```
AtRBOHF      ------------------------------------MKPFSKNDR-----RRWSFDSV   17
EsRBOHF      ------------------------------------MRPFSKNDR-----RRWSFDSV   17
AtRBOHD      MKMRRGNSSNDHELGILRGANSDTNSDTESIASDRGAPSGPLGRPKRASKKNARFADDLP   60
EsRBOHD      --MRRGNSGTDHELGILRGANSDTNSDNESIASDRTAFSGPLGRPKRASKKNARFAENLP   58
                                                     *:.: .*      *:: :

AtRBOHF      SAGKTAVGSASTSPGTEYSING-DQEFVEVTIDLQDDDTIVLRSVEPATAINVIGDISDD   76
EsRBOHF      SAGRTAVGSASSSPGTECSNGGYGEEFVEVTIDLQDDDTIVLRSVEPATAINVDISD-EI   76
AtRBOHD      KRSN---SVAGG--------RGDDDEYVEITLDIRDDSVAVHSVQ----------------Q   95
EsRBOHD      RRSN---SVSGGGSGGGRGRGGEDDEYVEITLDIRDDSVAVHSVQ----------------Q   101
               ..   . :.         * .:*:**:*:*::**.. *

AtRBOHF      NTGIMTPVSIRSPTMKRTSSNRFRQFSQELKAEAVAKAKQLSQELKRFSWSRSFSGNLT   136
EsRBOHF      AVGGGGSASIRSRPTMKRTSSNRLRQFSQELKAEAVAKARQLSHELKRFSWSRSLSGTLS   136
AtRBOHD      AAGGGG---HLEDPELALLTKKTLES-------SL-------NNTTSLSFFRSTSSRIK   137
EsRBOHD      AGGGGGGAQHLEDPELTLLTKKTLES--------SL-------NNSTSLSFFRSTSSRIK   146
               *         ..* :   :.: :..         ::       :: . :*: ** *. :.
                                                 Respiratory burst NADPH oxidase
AtRBOHF      TTSTAANQSGGAGGGLVNSALEARALRKQRAQLDFDFSSAQRALRGLRFISNKQKNVDGW   196
EsRBOHF      A---ANQNGGGGGGGLVNSALEARALRKQRAQLDFDFSSAQRALRGLRFISNNNKNVDGW   193
AtRBOHD      NASR----------E-LR-RVFSRRPSPAVRRFDFDSSAAIHALKGLKFIATK---TAAW   182
EsRBOHD      NASR----------E-LR-RVFSRRPSPAVRRFDFDSSAAIHALKGLKFIATK---TAAW   191
                             :.  : :*       ::*** *:* :**:**:**:.:   . .*

AtRBOHF      NDVQSNFEKFE--KNGYIYRSDFAQCIGMK-DSKEFALELFDALSRRRRLKVEKINHDEL   253
EsRBOHF      NHVQTNFEKLS--KNGFIYRSDFAQCIGMK-DSKEFALELFDALSRRRRLKVEKISHDEL   250
AtRBOHD      PAVDQRFDKLSADSNGLLLSAKFWECLGMNKESKDFADQLFRALARRNNVSGDPITTEQL   242
EsRBOHD      PAVDERFEKLSLDSNGLLLSSKFWECLGMNKESKEFADQLFRALARRNNISGDPITTEQL   251
              *: .*:*:.  .** :  :.* :*:**: :**:** :** **:**..:. : *.:::*
                                Calcium binding motif
AtRBOHF      YEYWSQINDESF SRLQIFFDIVDKNEDGRITEEEVKEIIMLSASANKLSRLKEQAEEYA   313
EsRBOHF      YEYWSQINDESFDSRLQIFFDIVDKNEDGRITEEEVKEIIMLSASANKLSRLKEQAEEYA   310
AtRBOHD      RIFWEQISDESFDAKLQVFFDMVDKDEDGRVTEEEVAEIISLSASANKLSNIQKQAKEYA   302
EsRBOHD      RLFWEQISDESFDAKLQVFFDMVDKDEDGRVTEEEVAEIISLSASANKLSNIQKQAKEYA   311
               :*.**.*****::**:***:***:*****:***** *** *********.:::**:***

AtRBOHF      ALIMEELDPERLGYIELWQLETLLLQKDTYLNYSQALSYTSQALSQNLQGLRGKSRIHRM   373
EsRBOHF      ALIMEELDPERLGYIELWQLETLLLQKDTYINYSQALSYTSQALSQNLQGLRKKSRIHRM   370
AtRBOHD      ALIMEELDPDNAGFIMIENLEMLLLQAPNQSVRMGDSRILSQMLSQKLRPAKESNPLVRW   362
EsRBOHD      ALIMEELDPDNAGYIMIENLEMLLLQAPNQSVRIGDSRILSQMLSQKLKPAQESNALMRW   371
             *********:. *:* : :** ****  .           ** ***:*:  : .. : *

AtRBOHF      SSDFVYIMQENWKRIWVLSLWIMIMIGLFLWKFFQYKQKDAFHVMGYCLLTAKGAAETLK   433
EsRBOHF      SSDCVYFMQENWKRIWVLSLWILIMIGLFLWKFFQYKQKDAFHVMGYCLLTAKGAAEILK   430
AtRBOHD      SEKIKYFILDNWQRLWIMMLWLGICGGLFTYKFIQYKNKAAYGVMGYCVCVAKGGAETLK   422
EsRBOHD      SEKIKYFVLDNWQRLWIMMLWLGICAGLFTYKFIQYRNREAYKVMGYCVCIAKGGAETLK   431
             *..  *:: :**:*:*:: **: *  *** :**:**::: *: *****:  ***.** **

AtRBOHF      FNMALILFPVCRNTITWLRS-TRLSYFVPFDDNINFHKTIAGAIVVAVILHIGDHLACDF   492
EsRBOHF      FNMALILFPVCRNTITWLRS-TRLSYFVPFDDNINFHKTIAGAIVVAVILHVGDHLACDF   489
AtRBOHD      FNMALILLPVCRNTITWLRNKTKLGTVVPFDDSLNFHKVIASGIVVGVLLHAGAHLTCDF   482
EsRBOHD      FNMALILLPVCRNTITWLRNKTKLGVVVPFDDNLNFHKVIASGIGVGVLLHAVSHLTCDF   491
             *******:***********. *:*. .*****.:****.**..* *.*:**   **:***

AtRBOHF      PRIVRATEYDYNRYLFHYFQTKQPTYFDLVKGPEGITGILMVILMIISFTLATRWFRRNL   552
EsRBOHF      PRIVRATEYDYNRYLFHYFQQKQPTYFDLVKGPEGITGILMIILMTISFTLATRWFRRNL   549
AtRBOHD      PRLIAADEDTYEP-MEKYFGDQPTSYWWFVKGVEGWTGIVMVVLMAIAFTLATPWFRRNK   541
EsRBOHD      PRLLAADEDTYEP-MEKYFGEQPESYWWFVKGVEGWTGIVMVVLMAIAFTLATPWFRRNK   550
             **:: * *  *:  : :**  :  :*: :*** ** ***:*::** *:***** *****

AtRBOHF      VKLPKPFDRLTGFNAFWYSHHLFVIVYILLILHGIFLYFAKPWYVRTTWMYLAVPVLLYG   612
EsRBOHF      VKLPKPFDRLTGFNAFWYSHHLFVIVYILLILHGIFLYFAKPWYVHTTWMYLSVPILLYG   609
AtRBOHD      LNLPNFLKKLTGFNAFWYTHHLFIIVYALLIVHGIKLYLTKIWYQKTTWMYLAVPILLYA   601
EsRBOHD      LNLPKFLKKLTGFNAFWYSHHLFIIVYALLIVHGIKLYLTKIWYQKTTWMYLAVPILLYA   610
             ::**: :.:*********:****:*** ***:*** **::* ** :******:**:***.
                      FAD-binding domain
AtRBOHF      GERTLRYFRSGSYSVRLLKVAIYPGNVLTLQMSKPTQFRYKSGQYMFVQCPAVSPFEWHP   672
EsRBOHF      GERTLRYFRSGSYSVRLLKVAIYPGNVLTLQMSKPSQFRYKSGQYMFVQCPAVSPFEWHP   669
AtRBOHD      SERLLRAFRSSIKPVKMIKVAVYPGNVLSLHMTKPQGFKYKSGQFMLVNCRAVSPFEWHP   661
EsRBOHD      SERLIRAFRSSIKPVKMLKVAVYPGNVLSLHMTKPQGFKYKSGQYMFVNCRAVSPFEWHP   670
             .** :* ***.   *:::***:******:*:*:**  *:*****:*:*:* *********

AtRBOHF      FSITSAPEDDYISIHIRQLGDWTQELKRVFSEVCEPPVGGKSGLLRADETT-KKSLPKLL   731
EsRBOHF      FSITSAPEDDYISIHIRQLGDWTQELKRVFSEVCEPPVAGKSGLLRADETT-KKSLPKLL   728
AtRBOHD      FSITSAPGDDYLSVHIRTLGDWTRKLRTVFSEVCKPPTAGKSGLLRADGGDGNLPFPKVL   721
EsRBOHD      FSITSAPGDDYLSVHIRTLGDWTRKLRTVFSEVCKPPMAGKSGLLRADGE-DNIAFPKVL   729
             ******* ***:*:*** *****::*: ******:** .*********    :  :**:*
                      Ferric reductase NAD binding domain
AtRBOHF      IDGPYGAPAQDYRKYDVLLLVGLGIGATPFISILKDLLNNIVKMEEHADSISDFSRSSEY   791
EsRBOHF      IDGPYGAPAQDYRKYDVLLLVGLGIGATPFISILKDLLNNIIKMEEQADSISDFSRSSEP   788
AtRBOHD      IDGPYGAPAQDYKKYDVVLLVGLGIGATPMISILKDIINNMKGPDRDSDIE---------   772
EsRBOHD      IDGPYGAPAQDYKKYDVVLLVGLGIGATPMISIVKDIINNMKSHDSDIES----------   779
             ************:****:***********:***:**::**:   : . :

AtRBOHF      STGSNG--DTPRRKRILKTTNAYFYWVTREQGSFDWFKGVMNEVAELDQRGVIEMHNYLT   849
EsRBOHF      STGSNSDNNTPRRKRILKTTNAYFYWVTREQGSFDWFKGVMNEVAELDQRGVIEMHNYLT   848
AtRBOHD      ------NNNSNNNSKGFKTRKAYFYWVTREQGSFEWFKGIMDEISELDEEGIIELHNYCT   826
EsRBOHD      ------NTNSNGNSKGFKTTKAYFYWVTREQGSFEWFKGIMDEVSELDEEGVIELHNYCT   833
                   ::  ..: :** :*************:****:*:*::***:.*:**:*** *

AtRBOHF      SVYEEGDARSALITMVQALNHAKNGVDIVSGTRVRTHFARPNWKKVLTKLSSKHCNARIG   909
EsRBOHF      SVYEEGDARSALITMVQALNHAKNGVDIVSGTRVRTHFARPNWKKVLSKLSSKHCNARIG   908
AtRBOHD      SVYEEGDARVALIAMLQSLQHAKNGVDVVSGTRVKSHFAKPNWRQVYKKIAVQHPGKRIG   886
EsRBOHD      SVYEEGDARVALIAMLQSLQHAKNGVDVVSGTRVKSHFAKPNWRQVYKKIAVQYPGKRIG   893
             ********* ***:*:*:*:*******:******::***:***::* .*:: :: . ***

AtRBOHF      VFYCGVPVLGKELSKLCNTFNQKGSTKFEFHKEHF   944
EsRBOHF      VFYCGVPVLGKELSKLCNTFNQKGSTKFEFHKEHF   943
AtRBOHD      VFYCGMPGMIKELKNLALDFSRKTTTKFDFHKENF   921
EsRBOHD      VFYCGAPGLTKELKNLALDFSRKTTTKFDFHKENF   928
             ***** * : ***.:*.  *.:* :***:****:*
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Fig. S1. The multiple alignment of RBOHD and RBOHF amino acids in *Arabidopsis thaliana* and *Eutrema salsugineum* constructed using EMBL-EBI Clustal OMEGA tool (https://www.ebi.ac.uk/Tools/msa/clustalo/). (*) indicate full conservation among all sequences, (:) highly conservative exchanges and (.) conservative exchanges of amino acids. The black color highlights the Respiratory burst NADPH oxidase domain (PF08414). The FAD-binding domain (PF08022) is indicated with a straight line above the alignment. The grey color marks Ferric reductase NAD binding domain (PF08030) and the box identifies calcium binding motif (cd00051). The conserved motifs were identified using NCBI Batch CD-Search online tool (https://www.ncbi.nlm.nih.gov/Structure/bwrpsb/bwrpsb.cgi).

Table S1. Selected parameters of tap water used for irrigation according to the information provided by the Kraków waterworks (Wodociągi Miasta Krakowa S.A.) at website https://en.wodociagi.krakow.pl/.

pH	7.6
NH_4^+	0.017 mg/dm^3
NO_2^-	< 0,01 mg/dm^3
NO_3^-	15,6 mg/dm^3
Cl^-	39,7 mg/dm^3
Ca	96 mg/dm^3
Mg	12 mg/dm^3
Fe	< 0,025 mg/dm^3
Cu	< 0,003 mg/dm^3
Cr	< 0,002 mg/dm^3
Cd	< 0,00045 mg/dm^3
Chloroform	< 0,3 μg/dm^3

Table S2. PCR primers used for quantitative RT-PCR.

Gene name	**Gene reference**	**5´ – 3´ primer sequence**	**Product size (bp)**	**Amplific. Efficiency (%)**
AtRBOHD	At5g47910	GGTTAAGATGATCAAGGTGGCT TCCTTGTGGCTTCGTCATGT	70	100
AtRBOHF	At1g64060	ACGGGGTGTGATAGAGATGC GCAAAGTGTGTTCTGACCCT	150	104
AtAT5G	At5g13440	CTTTCCCGTGACCATACCCT AGCAAAACCTCTTATAACGCTCC	120	100
EsRBOHD	Thhalv10003619m	CACTTCGCCAAACCCAACTG GAAGACTCCGATTCGTTTGCC	78	99
EsRBOHF	Thhalv10023240m	ATGGAAGAGCAAGCGGATTC GCCTTGTTCTCTTGTGACCC	147	100
EsAPT1	Thhalv10008627m	GTCCGACTACTTGAGCGAGT CCCTTCCCTTACACTCTGGT	79	100