Supplementary Figure legends

Suppl. Figure 1

OsRac1 ^{1}H-^{15}N HSQC spectra.

Pairs of overlying OsRac1 spectra of OsRac1 are shown. Left, OsRac1 alone (red) and in the presence of the wild-type OsRbohB$^{138-313}$ (blue). Right, OsRac1 alone (red) and in the presence of the R273Q/Y277Q mutant of OsRbohB$^{138-313}$ (blue).

Suppl. Figure 2

The highly conserved N-terminal cytoplasmic regions of Rboh proteins.

Sequence alignment of Rboh proteins from Oryza sativa (OsRbohB, A, C, and D), Arabidopsis thaliana (AtRbohC, D, and F), Solanum tuberosum (StRbohA and B), Nicotiana benthamiana (NbRbohA and B), and Nicotiana tabacum (NtRbohD). Identical and homologous residues are shown on yellow and blue background, respectively. EF-hand motifs are indicated above the alignment.

Suppl. Figure 3

Model for the regulation of RbohB in rice innate immunity

The N-terminal cytoplasmic region takes part in an intramolecular interaction with the cytosolic C-terminal region that carries FAD- and NADPH-binding domains. The Rac1 immune complex is composed of several proteins. Rboh probably dimerizes through interaction of the cytoplasmic domains and is regulated by this dimerization and by Ca^{2+}.

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Supplementary Table 1

Structure validation by MolProbity	
clash score, all atoms (percentile)*	20.3 (63rd)
Rotamer outliers (%)	12.2
Cβ deviations > 0.25 Å	0
MolProbity score$^{\wedge}$ (percentile)*	2.9 (35th)
Residues with bad bonds (%)	0.0
Residues with bad angles (%)	0.0

* 100th percentile is the best of comparable resolution; 0th percentile is the worst.

$^{\wedge}$MolProbity score is defined as the following: 0.42574*log(1+clashscore) + 0.32996*log(1+max(0,pctRotOut-1)) + 0.24979*log(1+max(0,100-pctRamaFavored-2)) + 0.5
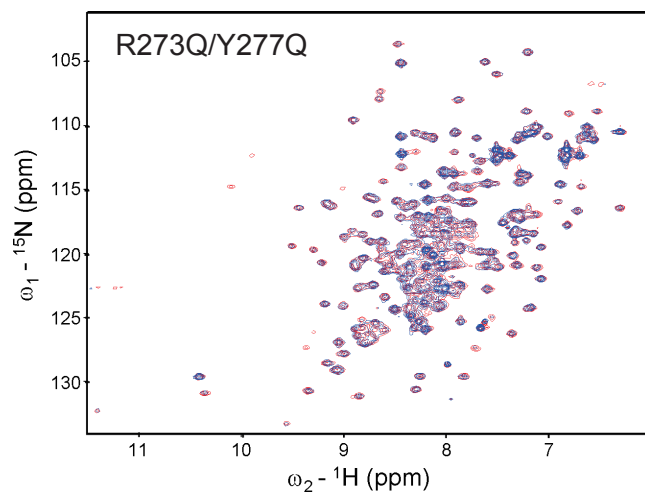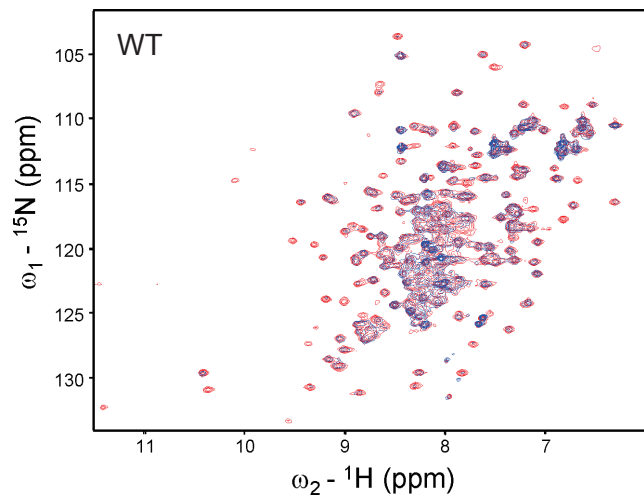
Supplementary figure.1 (Oda *et al.,*)

EF-like1 x   y   z   -y -x -z

	138 140	150	180	170	180	
OsRbohB	T K S S A A V A L K G L Q F V T - A K V G N - D G W A A V E K R F N Q L Q V D - - G V L L R S R F G K					184
OsRbohA	T R S G A H K A L R G L R F I S - S N K A N - N A W M E V Q A N F D R L A R D - - G Y L S R S D F A E					213
OsRbohC	T K S G A Q R A I R G L R F I S G P N K A S - N A W I E V Q A N F D R L A R D - - G Y L S R D D F P Q					221
OsRbohD	T H S S A Q P A L R G L R F L D K T S A G K - D G W K N V E K R F D E M S - A D - G R L P Q E S F A K					98
AtRbohC/RHD2	T K S A A S Q A L K G L K F I A - K T D G G - A G W S A V E K R F N Q I T A T T G G L L L R T K F G E					182
AtRbohD	T S S A A I H A L K G L K F I A - T K T - - - A A W P A V D Q R F D K L S A D S N G L L L S A K F W E					207
AtRbohF	T R S S A Q R A L R G L R F I S - N K Q K N V D G W N D V Q S N F E K F E K N - - G Y I Y R S D F A Q					219
StRbohA	T R S S A H K A L R G L K F I S - N N K - - T N G W N E V E N N F A K L A K D - - G Y L Y R S D F A Q					231
StRbohB	S K S G A A R A L R G L Q F M N - K N V G T - E G W S E V E S R F D Q L A V N - - G M L T K S L F G Q					153
NbRbohA	T R S S A H R A L R G L K F I S - N N K - - T N G W N E V E N N F S K L A K D - - G Y L Y R S D F A Q					229
NbRbohB	N K S A A A H A L K G L K F I S - K T D G G - A G W P A V E K R F D E I T A S T T G L L P R A K F G E					199
NtRbohD	N K S A A A H A L K G L K F I S - K T D G G - A G W A A V E K R F D E I T A S T T G L L P R A K F G E					199

EF-like2 x   y   z   -y   -x -z

	190	200	210	220	230	
OsRbohB	C I G M D - G S D E F A V Q M F D S L A R K R G I V K Q V - L T K D E L K D F Y E Q L T D Q G F D N R					233
OsRbohA	C I G M - T E S K E F A L E L F D T L S R R R Q M K V D T - I N K D E L R E I W Q Q I T D N S F D S R					262
OsRbohC	C I G M - T E S K E F A M E L F D T L S R R R Q M Q V D K - I N K E E L R E I W Q Q I T D N S F D S R					270
OsRbohD	C I G M - A D S K E F A S E V F V A L A R R S I K P E D G I T K E Q L K E F W E E L T D Q N F D S R					148
AtRbohC/RHD2	C I G M T - - S K D F A L E L F D A L A R R N I T G E V - I D G D Q L K E F W E Q I N D Q S F D S R					230
AtRbohD	C L G M N K E S K D F A D Q L F R A L A R R N N V S G D A - I T K E Q L R I F W E Q I S D E S F D A K					256
AtRbohF	C I G M - K D S K E F A L E L F D A L S R R R R L K V E K - I N H D E L Y E Y W S Q I N D E S F D S R					268
StRbohA	C I G M - K D S K E F A L E L F D A L S R R R R L K V D K - I S K E E L Y E Y W S Q I T D Q S F D S R					280
StRbohB	C I G M - K E S S E F A E E L F D A L A R K R C I T S P A - V T K D E L R E F W E Q I T D T S F D A R					202
NbRbohA	C I G M - K D S K E F A L E L F D A L S R R R R L K V D K - I S K E E L Y E Y W S Q I T D Q S F D S R					279
NbRbohB	C I G M N K E S K E F A V E L Y D A L A R R R N I T T D S - I N K A Q L K E F W D Q V A D Q S F D S R					250
NtRbohD	C I G M N K E S K E F A V E L Y D A L A R R R N I T T D S - I N K A Q L K E F W D Q V A D Q S F D S R					249

EF-1 x   y   z   -y -x -z

	240	250	260	270	280	
OsRbohB	L R T F F D M V D K N A D G R L T A E E V K E I I A L S A S A N K L S K I K E R A D E Y T A L I M E E					284
OsRbohA	L Q I F F E M V D K N A D G R I T E A E V K E I I M L S A S A N K L S R L K E Q A E E Y A A L I M E E					313
OsRbohC	L Q I F F D M V D K N A D G H I T E A E V K E I I M L S A S A N K L S R L K E Q A E E Y A A L I M E N					321
OsRbohD	L R I F F D M C D K N G D G Q L T E D E V K E V I V L S A A A N K L A K L K S H A A T Y A S L I M E E					199
AtRbohC/RHD2	L K T F F D M V D K D A D G R L T E D E V R E I I S L S A S A N N L S T I Q K R A D E Y A A L I M E E					281
AtRbohD	L Q V F F D M V D K D E D G R V T E E E V A E I I S L S A S A N K L S N I Q K Q A K E Y A A L I M E E					308
AtRbohF	L Q I F F D I V D K N E D G R I T E E E V K E I I M L S A S A N K L S R L K E Q A E E Y A A L I M E E					319
StRbohA	L Q I F F D M V D K N E D G R I G E E E V K E I I M L S A S A N K L S R L K E Q A E E Y A A L I M E E					331
StRbohB	L Q T F F D M V D K D A D G R I T Q E E V K E I I S L S A S A N K L S K I Q D N S D E Y A A L I M E E					253
NbRbohA	L Q I F F D M V D K N E D G Q I A E E E V K E I I M L S A S A N K L S R L K E Q A E E Y A A L I M E E					330
NbRbohB	L Q T F F D M V D K D A D G R I T E E E V R E I I G L S A S A N R L S T I Q K Q A D E Y A A M I M E E					301
NtRbohD	L Q T F F D M V D K D A D G R I T E E E V R E I I G L S A S A N R L S T I Q K Q A D E Y A A M I M E E					300

EF-2 x   y   z   -y -x -z

	290	300	310	
OsRbohB	L D P T N L G Y I E M E D L E A L L L Q S P S E A A A R S			313
OsRbohA	L D P E G L G Y I E L W Q L E T L L L Q K D T Y M N Y S Q			342
OsRbohC	L N P E Q L G Y I E L W Q L E T L L L Q K D T Y V N Y S Q			350
OsRbohD	L D P D H R G Y I E I W Q L E T L L R G M V T A Q G P P E			228
AtRbohC/RHD2	L D P D N I G Y I M L E S L E T L L L Q A A T Q S V I T S			310
AtRbohD	L D P D N A G F I M I E N L E M L L L Q A P N Q S V R - M			336
AtRbohF	L D P E R L G Y I E L W Q L E T L L L Q K D T Y L N Y S Q			348
StRbohA	L D P E R L G Y I E L W Q L E T L L L Q K D T Y L N Y S Q			360
StRbohB	L D P G N V G Y I E L Y N L E T L L L Q A P S H S M N - -			280
NbRbohA	L D P E R L G Y I E L W Q L E T L L L Q K D T Y L N Y S Q			359
NbRbohB	L D P N N L G Y I M I E N L E M L L L Q A P N Q S V Q R G			330
NtRbohD	L D P N N L G Y I M I E N L E M L L L Q A P N Q S V Q R G			329

Supplementary figure.2 (Oda *et al.,*)

O_2^- O_2

OsRbohB   OsRbohB

EF   EF

FAD   FAD

NADPH   NADPH

C   N   Ⓟ   N   C

OsRac1

Immune complex

Ca^{2+}

?

CDPK
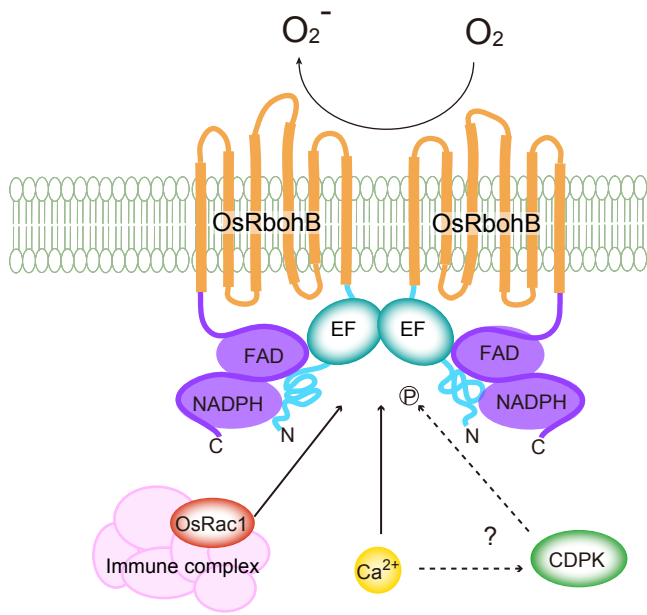
Supplementary figure.3 (Oda *et al.,*)