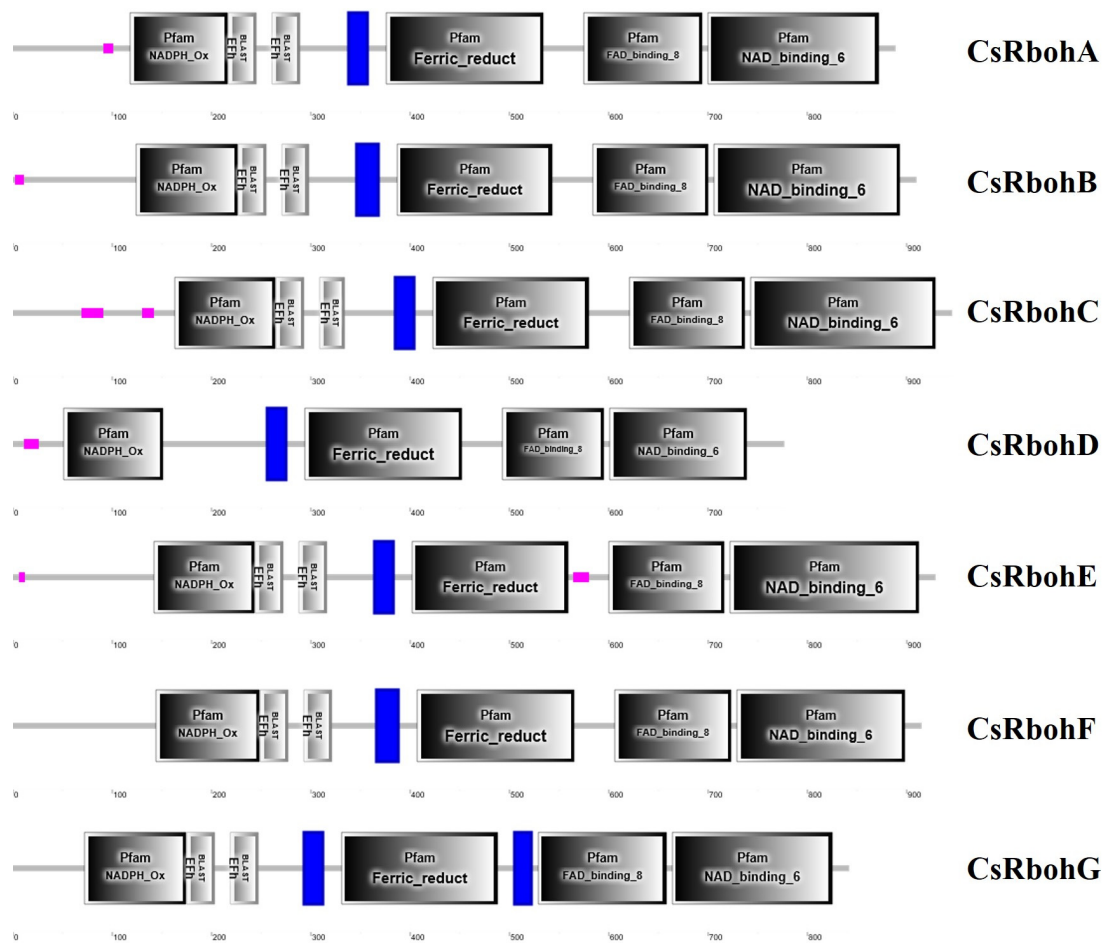
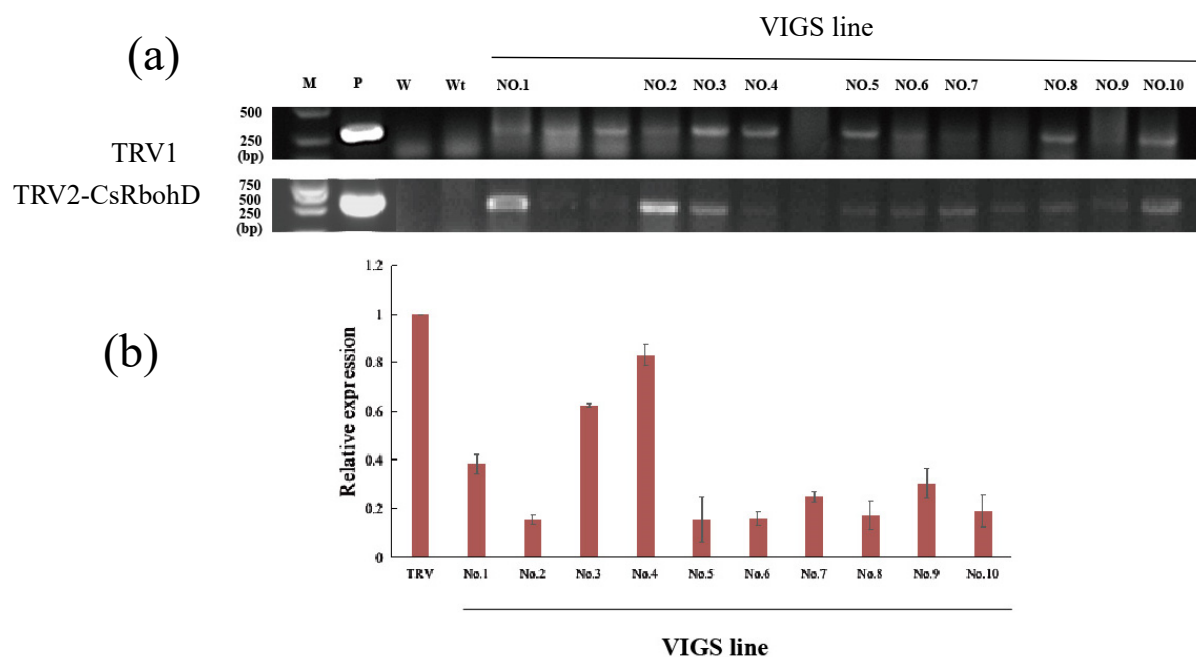


AtRbohA	LNHNEEMQK.....LGFENVRVYTT-ESFVNR.....QSSASNV.....ATTSYVNGVE-DEPVVEITLSINDSS-VSVYVQKSPNHRGAGS-N.....YEDDSLRGQ.....RSGRNSVLKRLA	96
CaRbohA	MDIQDYKDD.....SLSEGTSTSSRVGVSGLPSGLPVT.....TNKKK.....SSRKARFQDQ-DECVVEITLVDDDS-VSVONI R6D.....SETAFLAGR.....LER.....KPS	93
CaRbohB	MRSLRSRSSRS.....NYQRTFF.....ELPDQC-EDPOSRTSDYVGGAAMPVFLN.....DLSRNSQDQG-ADQLVELTIELEHA-VVLVSYSTPTAPA.....RVG	87
CaRbohC	MRGSASHRRW.....ASDTPGRAVVS.....S-ASSPGETSNG-AEEVVEITBLODDTIVLRSEVAP-PHVFSIEDGAGAGSETPSSA.....SPSP	87
CaRbohD	MHAESQETLS.....C-SSSSSSSSSSPSCSACVPLAFSPVOGT-VTV.....	43
CaRbohE	MGTEHHQW.....HHNSDTEVLNERIPVSGPLSGLNKR.....VGRKSTFML.....ATSSSSSSPH-DEPVVEITLVDDDS-VAVHSVKAAGSDNSMLQE.....DPEITLLAKG.....LEKSTSTGSEA	113
CaRbohF	NKMRSEEGRGVYIENNSDTEISQDSKSAFSOPLA.....NKR.....ASKKSARFNLPEAAVTSNNND-DGQVVEITLDRDS-VAVHSVQALH-H.....E.....DPELSLLAKKTLEINKNSSSRSLF	116
CaRbohG	MYGSNSRKHA.....DS.....RSVLESLE-VDRM-VDVPINDRT-SGRVSVKPTT.....APSLR	40
Respiratory burst NADPH oxidase		
AtRbohA	SSVSTQITRVASSVSSSSR.....KPPR-POLAKLR-SK-SRRELALKGLKFTKTDGV.....TQWPEKRFVYVMTMT-TNG.....LHRS	173
CaRbohA	SALSARLRQVSEKLRM-AS.....S.....KRFDKVBR-TK-SQARALKGLKFTKNVGT.....ENQVEKRFDELA.....VDR.....MLPKS	164
CaRbohB	ESGSGSRIFG-WLRD.....SSSDIE.....ERTISARDE-RIKERLOS-AR-SQKRALNGLRFSKTABASDAEQLNKLVSREELA.....EDG.....LLARE	174
CaRbohC	RSSEKKLRHFQELKAE-VAKAKQFSQELKAE LRFSWSHGQASRVLSASTSSSAQNGNFDALAAARAL-KORALDR-TR-SQAKALRLRFSNSSKT-NGVDANNEVOSNKLKLA-KG.....FLYRA	212
CaRbohD	.....PFSAGWNRHYRDASGENLITGLEIIPLRFTN.....LEWTDVEARFORLAYT-KNTEPEVIKWS	101
CaRbohE	RTABAKIRQVSEKLR-AS.....FAKKPOPPARFDR-NK-SAAAYALKGLKFTSKTDG.....ADHANKEKREDEITAS-TNG.....VYRA	190
CaRbohF	RNTSHIVQVSELEKRF-AS.....LTRR-PSRRFDR-TK-SAAAHALKGLKFTTKTSAAG-ONGNPAKFNKYNELAITSDG.....LHCS	195
CaRbohG	RNASITAIRSQA-ML.....QT.....N-SI-RNPAKMR-TA-SGARQGLRLRLDTVTG-KENDAWRSIERZQFA.....VNG.....RLPKD	121
EF-hand domain		
AtRbohA	RFGECIQMK-STEFALALDALARRENVSG-DSINIELKFWKQITDGOFSRLRTFRAMVDKSDGRLEAEVREIITLSASANEKNIRRAQDEYAAIMIELDPRHYHYMIENLEILLQAPMQDVR-DG	305
CaRbohA	SFGQCIQMN-ESKQFASLFDALARRRGLTS-SSITKSELRFQWEDITDOSTFARLETFIDMVQKNLDORITEEVKEIIALSASANKLKIQRVEEYAAIMIELDPHNLQVIELYNLEMLLQAPSGANLLT	298
CaRbohB	DFGECIQMV-DTEKFAVIFDALARRQDKI-OKIMELREEMEDIDOSTFARLQIFDQABSGVDGRIIEVEDELLMSASANKLKEGAEYAAIMIELDPENLVIELWELTLLQDQTYMNY-SR	307
CaRbohC	DQACIQMR-DSKEFALFELDALRRRLKLV-QK-SREELVEYMSQITDOSTFASRLQIFDQVKNNDORIAIEEVEKIIIMLSASANKLRLHQAEYAAIMIELDPRGLQVLEWDELTLQDQTYLNY-SQ	345
CaRbohD	DFFSICIAMQ-OTPEFANEILRALRGSEWKV-DITKHELFDYNNHMA-QEVSRIQLFTYMCORFQKIDQIDMKQITLOSASANKLMTHEAEYAAIMIELDKKRVLELDTFKVSPRASYGRS-SP	322
CaRbohE	DFSGIQMNSDKDFAVELFDALTRRNIGQ-DITKQDLREFWQIDSDOSTFASRLQTFIDMVQKQADGRITTEVEVEIITLSASANKLNIQKAEYAAIMIELDPHLYIIMIDNLEMLLQAPAGSVK-GG	324
CaRbohF	DFFSGIQMKESKEAQLPOLGRKHNIIGQ-DSINKAQLREFWQIDSESTFASRLQTFIDMVQKQADGRITTEVEVEIITLSASANKLNIQKAEYAAIMIELDPHAGVIMIHNLLEMLLQAPAGSVR-VQ	329
CaRbohG	MEGIVQMG-ESTESVQVELEKRRKRVNTENG-LEVEVRFEDMTKKQILBALQ-LEEDICDKDQSG-LTEDVEVEIITLSASANKLNLKENSSTYAAIMIELDQCKQVTEWDELLELMQVNEEPP-...	253
Transmembrane domain		
AtRbohA	EG---KKLSKMLSQNLMPVQSRNLGARFCRGMKYFLDNKKRVVWMLVIGAMAGLTWKFMEKKRSAYEVHMGVQCIKAGAAETLKLMMAILLPVCRNTITWLRTKTLKSAIVPFDRLNFHVIAGIGSVGV	439
CaRbohA	DS---RVLSQMSLSQRLVFTKDRNPRIKCCRGLSYFVODNKKRIWVMLLWLSICAGLTWKFQVKKHRAVFMVGVCTTAKGAAETLKLMMAILLPVCRNTITWLRSRTKLQRVVPFDNINFHVIAGVAGIGV	432
CaRbohB	PLSTSTKSNWSQNLSEFTPKGALRKLSTFTKCLVLEWQDRIWILLWMMAMAGLFAWKTIOYKNMAAFQVGVGLTTAKGAAETLKLMMAILLPVCRNTITWLRS-TRARYVPFDNINFHVIAGVAGIGV	442
CaRbohC	AL---SVTSGALSQNLQDLKKRRIKRMSTFVVEQEWPRRLVLSWILIMDQTTWKFQVKKHRAVFMVGLTTAKGAAETLKLMMAILLPVCRNTITWLRS-TRARYVPFDNINFHVIAGVAGIGV	478
CaRbohD	TF-DLLYHEPMKN.....EVFRSRYWRANVLFVLLCLQVLTWKFQVSHRPAQFQVGVGLSTAKGAAETLKLMMAILLPVCRNTVWLKRWKSSIIIFENDNFHKLACGVGVGV	350
CaRbohE	ES---RNLSHMLSKKKFTQFNPIRCCDSTMYFLLDNRQVWVMAQVIGMAGLTWKTIOYKNRAAFQVHGLVGMKAGAAETLKLMMAILLPVCRNTITWLNRKTLQGVVPFDNINFHVIAGVAGIGV	468
CaRbohF	DS---RLSLSQMSLSQNLQDLKKRRIKRMSTFVVEQEWPRRLVLSWILIMDQTTWKFQVKKHRAVFMVGLTTAKGAAETLKLMMAILLPVCRNTITWLNRKTLQGVVPFDNINFHVIAGVAGIGV	468
CaRbohG	KM---NNRTSTLTKAMIRONYNPTTKFFSMITTEIFIDFKFNIIVTLQVNLVGLTWKTELOSQVGVCTTAKGAAETLKLMMAILLPVCRNTITWLNRKTLQGVVPFDNINFHVIAGVAGIGV	386
Ferric reduct		
AtRbohA	IAATSHLACDPPRLAHADQDEVE-PMKRYFGQPTK-RPLDFQSVGVGVGVGVVULMTAETLATWFRNN-LNPLRLKKITQFNATWYSHHLFVIVVGLFIVHGVFVVLIEPWHKRTWMYLAVPVLVYACER	573
CaRbohA	LHAHAHLCDDPRLAHADQDEVE-PMKRYFGQPTK-RPLDFQSVGVGVGVGVVULMTAETLATWFRNN-LNPLRLKKITQFNATWYSHHLFVIVVGLFIVHGVFVVLIEPWHKRTWMYLAVPVLVYACER	566
CaRbohB	LHGVNHLACDPPRLVNSPPEFA-PMSTQFNHKKP-TYKYLTTQVEQVTOIVMVULMAIAFTLATHKFRNGVRLPSFFNRLTQFNATWYSHHLTAIVVILLIVHGNFLVLA-HEWYKRTWMYLAVPVLVYACER	575
CaRbohC	LHGVNHLACDPPRLVNSPPEFA-PMSTQFNHKKP-TYKYLTTQVEQVTOIVMVULMAIAFTLATHKFRNGVRLPSFFNRLTQFNATWYSHHLTAIVVILLIVHGNFLVLA-HEWYKRTWMYLAVPVLVYACER	612
CaRbohD	LHGVNHLACDPPRLVNSPPEFA-PMSTQFNHKKP-TYKYLTTQVEQVTOIVMVULMAIAFTLATHKFRNGVRLPSFFNRLTQFNATWYSHHLTAIVVILLIVHGNFLVLA-HEWYKRTWMYLAVPVLVYACER	484
CaRbohE	IAHAHLACDPPRLVNSPPEFA-PMSTQFNHKKP-TYKYLTTQVEQVTOIVMVULMAIAFTLATHKFRNGVRLPSFFNRLTQFNATWYSHHLTAIVVILLIVHGNFLVLA-HEWYKRTWMYLAVPVLVYACER	561
CaRbohF	LHAHAHLCDDPRLAHADQDEVE-PMKRYFGQPTK-RPLDFQSVGVGVGVGVVULMTAETLATWFRNN-LNPLRLKKITQFNATWYSHHLFVIVVGLFIVHGVFVVLIEPWHKRTWMYLAVPVLVYACER	567
CaRbohG	VITLTHLLNLY-SSCRPFRKMYLGLPALNVHQR-TYVDLMHTVRYGVGLVLMIAISFSLATSHSENNIKLWIFHRFAENQFWAKHLLVLAVLFMHGQVITFD-KPWMDKTTNIFFRVLFANER	520
FAD-binding domain 8		
AtRbohA	LIARFQEVGAQVLRVAVLPQWGLHLEPQFNRTSSQWVNLGAVTLNHPFSITSAPODDVLSVHIRTLDQWTLQELSLSEVGRPPPP---DEHRFNRRDSKH-----WDVIPQRFILIDGPYGA	609
CaRbohA	LIARFQEVGSYRIKLVAVYFQWNLALQSKRQPFNTSGOQVFNNAAGVQKHPFSITSAPODDVLSHIRTLDQWTLQELSLSEVGRPPPP---ADNRPRPKLLIDGPYGA	602
CaRbohB	LNHTRRSQHSKADKXVSLPQWGLVMSKRNQFRVRSQOYFLOQPTIESFEWHPFSITSAPODDVLSVHIRTLDQWTLQELSLSEVGRPPPP---GATNRRIKRLIDGPYGA	608
CaRbohC	TLHFRRSQHSKADKXVSLPQWGLVMSKRNQFRVRSQOYFLOQPTIESFEWHPFSITSAPODDVLSVHIRTLDQWTLQELSLSEVGRPPPP---GATNRRIKRLIDGPYGA	735
CaRbohD	LYRVRSQIYELINKETPSLVPGLVLSMKKQEFNRYRABVMVFQCPREISFEWHPFSITSAPODDVLSVHIRTLDQWTLQELSLSEVGRPPPP---GATNRRIKRLIDGPYGA	593
CaRbohE	LIARFQEVGAQVLRVAVLPQWGLHLEPQFNRTSSQWVNLGAVTLNHPFSITSAPODDVLSVHIRTLDQWTLQELSLSEVGRPPPP---DEHRFNRRDSKH-----WDVIPQRFILIDGPYGA	714
CaRbohF	LTBALRSIEIPKILKLVAVYFQWNLALHMSKQPFNTSGOQVFNNAAGVQKHPFSITSAPODDVLSVHIRTLDQWTLQELSLSEVGRPPPP---GATNRRIKRLIDGPYGA	721
CaRbohG	FLAKFHLNHLKVEIVNAVITQNLVALYMTKRPQTKVQSGMLVKKRQPLPFEWHPFSITSAPODDVLSVHIRTLDQWTLQELSLSEVGRPPPP---GATNRRIKRLIDGPYGA	656
NAD-binding domain 6		
AtRbohA	PAQDYKFEVLLVLQGLQIATGTFISIVSDIINNLKQVEGSS-N-RROSPH-----NMVTPPVSPSRKSETFRTRKAYFVWVTRQGGSDFWKGMVDEVTETRR-KNVIELHNYQTSVYEEGARSALITN	822
CaRbohA	PAQDYKFEVLLVLQGLQIATGTFISIVSDIINNLKQVEGSS-N-RROSPH-----NMVTPPVSPSRKSETFRTRKAYFVWVTRQGGSDFWKGMVDEVTETRR-KNVIELHNYQTSVYEEGARSALITN	830
CaRbohB	PAQDYKFEVLLVLQGLQIATGTFISIVSDIINNLKQVEGSS-N-RROSPH-----NMVTPPVSPSRKSETFRTRKAYFVWVTRQGGSDFWKGMVDEVTETRR-KNVIELHNYQTSVYEEGARSALITN	830
CaRbohC	PAQDYKFEVLLVLQGLQIATGTFISIVSDIINNLKQVEGSS-N-RROSPH-----NMVTPPVSPSRKSETFRTRKAYFVWVTRQGGSDFWKGMVDEVTETRR-KNVIELHNYQTSVYEEGARSALITN	896
CaRbohD	SSQDYVYKDVLLVLQGLQIATGTFISIVSDIINNLKQVEGSS-N-RROSPH-----NMVTPPVSPSRKSETFRTRKAYFVWVTRQGGSDFWKGMVDEVTETRR-KNVIELHNYQTSVYEEGARSALITN	896
CaRbohE	PAQDYKFEVLLVLQGLQIATGTFISIVSDIINNLKQVEGSS-N-RROSPH-----NMVTPPVSPSRKSETFRTRKAYFVWVTRQGGSDFWKGMVDEVTETRR-KNVIELHNYQTSVYEEGARSALITN	849
CaRbohF	PAQDYKFEVLLVLQGLQIATGTFISIVSDIINNLKQVEGSS-N-RROSPH-----NMVTPPVSPSRKSETFRTRKAYFVWVTRQGGSDFWKGMVDEVTETRR-KNVIELHNYQTSVYEEGARSALITN	835
CaRbohG	PAQDYKFEVLLVLQGLQIATGTFISIVSDIINNLKQVEGSS-N-RROSPH-----NMVTPPVSPSRKSETFRTRKAYFVWVTRQGGSDFWKGMVDEVTETRR-KNVIELHNYQTSVYEEGARSALITN	782
NAD-binding domain 6		
AtRbohA	LSLSNKAHNDVDSVQTRVMSHFAPNWRSGFKRIAVNN.....PKTRVGVFYCGAAGLVKELRHSLDFSHKSTKTFPHKEN	902
CaRbohA	LSLSNKAHNDVDSVQTRVMSHFAPNWRSGFKRIAVNN.....PKTRVGVFYCGAAGLVKELRHSLDFSHKSTKTFPHKEN	889
CaRbohB	LSLSNKAHNDVDSVQTRVMSHFAPNWRSGFKRIAVNN.....PKTRVGVFYCGAAGLVKELRHSLDFSHKSTKTFPHKEN	910
CaRbohC	LSLSNKAHNDVDSVQTRVMSHFAPNWRSGFKRIAVNN.....PKTRVGVFYCGAAGLVKELRHSLDFSHKSTKTFPHKEN	940
CaRbohD	LSLSNKAHNDVDSVQTRVMSHFAPNWRSGFKRIAVNN.....PKTRVGVFYCGAAGLVKELRHSLDFSHKSTKTFPHKEN	777
CaRbohE	LSLSNKAHNDVDSVQTRVMSHFAPNWRSGFKRIAVNN.....PKTRVGVFYCGAAGLVKELRHSLDFSHKSTKTFPHKEN	929
CaRbohF	LSLSNKAHNDVDSVQTRVMSHFAPNWRSGFKRIAVNN.....PKTRVGVFYCGAAGLVKELRHSLDFSHKSTKTFPHKEN	915
CaRbohG	LSLSNKAHNDVDSVQTRVMSHFAPNWRSGFKRIAVNN.....PKTRVGVFYCGAAGLVKELRHSLDFSHKSTKTFPHKEN	842

Supplementary Figure S1. Alignment of the CsRboh protein sequences. The *Arabidopsis* AtRbohA is also included in this analysis. Conserved domains in alignment are highlighted with colored lines, and their names are given above the conserved regions.



Supplementary Figure S2. Domain compositions of CsRboh proteins by SMART analysis. Only major domains (NADPH\_Ox, Ferric\_reduct, FAD\_binding\_8, and NAD\_binding\_6) were presented here. Blue box in figure indicates the trans-membrane domain while pink indicates low complexity region.



Supplementary Figure S3. Molecular characterization of the VIGS plants by genomic PCR and qRT-PCR. (a) Characterization of positive VIGS plants by genomic PCR amplification. (b) Analysis of *CsRbohD* expression in the control (TRV) and VIGS plants using qRT-PCR.