

Figure S1. Multiple sequence alignment of *HIR1*, *HIR2*, *HIR3*, *HIR4*, *EDS1* and *PAD4* genes of *Coffea* spp. Alignments were carried out using T-coffee server (<http://tcoffee.crg.cat>). Nucleotide and amino acid differences are encircled by orange boxes, the first ATG by a yellow box and the STOP codon by a blue box. Genes appear in the following order:

1. [HIR1](#);
2. [HIR2](#);
3. [HIR3](#);
4. [HIR4](#);
5. [EDS1](#);
6. [PAD4](#).

Figure S2. A. Motifs identified by the MEME algorithm (<https://meme-suite.org/meme/>) using complete amino acids sequences of 25 HIR genes from *Coffea* spp. and *Arabidopsis thaliana*. Motifs are numbered according with their position in the protein sequences. **B.** Distribution of the conserved motifs identified in MEME algorithm in a scheme representing a generic HIR protein. Different motifs are indicated by different colors and numbered 1 to 7 corresponding to the numbers in the table above.

Figure S3. Phylogenetic analysis of putative *Coffea* spp. EDS1 and PAD4 with AtEDS1 and AtPAD4 and orthologs from a select group of species.

HDT M2043762 T-AATCAGAAAGTCTACATGGATAGCCATCTGCGTGTCTTAAACCTTCGACCTTCCTCGTGTGCCCCCAAGCAAAAAA
M2043761 TAAATCTAATGAGTAAAGCATTCTGCTTTTATAAAGAAA
Ca_e XM_027241529 GAATATCAGAAAGTAAAGCATTCTGCTTTTATAAAGT
XM_027241530 TAAATCTAATGAGTAAAGCATTCTGCTTTTATAAAGT
Ca_e XM_027241531 GAATATCAGAAAGTAAAGCATTCTGCTTTTATAAAGT
XM_027241532 TAAATCTAATGAGTAAAGCATTCTGCTTTTATAAAGT
XM_027241533 TAAATCTAATGAGTCTACATGGATAGCCATCTGCTTTTATAAAGT
XM_027242349 T-AATCAGAAAGTCTACATGGATAGCCATCTGCTTTTATAAAGT
XM_027242350 T-AATCAGAAAGTCTACATGGATAGCCATCTGCTTTTATAAAGT
* * * * *

B - Coffee HIR1 Protein sequences

HDT M2043762 HQDALGCIQVQSTVAIKRIFKPKGNFDVLEPGCHVPMCVGSGQAGGILSLRWQLDICKETKTKNFPTVVA
M2043761 HQDALGCIQVQSTVAIKRIFKPKGNFDVLEPGCHVPMCVGSGQAGGILSLRWQLDICKETKTKNFPTVVA
Ca_e XP_027097331 HQDALGCIQVQSTVAIKRIFKPKGNFDVLEPGCHVPMCVGSGQAGGILSLRWQLDICKETKTKNFPTVVA
XP_027097332 HQDALGCIQVQSTVAIKRIFKPKGNFDVLEPGCHVPMCVGSGQAGGILSLRWQLDICKETKTKNFPTVVA
XP_027097333 HQDALGCIQVQSTVAIKRIFKPKGNFDVLEPGCHVPMCVGSGQAGGILSLRWQLDICKETKTKNFPTVVA
Ca_e XP_027098149 HQDALGCIQVQSTVAIKRIFKPKGNFDVLEPGCHVPMCVGSGQAGGILSLRWQLDICKETKTKNFPTVVA
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M2043761 HXINIAASRLREAAASEKAAEKILQLKRAEGEAAKYLGLGILARQQAIVDGLRSLVGFASNVPGTSSKVDHMDVLV
Ca_e XP_027097331 HXINIAASRLREAAASEKAAEKILQLKRAEGEAAKYLGLGILARQQAIVDGLRSLVGFASNVPGTSSKVDHMDVLV
XP_027097332 HXINIAASRLREAAASEKAAEKILQLKRAEGEAAKYLGLGILARQQAIVDGLRSLVGFASNVPGTSSKVDHMDVLV
XP_027097333 HXINIAASRLREAAASEKAAEKILQLKRAEGEAAKYLGLGILARQQAIVDGLRSLVGFASNVPGTSSKVDHMDVLV
Ca_e XP_027098149 HXINIAASRLREAAASEKAAEKILQLKRAEGEAAKYLGLGILARQQAIVDGLRSLVGFASNVPGTSSKVDHMDVLV
XP_027098150 HXINIAASRLREAAASEKAAEKILQLKRAEGEAAKYLGLGILARQQAIVDGLRSLVGFASNVPGTSSKVDHMDVLV
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XP 027097330 MNKINAAASHLHPAASEKKAHAKILQIKRABGEAEAKYLACGLGARQRO

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	M2043761	MGDGLCIGQVDSVTAIKENFGKFDVLEGGCCHVPCVCGSGDGLGGLSLRVQLDLDKCTTKTKVNVPTVVA	QYRALAKAKSDAYYRLSNTKDIQYAVYDVVRASVPKSLDKVFKPKQNKITAKAVRRLIKAMH	GYEVTTLVDTLVDIEPQVQVKA
	XP_027097330	MGDGLCIGQVDSVTAIKENFGKFDVLEGGCCHVPCVCGSGDGLGGLSLRVQLDLDKCTTKTKVNVPTVVA	QYRALAKAKSDAYYRLSNTKDIQYAVYDVVRASVPKSLDKVFKPKQNKITAKAVRRLIKAMH	GYEVTTLVDTLVDIEPQVQVKA
	XP_027097331	MGDGLCIGQVDSVTAIKENFGKFDVLEGGCCHVPCVCGSGDGLGGLSLRVQLDLDKCTTKTKVNVPTVVA	QYRALAKAKSDAYYRLSNTKDIQYAVYDVVRASVPKSLDKVFKPKQNKITAKAVRRLIKAMH	GYEVTTLVDTLVDIEPQVQVKA
	XP_027097332	MGDGLCIGQVDSVTAIKENFGKFDVLEGGCCHVPCVCGSGDGLGGLSLRVQLDLDKCTTKTKVNVPTVVA	QYRALAKAKSDAYYRLSNTKDIQYAVYDVVRASVPKSLDKVFKPKQNKITAKAVRRLIKAMH	GYEVTTLVDTLVDIEPQVQVKA
Ca _c	XP_027097331	MGDGLCIGQVDSVTAIKENFGKFDVLEGGCCHVPCVCGSGDGLGGLSLRVQLDLDKCTTKTKVNVPTVVA	QYRALAKAKSDAYYRLSNTKDIQYAVYDVVRASVPKSLDKVFKPKQNKITAKAVRRLIKAMH	GYEVTTLVDTLVDIEPQVQVKA
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	XP_027097333	MGDGLCIGQVDSVTAIKENFGKFDVLEGGCCHVPCVCGSGDGLGGLSLRVQLDLDKCTTKTKVNVPTVVA	QYRALAKAKSDAYYRLSNTKDIQYAVYDVVRASVPKSLDKVFKPKQNKITAKAVRRLIKAMH	GYEVTTLVDTLVDIEPQVQVKA
	XP_027098149	MGDGLCIGQVDSVTAIKENFGKFDVLEGGCCHVPCVCGSGDGLGGLSLRVQLDLDKCTTKTKVNVPTVVA	QYRALAKAKSDAYYRLSNTKDIQYAVYDVVRASVPKSLDKVFKPKQNKITAKAVRRLIKAMH	GYEVTTLVDTLVDIEPQVQVKA
	XP_027098150	MGDGLCIGQVDSVTAIKENFGKFDVLEGGCCHVPCVCGSGDGLGGLSLRVQLDLDKCTTKTKVNVPTVVA	QYRALAKAKSDAYYRLSNTKDIQYAVYDVVRASVPKSLDKVFKPKQNKITAKAVRRLIKAMH	GYEVTTLVDTLVDIEPQVQVKA
Ca _e	XP_027098151	MGDGLCIGQVDSVTAIKENFGKFDVLEGGCCHVPCVCGSGDGLGGLSLRVQLDLDKCTTKTKVNVPTVVA	QYRALAKAKSDAYYRLSNTKDIQYAVYDVVRASVPKSLDKVFKPKQNKITAKAVRRLIKAMH	GYEVTTLVDTLVDIEPQVQVKA
	*****	*****	*****	*****
	M2043762	MHEINAAASRLREAASFEAKADKILQIKRABGEAEAKYLGLGIARQQAIVDGLRDSVLGPAASNVPGTSSKDVMDNVLT	QYDTMKRIGASSSSSEVFPIHGPGAVDIAQCRDGLLQGRIDEV	
	M2043761	MHEINAAASRLREAASFEAKADKILQIKRABGEAEAKYLGLGIARQQAIVDGLRDSVLGPAASNVPGTSSKDVMDNVLT	QYDTMKRIGASSSSSEVFPIHGPGAVDIAQCRDGLLQGRIDEV	
	XP_027097330	MHEINAAASRLREAASFEAKADKILQIKRABGEAEAKYLGLGIARQQAIVDGLRDSVLGPAASNVPGTSSKDVMDNVLT	QYDTMKRIGASSSSSEVFPIHGPGAVDIAQCRDGLLQGRIDEV	
Ca _c	XP_027097331	MHEINAAASRLREAASFEAKADKILQIKRABGEAEAKYLGLGIARQQAIVDGLRDSVLGPAASNVPGTSSKDVMDNVLT	QYDTMKRIGASSSSSEVFPIHGPGAVDIAQCRDGLLQGRIDEV	
	XP_027097332	MHEINAAASRLREAASFEAKADKILQIKRABGEAEAKYLGLGIARQQAIVDGLRDSVLGPAASNVPGTSSKDVMDNVLT	QYDTMKRIGASSSSSEVFPIHGPGAVDIAQCRDGLLQGRIDEV	
	XP_027097333	MHEINAAASRLREAASFEAKADKILQIKRABGEAEAKYLGLGIARQQAIVDGLRDSVLGPAASNVPGTSSKDVMDNVLT	QYDTMKRIGASSSSSEVFPIHGPGAVDIAQCRDGLLQGRIDEV	
	XP_027098149	MHEINAAASRLREAASFEAKADKILQIKRABGEAEAKYLGLGIARQQAIVDGLRDSVLGPAASNVPGTSSKDVMDNVLT	QYDTMKRIGASSSSSEVFPIHGPGAVDIAQCRDGLLQGRIDEV	
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Ca _e	XP_027098151	MHEINAAASRLREAASFEAKADKILQIKRABGEAEAKYLGLGIARQQAIVDGLRDSVLGPAASNVPGTSSKDVMDNVLT	QYDTMKRIGASSSSSEVFPIHGPGAVDIAQCRDGLLQGRIDEV	
	*****	*****	*****	*****

HDT M2043763 MNI1AAARLRPLVAANEAEAEAKKLLQIKRAEAGEAEAKYLSGNGIARQQAIVDGLRDSVLGFSVVPVPTTAKDVDMXVLVLYQYFDCKMEGAASKSSAVFTIHGPGAVRQVATQIRDGLQAS **SSS**
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Ca_c M2043766 MNI1AAARLRPLVAANRKAARFKKLLQIKRAEAGEAEAKYLSGNGIARQQAIVDGLRDSVLGFSVVPVPTTAKDVDMXVLVLYQYFDCKMEGAASKSSAVFTIHGPGAVRQVATQIRDGLQAS **EH**
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HDT = MZ043768 -----

[illegible]

B - Coffea *HIR4* Protein sequences

HDT M2043768 -----KGMILLCCQAQDGSVAITEKFGKFOVLEPGCHFLPCLCGSQIAGTSLRLQQLDWRCEHTKKNQVPTVASIQYRALAKASAFYRCSHTTQIATYVPTVIRTPFLNLDCAFQKRIAKAVDEDLKASMSYGYIQTLLVD
Ca_c XM 027220426 -----KGMILLCCQAQDGSVAITEKFGKFOVLEPGCHFLPCLCGSQIAGTSLRLQQLDWRCEHTKKNQVPTVASIQYRALAKASAFYRCSHTTQIATYVPTVIRTPFLNLDCAFQKRIAKAVDEDLKASMSYGYIQTLLVD
 XM 027220425 -----KGMILLCCQAQDGSVAITEKFGKFOVLEPGCHFLPCLCGSQIAGTSLRLQQLDWRCEHTKKNQVPTVASIQYRALAKASAFYRCSHTTQIATYVPTVIRTPFLNLDCAFQKRIAKAVDEDLKASMSYGYIQTLLVD
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Cc XM 027297650 -----KGMILLCCQAQDGSVAITEKFGKFOVLEPGCHFLPCLCGSQIAGTSLRLQQLDWRCEHTKKNQVPTVASIQYRALAKASAFYRCSHTTQIATYVPTVIRTPFLNLDCAFQKRIAKAVDEDLKASMSYGYIQTLLVD
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Ca_c XM 027220426 -----KGMILLCCQAQDGSVAITEKFGKFOVLEPGCHFLPCLCGSQIAGTSLRLQQLDWRCEHTKKNQVPTVASIQYRALAKASAFYRCSHTTQIATYVPTVIRTPFLNLDCAFQKRIAKAVDEDLKASMSYGYIQTLLVD
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Formin-
Domain

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Coffea PAD4 Protein sequences

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Cc — Cc02_g33900 M-----
Ce — XP_027178560 MEAEASSFECSEMLATLLASTPLLEESWKLCGQANAEAPQSYGTKQMGHVSYVAFSGIQMLAGLDPSCSNLVPIESSANG
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Cc — Cc02_g33900 AEYYRSGEHLKKGHYMEHGRERRYKIFDKWWRDRKVEGNPGNSRSKFASLTQDSCFWARVEEARDWLNVRVSEGDTRTQS
Ce — XP_027178560 AEYYRSGEHLKKGHYMEHGRERRYKIFDKWWRDRKVEGNPGNSRSKFASLTQDSCFWARVEEARDWLNVRVSEGDTRTQS

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Ce — XP_027178560 LLWENIEKFDQYARGMVD RKEVSIDVLAKNSSYNLFVEEWKDLKSQLQLFPFHPFSLDGGGSSSFDYIVGK
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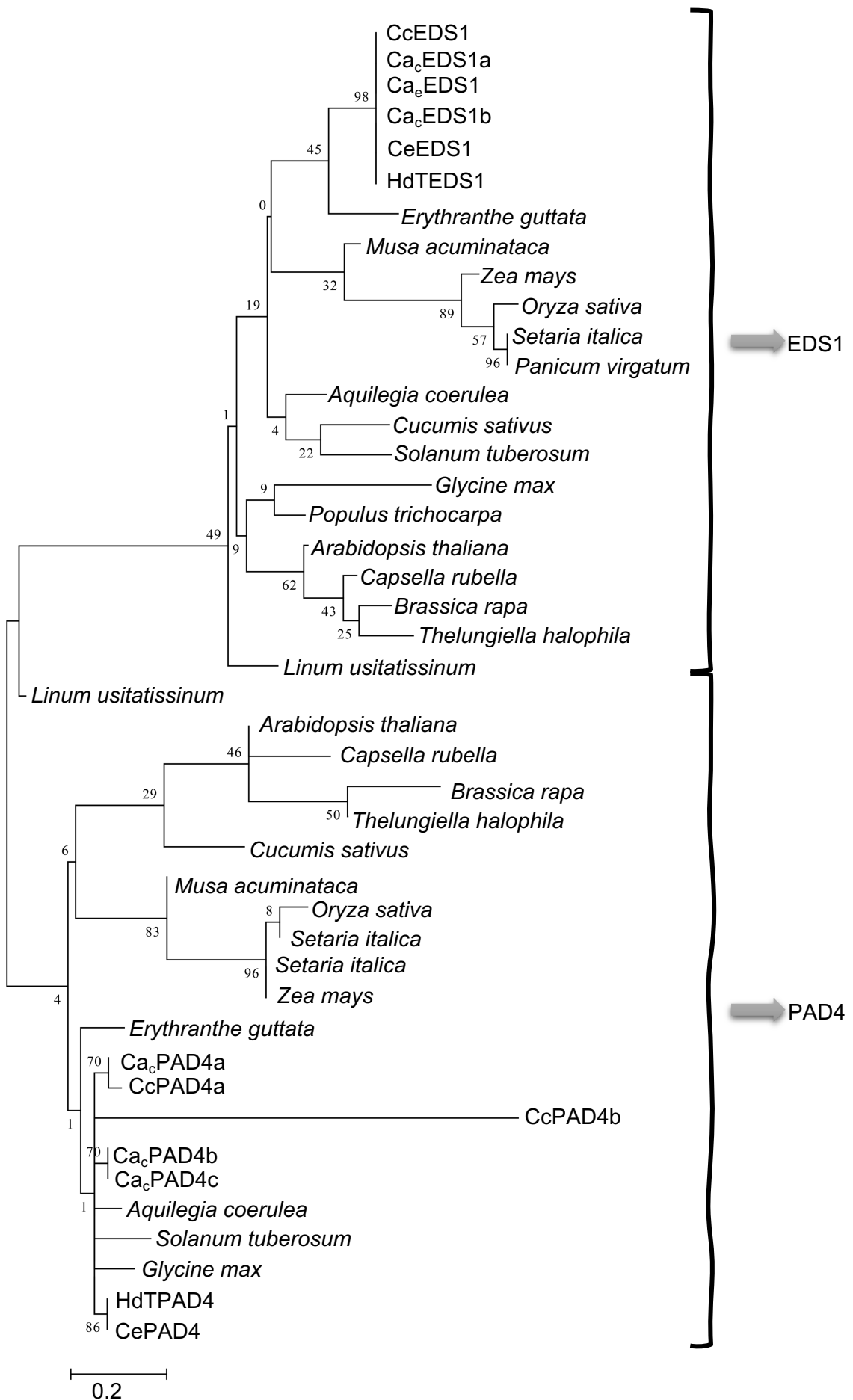


Figure S3 Phylogenetic analysis of putative *Coffea* spp. EDS1 and PAD4 with AtEDS1 and AtPAD4 and a orthologs from a select group of species.