. Bars represent means \pm SD, $n = 3$. Means with different small and capital letters are significantly different at $P < 0.05$ (Tukey test) for the comparison of Al treatments within soil moisture and comparison of soil-moisture treatments within Al treatments, respectively. For the ANOVA, *, *** denote significant at $P < 0.05$, $P < 0.001$, respectively. ns = not significant.

Table S1. List of genes and specific primer pairs used for quantitative gene expression analysis.

Candidate genes	Primer pairs (5'→3') ^a		Amplicon size (bp)	TC/GB ^b	Accession No.
<i>P5CS</i> (VuP5CS protein)	(+) GACAGTGCTGCTGTTTTCCA	(-) AAACCCCTACTCCCACAGGA	128		TC14708
<i>SUS</i> (Sucrose synthase 2)	(+) GCATGGCCTCATGAAAGAGT	(-) GAAAGCAGGTGAACGAAAG	133		TC11609
<i>AQP</i> (Aquaporin)	(+) CCACATCACCATCCTCACTG	(-) ATTGCCAAACCTCCTGTGAC	102		TC14630
<i>KS-DHN</i> (KS-type dehydrin SLTI629)	(+) CATAGCAGTGAGGGCTGTGA	(-) CAAAGCAGTGGGGTTACACA	157		TC23304
<i>CYP701A</i> (Cytochrome P450 monooxygenase CYP701A16)	(+) GGATGCAACATGGACAAGAA	(-) AACCTGCACACACCCTCTTC	136		TC18728
<i>PvLEA18</i> (PvLEA-18)	(+) ACCAAAGACTGGTCGAGGTG	(-) GGCAGTGTAGGAGGTGGTGT	141		TC17584
<i>BEG</i> (Glucan endo-1, 3-beta-glucosidase precursor)	(+) ATGGAAGACTTGGCAACGAC	(-) GCCTCTCAAAGCTCCAAGAA	122		TC11172
<i>HRGP</i> (Hydroxyproline-rich glycoprotein)	(+) CCTGTCTTGATGGTGAAGCA	(-) TTCATTTGTTGCAGGCTGAC	114		CV543261
<i>PRP</i> (Proline-rich protein)	(+) GCAAGTGTGTGCATTGCTT	(-) TGGAAGCCAGAAGGAAGTGT	160		TC12228
<i>LTP</i> (Protease inhibitor/seed storage/lipid transfer protein family protein)	(+) CCTCAGCAGCACAAGATGAG	(-) TGACAGCAATCTGAGGGTTG	147		CV542382
<i>XTHa</i> (Xyloglucan endotransglycosylase precursor)	(+) ATATGTCATCGGAGGGTCCA	(-) TTGGTAGGGTCGAACCAAAG	151		TC12227
<i>XTHb</i> (Xyloglucan endotransglycosylase/hydrolase)	(+) TTTGACCAACCCATGAAGGT	(-) GCATTCACTGAGGCTTACACA	153		CV542742
<i>bZIP</i> (bZip transcription factor)	(+) AAAGTCCACTTCCTCCTT	(-) TCTCCTGTGCTTCCTTTCGT	127		TC17978
<i>MYB</i> (MYB transcription factor MYB134)	(+) CCGATTCCGACAAAATGAAC	(-) GCATCAGGTGTGTTTCAGCTC	136		TC13287
<i>NCED</i> (9-cis-epoxycarotenoid dioxygenase)	(+) GCTCGAAGCTTCCATCAAAC	(-) ATCTGCAAGCATCCCTCAGT	143		AF190462
<i>ZEP</i> (Zeaxanthin epoxidase)	(+) CCTCATCACAAAGGTGGGAGT	(-) CCTTCTCTTTGCAGCCAAC	108		TC20513
<i>AAO1</i> (Abscisic aldehyde oxidase 1)	(+) TGCAACATCTTGGTCGAGAG	(-) AAGTTCACAGCTCGCAGGTT	113		TC30901
<i>AAO2</i> (Abscisic aldehyde oxidase 2)	(+) TGCTGGGAGCACTACATCAG	(-) TTGACAGAGCCATTTCCTC	117		TC25061
<i>IPT1</i> (Isopentenyltransferase 1)	(+) AAGGACAAGGTGGTGGTGAT	(-) TTGCATTTTGTGCGAGTTGA	114		BW662125
<i>IPT2</i> (Isopentenyltransferase 2)	(+) TGCCAGGATCAAGATCAACA	(-) GCTCTTAGCGAGAACGTGGT	160		CV543443
<i>IPT3</i> (Isopentenyltransferase 3)	(+) GTCAACTCAGACAAAATGCAA	(-) ACAGTGCCAAGCAGATGATG	104		CA784528
<i>CYP735A</i> (cytochrome P450 monooxygenase 735A)	(+) TCGTTGTGCTCAAGCAAGTC	(-) GCAGAGTCTCCACCTCCATC	107		CV535867
<i>ZOGT</i> (Zeatin O-glucosyltransferase)	(+) GTTCTCCTCCTCCCAATCC	(-) GCCATGAGGGAGTCATTGAT	155		AF116858
<i>βGlc</i> (β-glucosidase)	(+) GGAGGTGTGAACAAGGAAGG	(-) CTTGAGGAAGGTCCCAATGA	109		TC27431
<i>CKX1</i> (Cytokinin oxidase/dehydrogenase 1)	(+) GGAAGAAACCTTGTGGTGA	(-) ACAAGCCTTTTGAACGCAAC	152		FE674332
<i>CKX2</i> (Cytokinin oxidase/dehydrogenase 2)	(+) CCAATGGTCTGATGGACTT	(-) GCACTCTCCATGCTTCTCT	129		FE709123
<i>MATE</i> (Citrate transporter family) (Eticha et al., 2010)	(+) CTGGATGCAGTTTCAAGAGAG	(-) ACTCCAGCAGCTGCAAGTTC	138		CV535133
<i>ACCO</i> (ACC-oxidase) (Eticha et al., 2010)	(+) GAAGATGGCGCAAGAAGAAG	(-) TGGAGCAAAGGTTCAAGGAG	105		AB002667
<i>β-Tubulin</i> (Eticha et al., 2010)	(+) CCGTTGTGGAGCCTTACAAT	(-) GCTTGAGGGTCTGAAACAA	117		CV530631

^a (+) and (-) indicate forward and reverse primers, respectively; ^bTC/GB, Tentative Consensus/GenBank®.