

Figure S1. Sequence alignment of alcohol-forming FARs from Arabidopsis. The coding sequences for the eight Arabidopsis FARs were obtained from annotated gene databases and then, when necessary, manually reannotated to obtain the likely coding sequences. Identical residues are highlighted on black background; similar amino acids are shown on a gray background.

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At3g44540      1  -----
At5g22500      1  -----
At3g44550      1  -----
At3g44560      1  -----
At5g22420      1  -----
At4g33790      1  -----
At3g11980      1  MEALFLSSSSSSIVASNKLTRLHNHCVWSTVIRDKKRFGPTWCRVGGGGDGRNSNAERP
At3g56700      1  -----MATTNVLATSHAFKLNQVSYFSSFPKPNHYMP-----RRRLSHTTRR

At3g44540      1  -----MDSN-----
At5g22500      1  -----MESN-----
At3g44550      1  -----MELN-----
At3g44560      1  -----MEFS-----
At5g22420      1  -----MEPN-----
At4g33790      1  -----MSTEMEVVS-----
At3g11980      61  IRVSSLLKDRGQVLIREQSSPAMDAETLVLSPNGNGRTIEINGVKTLMPFSGASMVGMKE
At3g56700      44  VQTSCFYG-----ETSFEAVTSLVTP-----KTETSRLN-----SD

At3g44540      5  ---CIQFLHDKTILVTGVPGFFLAKVFVEKILRIQPKVKKLFLLLRAADNESAMQRFHSEV
At5g22500      5  ---CVQFLGNKTILITGAPGFFLAKVFVEKILRLQPNVKKIYLLRAPDEKSAMQRLRSEV
At3g44550      5  ---CVQFLRNKTILVTGATGFLAKVFVEKILRVQPNVKKLYLLVRASDNEAATKRLRTEV
At3g44560      5  ---CVHFLONKTILVTGATGFLAKVFVEKILRVQPNVKKLYLLVRASDNEAATKRLRTEA
At5g22420      5  ---CVQFLERNKTILVTGASGFLAKVFVEKILRLQPNVKKLYLLVRASDKKSAEQRLRREV
At4g33790      10  ---VLRKYLDNKSILVVGAAGFLANFVEKILRVAPNVKKLYLLRASKGKSATQRFNDEI
At3g11980      121  GLGIISFLQGGKFLITGSGFLAKVLTEKVLMAPDVSKTYLLIKAKSKEAAIERLKNEV
At3g56700      74  GIGIVRFLEGKSYLVTGATGFLAKVLTEKLLRESLEIGKIFLLMRSKDQESANKRLYDEI

At3g44540      62  LEKDLFRVLKNALGDENLKAFITEKVVPIPGDISVDNLGVKCSDLLOQHMWNEIDIIVNVA
At5g22500      62  MEIDLFKVLRNNLGEDNLNALMREKIVPVPGDISIDNLGLKDTDLIQRMWSEIDIINIA
At3g44550      62  FEKDLFKVLRQNLGDEKLNTLLEYKVVSVPGDIATDOLGINDSHLRERMQKEIDIIVNVA
At3g44560      62  FEKDLFKVLRDNLGDEKLNTLLSEKVVVAGDIAMDHLGMKDSNLRERMQKEIDIIVNVA
At5g22420      62  FEKDLFRVLRRVGDESLNALISEKVVVPGDISLTDIGVHDSNLLQDMMQDIDIISSA
At4g33790      67  LKDLFKVLKEKYG-PNLNQLTSEKITTIVDGDICLEDLGLQDFDLAHEMIHOVDIVNLA
At3g11980      181  LDAELFNTLKETHG-ASYMSFMLTKLIPVTGNICDSNIGLQ-ADSAEEIAKEVDVIINSA
At3g56700      134  ISSDLFKLLKQMHG-SSYEAFMRKLIPVIIGDIEEDNLGLK-SEIANMISEEIDVIISCG

At3g44540      122  ATTNFDERYDVGLSVNTFGPLNVLNFAKKCVKQLLLLHVSTAYVRGEKSGLLHEKTFHMG
At5g22500      122  ATTNFDERYDIGLGINTFGALNVLNFAKKCVKQLLLLHVSTAYISGEQPGLLLEKPFKMG
At3g44550      122  ATTNFDERYDVGLGINTFGALNVLNFAKKCVKVLLLLHVSTAYVCGEKPGLIPEKPFIME
At3g44560      122  ATTNFDERYDIGLGINTFGALNVLNFAKKCVKALLLLHVSTAYVCGEKPGLLPEKPFVME
At5g22420      122  ATTRFDERYDVALGINTFGALNVLNFAKKCVKPKLLLLHVSTVYVCGERPGHIVEKHFAMG
At4g33790      126  ATTKFDERYDVALGINTLGANVLNFAKRCAKVKILVHVSTAYVCGEKSGLIMETPFRMG
At3g11980      239  ANTFNFDERYDVALDINTRGPNLMGFAKKCKKLKFLQVSTAYVNGORQGRIMEKPFSMG
At3g56700      192  GRTTFDDRYDSALSVNALGPGRLLSFGKGCRKLKFLHFSTAYVITGKREGTVLETPLCTG

At3g44540      182  ETLNGH-----RKLVIETEMELMKQKLKELQKQNCSEEEISQSMKDLGMSRAKLHGW
At5g22500      182  ETLSGD-----RELDINIEHDLMKQKLKELQ--DCSDEEISQTMKDFGMARAKLHGW
At3g44550      182  EIRNENG-----LQLDINLERELMKQRLKELNEQDCSEEDITLSMKELGMERAKLHGW
At3g44560      182  EICNENG-----LQLDINLERELMKQRLKELNEQGCSEEGTFYMKELGMERAKLHGW
At5g22420      182  ESLNGK-----NKVDINTERELADQKSKQFKEQGCSEEETEQAMKDFGLKRRLYGW
At4g33790      186  ETLNGT-----TGLDINYEKLVQEKLDQLRVIGAAPETTETETMKDLGLRRAKLYGW
At3g11980      299  DCIATENFLEGNRKALDVREMKLAL----EAARKGTQNQEAQQMKDLGLERARSYGWQ
At3g56700      252  ENITSD-----LNIKSELKLAS----EAVRK-FRGREEIKKLELGFERAQHYGWE

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At3g44540 235 NTYVFTKSMGEMLLGNYRENLPVIIRPTMITSTFSEPFPGWIEGLRTIDSVIVAYGKGR
At5g22500 233 NTYVFTKAMGEMLLMGKYRENLPVIIRPTMITSTIAEPFPGWIEGLKTLDSVIVAYGKGR
At3g44550 236 NTYVFTKSMGEMLLGKHKENLPLVLIIRPTMITSTLSEPFPGWIEGLRTVDSVIIAYGKGV
At3g44560 236 NTYVFTKSMGEMLLGNHKENLPLVLIIRPTMITSTLSEPFPGWIEGLRTVDSVIIAYGKGV
At5g22420 235 NTYVFTKAMGEMLLGHYRETPVIIRPTIITSTFSDPFPGWIEGLKTVDSVIIIFYGKGI
At4g33790 239 NTYVFTKAMGEMMVGTKRENLSLVLLRPSIITSTFKEPFPGWIEGIRTIDSLAVGYGK GK
At3g11980 355 DTYVFTKAMGEMMINSTRGDVPLVLIIRPSVIESTYKDPFPGWIEGNRMMDPIVLCYGK GQ
At3g56700 298 NSYTFTKATGEAVIHSKRGNLPLVLIIRPSIIESSYNEPFPGWIOGTRMADPIILAYAKGQ

At3g44540 295 LKCFLADPNSVLDLIPVDMVANAMVIAAAIHAGKLGSGS----QTVYHVGSS-CKNPITTFEQ
At5g22500 293 LKCFLADSNSVFDLIPADMVNVAMVAAATAHSGDTIGI----QATYHVGSS-CKNPVTFGQ
At3g44550 296 LKCFLDVNSVCDMIPVDMVANAMITAAAKHAGGSGV----HMVYHVGSS-HQNPVTFGE
At3g44560 296 LKCFLDVNSVCDMIPADMVANAMIAAAAATHAGGSKV----HMVYQVGS-HQNPITTYGE
At5g22420 295 LKCFLDVQKTVCDIIPVDMVNVAMIAAADHCHDSGSGS----HTVYHVGSS-NQNPVIMKQ
At4g33790 299 LTCFLCDLDAVSDVMPADMVNVNLIIVSMAAQAGKQE-----EITVYHVGSS-LRNP MKNSK
At3g11980 415 LTGFLVDPKGVLDVVPADMVNVNATLAAIAKHGMAMSDPEPEINVYQIASS-AINPLVTFED
At3g56700 358 ISDFWADPQSLMDIIPVDMVANAAIAAMAKHGCGV----PEFKVYNLTSSSHVNPVRACK

At3g44540 350 IHDLAASYFTKNPLVRRDGSIIIVSKGTILSTMAQFSFYMTLRYKLPQLMLRLIYIYIPW
At5g22500 348 LHDFTARYFAKRPLIGRNGSPIIVVKGTILSTMAQFSLYMTLRYKLPQLILRLINIYIPW
At3g44550 351 IHEIAYRYFTKNPLRSRNGSLITVSKVRFIPTMALFSLYMTLRYKLPQLLKLVDIYIPW
At3g44560 351 IREILFCYFTKNPLRSRNGSMITVSKMKLIPTLALFSLYMTLRYKLPVQLLKLVDIYIPS
At5g22420 350 IYEMMSRYFMKSPLVGRNG-MLIVPKVTRISTLARFRVYTNLRYKLPILQILGLLSVIS-L
At4g33790 353 FPELAYRYFSIKPWTNKEGKVVVKGATEILSSMRSFHRVMTLRYLIALKGLELVNITLCK
At3g11980 474 LAELLYNHVKTSPCMDSKGDPIMVRLMKLFNSVDDFSDHWRDAQERSGLMSGMSS-VDS
At3g56700 414 LIDLSHQHLCDFPLEET---VIDLEHMKIHS SLEGFISALSNTIIKQERVIDNEGGGLST

At3g44540 410 WNGNKYKDIIDRK-IKIAMRLVDLYRPVYVLFKGFDDINTEKLRILKRKE--INKEMYGLFE
At5g22500 408 SHGDNYSDLSRK-IKIAMRLVELYQPYLLFKGFDDLNTERLRMKRKE--NIKELDGSFE
At3g44550 411 RNGDKYGDKNRK-IELVMRLVELYEPYVLFKGFDDRNTKSLCANQKEEIKNTEKLMFD
At3g44560 411 REGDEYKKNRKR-IDMVMRLVKLYEPYVLFKGFDDRNTKNLCAKQKEEDNRNSENFMFD
At5g22420 408 SQDKFALHNKR-FKMAMRLVKLYKPYVLFKGFDDKNMETLRLIKNEA----KDMEKLF G
At4g33790 413 LFEKEFYQFNKK- INFIFRLVDLYQPYLFFYGFDDSNTEKLRKMSVSK---TGVENEMFY
At3g11980 533 KMMQKLFICKKSVEQAKHLATIYEPYTFYGGFRFDNSNTQRLMENMSE-----DEKREFG
At3g56700 471 KGKRKLN YFVS-----LAKTYEPYTFEQARFDNINTTSLIQEMSM-----EKKTFG

At3g44540 467 FDPKSIDWEDYMTTIHHPGLITTVLKK----
At5g22500 465 FDPKSIDWDNYITNTHIPGLITHVLKQ----
At3g44550 470 FDPKGINWGDYLTNIHISGLVTHVLKK----
At3g44560 470 FDPKIIKWKDYLINVHHPGLITHVLKK----
At5g22420 463 TNPKCIDWEDYFM-IRIS-LAS-----
At4g33790 469 FDPKVIDWDDYFLNTHVIGLKYVF-----
At3g11980 588 FDVGSINWTDYITNVHHPGLRRHVLKGRA--
At3g56700 518 FDIKGLDWEHYIVNVHLPGLKKEFLSKKKTE