

Supporting Information

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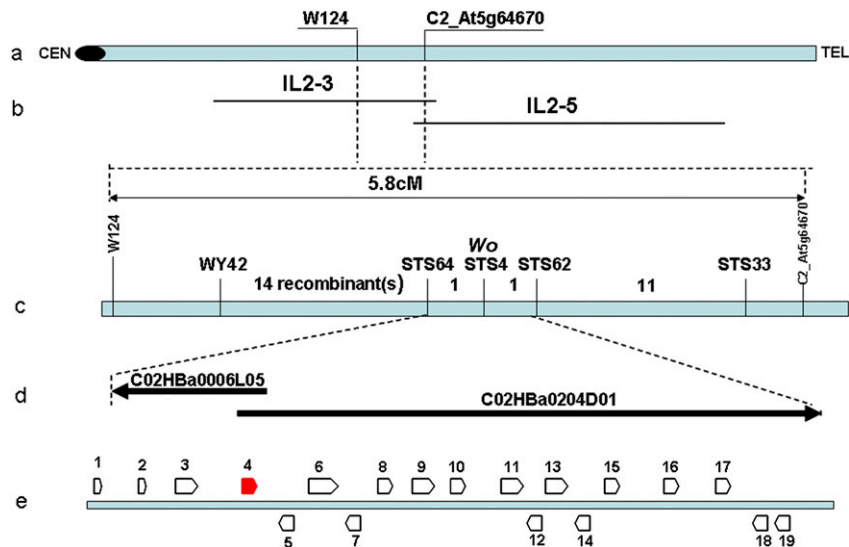


Fig. S1. Genetic physical map and predicted ORFs in the *Wo* region (1). It was reported that *Wo* is located near the midpoint of the long arm of chromosome 2 (2). Thus, we constructed mapping populations by crossing IL2-3 and IL2-5 with LA3186. Then, we delimited *Wo* to a 5.8-cM interval between W124 and C2_At5g64670 by using an F₂ population from the cross IL2-5 × LA3186 (A). This interval was located in the introgression segment of IL2-3 (B). Therefore, we carried out fine mapping by using F₂ progenies from the cross IL2-3 × LA3186. *Wo* was delimited in the region between STS64 and STS62, respectively, with one recombination event (C). STS4 was cosegregated with *Wo* (C). As STS64 and STS62 were exploited based on the sequences of C02HBa0006L05 and C02HBa0204D01 separately, we tried to align these two BAC sequences. These two BACs formed an approximately 200-kb contig with 15,328-bp overlapping ends, indicating that *Wo* was located in this approximately 200-kb region (D). Gene prediction by using FGENESH (<http://softberry.com>) demonstrated that this region contains 19 putative ORFs (E). The homologues of these ORFs include copia LTR rider (*S. lycopersicum*), COBRA-LIKE PROTEIN 10 PRECURSOR (*A. thaliana*), hypothetical protein (*Populus trichocarpa*), PDF2 (ORF4) (*A. thaliana*), VPS28-2 (*A. thaliana*), and β-glucosidase (*Oryza sativa*).

1. Yang C, Li H, Zhang J, Wang T, Ye Z (2011) Bayesian functional mapping of dynamic quantitative traits. *Theor Appl Genet*, 10.1007/s00122-011-1601-0.
2. Rick CM, Butler L (1956) Cytogenetics of the tomato. *Adv Genet* 8:267–382.

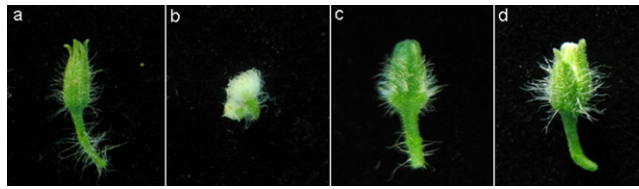


Fig. 53. Flower buds of negative plants (A) and transgenic lines (L1, L2, L3) overexpressing ORF4 (B–D).

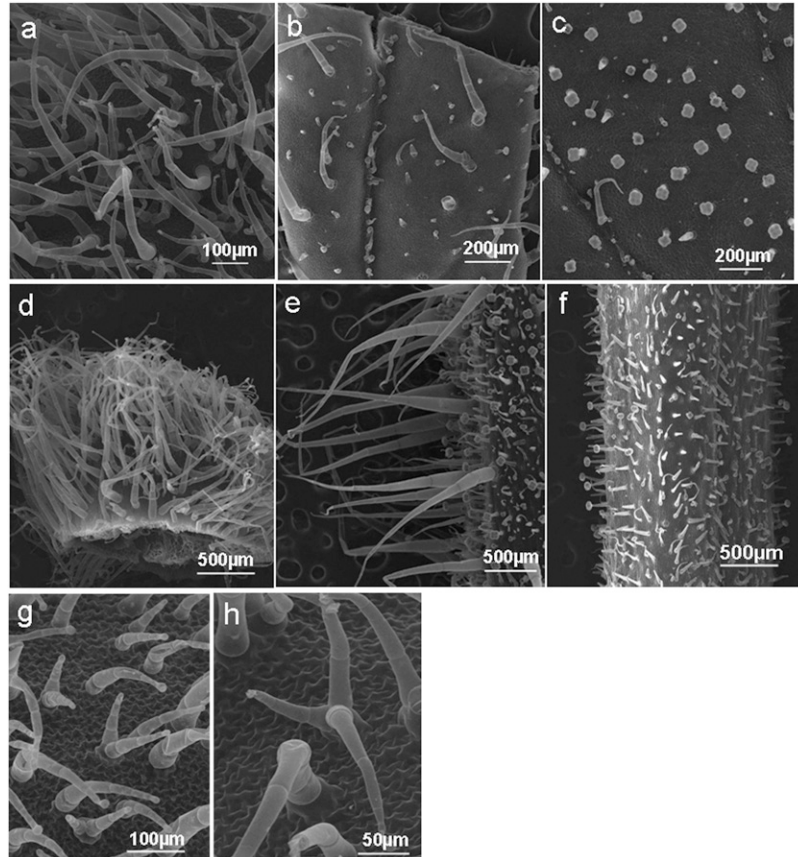


Fig. 54. Trichomes on the epidermis of LA3186 (A and D), its nonwoolly segregants (B and E), and RNAi transgenic plants (C and F). Clusters consist of two trichomes (G) and three trichomes (H) on LA3186.

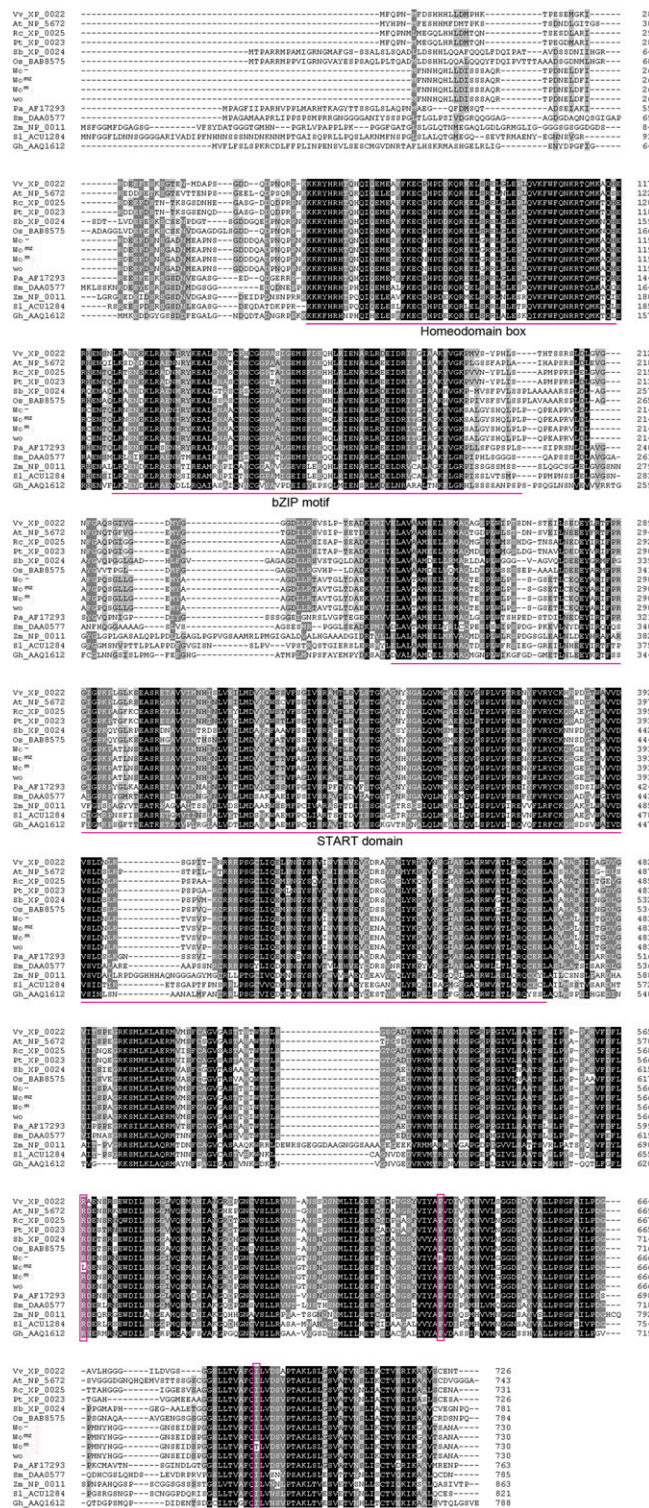


Fig. 55. Amino acid alignments of the predicted proteins of *Wo* alleles with 11 HD proteins from other species. Three conserved domains, a HD domain, a bZIP motif, and a START domain, are represented, respectively, by three red lines. Sites of amino acid substitution in *Wo* alleles indicated by three red rectangles are highly conserved among their homologues.

Table S1. Wo positively regulated genes

Accession no.	Annotation	e value	Fold change (woolly vs. nonwoolly)
SGN-U213590	Pepper esterase	1.00E-140	15.26
SGN-U218869	Microsomal omega-6-desaturase	1.00E-156	6.26
SGN-U223134	DC1 domain containing protein	4.00E-109	5.22
SGN-U217123	Cytochrome P450	9.00E-164	5.11
SGN-U214460	Pathogenesis-related protein STH-2	9.00E-83	5.09
SGN-U223742	Peroxidase 72 precursor	3.00E-41	5.04
SGN-U213891	Peroxidase	3.00E-110	4.92
SGN-U215958	Glucan endo-1,3- β -glucosidase A	5.00E-185	4.78
SGN-U233094	Pathogenesis-related protein P2	2.00E-35	4.7
SGN-U216027	KED	5.00E-11	4.55
SGN-U222505	Unnamed protein	7.00E-77	4.38
SGN-U215392	Suberization-associated anionic peroxidase 1	4.00E-185	4.37
SGN-U217569	Anionic peroxidase swpb2	2.00E-92	4.34
SGN-U212751	Probable GST	4.00E-59	4.29
SGN-U227243	Hypothetical protein	4.00E-30	4.28
SGN-U226950	B-type cyclin	2.00E-21	4.25
SGN-U219809	UDP-glucose:glucosyltransferase	4.00E-104	4.22
SGN-U232815	Lipid desaturase-like protein	3.00E-48	4.15
SGN-U217180	Predicted protein	1.00E-49	4.12
SGN-U226089	TCP protein	2.00E-34	4.1
SGN-U215639	NtEIG-A1	4.00E-48	4.02
SGN-U214192	Fatty acid desaturase	1.00E-164	3.92
SGN-U212989	Pathogenesis-related protein 10	1.00E-74	3.92
SGN-U214493	Peroxidase	2.00E-155	3.82
SGN-U221367	Hypothetical protein	2.00E-12	3.75
SGN-U213641	Lipid transfer protein LTP1 precursor	7.00E-51	3.71
SGN-U242427	MYB60	3.00E-42	3.69
SGN-U222533	Hypothetical protei	2.00E-33	3.6
SGN-U216630	Hypothetical protein	8.00E-74	3.59
SGN-U213101	Abscisic stress-ripening protein 1	4.00E-11	3.58
SGN-U216491	Putative membrane protein	2.00E-212	3.58
SGN-U222539	Leucine-rich repeat protein	4.00E-88	3.55
SGN-U214985	Pathogenesis-related protein P2	4.00E-82	3.54
SGN-U231227	Predicted protein	2.00E-58	3.51
SGN-U214902	Class IV chitinase	3.00E-136	3.5
SGN-U231098	CYP98A33v1	3.00E-85	3.47
SGN-U214186	Myo-inositol oxygenase	2.00E-178	3.47
SGN-U216964	Sn-1	5.00E-49	3.42
SGN-U221372	White-brown-complex ABC transporter family	7.00E-52	3.39
SGN-U220637	MYB12	6.00E-101	3.35
SGN-U212747	Probable GST	7.00E-105	3.33
SGN-U222800	Hypothetical protein	2.00E-78	3.32
SGN-U212990	Pathogenesis-related protein STH-2	1.00E-85	3.26
SGN-U214241	Predicted protein	2.00E-53	3.25
SGN-U212783	Lipoxygenase	0	3.23
SGN-U212850	Peroxidase	3.00E-136	3.21
SGN-U214304	Ethylene-responsive late embryogenesis-like protein	5.00E-48	3.2
SGN-U221457	Peroxidase	2.00E-159	3.2
SGN-U235070	Putative ROX1	1.00E-30	3.17
SGN-U216010	Alkaline alpha-galactosidase seed imbibition protein	0	3.16
SGN-U213299	Hypothetical protein	1.00E-120	3.1
SGN-U236390	Unnamed protein	4.00E-22	3.05
SGN-U219794	Unnamed protein	1.00E-117	3.03
SGN-U214672	Hypothetical protein	5.00E-200	3.01
SGN-U216420	Putative nonspecific lipid transfer protein StnsLTP	2.00E-52	2.97
SGN-U223970	Predicted protein	2.00E-83	2.94
SGN-U226166	GST	2.00E-37	2.93
SGN-U215098	Unnamed protein product	3.00E-232	2.92
SGN-U213104	ASR4	2.00E-91	2.91
SGN-U218860	Auxin-regulated dual specificity cytosolic kinase	3.00E-186	2.91
SGN-U217904	Chitinase, class II	3.00E-135	2.9
SGN-U219528	Phosphate transporter 3	6.00E-24	2.88
SGN-U214961	Flavonol synthase	2.00E-174	2.84

Table S1. Cont.

Accession no.	Annotation	e value	Fold change (woolly vs. nonwoolly)
SGN-U226297	Alkaline α -galactosidase seed imbibition protein	2.00E-109	2.82
SGN-U215001	BURP domain-containing protein	2.00E-157	2.78
SGN-U215393	Suberization-associated anionic peroxidase 2	1.00E-174	2.76
SGN-U223748	2-Hydroxyisoflavanone dehydratase	2.00E-71	2.73
SGN-U220694	Hypothetical protein	1.00E-151	2.71
SGN-U213790	Acidic 26 kDa endochitinase	8.00E-149	2.7
SGN-U227536	Predicted protein	4.00E-11	2.69
SGN-U226247	Unknown	3.00E-24	2.68
SGN-U222218	Nonspecific lipid-transfer protein 2	3.00E-38	2.67
SGN-U215088	MtN19-like protein	1.00E-158	2.64
SGN-U217302	Glycine-rich protein	5.00E-06	2.62
SGN-U213541	Cationic peroxidase	2.00E-165	2.62
SGN-U226141	Heat shock factor protein	4.00E-12	2.61
SGN-U214090	Caffeoyl-CoA O-methyltransferase	2.00E-135	2.61
SGN-U215231	Cell wall peroxidase	9.00E-161	2.59
SGN-U216828	HAT22	1.00E-49	2.56
SGN-U223342	Hypothetical protein	9.00E-68	2.55
SGN-U226976	Ubiquitin-conjugating enzyme	1.00E-75	2.54
SGN-U216827	Phytophthora-inhibited protease 1	7.00E-194	2.51
SGN-U223775	Hypothetical protein	1.00E-109	2.5
SGN-U218425	Hypothetical protein	4.00E-23	2.47
SGN-U233542	Nonspecific lipid transfer protein StnsLTP	7.00E-19	2.47
SGN-U223651	Hypothetical protein	1.00E-118	2.45
SGN-U217224	Protein SSM1	1.00E-93	2.44
SGN-U212775	Pectate lyase	1.00E-196	2.43
SGN-U214145	Hypothetical protein	5.00E-103	2.43
SGN-U219224	Hypothetical protein	2.00E-170	2.43
SGN-U219786	WRKY-type DNA binding protein	5.00E-83	2.42
SGN-U242588	Conserved hypothetical protein	1.00E-54	2.41
SGN-U214242	Hypothetical protein	2.00E-129	2.4
SGN-U240637	Nam-like protein 11	1.00E-21	2.39
SGN-U214663	Subtilisin-like protease	2.00E-173	2.37
SGN-U223262	Ring domain containing protein isoform 2	6.00E-32	2.37
SGN-U230206	Predicted protein	7.00E-83	2.36
SGN-U223136	Actin-100	1.00E-110	2.35
SGN-U218395	Unnamed protein product	2.00E-65	2.34
SGN-U212753	GST-like protein	2.00E-123	2.3
SGN-U219778	Protein binding protein	1.00E-42	2.29
SGN-U213103	ASR4	6.00E-100	2.27
SGN-U216860	Conserved hypothetical protein	3.00E-23	2.26
SGN-U217364	Hypothetical protein	1.00E-61	2.26
SGN-U212754	GST	3.00E-85	2.26
SGN-U232526	Peroxidase cevi16	3.00E-67	2.25
SGN-U214945	Serine acetyltransferase	1.00E-161	2.24
SGN-U215860	Xyloglucan endotransglucosylase-hydrolase XTH6	2.00E-147	2.24
SGN-U215369	Predicted protein	6.00E-105	2.23
SGN-U215219	CYP92B3	4.00E-184	2.23
SGN-U214088	Caffeoyl-CoA O-methyltransferase	7.00E-135	2.22
SGN-U213377	Dicyanin	1.00E-28	2.2
SGN-U212752	Probable GST	8.00E-84	2.18
SGN-U216984	Arabinogalactan-protein	5.00E-14	2.18
SGN-U215123	WRKY protein	8.00E-255	2.17
SGN-U217650	Myb-related protein	1.00E-68	2.17
SGN-U217525	Predicted protein	8.00E-112	2.17
SGN-U213200	<i>N</i> -hydroxycinnamoyl-CoA:tyramine <i>N</i> -hydroxycinnamoyl transferase THT1-3	5.00E-132	2.17
SGN-U225036	Hypothetical protein	9.00E-51	2.16
SGN-U215122	Transcription factor WRKY	1.00E-131	2.16
SGN-U215220	CYP92B2v1	1.00E-80	2.16
SGN-U215329	Hypothetical protein	4.00E-79	2.15
SGN-U212799	1-aminocyclopropane-1-carboxylate oxidase homolog	5.00E-97	2.15
SGN-U213099	Abscisic stress-ripening protein 3	3.00E-34	2.15

Table S1. Cont.

Accession no.	Annotation	e value	Fold change (woolly vs. nonwoolly)
SGN-U219448	Predicted protein	4.00E-72	2.14
SGN-U215689	Hypothetical protein	6.00E-33	2.13
SGN-U217841	UDP-glucose:glucosyltransferase	2.00E-48	2.12
SGN-U242267	Metal transporter	1.00E-67	2.12
SGN-U213376	Dicyanin	3.00E-130	2.12
SGN-U213688	Hypothetical protein	5.00E-26	2.11
SGN-U216552	Hypothetical protein	2.00E-43	2.11
SGN-U215524	Avr9/Cf-9 rapidly elicited protein 216	1.00E-100	2.11
SGN-U220541	Unnamed protein	2.00E-113	2.11
SGN-U215204	CER6	3.00E-287	2.09
SGN-U215387	Metal ion binding protein	2.00E-47	2.09
SGN-U213895	Early light inducible protein	2.00E-58	2.09
SGN-U216640	Predicted protein	2.00E-259	2.09
SGN-U215688	Hypothetical protein	1.00E-106	2.07
SGN-U222710	Unknown	6.00E-15	2.07
SGN-U235018	Ubiquitin-conjugating enzyme	2.00E-23	2.07
SGN-U226863	Hypothetical protein	2.00E-50	2.06
SGN-U226730	AP2 (APETALA 2)	2.00E-10	2.06
SGN-U219896	CYP72A54	1.00E-183	2.04
SGN-U222665	Receptor-like protein kinase	5.00E-47	2.03
SGN-U213391	Predicted protein	2.00E-39	2.03
SGN-U216631	NAC domain protein	9.00E-07	2.03
SGN-U214773	Peroxisomal membrane protein pmp34	7.00E-116	2.02
SGN-U216383	Wound-induced protein 1	6.00E-51	2.01
SGN-U233379	ABA-induced MYB transcription factor	6.00E-75	2.01
SGN-U216869	Predicted protein	1.00E-92	2.01
SGN-U215161	Auxin-regulated protein	5.00E-223	2
SGN-U223447	DNA binding protein	1.00E-49	2
SGN-U215935	NAD(P)H:quinone oxidoreductase	3.00E-85	2
SGN-U222613	Predicted protein	7.00E-75	2
SGN-U217320	Unknown	2.00E-25	2

Table S2. Primers used for function and expression analysis of *Wo* and *SlCycB2*

Name	Forward primer (5'-3')	Reverse primer (5'-3')
Full-length <i>Wo</i> cDNA	TTCAAGATGTTTAATAACCACCAGC	ACCTTTCATGCATTGCGGAAGTTAC
Full-length <i>Wo</i> gDNA	AAATCATAAACATGGGCGTTT	TGGGATAAAGGAAGTAAACACA
Full-length <i>Wo</i> for subcellular localization	GCGTCGACTTCAAGATGTTTAATAACCACCAGC	GCGTCGACACCTTTCATGCATTGCGGATAC
Full-length <i>Wo</i> for BiFC	GCGGATCCATGTTTAATAACCACCAGCACTTG	GCGGTACCGAGTGCATTGCGGAAGTTAC
<i>Wo</i> for RT-PCR	TGGAGAAATGTACGCTGCTG	TTGCAATGCTCCATTGTGAT
<i>Wo</i> promoter for GFP analysis	GCGCGCCGCCATCCTATTAGCCATAAGTGTGA	GCCTCGAGAATACCTTCTCGATCTTCTCAAAA
Fragment of <i>Wo</i> for RNAi vector and in situ hybridization	AATGGTGGGATTGTTCAGGA	TGCATTGCGGAAGTTACAG
Full-length <i>SlCycB2</i> cDNA	ATGAGCAGGAGAAATGGAAATG	TTATTTTTTCTCATAGATAACTTCA
Full-length <i>SlCycB2</i> for BiFC	GCGGATCCATGAGCAGGAGAAATGGAAATG	GCGGTACCGCGTTTTTCTCATAGATAACTTCA
<i>SlCycB2</i> for RT-PCR	AAACCCCTCACTTCCGATCT	GCCCTATAGAAGTCCAAAATTC
<i>SlCycB2</i> for real-time PCR	TGAGCAGGAGAAATGGAA	CATTGTCAGCGACCTTGT
Fragment of <i>SlCycB2</i> for RNAi vector	AATGAGCAGGAGAAATGGAAA	GGGCGGTGATATTGATAAACC
<i>NPTII</i>	AGACAATCGGCTGCTCTGAT	TCATTTGAAACCCAGAGTC
<i>Actin</i> for RT-PCR	ATGGCAGACGGAGAGGATATTCA	GCCTTGGCAATCCACATCTGCTG
<i>Actin</i> for real-time PCR	GTCCTCTCCAGCCATCCAT	ACCACTGAGCACAATGTTACCG