

Supplement to

A novel target (Oxidation Resistant 2) in *Arabidopsis thaliana* to reduce clubroot disease symptoms via the salicylic acid pathway without growth penalties

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Supplementary Tables

Tables S1 and S2 can be found as separate excel files. The legends are in the following:

Table S1. Genesect interaction and GO analysis between the transcriptomic data of *AtOXR2-OE* plants (Colombatti et al. [39]) and different clubroot transcriptome data. **A.** Data available in Siemens et al. [50], **B.** Data available in Agarwal et al. [24], **C.** Data available in Jubault et al. [53], **D.** Data available from Siemens [51], **E.** Data available in Irani et al. [54].

Table S2. Genesect interaction and GO analysis between the transcriptomic data of *AtOXR2-OE* plants (Colombatti et al. [39]) and *AtKIN10-OE* plants (=SnRK1) [56]. **A.** Genesect *KIN10-OE* up-regulated and *AtOXR2-OE* up-regulated ($p < 0.001$), **B.** GO enrichment (Molecular Function) in the Genesect list present in (A) from *KIN10-OE* up-regulated and *AtOXR2-OE* up-regulated ($p < 0.001$).

Supplementary Figures

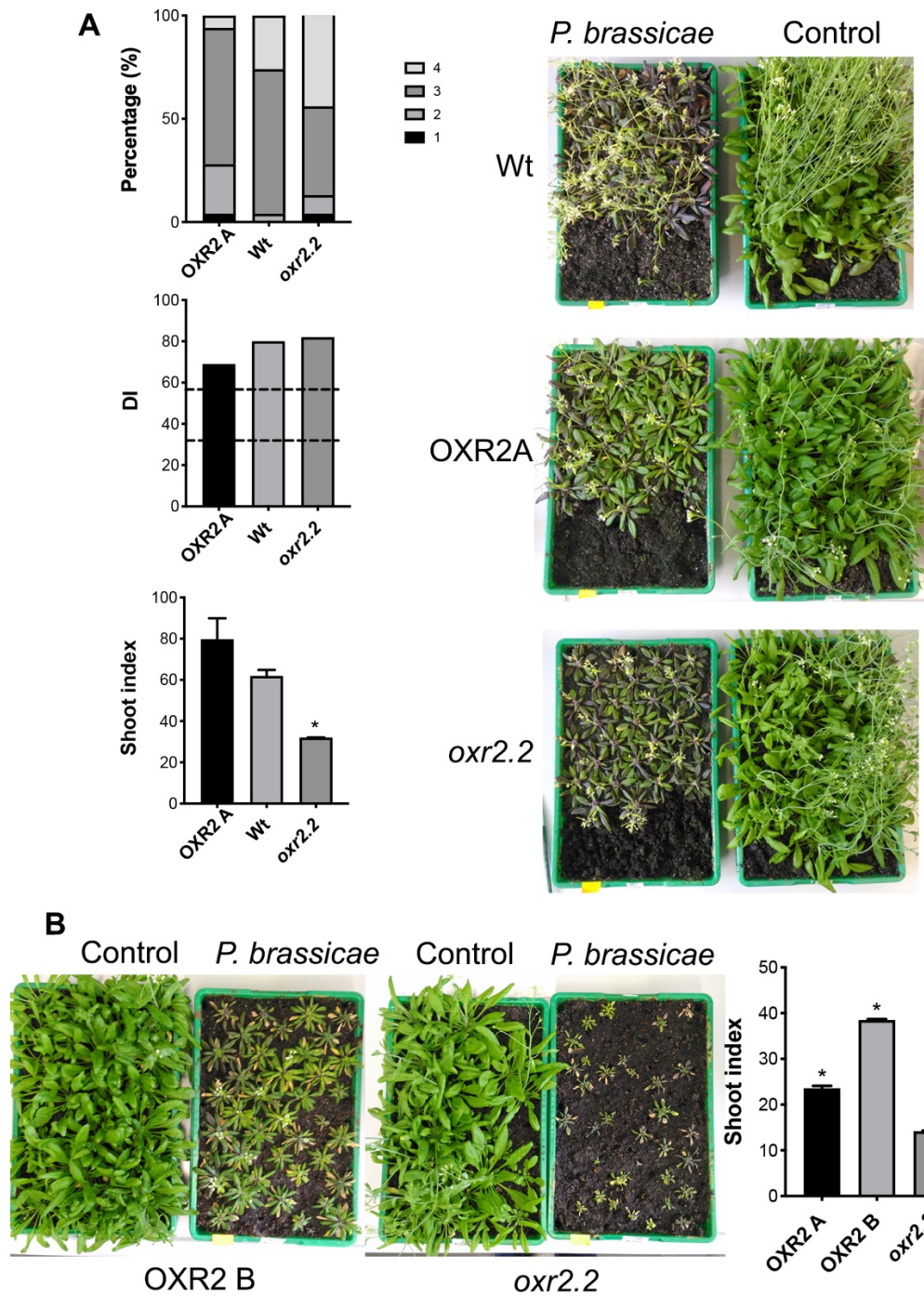


Figure S1. Data from the individual additional infection experiments. Upper plant parts of representative trays after inoculation of Col-0, *oxr2*, OXR2-OE plants with 10^6 spores ml^{-1} of *P. brassicae*. The controls were inoculated with the buffer only that had been used to resuspend the resting spores of the pathogen (see methods). The data were evaluated 28 dai. As a measure for disease severity the Disease Index (DI), the percentage of plants in individual disease classes and the shoot index (shoot dry weight of infected vs control plants) are given. A low disease index and high shoot index stands for more tolerant plants. For calculation of the DI see methods. Disease class 2 = small galls; class 3 = large galls, but roots still present, 4 = large galls and no roots present. Results are expressed as mean \pm SD (n=20). Asterisks indicate significant differences between genotypes at $p < 0.01$ (*) (ANOVA, LSD Fisher test).

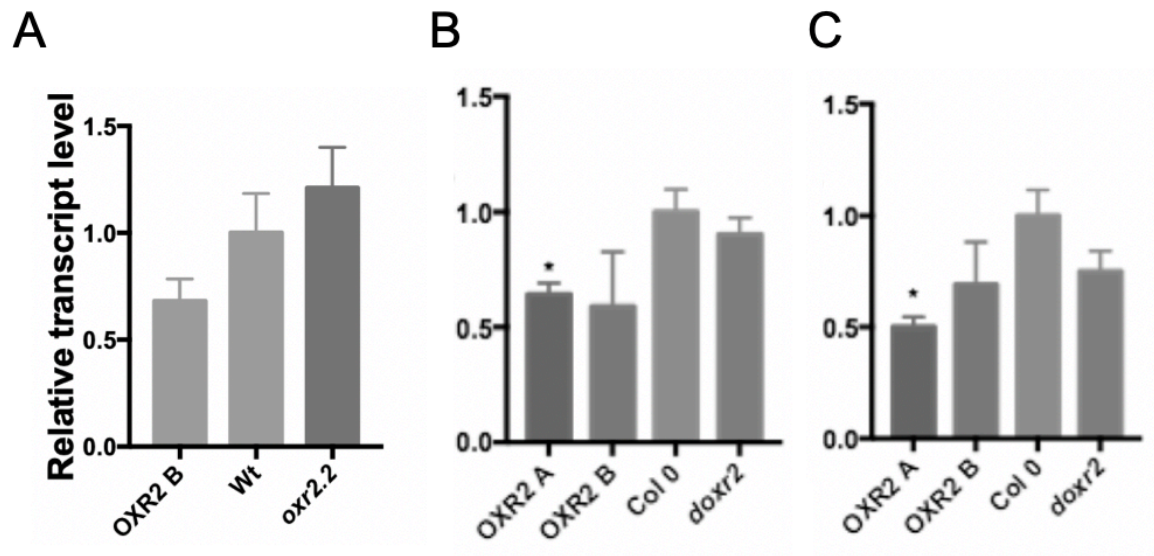


Figure S2. *PbBSMT* expression normalized to the plant genes *AtActin* (A), *AtYLS8* (B) and *AtE2FB* (C) in roots 20 dai in *OXR2 A* and *B* overexpressor lines and mutant *oxr2* plants. Results are expressed as mean \pm SD. Asterisks (*) indicate significant differences of thres biological replicates of each genotype at $p < 0.01$ (ANOVA, LSD Fisher test).

AT2G05590.2	MHALKDKVSQ	KLSNLFADSP	SQSASPRYS	---	NSDSPKA	RLNSSVGKSL	SSYFSFVVPQ
KAG2307096.1:1-289	MHALKDKVSQ	KLSNIFADSA	SQSASPRYS	---	LANSPPKA	RLHSNSGKTI	SSYFSGGGRQ
XP_013630309.1:1-281	MHALKDKVSQ	KLSNLFADSP	SQSASPRHS	---	LTDSPKA	S-----AKSF	TSYFSFGARN
VDC94483.1:51-336	MHALKDKVSQ	KLSNLFADSP	SQSASPRHS	---	LTDSPKA	S-----AKSF	TSYFSFGARN
KAG2298031.1:1-285	MHALKDKVSQ	KLSNLFADSP	SQSASPRHS	---	LTDSPKA	S-----GKSF	TSYFSFGAGN
XP_013736753.1:1-279	MHALKDKVSQ	KLSNLFADSP	SQSASPRHS	---	LTDSPK	-----ASGKSF	TSYFSFGARN
CAF1706006.1:1-280	MHALKDKVSQ	KLSNLFADSP	SQSASPRHS	---	LTDSPKA	S-----GKSF	TSYFSFGARN
KAH0892022.1:1-293	MHALKDKVSQ	KLSNLFADSP	SQSASPRHS	---	LTDSPKA	S-----AKSF	TSYFSFGARN
XP_009136175.1:47-322	MHALKDKVSQ	KLSNLFADSP	SQSASPRHS	---	LTDSPK	-----ASGKSF	TSYFSFGARN
VDC82381.1:1-286	MHALKDKVSQ	KLSNLFADSP	SQSASPRHS	---	LTDSPKV	YLLHASGKSF	TSYFSFGARN
KAH0934687.1:1-284	MHALKDKVSQ	KLSNLFADSP	SQSASPRHS	---	LTDSPK	-----ASGKSF	TSYFSFGARN
CAG7883155.1:1-281	MHALKDKVSQ	KLSNLFADSP	SQSASPRHS	---	LTDSPK	-----ASGKSF	TSYFSFGARN
KAG2266312.1:1-273	MHALKDKVSQ	KLSNLFAD--	-SASSPGYS	---	LTDSPKA	RLDSSNGKTF	SSYFPFGVRO
KAG5406516.1:47-304	MHALKDKVSQ	KLSNLFADSP	SQSASPRHS	---	LTDSPKA	S-----GKSF	TSYFSFGARN
KAF3486982.1:89-321	-----	-----	-----	---	---	A RLDSSSGKTF	SSYFPFGVRO
KAF2577258.1:4-152	-----	-----	-----	---	-----	-----	-----
KAF3597939.1:40-359	-----	-----	SSPLFST	---	DNPNLGTIFA	RLDSSSGKTF	SSYFLFGVRO
VDD35845.1:1-237	MHALKDKVSQ	KLSNLFADSA	S-----SPGYS	---	LTDSPKA	RLDSSSGKTF	SSYFPFGVRO
CAF1958953.1:1-236	MHALKDKVSQ	KLSNPFAD--	-SASSPGYS	---	LTDSPKA	RFK-FSGKTF	SSYFPFGVRO
KAF3544870.1:1-125	-----	-----	-----	---	-----	-----	-----
KAH0867696.1:1-227	MHALKDKVSQ	KLSNPFAD--	-SASSPGYS	---	LTDSPKA	RFK-FSGKTF	SSYFPFGVRO
XP_013593492.1:134-355	-----	-----	-----	---	-----	-----	-----
VDD41136.1:134-355	-----	-----	-----	---	-----	-----	-----
XP_013707691.1:134-355	-----	-----	-----	---	-----	-----	-----
KAG2245011.1:134-355	-----	-----	-----	---	-----	-----	-----
KAF2550874.1:176-349	-----	-----	-----	---	-----	-----	-----
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XP_009138553.1:131-330	-----	-----	-----	---	-----	-----	-----
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RIA05694.1:157-330	-----	-----	-----	---	-----	-----	-----
CAF2032809.1:134-356	-----	-----	-----	---	-----	-----	-----
KAF3600741.1:110-283	-----	-----	-----	---	-----	-----	-----
XP_013591161.1:134-307	-----	-----	-----	---	-----	-----	-----
KAF3601288.1:111-286	-----	-----	-----	---	-----	-----	-----
KAF2587732.1:205-386	-----	-----	-----	---	-----	-----	-----
XP_009128589.1:96-269	-----	-----	-----	---	-----	-----	-----
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KAH0867697.1:42-180	-----	FC ASHPLFADSA	SQSASPRYS	---	LTDSPKA	RLNSNSGKTF	SSYFSFGVRO
KAG2266311.1:29-128	-----	-----	LFADSA	---	LTDSPKA	RLNSNSGKTF	SSYFSFGVRO
CAF1958958.1:28-127	-----	-----	LFADSA	---	LTDSPKA	RLNSNSGKTF	SSYFSFGVRO
KAF3597932.1:164-263	-----	-----	LFADSA	---	LTDSPKA	RLISNSGKTF	SSYFSFGVRO
XP_022562822.1:1-105	MHALKDKVSQ	KLSNPFAD--	-SASSPGYS	---	LTDSPKA	RFK-FSGKTF	SSYFPFGVRO
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KAF3590199.1:179-216	-----	-----	-----	---	-----	-----	-----
KAG2306043.1:144-182	-----	-----	-----	---	-----	-----	-----

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XP_013630309.1:1-281	VFGAMLECPL	ITT	-----	-----	PKRKYC	-----	-----
VDC94483.1:51-336	VFGAMLECPL	ITT	-----	-----	PKRKYCA	CL	U
KAG2298031.1:1-285	VFGALVECPL	ITT	-----	-----	PKRKYC	-----	-----
XP_013736753.1:1-279	VFGAMLECPL	ITT	-----	-----	PKRKYC	-----	-----
CAF1706006.1:1-280	VFGAMLECPL	ITT	-----	-----	PKRKYCA	CL	U
KAH0892022.1:1-293	VFGAMLECPL	ITT	-----	-----	PKRKYCA	CL	LLVVMIFA
XP_009136175.1:47-322	VFGAMLECPL	ITT	-----	-----	PKRKYC	-----	-----
VDC82381.1:1-286	VFGAMLECPL	ITT	-----	-----	PKRKYCA	CLLL	-----
KAH0934687.1:1-284	VFGAMLECPL	ITT	-----	-----	PKRKYCA	CLLL	-----
CAG7883155.1:1-281	VFGAMLECPL	ITT	-----	-----	PKRKYCA	CLLL	-----
KAG2266312.1:1-273	VFGAMLECPL	RIT	-----	-----	PKRKYC	-----	-----
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XP_013707691.1:134-355	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
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KAF2550874.1:176-349	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
XP_013738555.1:154-327	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
XP_009138553.1:131-330	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
KAF3590200.1:291-512	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
KAF3590200.1:134-271	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
KAG5407885.1:130-326	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
KAG2238657.1:197-370	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
RIA05694.1:157-330	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
CAF2032809.1:134-356	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
KAF3600741.1:110-283	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
XP_013591161.1:134-307	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
KAF3601288.1:111-286	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
KAF2587732.1:205-386	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
XP_009128589.1:96-269	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
RID77147.1:96-269	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
KAF2543411.1:114-287	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
KAG2242019.1:110-284	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
KAH0940452.1:96-270	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
CAG7886012.1:59-273	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
XP_022550071.1:132-305	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
XP_033143637.1:131-351	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
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VDD47700.1:117-291	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
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CAF2067211.1:117-291	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
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XP_022572850.1:154-289	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
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KAF3542567.1:7-75	-----	-----	-----	-----	-----	-----	-----
KAH0900489.1:136-305	VFGGLVEAPL	IPDCK	-----	-----	YC	-----	-----
KAF3511568.1:1-61	-----	-----	-----	-----	-----	-----	-----
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KAG2266311.1:29-128	-----	-----	-----	-----	-----	-----	-----
CAF1958958.1:28-127	-----	-----	-----	-----	-----	-----	-----
KAF3597932.1:164-263	-----	-----	-----	-----	-----	-----	-----
XP_022562822.1:1-105	-----	-----	-----	-----	-----	-----	-----
KAG2325584.1:107-169	-----	-----	-----	-----	-----	-----	-----
KAF3590199.1:179-216	-----	-----	-----	-----	-----	-----	-----
KAG2306043.1:144-182	LVKAPL	IPDCK	-----	-----	YC	-----	-----

Accession	Position	Sequence	Accession	Position	Sequence	Accession	Position	Sequence
AT2G05590.2		-GTSQTFLFT			-TIYG	EPRIFRPT		-GANNYYLMC
KAG2307096.1:1-289		-GSNOTFMFT			-TIYG	QPRIFRPT		-GANNYYMYC
XP_013630309.1:1-281		-GTSQTFLFT			-TIYG	QPRIFRPT		-GANNYYMYC
VDC94483.1:51-336		LGTSTQFLFT			-TIYG	QPRIFRPT		-GANNYYMYC
KAG2298031.1:1-285		-GTSQTFLFT			-TIYG	QPRIFRPT		-GANNYYMYC
XP_013736753.1:1-279		-GTSQTFLFT			-TIYG	QPRIFRPT		-GANNYYMYC
CAP1706006.1:1-280		LGTSTQFLFT			-TIYG	QPRIFRPT		-GANNYYMYC
KAH0892022.1:1-293		LGTSTQFLFT			-TIYG	QPRIFRPT		-GANNYYMYC
XP_009136175.1:47-322		-GTSQTFLFT			-TIYG	QPRIFRPT		-GANNYYMYC
VDC82381.1:1-286		-GTSQTFLFT			-TIYG	QPRIFRPT		-GANNYYMYC
KAH0934687.1:1-284		-GTSQTFLFT			-TIYG	QPRIFRPT		-GANNYYMYC
CAG7883155.1:1-281		-GTSQTFLFT			-TIYG	QPRIFRPT		-GANNYYMYC
KAG2266312.1:1-273		-GTNQTFLFT			-T	-LY		-GQPRIF
KAG5406516.1:47-304		-GTSQTFLFT			-TIYG	QPRIFRPT		-GANNYYMYC
KAP3486982.1:89-321								-ANNYYMYC
KAP2577258.1:4-152		-GTSQTFLFT			-TIYG	QPRIFRPT		-GANNYYMYC
KAP3597939.1:40-359		-AVSPSPFLLE			-QSYG	QLNCCYKPKK	DRVSLVDDGK	GVPTDITC
VDD35845.1:1-237		-SSPCFFMI			-PKQL	NLPINLGA		-GANNYYMYC
CAP1958953.1:1-236		-SSPCFFMI			-PKQL	NLPINLGA		-GANNYYMYC
KAP3544870.1:1-125		-GTSQTFLFT			-TIYG	QPRIFRPT		-GANNYYMYC
KAH0867696.1:1-227		-SSPCFFMI			-PKQL	QPRIFRPT		-ANNYYMYC
XP_013593492.1:134-355		-GTNSTFVFT			-DKSG	OPTIYRPT		-GANNFYTLC
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XP_013707691.1:134-355		-GTNSTFVFT			-DKSG	OPTIYRPT		-GANNFYTLC
KAG2245011.1:134-355		-GTNSTFVFT			-DKSG	OPTIYRPT		-GANNFYTLC
KAP2550874.1:176-349		-GTNSTFVFT			-DKSG	OPTIYRPT		-GANNFYTLC
XP_013738555.1:154-327		-GTNSTFVFT			-DKSG	OPTIYRPT		-GANNFYTLC
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KAP3590200.1:291-512		-GTNSTFVFT			-DKSG	OPTIYRPT		-GANNFYTLC
KAP3590200.1:134-271		-ETT						
KAG5407885.1:130-326		-GTNSTFVFT			-DKSG	OPTIYRPT		-GANNFYTLC
KAG2238657.1:197-370		-GTNSTFVFT			-DKSG	OPTIYRPT		-GANNFYTLC
RIA05694.1:157-330		-GTNSTFVFT			-DKSG	OPTIYRPT		-GANNFYTLC
CAP2032809.1:134-356		-GTNSTFVFT			-DKSG	OPTIYRPT		-GANNFYTLC
KAP3600741.1:110-283		-GTNNFVFT			-TDKSG	OPTVYHP		-GANNFYTLC
XP_013591161.1:134-307		-GTNNFVFT			-TDKSG	OPTVYHP		-GANNFYTLC
KAP3601288.1:111-286		-GTNNFVFT			-TDKSG	OPTVYHP		-GANNFYTLC
KAP2587732.1:205-386		-GTNNFVFT			-TDKSG	OPTVYHS		-GANNFYTLC
XP_009128589.1:96-269		-GTNNFVFT			-TDKSG	OPTIYHS		-GANNFYTLC
RID77147.1:96-269		-GTNNFVFT			-TDKSG	OPTVYHS		-GANNFYTLC
KAP2543411.1:114-287		-GTNNFVFT			-TDKSG	OPTVYHS		-GANNFYTLC
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KAH0940452.1:96-270		-GTNNFVFT			-DKSG	OPTVYHST		-GANNFYTLC
CAG7886012.1:59-273		-GTNNFVFT			-DKSG	OPTVYHST		-GANNFYTLC
XP_022550071.1:132-305								

AT2G05590.2	MNEFLAFGGG	GSPALCLDED	LLKATSGPSE	TFGNECLASS	TEFELKNVEL	NGFAHASQYL
KAG2307096.1:1-289	MNEFLAFGGG	GSPALCLDED	LLKATSGPSE	TFGNECLASS	TEFELKNVEL	NGFAHASQYL
XP_013630309.1:1-281	MNEFLAFGGG	GSPALCLDED	LLKATSGPSE	TFGNECLASS	TEFELKNVEL	NGFAHASQYL
VDC94483.1:51-336	MNEFLAFGGG	GSPALCLDED	LLKATSGPSE	TFGNECLASS	TEFELKNVEL	NGFAHASQYL
KAG2298031.1:1-285	MNEFLAFGGG	GSPALCLDED	LLKATSGPSE	TFGNECLASS	TEFELKNVEL	NGFAHASQYL
XP_013736753.1:1-279	MNEFLAFGGG	GSPALCLDED	LLKATSGPSE	TFGNECLASS	TEFELKNVEL	NGFAHASQYL
CAF1706006.1:1-280	MNEFLAFGGG	GSPALCLDED	LLKATSGPSE	TFGNECLASS	TEFELKNVEL	NGFAHASQYL
KAH0892022.1:1-293	MNEFLAFGGG	GSPALCLDED	LLKATSGPSE	TFGNECLASS	TEFELKNVEL	NGFAHASQYL
XP_009136175.1:47-322	MNEFLAFGGG	GSPALCLDED	LLKATSGPSE	TFGNECLASS	TEFELKNVEL	NGFAHASQYL
VDC82381.1:1-286	MNEFLAFGGG	GSPALCLDED	LLKATSGPSE	TFGNECLASS	TEFELKNVEL	NGFAHASQYL
KAH0934687.1:1-284	MNEFLAFGGG	GSPALCLDED	LLKATSGPSE	TFGNECLASS	TEFELKNVEL	NGFAHASQYL
CAG7883155.1:1-281	MNEFLAFGGG	GSPALCLDED	LLKATSGPSE	TFGNECLASS	TEFELKNVEL	NGFAHASQYL
KAG2266312.1:1-273	MNEFLAFGGG	GSPALCLDED	LLKATSGPSE	TFGNECLASS	TEFELKNVEL	NGFAHASQYL
KAG5406516.1:47-304	MNEFLAFGGG	GSPALCLDED	LLKATSGPSE	TFGNECLASS	TEFELKNVEL	NGFAHASQYL
KAF3486982.1:89-321	MNEFLAFGGG	GSPALCLDED	LLKATSGPSE	TFGNECLASS	TEFELKNVEL	NGFAHASQYL
KAF2577258.1:4-152	MNEFLAFGGG	GSPALCLDED	LLKATSGPSE	TFGNECLASS	TEFELKNVEL	NGFAHASQYL
KAF3597939.1:40-359	MNEFLAFGGG	GSPALCLDED	LLKATSGPSE	TFGNECLASS	TEFELKNVEL	NGFAHASQYL
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KAH0867696.1:1-227	MNEFLAFGGG	GSPALCLDED	LLKATSGPSE	TFGNECLASS	TEFELKNVEL	NGFAHASQYL
XP_013593492.1:134-355	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
VDD41136.1:134-355	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
XP_013707691.1:134-355	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
KAG2245011.1:134-355	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
KAF2550874.1:176-349	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
XP_013738555.1:154-327	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
XP_009138553.1:131-330	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
KAF3590200.1:291-512	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
KAF3590200.1:134-271	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
KAG5407885.1:130-326	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
KAG2238657.1:197-370	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
RIA05694.1:157-330	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
CAF2032809.1:134-356	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
KAF3600741.1:110-283	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
XP_013591161.1:134-307	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
KAF3601288.1:111-286	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
KAF2587732.1:205-386	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
XP_009128589.1:96-269	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
RID77147.1:96-269	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
KAF2543411.1:114-287	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
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KAG5412509.1:371-544	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
KAG2238658.1:148-367	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
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KAF3528724.1:114-303	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
XP_022572850.1:154-289	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
XP_022568108.1:96-231	SKDFLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
KAF2615699.1:16-84	MNEFLAFGGG	GSPALCLDED	LLKATSGPSE	TFGNECLASS	TEFELKNVEL	NGFAHASQYL
KAF3542567.1:7-75	MNEFLAFGGG	GSPALCLDED	LLKATSGPSE	TFGNECLASS	TEFELKNVEL	NGFAHASQYL
KAH0900489.1:136-305	SKDLLALGGG	GRFALYLDSE	LLSGSSAYSE	TYGNACLATS	QDFDVKEVEL	NGFVYGSXY
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KAG2306043.1:144-182	---	---	---	---	---	---

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VDD35845.1:1-237
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KAH0867696.1:1-227
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VDD41136.1:134-355
XP_013707691.1:134-355
KAG2245011.1:134-355
KAF2550874.1:176-349
XP_013738555.1:154-327
XP_009138553.1:131-330
KAF3590200.1:291-512
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KAG5407885.1:130-326
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XP_022568108.1:96-231
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XP_022562822.1:1-105
KAG2325584.1:107-169
KAF3590199.1:179-216
KAG2306043.1:144-182

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Figure S3. Multiple sequence alignment for *Brassica* OXR2 homologs in comparison with *Arabidopsis thaliana*. Protein sequence alignment and the phylogenetic tree were built using the Seaview 4.5.0 software and the PhyML-aLRT-SH-LIKE algorithm [48] with maximum likelihood tree reconstruction. *Brassica* TLDC containing proteins were identified from the Brassica database (<http://brassicadb.cn/#/>) and the Blastp tool [46,47]. A total of sixty six homologous sequences from *B. oleracea* (taxid:3712), *B. napus* (taxid:3708), *B. rapa* (taxid:3711), *B. cretica* (taxid:69181) and *B. carinata* (taxid:52824) were used for the analysis.