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      *           20           *           40           *           60           *           80           *           100          *           120          *           140
Cc : MKIEVKESTMVRPAQETPGRNLWNSNVDLVPNFHTPSVYFYRPTGS-----SNFFDAKVLKDALSRLVPFYPMAGRLKRDEDGRIEIECNAGEVLFVEAES-DGVVDDFGDFAPTLELRRLIPAVDYSQGISSYALLVLQV : 137
Ca : MKIEVKESTMVRPAHETPRRNLWNSNVDLVPNFHTPSVYFYRPTGS-----SNFFDAKVLKDALSRLVPFYPMAGRLKRDEDGRIEIECNAGEVLFVEAES-DGVVDDFGDFAPTLELRRLIPAVDYSQGISSYALLVLQV : 137
Nt : MKIEVKESTMVRKPAETPQQRNLWNSNVDLVPNFHTPSVYFYRPTGS-----PNFFDGKVLKEALSALVPFYPMAGRLCRDEDGRIEIDCKGQGVLFVEAES-DGVVDDFGDFAPTLELRQLIPAVDYSQGIQSYALLVLQI : 137
Cca : MKIEVRESTMVRPAEETPRINLWNSNVDLVPNFHTPSVYFYRPNGA-----ANFFDPKVMKDALSRLVPFYPMGRLKRDEDGRIEIDCQGGVLFVEAES-DGVVDDFGDFAPTLELRKLIIPAVDYTLGIESYLLVLQV : 137
Sb : MKITVRGSEMVPYPAETPRRRLWNSGPDLVVPRFHTPSVYFRRRDADGNDLTAADGSAFFDGARMRRALAEALVPFYPMAGRLARDEDGRVEIDCNAAGVLFQEADAPDATIDYFGDFAPTMELKRLIPTVDFSD-DTAFPLLVLQV : 146
      MKIEv eStMV PA ETP      LWNSnvDLVVPnFHTPSVYFyRp g              nFFD kv k ALs ALVPFYPMaGRL RDEDGRiEI C g GVLFvEAes Dgv DdFGDFAPTLELr LIpAVDys gi sy LLLVLQv

      *           160          *           180          *           200          *           220          *           240          *           260          *           280          *
Cc : TYFKCGGVSLGVGMRHHAADGFSGLHFINSWSDMARGLDVTLPPFIDRTLRLRARDPPQPQFQHIEYQPPFALKVSPQ---TAKSD-SVPETAVSIFKLTREQISALKAKS--KEDGNTISYSSYEMLAGHVWRCACKARGLEVDQGT : 278
Ca : TYFKCGGVSLGVGMQHHAADGFSGLHFINSWSDMARGLDVTLPPFIDRTLRLRARDPPQPQFQHIEYQPPFALKVSPQ---TAKSD-SVPETAVSIFKLTREQISALKAKS--KEDGNTISYSSYEMLAGHVWRCACKARGLEVDQGT : 278
Nt : THFKCGGVSLGVGMQHHAADGASGLHFINTWSDMARGLDLTIPPFIDRTLRLRARDPPQPQFPHVEYQPPFALKVTPEN--TPISE-AVPETSVSIFKLTREQISALKAKS--KEDGNTVNYSSYEMLAGHVWRSTCMARGLAHDQET : 279
Cca : TYFKCGGVSLGVGMQHHAADGASGLHFINTWSDLARGLDLAVPPFIDRTLRLRSRDPQPQAFDHIEYQAPPMPKTAETP--TPTDDESVPETTVSIFKLTREQVNAKAKS--KEDGNTVNYSSYEMLSGHVWRCVCKARGLPDDQDT : 280
Sb : THFKCGGVVAIGVGMQHHAADGFSGLHFINSWADLCRGVPIAVMPFIDRSLRLRARDPPAPVYPHVEYQAPAMLSSEPPQAALTAKPATPPAAVAIFKLSRAELGRILRSQVPAREREGAPRFSTYAVLAHVWRCASLARGLPADQPT : 293
      T FKCGGVslGVGMqHhAaADG SGLHFIN WsD aRGld  pPFIDRtLLRaRDPPqP f H EYQP P k p t          vPet VsIFKLtR q Lk ks kEdgnt ySsYemLagHVWRC c ARGL DQ T

      *           300          *           320          *           340          *           360          *           380          *           400          *           420          *           440
Cc : KIYIATDGRARLRPSLPPGYFGNVIFTATPIAIAIGDLEFKPVWYAASKIHDALARMDNDYLRSA LDYLELQPD LKALVRGAHTFKCPNLGITSWVRLPIHDADFGWGRPIFMGPGGIAYEGLSFILPSPTNDGSM SVAISLQGEHMK : 425
Ca : KIYIATDGRARLRPSLPPGYFGNVIFTATLIAIAIGDLEFKPVWYAASKIHDALARMDNDYLRSA LDYLELQPD LKALVRGAHTFKCPNLGITSWVRLPIHDADFGWGRPIFMGPGGIAYEGLSFILPSPTNDGSM SVAISLQGEHMK : 425
Nt : KIYIATDGRSRLRPSLPPGYFGNVIFTTPIAVAGDIQSKPIWYAASKLHDALARMDNDYLRSA LDYLELQPD LKALVRGAHTFKCPNLGITSWVRLPIHDADFGWGRPIFMGPGGIAYEGLSFILPSPTNDGSSVAISLQAEHMK : 426
Cca : KIYIATDGRARLRPSLPRGYFGNVIFTTPIAVAGDLQSKPTWYAASKIHDALARMDNDYLRSA LDYLELQPD LKALVRGAHTFKCPNLGITSWARLPIHDADFGWGRPIFMGPGGIAYEGLSFVLPSPINDGSL SIVISLQAEHMK : 427
Sb : KIYCATDGRQLRQLPPLPEGYFGNVIFTATPLANAGTVTAG-VAEGA AVIQAAALDRMD DGYCRSALDYLELQPD LKALVRGAHTFKCPNLGLT SWVRLPIHDADFGWGRPIFMGPGGIAYEGLAFVLP SANRDGSL SVAISLQAEHME : 439
      KIYIATDGR RLrPsLP GYFGNVIFT TpiA AGd  kp wyaAskihdALaRMD dYlrsALDYLELQPD LkALVRGAHTfKCPNLGiTSW RLPiHDADFGWGRPiFMGPGGIAYEGLsF LPSp nDGS SvaISLQ EHMk

      *
Cc : LFQSFLYDI : 434
Ca : LFQSFLYDI : 434
Nt : LFEKFLYDF : 435
Cca : LFSKFLYDI : 436
Sb : KERKLIYDF : 448
      lF flyD

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Figure S6. Sequence alignment of sequences belonging to the plant hydroxycinnamoyl CoA shikimate/quinic acid hydroxycinnamoyltransferase (HCT) family. 499142250 from *Sorghum Bicolor* (Sb), AAZ80046 from *Cynara cardunculus* (Cca), ABO47805 from *Coffea canephora* (Cc), ABO40491 from *Coffea arabica* (Ca), Q8GSM7 from *Nicotiana tabacum* (Nt). Red box indicates Tyr 296 in SbHCT and equivalent residues in HCT enzymes from other plant species.