

University of Groningen

## NARROW LEAF 7 controls leaf shape mediated by auxin in rice

Fujino, Kenji; Matsuda, Yasuyuki; Ozawa, Kenjiro; Nishimura, Takeshi; Koshiba, Tomokazu; Fraaije, Marco W.; Sekiguchi, Hiroshi

*Published in:*  
MOLECULAR GENETICS AND GENOMICS

*DOI:*

[10.1007/s00438-008-0328-3](https://doi.org/10.1007/s00438-008-0328-3)

**IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.**

*Document Version*  
Publisher's PDF, also known as Version of record

*Publication date:*  
2008

[Link to publication in University of Groningen/UMCG research database](#)

*Citation for published version (APA):*

Fujino, K., Matsuda, Y., Ozawa, K., Nishimura, T., Koshiba, T., Fraaije, M. W., & Sekiguchi, H. (2008). NARROW LEAF 7 controls leaf shape mediated by auxin in rice. *MOLECULAR GENETICS AND GENOMICS*, 279(5), 499-507. <https://doi.org/10.1007/s00438-008-0328-3>

### Copyright

Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

The publication may also be distributed here under the terms of Article 25fa of the Dutch Copyright Act, indicated by the "Taveme" license. More information can be found on the University of Groningen website: <https://www.rug.nl/library/open-access/self-archiving-pure/taveme-amendment>.

### Take-down policy

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

*Downloaded from the University of Groningen/UMCG research database (Pure). <http://www.rug.nl/research/portal>. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.*

**Table S1** List of PCR primers for high resolution mapping of the *NAL7* gene

Marker	Position <sup>a</sup>	Forward		Reverse		Size(bp)
		Name	Sequence	Name	Sequence	
AC122149_1	2284350	AC122149_1U	TAGCTCCCAACTGAGGAAAT	AC122149_1L	GCCCCATATGAGTGTTGAAA	224
AC105734_1	2723835	AC105734_1U	GAGCAGGTACATCTGGAGTATTTT	AC105734_1L	CTAAGACACGAAATCTGGAATACC	197
AC105730_1	3028233	AC105730_1U	CCTGAAACGGATGGAGTATC	AC105730_1L	TCCCAAATTATAGGGCGCTT	221
AC119797_1	3204674	AC119797_1U	CTCATTTGAATTGGGTATATACTCA	AC119797_1L	CGGTATTTTCATGCAGTTTCG	213
AC105729_22	3385888	AC105729_22U	ATCTAAACATTTAAAAAAA	AC105729_22L	CAATTAATGAATCTATTGAT	252
SNP5	3234611	nal7_5AU	GAGATGGTGATTTTGGGTCGTT	nal7_5AL	CTGACCGTTTTCAACCGATAAA	183
SNP98	3325690	nal7_98AU	CCTCGTCCTCTTCTTCGAGAAT	nal7_98AL	CAAAGCACGAAAGCCAATATG	183
SNP165	3339836	nal7_165A1U	ACGTCTGTGATCACCGAGTACG	nal7_165A1L	TCGTTAGTACTTACCCACTCCTGAC	266

<sup>a</sup> Position of primer is in PseudoMolecule 3.0 in RAP-DB (<http://rapdb.lab.nig.ac.jp/index.html>)

**Table S2** List of PCR primers for semi-quantitative RT-PCR analysis

Gene	Chr	Accession		Primer		Annealing Temp.	Cycle	Size	Reference
		RAP-DB	KOME	Forward	Reverse				
<i>O.s</i> YUCCA1	1	O.s01g0645400	AKI05488	TGCATACTCCGAGTACAAGTCC	GGTGAGGTCTTGAGCTCGAT	61	35	329	this study
<i>O.s</i> YUCCA2	5	O.s05g0528600	NA	AGGAAAAGTGCCTTTGAGCA	GTCGGCTGACCTAGCATCTC	61	38	488	this study
<i>O.s</i> YUCCA3	1	O.s01g0732700	NA	AGAGATTGATGGCCTAGACGAC	TGGTCTGAGCTATGAGCAGTAGAA	61	35	284	this study
<i>O.s</i> YUCCA4	1	O.s01g0224700	AKD70386	CCTCGACCTCTGCAACCACAA	GGACTTGATCTTGCTAGGGTT	61	35	298	this study
<i>O.s</i> YUCCA5	12	O.s12g0512000	NA	GATGCACACCAGCAGCTACAA	ATCTGGAGTGGACCAATCTTAGG	61	35	318	this study
<i>O.s</i> YUCCA6	7	O.s07g0437000	NA	ACCGGATACCAAAGCAACGTC	GCAAATGTCCTGTGCAACCTTAA	61	33	185	this study
<i>O.s</i> YUCCA7	4	O.s04g0128900	AKD68976	AACACAGTGATGCGATGGACA	TCGAGGTAGTCGATGAACTGG	61	35	292	this study
<i>O.s</i> YUCCA8 ( <i>NAL7</i> )	3	O.s03g0162000	AKD72466	ACTGTAGTGCATGCAAGAGGAGA	CCCAAGAACCGATGAGCTAAG	61	35	319	this study
<i>O.s</i> YUCCA9	1	O.s01g0273800	AKI09645	ATGGAGATCGCCTACGACCTC	GACCTGATCTTGCGAAGGTG	64	35	287	this study
<i>UBQ2</i>	2	O.s02g0161900	AKI01547	GTCTGATCTTCGCTGGCAAGCAGC	GCATACTGCTGTCCCACAGGAAACTG	63	25	271	Yang et al. (2005)

NA; not available.