Supporting Information

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SI Materials and Methods

Culture Conditions for *Penicillium chrysogenum.* All strains investigated in this study were grown at 27 °C and 120 rpm in liquid complete culture medium (CCM); in case of the liquid-static cultures, shaking was avoided. For solid media, CCM, M322, or minimal medium (MM) was used as previously described (1, 2). For microarray analysis, strains were grown on sterile membranes (Pall Life Sciences) layered on solid M322 medium. All liquid media were inoculated with 5.0×10^6 spores from freshly prepared spore suspensions derived from cultures grown on M322 medium for 4–5 d. For quantitative real-time analysis, CCM was inoculated with 2×10^8 spores. Solid media were grown on CCM for 168 h.

Light Microscopy. The microscopic observations of hyphal morphology at different growth phases were performed as described previously (3). For pellet quantification assays, strains were grown at 27 °C and 120 rpm in CCM, and samples were taken at different time points. The flasks were inoculated with 1×10^7 spores/mL freshly prepared spore suspensions. For each time point, three 2-mL samples were taken from the culture. Images were obtained with a stereomicroscope (Stemi 2000-C; Zeiss) equipped with a digital camera (AxioCamERc 5s) and digitally processed using Adobe Photoshop CS4. Pellet sizes were measured using the programs ImageJ (http://rsbweb.nih.gov/ij/) and Microsoft Excel 2010.

Scanning Electron Microscopy. Cleistothecia were removed with a sterile needle tip. The samples were fixed as described (4) for at least 24 h at room temperature, dehydrated in an ascending ethanol series, transferred to formaldehyde–dimethylacetal for 48 h, critical point dried, and mounted on metal stubs, sputter coated with gold for 180 s using an SEM Coating Unit E 5100 (Polaron Equipment Ltd), and examined on a Zeiss DSM 950 scanning electron microscope. Recorded images were processed with Adobe Photoshop CS4 software.

Examination of Crosses and Ascospore Isolates. The crosses were examined for cleistothecial production periodically with a Zeiss Stemi 2000 stereomicroscope. Cleistothecia were removed with a sterile needle tip, cleaned of adhering conidia by rolling on preparation agar [7% (wt/vol) agar], and then squashed with a needle tip in 200 µL of sterile water. Aliquots of 50 µL were plated on oatmeal agar medium or Köllnflocken agar supplemented with biotin (6.4 µg/L), incubated at 27 °C, and examined daily for germinating ascospores. Ascospore isolates were grown on CCM and characterized phenotypically with respect to spore color, chrysogenin production, and penicillin biosynthesis (3). Two different types of genetic markers were chosen for molecular characterization. First, mating type was determined by Southern hybridization. EcoRI-restricted genomic DNA from individual strains was blotted and hybridized with probes specific for the MAT1-1-1 or MAT1-2-1 gene. In a second approach, genome databases (www.ncbi.nlm.nih.gov) were searched with BLASTn to identify suitable molecular markers from the major contigs. Selected genes from the parental strains Q176 and IB 08/921 were amplified by PCR and sequenced for comparison. Finally, restriction fragment length polymorphisms (RFLPs) of 11 gene sequences were chosen and used to identify single point mutations by endonuclease restriction of amplified genomic DNA. As listed in Table S5, oligonucleotide pairs were used to amplify the corresponding gene fragments from the two parental strains.

Böhm et al. www.pnas.org/cgi/content/short/1217943110

Sequencing of both amplicons identified RFLPs for differential restriction enzyme analysis. In a subsequent step, amplified DNA from each ascospore group was cut with the selected restriction enzymes (Fig. S1A) to detect which parental gene copy was present.

Transformation. DNA-mediated transformation of *P. chrysogenum* strains was performed as recently described (3, 5). The *ergA* gene was used as a selection marker as described (6) with some modifications: for regeneration of protoplasts, solid MM was used containing 5% (wt/vol) KCl and 2% (wt/vol) glucose as the sole carbon source. Twenty-four hours after transformation, the medium was overlaid with agar containing 0.7 µg/mL terbinafine.

Construction of MAT1-1–1 Deletion Strains. The sequences of all plasmids and oligonucleotides used for construction of the gene deletion cassette are listed in Tables S4 and S5. For construction of the deletion vector, the strategy recently described by Hoff et al. (3) was used to generate the recombinant plasmid pKOMAT-1, containing the Tn5Phleo marker gene, flanked by sequences located 5' and 3' of the *MAT1-1–1* gene. This plasmid was used as a template to amplify the linear KO-MAT-1 cassette with primers 5'-Mat_sense and 3'-MAT_anti. The PCR fragment was used for transformation of Δ Pcku70 (7), which facilitates homologous recombination (7). Resulting transformants were screened and analyzed as previously described (3). DNA from single spore isolates was used to verify the complete lack of the *MAT1-1–1* gene by Southern hybridization analysis (Fig. S24).

Rescue of MAT1-1–1 Deletion Strains. For complementation analysis, Δ MAT1-1–1 EK5 and EK6 were transformed with plasmid pKompMAT-1_ergA. This plasmid carries the *MAT1-1–1* gene with the native 5' and 3' regions using the *ergA* gene as a selectable marker, under the control of the strong Pacn-promoter of *P. chrysogenum* (6). The successful rescue of the *MAT1-1–1* gene was verified by Southern hybridization, and the corresponding strains were designated Δ MAT1-1–1::MAT1-1–1 (Fig. S2C).

Construction of MAT1-1–1 Overexpression Strains. For generating *MAT1-1–1* overexpression strains, plasmid pPgpd-MAT-1-ptrA was transformed into strain P2niaD18. Here, the *MAT1-1–1* gene is under the control of the strong constitutive *gpd* promoter of *Aspergillus nidulans*. Resulting transformants were selected using pyrithiamine-supplemented agar plates, as the constructs carry the *ptrA* resistance gene and were named P2::MAT1-1–1. Copy numbers of integrated plasmids were tested by Southern hybridization using a ³²P-radiolabeled *MAT1-1–1* probe (Fig. S2B).

Interaction Studies with Pheromones and Receptors from *P. chrysogenum*. For the heterologous expression of the *P. chrysogenum* pheromone receptor gene *Pcpre2* in *Saccharomyces cerevisiae*, we used the yeast expression vector pPGK (8). The ORF of *Pcpre2* was amplified by PCR with the oligonucleotides Pre2-hom-f and Pre2-hom-r (Table S5) and inserted into the BamHI linearized vector pPGK by homologous recombination (9) to obtain the desired plasmid pPGK-PcPRE2. Plasmid pPGK-PcPRE2 was transformed into the yeast strain YDB103 (MATa *ste2* Δ *sst2:: KanMX4*) (1). Shmoo formation (Fig. 4A) was assayed as described previously (10).

Yeast halo assays were conducted as described previously (10). YDB103 containing pPGK-PcPRE2 or strain Y06055 [MATa, his3 Δ 1, leu2 Δ 0, lys2 Δ 0, ura3 Δ 0, YLR452c::kanMX4 (sst2 Δ); Euroscarf] were used. Five microliters of synthetic pheromone from either *Sordaria macrospora* (SmPPG1; GeneScript Corporation), *P. chrysogenum* (PcPPG1; GeneScript Corporation) or *S. cerevisiae* (α -factor; Sigma-Aldrich) were applied to filter disks (6 mm; Sartorius Stedim) at a concentration of 3 nmol. No halo formation was seen when synthetic *S. cerevisiae* α -factor or DMSO was added in control experiments. As a positive control, we applied the synthetic *S. cerevisiae* α -factor to strain Y06055, which produces the *S. cerevisiae* α -factor receptor Ste2p.

Identification of *P. chrysogenum* **Genes and Sequence Analysis.** The sequences for all genes in this study were obtained from the public National Center for Biotechnology Information Entrez database (www.ncbi.nlm.nih.gov/entrez/). The genome sequence of *P. chrysogenum* ATCC28089 (Wisconsin 54–1255) served as the source. Sequence alignments were performed with the program MultAlign (http://multalin.toulouse.inra.fr/multalin/) and displayed using GeneDoc (www.nrbsc.org/gfx/genedoc/index.html).

Penicillin Bioassay and HPLC Analysis. For penicillin bioassays with *Staphylococcus aureus* as a sensitive indicator bacterium, $30 \ \mu$ L of supernatant from the culture broth was used in a halo test. For

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calibration of penicillin activity, the area of the inhibition zone was normalized to the dry weight of the mycelium. Media were buffered to pH 6 to obtain optimal conditions for penicillin biosynthesis. Penicillin titers were also determined using HPLC as described (11). The standard protocol involved measurement of penicillin production in liquid shaking cultures after 72 h growth, as this is the optimal time point for penicillin biosynthesis.

Nucleic Acids Isolation, cDNA Synthesis, Microarray, and Quantitative Real-Time PCR. Preparation of nucleic acids, hybridizations, and cDNA synthesis for microarray and quantitative real-time PCR (qRT-PCR) analysis were carried out as described recently (7). The time-course microarray analysis was performed using Δ Pcku70 as the reference strain (7). qRT-PCR was carried out as described previously (7) with the following modifications: The Promega GoTaq qPCR Master Mix was used as recommended by the manufacturer, and incubation cycles were performed on a StepOnePlus Real-Time PCR System (Applied Biosystems) with the primers listed in Table S5.

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	Chry.syn.	flbB	flbC	fluG	hypo.	nsdD	pcbC	pcIA	penDE	stuA	UDP
Marker	Pc21g	Pc12g	Pc12g	Pc20g	Pc24g	Pc13g	Pc21g	Pc22g	Pc21g	Pc13g	Pc19g
	16000	01640	12190	02420	01940	15350	21380	14900	21370	04920	00330
Restriction enzyme	Sspl	HpyAV	Mnll	Hin111	Hinfl	Pdml	Taql	Mval	Alul	Nael	Hpall
Q176 # of fragments	2	4	13	6	3	2	7	5	3	3	3
IB 08/921 # of fragments	3	3	12	5	2	3	6	4	2	4	4

в



Fig. S1. Analysis of recombinant ascospore lineages. (A) RFLP analysis with different marker genes to detect genetic recombination. Sequence analysis identified point mutations in different genes derived from both parental strains Q176 and IB 08/921. In some cases, these point mutations generated new restriction sites, which were used to distinguish the two gene variants. Numbers indicate restriction fragments when PCR products were digested with the indicated endonucleases. (B) Location of marker genes used for RFLP analysis of recombinant ascospore groups displayed on contigs of the P. chrysogenum genome (www.ncbi.nlm.nih.gov/genbank/). All genes shown were tested for sequence polymorphisms between the two parental strains Q176 and IB 08/921. The genes with suitable polymorphisms are highlighted in bold. Only the genes highlighted in red were used in the RFLP analysis. (C) Phenotypes of parental Legend continued on following page

strains (AS 38 and AS 25) and ascospore progeny (AP 16, AP 20) as evidence of meiotic recombination during a sexual cross. The two parental strains are F1 progeny from a cross between Q176 and IB 08/921 that differed in spore color (light green versus dark green; *Top*), chrysogenin production (bright yellow versus fawn reverse coloration; *Middle*), and penicillin production (differential size of halo; *Bottom*). Recombinant ascospore progeny AP 16 and AP 20 have novel phenotypes of dark green conidia, chrysogenin production, and a reduced halo size. Strain designation color indicates either *MAT1-1* (blue) or *MAT1-2* (red) genotype. Molecular analysis of progeny was not performed.

DNAS



PcMAT1-1-1-probe

Fig. S2. Recombinant *P. chrysogenum MAT1-1–1* strains produced for functional analysis of the *MAT1-1–1* gene. Constructs to generate (*A*) deletion, (*B*) overexpression, and (*C*) complementing strains are shown, together with results of the corresponding Southern hybridizations used to characterize the recombinant fungal strains. Lane headings indicate results for specific control or recombinant *MAT1-1–1* strains. *ble*, phleomycin resistance gene; *ergA*, gene encoding squalene epoxidase (which confers resistance to terbinafine); Pacn, promoter sequence of the *P. chrysogenum* actin gene; Pgpd, promoter sequence of the *A. nidulans gpdA* gene; *ptrA*, pyrithiamine resistance gene.



Fig. S3. Penicillin biosynthesis and hyphal morphology of recombinant *P. chrysogenum* strains. (A) HPLC analysis of penicillin V production in Δ MAT1-1-1 deletion strains and their corresponding reference strains. Measurements were taken after 96 h cultivation. Error bars represent mean \pm SD (*n* = 3) from three independent experiments. (*B*) Representative examples of hyphal morphology and polarity of germinating conidia when parental and recombinant *MAT1-1-1* strains were grown in liquid shaking CCM for the times indicated. The morphology of the germinating conidia from the *MAT1-1-1* deletion strain is distinct from the reference strains as shown by the dichotomous branching of the hyphal tips and by the increased number of germ tubes. The P2::MAT1-1-1 overexpression strain shows elongated hyphae without branching, which is further evidenced by the quantitative analysis in C. These observations are identical to those seen on solid media, as shown in Fig. 2*B*. Scale bars: 20 µm (24 h) and 100 µm (36 h). (*C*) Quantification of hyphal length and (*D*) quantification of germ tubes from 50 germinating conidia. As an example, one out of two independent *MAT1-1-1* knockout and overexpression strains is shown. (*E*) Quantification of points as indicated. Error bars represent mean \pm SD of 100 random pellets. One out of two independent *MAT1-1-1* knockout and overexpression strains is shown.



Fig. 54. qRT-PCR analysis to quantify transcriptional expression of genes for pheromone and pheromone receptor genes. Values are the log_2 -transformed average expression ratios of at least three biological replicates of two independently derived deletion strains (mean Δ MAT1-1–1 EK5/EK6, $n \ge 3$), relative to the Δ Pcku70 parental strain. Strains were grown in liquid shaking (*Upper*) or surface (*Lower*) cultures.

Table S1.	Р.	chrysogenum	isolates	that were	crossed in	n various	combinations
	•••						

		MAT1-2*'										
		IB 08/921	PC 0814C	PC 0819C	PC 0826A	DAOM 155628	DAOM 59494C	IBT 30738	Pc 131	US 68	Pc 105	AS 25
MAT1-1	P2niaD18 ATCC 10106	4, 5, 6, 8, 9 – (1, 2, 3, 12, 13) 7 – (4)	- (3)	- (3)		- (3)		10, 11				
	Q176 ΔMAT1 EK5 P2::MAT1 T5 P2::MAT2 T2 P2::MAT2 T5 D4:0M 193710	6, [‡] 7, 8 – (1, 2, 3, 4) 1, 12, 13 – (2, 3, 4, 5) 4, 5, 7 – (1, 2, 3, 12, 13) 3 4	- (3) - (3)	- (3)		- (3)						
	PC0820A PC088B		1, 2, 3 3 – (1, 2)	3 – (1, 2)		3 – (1, 2) 3 – (1, 2)	3 – (1, 2)					
	DAOM 155627 PC08105C IBT 14508 IBT 30427 IBT 22703 US 49	- (4)	3	1, 3 – (2)	3 – (1)	3 – (1, 2)	3	10, 11 10, 11	- (10) - (10) 10	- (10) - (10)	- (10) - (10) - (10)	
	AS 38											6 [‡]

Numbers represent different growth conditions where the formation of cleistothecia was observed. Numbers in parentheses indicate conditions where no fruiting bodies were detected (see *Materials and Methods, Mating and Analysis of Recombinant Ascospore Lines* for full details): 1, OA at 15 °C; 2, OA at 18 °C, 3, OA at 20 °C, 4, OA at 27 °C; 5, Kölln at 27 °C; 6, OA + biotin at 20 °C; 7, OA + Var at 27 °C; 8, OA + Sil at 27 °C; 9, OA + biotin at 27 °C; 10, OA (U.K.) at 20 °C; 11, OA (U.K.) + biotin at 20 °C; 12, Kölln at 15 °C; 13, Schmelz at 15 °C. OA, oatmeal agar medium (Pinhead Oatmeal; Odlums Group); OA (U.K.), Traditional Rolled Oats (Quaker Oats); Kölln, Köllnflocken medium; Schmelz, Schmelzflocken medium (Peter Kölln KGaA); Sil, sildenafil citrate; Var, vardenafil citrate. *See Table S3 for isolate details.

[†]Shaded boxes indicate pairings that were not tested.

[‡]Cleistothecia contained viable ascospores under these conditions.

Gene	חו	36 h	60 h	96 h
		5011	00 11	50 11
Down-regulated at all time points	Bc12c02560	סר ר	1 07	1 /6
Hypothetical protein	Pc12g02300	-2.20	-1.07	-1.40
Tetratricopeptide repeat domain protein	Pc13g15900	-1.63	-2.21	-1.42
Hypothetical protein	Pc15q01560	-1.50	-1.38	-2.42
Hypothetical protein	Pc18q06580	-3.15	-2.74	-2.39
Hypothetical protein	Pc18g06600	-3.38	-4.06	-3.47
Hypothetical protein	Pc18g06610	-4.30	-5.13	-5.51
Hypothetical protein	Pc18g06620	-1.48	-1.36	-1.67
Hypothetical protein	Pc18g06660	-3.13	-1.37	-3.08
HMG box protein	Pc18g06680	-2.81	-2.20	-1.53
Vanillin dehydrogenase, putative	Pc20g02480	-1.04	-2.45	-1.15
Killer toxin sensitivity protein (lki1)	Pc20g12630	-2.28	-2.13	-2.11
Small oligopeptide transporter, OPT family	Pc20g15530	-1.00	-1.69	-1.20
ABC multidrug transporter, putative	Pc21g10850	-2.22	-1.30	-1.08
Putative Transcription factor	Pc21g17180	-1.15	-1.92	-1.99
Glyoxalase family protein	Pc21g21290	-6.09	-6.88	-6.41
FAD dependent oxidoreductase, putative	Pc21g21350	-1.06	-1.23	-1.03
Hypothetical protein	Pc21g21440	-7.04	-1.44	-1.45
Phosphotransferase enzyme family protein	Pc21g21580	-1.11	-1.11	-1.07
Putative Transcription factor	PC22g07530	-5.21	-2.27	-1.20
Hypothetical protein	PC22g16710	-1.02	-1.09	-1.27
Hypothetical protein	PC24901440	-1.51	-2.59	-1.51
In-regulated at all time points	FC24901000	-4.45	-2.99	-4.91
MES transporter putative	Pc03a00020	2 5 2	3 16	1 35
Arsenate reductase ArsC	Pc06g02220	1.03	2 43	1.55
MFS monosaccharide transporter, putative	Pc12g02140	1.90	1.92	1.25
Glycosyl hydrolase family protein	Pc12g024400	1.08	1.02	1.13
Hypothetical protein	Pc13q09280	1.04	1.56	1.16
MFS transporter, putative	Pc13g09900	3.72	3.14	3.17
Flavin-binding monooxygenase	Pc13g14930	3.06	1.21	3.34
MFS sugar transporter, putative	Pc15g00030	1.44	2.18	1.44
Hypothetical protein	Pc16g14900	1.01	1.47	1.71
Hypothetical protein	Pc17g00990	3.29	2.62	1.87
Hypothetical protein	Pc17g01090	1.20	1.05	1.85
Hypothetical protein	Pc18g06590	1.26	1.51	1.22
Hypothetical protein	Pc19g00170	1.61	1.79	1.63
MFS transporter, putative	Pc20g06200	1.76	1.70	3.91
Alpha-ketoglutarate-dependent taurine dioxygenase	Pc20g06210	2.38	1.63	4.23
High-affinity glucose transporter	Pc20g10820	2.05	1.35	1.48
sesA	Pc20g13730	1.24	1.24	1.52
Phytanoyl-CoA dioxygenase	Pc21g04130	1.40	1.97	1.41
Cyclin	Pc21g20530	1.39	1.28	1.48
Amino acid permease, putative	Pc21g20960	2.98	1.67	1.49
FAD dependent oxidoreductase	Pc21g21/50	1.86	1.89	3.29
Hypothetical protein	PCZZG13Z40	1.51	2.49	2.44
Hypothetical protein	PCZZYZ4550	1.02	2.25	2.05
Hypothetical protein	PC22g25960	1.54	2.70	1.49
C2H2 finger domain protein	Pc22g20500	1.52	2.02	2 02
Hypothetical protein	Pc22g27040	1.24	1 97	1.82
Hypothetical protein	Pc24g00020	1.67	1.37	7.02
Hypothetical protein	Pc24a00920	1.40	2.84	1.18
Penicillin biosynthesis	. <u>.</u>			
pcbAB	Pc21a21390	-0.87	-2.84	-2.27
pcbC	Pc21g21380	-0.82	-1.73	-1.28
penDE	Pc21g21370	-0.59	-2.1	-1.35
Asexual development	5			
brlA	Pc06g00470	-1.22	-0.23	-0.45
dewA	Pc16g06690	-4.28	0.02	0.05
dewB	Pc13q16010	-1.14	-0.09	-0.02

Table S2. List of differentially expressed genes in the Δ MAT1-1–1 mutant according to a microarray analysis

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Table S2. Cont.				
Gene	ID	36 h	60 h	96 h
flbA	Pc15g00600	1.45	-0.47	0.27
tmpA	Pc21g07830	-0.49	0.50	1.00
рроА	Pc22g06980	1.05	-2.54	-0.52
Cell wall				
agsD	Pc22g15390	-1.81	0.45	0.27
Fruit body lectin	Pc12g08560	0.20	2.19	2.62
Transcription factors				_
pacC	Pc18g00420	0.47	-1.24	-0.46
HMG box protein	Pc18g06680	-2.81	-2.2	-1.53
Hypothetical protein	Pc22g07530	-3.21	-2.27	-1.2
Hypothetical protein	Pc21g17180	-1.15	-1.92	-1.99
HLH transcription factor	Pc13g11100	-2.86	-1.18	-0.8
C6 zinc finger domain protein	Pc13g10310	-0.07	-2.8	-3.18
Phosphotransferase enzyme family protein	Pc18g03150	-0.16	-1.15	-1.02
C2H2 finger domain protein (Ezf)	Pc21g21760	0.65	-2.16	-1.14
Hypothetical protein	Pc17g01190	-4.16	-0.1	-1.13
Hypothetical protein	Pc24g01630	-3.47	-0.29	-1.3
C2H2 finger domain protein	Pc22g27040	1.24	2.03	3.08
bZIP transcription factor (Atf21) homolog	Pc22g26820	2.31	2.11	0.69
bZIP transcription factor (Atf21) homolog	Pc19g00240	2.42	2.68	0.92
Hypothetical protein	Pc04g00010	0.18	1.09	1.63
Hypothetical protein	Pc13g01210	-1.94	1.87	1.85
zf-fungal binuclear cluster type transcription factor	Pc16g05270	0.00	1.1	1.32
bZIP transcription factor JIbA	Pc20g15070	-0.06	1.84	1.35
C6 finger domain protein	Pc22g19540	-1.32	1.44	1.39

Values are mean \log_2 -transformed ratios relative to the Δ Pcku70 parental strain. Colored values indicate genes with at least a twofold transcriptional up-regulation (red) or down-regulation (green). Listed are genes down-regulated or up-regulated at all time points, as well as those that control conidiation or morphology.

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Table S3.	List of	bacterial	and	fungal	strains	used	in tl	his	study

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Strain	Characteristics and genotype	Mating type	Source
IB 08/921	Wild type	MAT1-2–1	M. Kirchmair*
Pc105	Wild type	MAT1-2–1	This study; indoor air
Pc131	Wild type	MAT1-2–1	This study; indoor air
US 49	Wild type	MAT1-1–1	BDUN Collection [†]
US 68	Wild type	MAT1-2–1	BDUN Collection [†]
IBT 14508	Wild type	MAT1-1–1	IBT Culture Collection of Fungi [‡]
IBT 30738	Wild type	MAT1-2–1	IBT Culture Collection of Fungi
IBT 30427	Wild type	MAT1-1–1	IBT Culture Collection of Fungi
IBT 22703	Wild type	MAT1-1–1	IBT Culture Collection of Fungi
PC0820A	Wild type	MAT1-1–1	(1)
PC088B	Wild type	MAT1-1–1	(1)
PC08105C	Wild type	MAT1-1–1	(1)
PC0814C	Wild type	MAT1-2–1	(1)
PC0819C	Wild type	MAT1-2–1	(1)
PC0826A	Wild type	MAT1-2–1	(1)
DAOM 193710	Wild type	MAT1-1–1	(2)
DAOM 155627	Wild type	MAT1-1–1	(2)
DAOM 155628	Wild type	MAT1-2–1	(2)
DAOM 59494C	Wild type	MAT1-2–1	(2)
ATCC 10106	Type strain; chrysogenin producer	MAT1-1–1	(3)
Q176	chrysogenin producer	MAT1-1–1	(3)
P2niaD18	niaD	MAT1-1–1	(4)
∆Pcku70	Pcku70∆::nat1; niaD ⁻	MAT1-1–1	(5)
ΔMAT1-1–1 EK5	MAT1-1–1 Δ ::ble; Pcku70 Δ ::nat1; niaD ⁻		This study
∆MAT1-1–1 EK6	MAT1-1–1∆::ble; Pcku70∆::nat1; niaD ⁻		This study
∆MAT1-1–1::MAT1-1–1	MAT1-1–1Δ::ble; Pcku70Δ::nat1; PMAT1-1–1::MAT1-1–1::TMAT1-1–1; ergA; niaD [–]	MAT1-1–1	This study
P2::MAT1-1-1 T2	Pgpd::MAT1-1–1; ptrA; niaD [–]	MAT1-1–1	This study
P2::MAT1-1-1 T5	Pgpd::MAT1-1−1; ptrA; niaD ⁻	MAT1-1–1	This study
P2::MAT1-2-1 T2	Pgpd::MAT1-2–1; ptrA; niaD ⁻	MAT1-1–1	This study
		MAT1-2–1	
P2::MAT1-2-1 T5	Pgpd::MAT1-2–1; ptrA; niaD [–]	MAT1-1–1	This study
		MAT1-2–1	
AS 38	F1 progeny from Q176 x IB 08/921	MAT1-1–1	This study
AS 25	F1 progeny from Q176 x IB 08/921	MAT1-2–1	This study
YDB103	sst2∆::KanMX4 ste2∆	<i>MAT</i> a	(6)
Y06055	his $3\Delta 1$, leu $2\Delta 0$, lys $2\Delta 0$, ura $3\Delta 0$, YLR452c::KanMX4, sst 2Δ	<i>MAT</i> a	Euroscarf
XL1-Blue K12	recA1, endA1, gyrA96, thi1, hsdR17, supE44, relA1, lac-, [F' proAB, laclqZ∆M15, Tn10(tetr)]		(7)

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Table S4. List of plasmids used in this study

PNAS PNAS

Plasmid	Characteristics	Source
pDrive/PtrpC-Tn5Phleo	trpC promoter of A. nidulans, ble resistance gene of Streptoalloteichus hindustanus	(1)
pTn5Phleo-3'-FlankeMAT	<i>trp</i> C promoter of <i>A. nidulans, ble</i> resistance gene of <i>S. hindustanus</i> , 3' flanking region of <i>MAT1-1–1</i>	This study
рКОМАТ-1	5' flanking region of MAT1-1–1, trpC promoter of A. nidulans, ble resistance gene of S. hindustanus, 3' flanking region of MAT1-1–1	This study
pT3T7-gpd	gpd promoter of A. nidulans	This study
pT3T7Pgpd-MAT1	gpd promoter of A. nidulans, MAT1-1–1 gene of P. chrysogenum	This study
pDrive-ptrA	ptrA resistance gene of Aspergillus oryzae	This study
pPgpd-MAT-1-ptrA	gpd promoter of A. nidulans, MAT1-1–1 gene of P. chrysogenum, ptrA resistance gene of A. oryzae	This study
pDrive-ergA	acnP promoter of P. chrysogenum, ergA gene of P. chrysogenum	(2)
ergA+3'FlankeMAT-1	acnP promoter of P. chrysogenum, ergA gene of P. chrysogenum, 3' flanking region of MAT1-1-1	This study
pKompMAT-1_ergA	5' flanking region of MAT1-1-1, MAT1-1-1 gene of P. chrysogenum, acnP promoter of P. chrysogenum, ergA gene of P. chrysogenum, 3' flanking region of MAT1-1-1	This study
pPGK-PcPRE2	Pcpre2 under control of the S. cerevisiae PGK promoter	This study

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Sigl C, Handler M, Sprenger G, Kürnsteiner H, Zadra I (2010) A novel homologous dominant selection marker for genetic transformation of *Penicillium chrysogenum*: overexpression of squalene epoxidase-encoding *ergA*. J Biotechnol 150(3):307–311.

Table S5. List of oligonucleotides used in this study

PNAS PNAS

SHATLISHNE ACCONTINUEAACAACCAACCA \$' flanking region of MAT1-1-1 S'MALISHNE ACCONTINUEAACAAACAACCACC \$' flanking region of MAT1-1-1 S'MALISHNE ACCONTINUEAACAAACAACACC \$' flanking region of MAT1-1-1 S'MALISHNE ACCONTINUEAACAACAACACC \$' flanking region of MAT1-1-1 S'MALISHNE GGECCEAACCOCCUCTUCTUCTUCATUREACC MAT1-1-1 GGECCEAACACACACACCC MAT1-1-1 gene MUMATI GGECCEAACACCACCACCCC MAT1-1-1 KMAT S'SENE GLECCEAACACCACACCCCCCCCCCCCCCCCCCCCCCCCC	Oligonucleotide	Sequence (5′–3′)	Specificity
S-Mat_anti GENERCEGETAACAATATRAGENCC S: flanking region of MAT1-1-1 S-Mat_anti GEGECCECACCACCTCOTEGETARA S: flanking region of MAT1-1-1 Aph-MAT1 GEGECCECACCACCTCOTEGETARA S: flanking region of MAT1-1-1 Aph-MAT1 ACCECACCACCACCTCOTEGETARA S: flanking region of MAT1-1-1 Aph-MAT1 ACCECACCACCCACCGACCCACCGACCC MAT1-1-1 gene KOMAT 3-sense CCICCCACACCCACCCACTAG TraC promoter ToS-phile GECACCCACACCCACCCACTAG TraC promoter ToS-phile GECACCCACACCCACCTAGACTCCCCCCCCAG TraC promoter MAT1_Linf. TRICACCCACCCCCCCCCACTAGACTCCCCCCCCAGA S: flanking region of MAT1-1-1 SMAT_Linf. TRICACCCACCACCCCCCCCCCCCCCCCCCCCCCCCCCCC	5'-Mat_sense	ACGCGTCTGTCAACAAGCAACGC	5' flanking region of MAT1-1-1
3-Mat, sense 3-Mat, anti CONCRECTION CONCRETACIONS 3' flanking region of MAT1-1-1 Apal-MAT1 GOGOCCALCETOCONSTRAT MAT1-1-1 gene Mulu-MAT1 ACCONTECTACTETERCECTAACATCC MAT1-1-1 gene Mulu-MAT1 GOGOCCALCETOCONSTRAT 5' flanking region of MAT1-1-1 koMAT 5-ensee GOCOCCALCETOCONSTRAT 5' flanking region of MAT1-1-1 koMAT 5-ensee GOCOCCATACTOCONSTRAT 5' flanking region of MAT1-1-1 trip-C_ant1 GOCOCTATACTACTACTOCONSTRA 5' flanking region of MAT1-1-1 SMAT-Linf-fw ATTOCATACTACTACTACTACTACTOCONSTRA 5' flanking region of MAT1-1-1 SMAT-Linf-fw ATTOCATACTACTACTACTACTACTOCONSTRA 5' flanking region of MAT1-1-1 SMAT-Linf-fw ATTOCATACTACTACTACTACTACTACTACTACTACTACTACTA	5'-Mat_anti	GGATCCGGTAAACAAATATAGGACC	5' flanking region of MAT1-1-1
3'-Mat, antiGCGGCCCCCCCCCCCCGGTTAG3' flanking region of MAT1-1-1ApaHMAT1AGGGCTCTGGTCTGGCTGGATGGMAT1-1-1 geneMuLMAT1AGGGCTCTGGTCTGGCCGAAGATCCMAT1-1-1 geneKoMAT 3'-antiCTGGCCTGCTGTGTATTGCGCGAS' flanking region of MAT1-1-1KoMAT 3'-antiCTGGCCTGCTGTGTATTGCGCGABresistance gene3'MAT-1_inf.ATTGCTGGACAAGCTTCCATTGCACAGCGCGC3' flanking region of MAT1-1-1Ximat-1_inf.TTGCTGGACAAGCTTCCATTGCACAGCTGCGCT3' flanking region of MAT1-1-1Ximat-1_inf.TTGCTGGACAAGCTTCCATTGCACAGCGCGC3' flanking region of MAT1-1-1Ximat-1_inf.TCGTGGACAAGCTTCCATTGCACAGCGGGC5' flanking region of MAT1-1-1Ximat-1_inf.CATGGTCGACAGCGGGGCTTGCACAGCTGGGGG5' flanking region of MAT1-1-1Simat-1_inf.GCGTGTGCGGACGGGGTTGTGGGGGGGGGGGGGGGGGGG	3'-Mat_sense	AAGCTTCCCATTCACAATTTCGAC	3' flanking region of MAT1-1-1
Apal-MATIGGGCCATEGETTACCTECCECTATACTECCMATI-1-1 genekoMAT 5'senseGCACEGARGACCCASCATCEG5' flanking region of MATI-1-1koMAT 3'antiCETTEGETERTERTACTECGEG3' flanking region of MATI-1-1koMAT 3'antiGCACEGARGACCCACCACTAGAthe promoterTh5-pheleGCGCCTGATACAGRACGAATTCCble resistance geneSMAT-L_Inf_fwATTCCCCCACACGCTCCCATTCACATTCCACTCCCCCT3' flanking region of MATI-1-1SMAT-L_Inf_fwATTCCCCCCACACGCTCCCATTCACATTCCACTCCCCCCT3' flanking region of MATI-1-1SMAT-L_Inf_fwCATCCCCACACGCTCCCCATTCCCCAGGCACCTCCCCCATTCCCCAGGCACCTCCCCCCATTCCCCAGGCACCTTCCCCCCACGCACCTTCCCCCCCC	3'-Mat_anti	GCGGCCGCCCAACCTCCGTGGTTAG	3' flanking region of MAT1-1-1
Miul-MAT1ACCCONCURATORSMAT1-1-1 genekoMAT 3-antiCTTGGCTGTCTGTRIATTCCGCG3' flanking region of MAT1-1-1PtpC_antilGGCATTCATCGTGTACATTCGCCGAGATTCCbe resistance gene3'MAT-1_inf,*vATCGTCGCCAAGAGCTCCCATTGACTTCGACTCGGCT3' flanking region of MAT1-1-1SMAT-1_inf,*vRATCGTCGCCAAGAGCTTCCCATTCGACTCGGCT3' flanking region of MAT1-1-1SMAT-1_inf,*vRATCGTCGCCAAGGCTGGAATTACTTTCCAGGAGGGGA5' flanking region of MAT1-1-1SMAT-1_inf,*vCATCGTCGCACGGGCGGAATTACTTTCCCAGGAGGGGA5' flanking region of MAT1-1-1SMAT-1_inf,*vCATCGTCGCAGGCGTGGAATTACTTTCCCAGGAGGGGA5' flanking region of MAT1-1-1SMAT-1_inf,*vCATCGTCGCAGCGAGCTTATTTTCCCCGGAGGGGA5' flanking region of MAT1-1-1SMAT-1_inf,*vCATCGTCGCGTCGGCCCCATTMAT1-1-1SCMAT-1_inf,*vCATCGTCGGCGCCCCCCCCCCCATCGCCCAAGGCGGGGAMAT1-1-1SCMAT-1_inf,*vCATCGCGTCGGCCCCCCCCCCCCCCCCCATGCCMAT1-1-1SCMAT-1_inf,*vCCTCGCCCCAAGGCGTCGCCCCCCAGGCGMAT1-1-1SCMAT-1_inf,*vCCTCGCCCCCAAGCCGCCCCCCCCCCCCCCCCCCCCCCC	Apal-MAT1	GGGCCCATGTCTACCTCTTGATGC	MAT1-1-1 gene
koMAT 3'-enteSCACEGRAMACCACEGATOTES' flanking region of MAT1-1-1koMAT 3'-antiCCATEGATEGTETERTATITECEGE3' flanking region of MAT1-1-1ptpC_antilGCACTEGATEACBAACGAATTCCble resistance geneSMAT-L_inf_fwATTCCTEGACAGACTECCAATTCCAATTCCAACTCCCCT3' flanking region of MAT1-1-1SMAT-L_inf_fwATTCCTEGACAGACTECCAATTCCAATTCCAACTCCCCT3' flanking region of MAT1-1-1SMAT-L_inf_fwCATCCTEGACAGACTECCAATTCCCAATTCCCAATTCCCACTCCCCT3' flanking region of MAT1-1-1SMAT-L_inf_fwCATCCTEGACAGACTECCACTCCCAATTCCCCACTCCCCCCCCCC	Mlul-MAT1	ACGCGTCTAGTTGTGCCCAAAGATCC	MAT1-1–1 gene
koMAT 3-antiCITEGECTERCENTRATECCEGE3' flanking region of MAT1-1-1PtrpC_antilCGCATCATTEGACTCOACTAGtrpC promoterTaS-phileCGCATCATTEGACTCOACTAGtrpC promoter3'MAT-Linf_MATTCGTCGACAGGATTCC3' flanking region of MAT1-1-13'MAT-Linf_MCATCCTCCAACCGACGACATTETATATTCCCCCC3' flanking region of MAT1-1-15'MAT-Linf_MCATCCTCCAACCGCGGACATTETATATTCTCCCCC3' flanking region of MAT1-1-15'MAT-Linf_MCATCCTCCAACCGCGGACATTETATATTCTCCCCC5' flanking region of MAT1-1-15'MAT-Linf_MCATCCTCCAACCTACTETACTCTCTCCCCAAGATCCCG5' flanking region of MAT1-1-1 and MAT1-1-1 gFCMAT1-1CCCTTCCCAACCAACCTMAT1-1-1 geneFCMAT1-3CCCTTCGCTCCCACCTCTCCCCCCCCCCCCCCCCCCCCC	koMAT 5'-sense	GCACGGAGAGCCACGGATGTG	5' flanking region of MAT1-1-1
PtrpC_antilGCCATTCATTGTTGACCTCCACTGtp/Th5-bileoGCCCTGATACAGAACGAATGCb/e resistance gene3MAT-1_inf_twATTCOTCGACAACCTTCCCATTCCACATTTCGACTGGCT3 flanking region of MAT1-1-13TMAT-1_inf_twCATCCTCCACACCCCCAGACCTTCCACATTTCGACTGGGCT3 flanking region of MAT1-1-13TMAT-1_inf_twCATCCTCCACACCCCCAGACCTTTCACATTTCGCCCAGGGGC5 flanking region of MAT1-1-13TMAT-1_inf_twCATCCGATACTTGTACGTCCACACATTMAT1-1-1GCCTTGTCGCTGACACCCACTTMAT1-1-1genePCMAT1-3GCCTTGCTGTCACCCAATTGTGCCGGGMAT1-2-1PCMAT1-4GCCTTGCTGTCACCCCAATTGTGTGCGGGAMAT1-2-1PCMAT1-4GCCTGCGTCGTGCGGCCCCCCCTGGGGMAT1-2-1PCMAT1-5GCGATGCCTTGCCCCACTTGTGCGGGAMAT1-2-1RAT1-1-1_GCAGTGCGTCTGCGCCCCCCCTGGGGCMAT1-2-1GCAGTGCGTCGTGCGGCCCCCCCCCCCCCCCCCCCCCCC	koMAT 3'-anti	CTTGGCTGTCTGTATATTCCGCG	3' flanking region of MAT1-1-1
Th5phlo0GCCCTCATACAGACGATTCCDesistance gene3'MAT-1_inf_fwATTCGTCGACAGCTTCCATTCGACTAGCTTCGACTGGACT3' flanking region of MATI-1-13'MAT-1_inf_rwTATCGTCGACAGCCGCGAGAGTTTGATATTGTCGGCG3' flanking region of MATI-1-15'MAT-1_inf_rwCATCGTCGACAGCCGCGAGATACTGTCGCCGAAGATCCGG5' flanking region of MATI-1-1 and MATI-1-15'MAT-1_inf_rwGCTGTCGCGACAGCGTGCACACTTGCACGCGAAGAGCGGA5' flanking region of MATI-1-1 and MATI-1-18'MAT-1_inf_rwGCTGTCGCGTCGTCGCCACACTTMATI-1-1RCMAT1GCTGTGCGTGTCGTGCCACTTMATI-1-1RCMAT1GCTGGCGTTCTTGGCCCACGTMATI-1-1RCMAT1-1GCTGCGCACAAGGGCGGMATI-2-1RCMAT1-1GCTGCGCACCAAGGTCGTCGGAGMATI-1-1RCALSenseCGAGGGCGTCTTGGCCCCCCCCCCCCCCCCCCCCCCCCC	PtrpCanti1	GGCATTCATTGTTGACCTCCACTAG	<i>trpC</i> promoter
3'MÅT-1_inf_iv ATTGETGEACAGETTICCATTTCACATTTGECGET 3' flanking region of MAT1-1-1 3'MÅT-1_inf_iv CATGETGEAGEGEGEGEGEGEGEGEGEGEGAGEATTGEATATTGETGEGEGT 3' flanking region of MAT1-1-1 3'MÅT-1_inf_iv CATGETGEAGEGEGEGEGEGEGEGAGEATTGEATATTGETCCEAGEAGEGEA 5' flanking region of MAT1-1-1 and MAT1-1-1 g 5'MÅT-1_inf_iv CATGETGEAGEGEGEGEGEGAGEATTGETGETCEGAGEAGEGEA 5' flanking region of MAT1-1-1 and MAT1-1-1 g FCMAT1-3 GGETATTCETTGEAGECAGETATT MAT1-1-1 gene PCMAT1-4 GETGEATCETTEGEGEGAGE MAT1-1-1 gene PCMAT1-5 GGETGEGETGETGEGEGEGEGEGEGEGE MAT1-1-1 gene PCMAT1-6 GEGEGEGETETTGEGEGAGE MAT1-1-1 gene RAMAT1-1-1_a CAGEATTGEGTTGETGEGEGEGE MAT1-1-1 gene MAT1-1-1_a CAGEATTGEGTTGETGEGEGEGE MAT1-1-1 gene MAT1-1-1_a CAGEATTGEGTGETGETGEGEGE MAT1-1-1 gene MAT1-1-1_a CAGEATTGEGTGETGETGEGEGEATT PAGIA MAT1-1-1_a CAGEATTGEGTGEGEACTCE PAGIA PCLA_ant CAGEATTGEGETGETGEGEGETCTGE PAGIA (PC2214900) gene Chy AGEACTTGEGEGETCTGEGECATTGE PAGID Gene PCPanDE_a CCTGECATAGEACATGECATGE PAGID Gene PCPanDE_A C	Tn5-phleo	GCGCCTGATACAGAACGAATTGC	ble resistance gene
3'MAT-Linf_rvTAGAATACAGGCCGCCAAGGAGTTCATATTOTCCTG3' flanking region of MAT1-1-15'MAT-Linf_rvCATGCGATACGGCGGAAATACGACGCGGAAATACGAGTGCGGGAA5' flanking region of MAT1-1-1 and MAT1-1-1 g5'MAT-Linf_rvGGCTATTCGTGCGAGGCGGAAATACGACGCGGAAATACGGCGGGAAGGGGA5' flanking region of MAT1-1-1 and MAT1-1-1 gPCMAT1-aGGCTGATCGTGTGGCGGCCACTTMAT1-1-1 genePCMAT1-aGGCTGACGATGCGTCGCGCCACTTMAT1-1-1 genePC,HMG_antiGCCTGACCAAAGGCAGGMAT1-1-1 geneMAT1-1-1_sCGCTGCGTCGCCCCAAGTGCGTCGGGGMAT1-1-1 geneMAT1-1-1_sGGCTGACGAAGGGAAGGMAT1-1-1 geneMAT1-1-1_sGAGATGCGCTTGCCCCCACTCCpCA (PC2214900) genePCLA,sensTGTGGTTGCCCCGCGCACTCCpCA (PC2214900) genePCLA,sensTGTGGTTGCCCCGCGCCCCCCCCCACGCCPC21g16000 geneChy1GAGTTGCACTGGGCGTTCGCCCCAAGCCCATCPc21g16000 geneChy4AGCCAATCCATCGCTCGCACCCPC21g16000 geneChy4AGCCAATCCATCGCTCGCACCCCPC21g16000 genePcpenDE_sCTGCCACCAAGGGCAATCTPcpenDEgenePcbC_sCCACCATGCGCTTCACCCCCAAGGCCAATCPcphC genepcbC_sCCACCATGCCCTAAGCCACCCCPC21G1600 genepcbC_sCCACCATGCCCTAAGCCACCCCCPC21G1600 genepcbC_sCCACCATGCCCTAAGCCACCCCPC21G1600 genepcbC_sCCACCATGCCCTCAAGCCACCCCPC21G1600 genepcbC_sCCACCATGCCCTCAAGCCACCCCCPC21G1600 genepcbC_sCCACCATGCCCTCAAGCCACCCCPC21G1600 genepcbC_sCCACCATGCCCTCAAGCCACCCCCPC21G1000 genepcbC_sC	3'MAT-1_inf_fw	ATTCGTCGACAAGCTTCCCATTCACAATTTCGACTCGGCT	3' flanking region of MAT1-1-1
STMAT-1_inf_rvCATCCTCCAGACCCCTCAAATCACTCTCCCGCAGACCCGAS' flanking region of MAT1-1-1 and MAT1-1-1 gS'MAT-1_inf_rvGATCCGATACTGACTACTACTAGTGTGTCCCCGAACGCGS' flanking region of MAT1-1-1 and MAT1-1-1 gPCMAT1-sGGCTATTCCGTCCGACCAAGTMAT1-1-1 genePCMAT1-sGGCTGATCGATCGACCAAGTMAT1-1-1 genePCMAT1-sGGCTGCCTCGACCAATGCTGCCGACGAGTMAT1-1-1 genePCMAT1-sGGCATGCCTCGCTCAACCGAATGCTGCTGGGGMAT1-1-1 genePCLMS_enseCGCTGCCTCACCCAATGCTGCTGGGGGMAT1-1-1 geneNAT1-1-1_sGGCATGCCTCACCTCGCCCCCTCTGTGCGMAT1-1-1 geneMAT1-1-1_sGGCATGCCCACTCTCCCCCCTCTGTGCGMAT1-1-1 geneMAT1-1-1_sGGCATGCCCACTCTCCCCCCTCTGTGCGMAT1-1-1 genePCd_senseTGTGGTATTACCGGGAGCTCTGGPC21g16000 geneChry1GAGTTGGCTCGCGGTCTTGGPC21g16000 geneChry1GAGTTGGCTCCACCGGGTCTTGGPC21g16000 geneChry1GAGTTGGCTCCACCGGGCGCATGGCCCCCAGGCCATGPcpenDEgenePcpenDE_aCCCGCGGGTGGAGCCATGPcpenDEgenepcbC_sCCACCGCCGAAGGCGAGCCCCPcphDEgenepcbC_sCCACCGCGCGCGGGCGCATGGACCCCCPCHLG genepcbC_sCCAACGCGCGTGGACCCCCCPCHLG genepcbC_sCCAACGCGCGTGGACCCCCPCHLG genepcbC_sCCAACGCGCGTGGACCCCCCPC300420 genepc23g00420_rvTGCAGGCGCCGAAGCCCCCCAAGGCPC300420 genePc23g00420_rvTGCAGGCCGCGAAGCCCCCCAAGCPC300420 genePc23g00420_rvTGCAGGCACGCGGAAGCCCCCPC300420 genePc23g00420_rvTGCAGGCACGCGGAAGCCCCCPC30	3'MAT-1_inf_rv	TAGAATACAGCGGCCGCCGAGGAGTTTGATATTGTCCGTG	3' flanking region of MAT1-1-1
STMAT1-1_inf_rvGATCCGATACTGTGCGCCAAGGTTMAT1-1-1 genePCMAT1-3GCGTATGGCGTGCGCCAGGTMAT1-1-1 genePCMAT1-4GTCTGATCGTGGCGCCACTTMAT1-1-1 genePC, HMG_senseCGATGGCGTTCTTGACTGGMAT1-2-1 genePC, HMG_senseCGATGGCGTTCTTGACCTGGMAT1-2-1 genePC, HMG_antiGCCTGACCAAMAGGCGGMAT1-1-1 geneMAT1-1-1_3GGAAATCGCCTGTGCCACCTGCGGGGMAT1-1-1 geneMAT1-1-1_4GGAAATCGCCTGCCCGGACGCpclA (Pc22g14900) genePCIA, senseTGGGTTTACCGGAGACTCCpcl2 [91000) genePCIA, antiACAATTCGCTGCGCGGACTCPc21g16000 geneChry4AGCCAATCCACTCGCCTGGCCGCAPc21g16000 geneChry4AGCCAATCCACTCGCCTGGCCGCAAGGCCAATGPcpenDEgenePcpenDE_3CCTGCCACAAAGAGATGATCCPcpenDEgenePcbC_3CCTGCCATGCACCTAAGGCCAAGCCAATGPcplD GenePcHuG-3GCCAATGCCCTTGCCCCTTGTTGTTATAGACPcpbC genePcHuG-3GCCAATGCCCTAAGCCAAGCCAATGPclbG genePcHuG-3GCCAATGCCCTAAGCCAAGCCAATGPclbG genePcHuG-3GCCAATGCCCATAGCCAAGCCAATGPclbG genePcHuG-3GCCAATGCCCATAGCCAAGCCAATGPclbG genePcHuG-4GCCCAATGCCCTAAGCCAAGCCACTCPclbG genePcHuG-5CCCCCACGCCGCGAAGCCACTCPclbG genePcHuG-5CCCCCACGCCGCGCAAGCCACCCPclbG genePc2300420_forTAGACCCACGCTGAAGGAGAGAPclbG genePc2300420_forTAGACCCACGCGCTAAGCCCACACPc2300420 genePc2300420_forTGAGCACCCAGCTGCCGAAGGPclbG genePc2300420_fo	5′MAT-1_inf_fw	CATGCTGCAGACGCGTGAAATACATGTTCCAGGAAGGGGA	5' flanking region of MAT1-1-1 and MAT1-1-1 gene
PCMAT1 -sGGCTATTGCTGTGCACCACTTMAT1-1-1 genePCMAT1-aGTCTGATCGTTGACTGGCTCACTTMAT1-2-1 genePC,HMG_senseCGATGGCTTTGACCTGGMAT1-2-1 geneR_LHMG_antiGCCTTGACAAAAGGCAGGMAT1-1-1 genePC,HMG_senseCGATGGCTTGTCGCCACACTCTGGTGCTGGAGMAT1-1-1 geneMAT1-1-1_aGAGAATGGTGCTGGCGCAATGGTGGCTGGAGMAT1-1-1 geneMAT1-1-1_aGAGAATGGTGCTGCCCACTCTGGTGCGGAMAT1-1-1 genePCA_senseTGTGGTATTACCGGGAAGTCpCA (Pc22g14900) genePCA_senseTGTGGTATTACCGGGACGTCTGGPC21g16000 geneChrydAGCTTGACTCGGCTGTGGCGGACGCPC21g16000 geneChrydAGCCAATTCGTGCTGGCGGTGCTGGGCGCAATGPCpenDEgenePcpenDE_sCTGCGCGTGGCGGCGGCGCTGTGTTGTGATTAGACPCpenDEgenepcbC_sCCCCCATGGCCTCAGCCCCAAGGCCAATGPcfuG genepcbC_sCCCCCATGGCCTGGCCGTGTTGTGTGATTAGACPcfuG genepcbC_sCCCCATGGCCTTGGCCGTATGGACGCAATGPcfuG genepcbC_sCCCCATGGCCTGGCCGTGCTGTGGCGGTCGTGGCGGTCGTGGCGGTCGTGGCGGTCGGCAATGPcfuB geneflbB_forGCCATGGCGTGCGCAACCCPcfuB genensdD_forTAGGGTGGCTCGCCAATGGCAACPcflbB genensdD_forTAGGGTGGCTGCGCAACCCPc3300420 genePc2300420_forTGAGACACCGGCCTAATGGAAGPcflbG genePc2300420_forGCACGCCCCTAAGGAAGCAPcflbG genePc2300420_forGCACGCCCCTAAGGAACCACCPc2300420 genePc2300420_forGCACGCCCCCCCCCCCCCCCAAGGCCCAATGPc1BG genePc1301940_forGCCCCCCCCCCCCCCCCCAAGGCCCCAAGGPc1BC genePc	5′MAT-1_inf_rv	GATCCGATACTGTACGTACTAGTTGTGCCCAAAGATCCGG	5' flanking region of MAT1-1-1 and MAT1-1-1 gene
PCMAT1-aGTCTGATCGATCGATCGATCGACTGGMAT1-2-1 genePC_HMG_antiGCCTGAACGAAAGGCAGGMAT1-2-1 geneMAT1-1-1_SGCCTGAACGAAAGGCAGGMAT1-2-1 geneMAT1-1-1_GGCGTGAACGAAAGGCAGGMAT1-1-1 geneMAT1-1-1_GGAGAATGTGCTGTCGCCACACTGTGCTGCGGpclA (Pc22g14900) geneMAT1-1-1_GGAGATGTGCTGTCCCCCCACTGCpclA (Pc22g14900) genePCA_antiACAATTCGTGCTGCGCACTCGpc16 (Pc22g14900) geneChry1ACCAATTCCATCGTGCTGCPc21g16000 geneChry1AGCCATTGCCTGCGCCCCAAGGCCATGPcpenDEgenePcpenDE_sCTGCCACCAAAGGGCAATCCPcpenDEgenePcpenDE_sCTGCCATCGCCTTACCAACGCAATGPcpbC genepdbC_sCACCCATGGCGTTGCGCCGACCCPcpbC genepdbC_sCACCATGGCGTGACCCCCAAGGCACTGPcfluG genepdbC_sCCACATGCCATGGCCGTTACCAAACCAACPcfluG genepdbLacGCCAATGCCATGGCTGCCCAAGGCACTGPcfluG genepdbLacGCCAATGCCATGGCTGCCCAATGCAACACCPcfluG genepdbLacCCACAGTGCGTGCGCGAACCACCCPc2300420 genepdbLacTAACGTGGCTGCCCGAACCACCGPc2300420 genepc2300420_forTAAGACCCGGATAGCACCGCGAACCACCCPc2300420 genepc2300420_forTAAGACCCCGGATAGCACCGPc2300420 genepc2300420_forGCCCCAGGCTGAGAGCACCACGCPc2300420 genepc2300420_forTCAGCACGCGCTAGAGCACCGPc2300420 genepc2300420_forTCAGCACGCGCTAGAGCACCGPc2300420 genepc2300420_forGCCCACGCCGCGAACCACGCCCGAACPc2300420 genepc300420_forTCAGCACGCGCTAGGAGCACGC <t< th=""><th>PcMAT1 -s</th><th>GGCTATTGCTGTCGACCAAGTT</th><th>MAT1-1–1 gene</th></t<>	PcMAT1 -s	GGCTATTGCTGTCGACCAAGTT	MAT1-1–1 gene
Pc_HMG_senseCGATGGCTTCTGACCTGGMAT1-2-1 genePc_HMG_antiGCCTGACAAAAGCCAGGMAT1-2-1 geneMAT1-1-1GCCTGACCAAAAGCCGCGAATGCTGCTGCGAGMAT1-1-1 geneMAT1-1-1_3GAGATGTGCTTGCCCCAATGCGTGCTGCGGMAT1-1-1 geneMAT1-1-1_3GAGATGTGCTTGCCCCACTCCTCGTGCGMAT1-1-1 genePclA_senseTGTGGTATTACCGGGAGTCpclA (Pc22g14900) genePclA_antiACAATTGCTGCGTCGTCGCpclA (Pc22g14900) geneChy1GAGTTGGACTGCGCGTGCTGCPc21g16000 geneChy4AGCAATTCCACTGGCTCGPc20pl5000 genePcpenDE_sCTGCCACCAAGGATGCTCCPcpenDEgeneCpcpnDE_sCTGCCACTGGCTGCAGCCCAATGGPcpenDEgenepcbC_sCACCCATGGCTTGCACCCCAAGGCCAATGPcpbC genepcbC_sCACCCATGGCTGCTGCGCCTTCTGCTGTTGTTGATTAGACPcfbLG genePcfluG-sCCCACTGGCTGCGCAACCACCPcfbLG genePcfluG-sCCCACTGGCTGCGCAATGGCPcfbLB geneflbB_forGCCATGGCACGCGCTAATGCAACCAACPcfbLB geneflbB_forTAGCGACGCGCTGAATGCPcfbD genepc23g00420_forTAGGCACCGGCTGAATGCACCACCPc23g0140 genePc23g00420_forTAGGCACGGCGTAATGCAACCAACPc23g0140 genePc23g01940_forGTCCACGCGGCTGAATGCAAGGPc23g0140 genePc13g1919_forGCCTCCACGTTGCTGCGCAAGCPc24g01940 genePc13g1919_forGCGCGCAGGGCGGAAGGAGAPc13g1990 genePc13g1919_forTCAAGCACCGGGCGGAAGCAGAGPc13g1990 genePc13g1919_forGCGCGCAGGGCGCGAAGGAGAGAGAPc13g1990 genePc13g1919_forTCAAGCACGGGGCGCGGAAGGAGA </th <th>PcMAT1-a</th> <th>GTCTGATCGTTGAGTCGTCCACTT</th> <th>MAT1-1–1 gene</th>	PcMAT1-a	GTCTGATCGTTGAGTCGTCCACTT	MAT1-1–1 gene
Pc_HMG_antiGCCTEAACAAAAGCACGMAT1-21MAT1-1-1_sCGCTTCACCAAAGCGCAATGCGTCGGAGMAT1-1-1MAT1-1-1_sCGCTTCACCGAATGCTCGTCGCGAGCMAT1-1-1PclA_senseTCTGGTATACCGGGAAGCpclA (Pc22g14900) genePclA_antiACAATTCGTCCCGGCTCTGpclA (Pc22g14900) genePclA_antiACAATTCGTCCGGCTCTGGPc21g16000 geneChry1GAGTTTGACTCCGGCTCTGGPc21g16000 geneChry4AGCCAATTCCATCGCTCTGPc21g16000 genePcpenDE_sCTGCCACAAAGAGATGATCCPcpenDEgenePcpenDE_sCCTGCCGCTAAGCGCAAGCCAATGPcphDC genepcbC_sCCTGCCATGACTCCTCTCTGTGTGTATTAGACPcphC genepcbC_sCCACCATGCCTGCCACAACCAACCAACPcfluG genePcHuG-sCCACCATGCCTGCCAAGAGAGACCACCPcfluG genepcbL_sCCACATGCCTGCCAAGAGCAACCACCACPcfluB genepcbL_sCCACATGCCTGCCAAGAGPcfluB genepcbL_sCCACATGCCTGCCAAGAGPcfluB genepcbL_sCCACATGCCTGCCAAGAGPcfluB genepcbL_sCCACCATGCCTGCCAAGAGPcfluB genepcbL_sCCACCATGCCTGCCAAGAGPcrisdD genepcbL_sCCACCAGGCTGCCAAGAGPcrisdD genepcbL_sCCACCAGGCTGCCGAACPc23g00420 genepc23g00420 forTTGAGACACCAGGCTCAAGAGPc23g00420 genepc23g00420 forCTGAGCAACCAGGCTCAAGGAPc23g00420 genepc23g00420 forGTGAGCACCAGCGCTAAGGAAGAGPc13g1290 genepc23g01940 forGTGAGCACCAGCGCTAAGGAGAGAPc13g1290 genepc23g01940 forGTGAGCACCAGCGCTAAGGAGAGAPc13g	Pc_HMG_sense	CGATGGCGTTCTTGACCTGG	MAT1-2–1 gene
MATI-1-1_sCGCTTCGTCTACGCAAATGGTGTGCTGGAGMATI-1-1 geneMATI-1-1_sGAGAATGTCGTTCTCCCCCTCTTCGTTCGGMATI-1-1 genePCIA_senseTGTGTATTACGGGAAGTCpCIA (P22214900) genePCIA_antiACAATGGTGCCTGGACTCCpC21g16000 geneChry1GAGTTTGACTCGGTCTTGGP21g16000 genePcpenDE_sCTGCCACCAAAGAGTGATCCPCpenDEgenePcpenDE_sCTGCCACCAAGGCTGTCTGGTCGTGGCGCAATGPcpenDEgenepcbC_sCACCCATGCGTCTGCCCCAAGGCCAATGPcphC genepcbC_sCGCCCATGCGCTGTCTGGCCGTCTTGTTGATTAGACPcfulG genePcfluG-sCCACCATGCGCTATACCAACCACACPcfulG genePcfluG-sCCACCATGGCCTATACCAACCACACPcfluB geneflbB_revTGACAAGTGCTCTCAGGCAATGPcfluB genersdD_revTGACCACGGGCTGTCTGGCCGAACPcrisD genePc23g00420_revTGACACGCGGATAGGGAAGPcrisD genePc23g00420_revCTACGCAGGTCTCAGGGAAGPc23g00420 genePc23g00420_revCTACGCAGGGCTCAAGGGAAGPc242g01940 genePc23g00420_revCTACGCAGGGCTCAAGGGAAGPc242g01940 genePc23g00420_revCTACGCAGGGCTAAGCGAAGPc242g01940 genePc23g00420_revCTACGCAGGGCTCAAGGGAAGPc1b genePc13g12190_rovAGGCCAGGGCTCAAGGGAAGPc1b genePc13g12190_rovTGAGCAACGGGGTAATTCPc242g01940 genePc13g12190_rovCTGCGCGACGCTCAAGGGAAGAPc1b genePc33g00420_revCTCCAGCGAGGTCAAGGGAAGAPc1b genePc13g12190_rovTGAGCAACGGGGAAACCAGGCPc300420 genePc13g12190_rovTGAGCAACGGGGAGACAGG	Pc_HMG_anti	GCCTGAACAAAAGGCAGG	MAT1-2–1 gene
MATI-1-1_aGAGAATGTGCTGTGTCCCACTCTTGGTGCGMATI-1-1_genePclA_senseTGTGGTATTACCGGGAAGTCpclA (Pc22g14900) genePclA_antiGAGTTGACTCGGGTCTGCPc21g16000 geneChry1GAGTTGACTCGGGTCTGCPc21g16000 geneChry4AGCCAATGCGTCGGCTGTGGPc21g16000 genePcpenDE_sCTGCGCGTGAGGCCAGACCTPcpenDEgenepcbC_sCACCCATGGCTTCCACCCCAAGCCCAAGCCAATGPcpcbC genepcbC_sCACCCATGGCTGCGCGCGTCTGTGTGTGATTAGACPcfuG genePcfluG-sCCCACTGGCTGCCCCATAGCCAATGCPcfluG genePcfluG-sCCCACTGGCTGCCCCTAACCCATTGGAAPcfluG genepcbC_aGCAAATTCCGCATAACCAACCAACPcfluB genepcbLg-sTGACCAATGCCTGCCCTAATGAAACCAACPcfluB genepcbLg-sTGACCAAGGCTGCCCCATAGGAGAGACPcflbB genepcbLg-sTGACCAAGGCTGCCCCATAGGAGAGACPcflbB genepcbLg-sTGACCAAGGCTGCCGAAGACCACCPcflbB genepcbLg-sTGACCAAGGCTGCCGAACCPc300420 genepc23g00420_forTAAGCACGCGGTAGATCCPc23g00420 genePc23g00420_forGCCTCCAGCGCTAAGACCACCPc24g01940 genePc24g01940_forGCCAGCGCCTAAGACCACCACCPc24g01940 genePc24g01940_forGCCAGCGCCTAAGACCACCACCACCACCACCPc24g01940 genePc24g01940_forGCCAGCGCCTAAGACCACCACCACCACCACCACCACCACCACCACCACCA	MAT1-1-1_s	CGCTTCGTCTACGCAAATGGTGTGCTGGAG	MAT1-1–1 gene
PclA_senseTGTGGTATTACCGGGAAGTCpclA (Pc22g14900) genePclA_antiACAATTCGTCGCTCGGCTCTCGpclA (Pc22g14900) genePchy1GACATTCGTCGGGTCTCGGGGTCTCGPc21g16000 geneChny4AGCCAATTCGATCGCTCGGGCTCTGGPc21g16000 genePcpenDE_sCTGCCACCAAGGGCCAAGCTPcpenDEgenepcbC_sCACCCATGGCTGCGCGCGTCTTGTGTTGGATTAGACPcpcbC genepcbC_sCACCCATGGCTGCGCGCGTCTTGTGTTGGATTAGACPcfuG genePcFluG-aGCCAATGGCTGTCGCGCGTTCTTGTGGATTAGACPcfluG genePcFluG-aGCCAATGGCTGGCAGACCACCPcfluG genepcbC_sGCCAATGGCTGGCCGTAAGCAATGPcfluG genepcbC_sGCCAATGGCTGGCCGAAGGPcfluG genepcbL_aCCCACTGGCCTGTCAAGGACPcfluG genepcbLg-aGCCAATGGCGTGGCGCAAGAPcfluG genepcbLg-aGCCAATGGCGTGGCGCAAGCPcfluG genepcbLg-aGCCAATGGCGGGGGGAGAPcfluG genepcbLg-aGCCAATGGCGTGGCGAAGCPcfluG genepcbLg-aTAGCGGGGGGGGGGAACCPc300420 genepc23g00420_frorTAGAGCACGCGTATGGCCTAAGCCPc23g0420 genepc23g00420_frorGCCAACGGGGTGAAGCCPc24g01940 genepc23g00420_frorGCCAGCGGGGGAAGACPc24g01940 genepc23g00420_frorGCCAGCGGGTGAAGCCPc24g01940 genepc23g00420_frorGCCGCAGGCGCAAGGPc1bC genepc23g00420_frorGCCGCCTGCGCGAAGACPc24g01940 genepc23g00420_frorGCCGCAGGCGCGAAGACPc24g01940 genepc13g04320_frorGCCGCGCGGGGCGAAGACPc1bC genepc13g04320_frorG	MAT1-1-1_a	GAGAATGTGCTTGTCCCACTCTTCGTTGCG	MAT1-1–1 gene
PclA_antiACAATTCGTGCCTGGACTCCpclA (Pc22g14900) geneChry1GACTTTGACTCGGCTCTTCGPc21g16000 genePcpenDE_sCTGCCACTCTCTCTGPc21g16000 genePcpenDE_aCTGCCACCAAGGATGGTCCPcpenDEgenepcbC_sCACCCATGCCTTCACCCCCAAGGCCAATGPcpcbC genepcbC_sCACCCATGCCCTATGCACCCCCATAGCCAATGPcpcbC genepcbC_sCCCCCATGCCCATAACCTATTGAAPcfluG genePcfluG-aGCCAATGCCCATAACCAACCACCPcfluG geneflbB_forGCCAATGCCATGACCACTCCPcfluG geneflbB_revTGACCAAGTGCTGTCAACCACCCPcfluG geneflbB_revTGACCAAGGCATGAGCAACCACCACPcfluG generbdC_sCCACCAGTGCCTTGCCAAGAGPcfluG geneflbB_revTGACCACGGATGAGCAACCACCCPcfluG generbdD_revTAGGCACCGGTAGCGAAGPcrsdD genePc23g00420_forTAGGCACCGGTAAGACACCACCPc2300420 genePc23g00420_forCTCAGCAACCGGTGCTAAGACCACCGCPc2300420 genePc23g00420_forGCCACCGGTCTAAGACACCPc2300420 genePc24g01940_revCTCAGCAACCGGGTAAGCACACCPc24g01940 genePc24g01940_revCTCAGCAGCCTATAGACACPc24g01940 genePc12g12190_forGCCTCCCAGCTAGCGAAAGPcflbC genePc13g04320_forTGAGCACCAGGCTAATGGAAGACPcstuA genePc13g04320_forTGAGCAACCAGGCTCAATGCACPcbAB genePcbAB-RT-3GCCTCCCAGCGAAGACCAGACpcbA genePcbAB-RT-4CCCCCCGTCTCGCGAAGACACAGACpcbA genePcbAB-RT-5GCCTCCCGCTCTCGCGAAGACACAGACpcbA genePcbAB-RT-5GC	PcIA_sense	TGTGGTATTACCGGGAAGTC	<i>pclA</i> (<i>Pc22g14900</i>) gene
Chry1GAGTTTGACTCGGGTCTTCGPc21g16000 geneChry4AGCCAATTCCATCTGCTCTGPc21g16000 genePcpenDE_sCTGCGCCAAAGAGATGATCCPcpenDEgenePcpenDE_aCCTGCGTTGAGCCCAAAGCATPcpenDEgenepcbC_sCACCATGGCTTCACCCCAAGGCCATGPcpcbC genepcbC_aGTGCCATGGCTGTGCGCGTTCTTGTTGATTAGACPcfbuG genePcFluG-sCCACCATGCCTGCGCATTCTGACAAAACCAACPcfbuG genepcbL_aGCAAATTCCGATAACAAAACCAACPcfbuG genepcbL_aGCAAATTCCGATGCATGGACACTCPcfbuG genepcbL_aGCAAATTCCGATGCACACACCPcfbuG genepcbL_aGCAAATTCCGATGCACACACCPcfbuG genepcbL_aGCAAATTCCGATGCACACACCPcfbuG genepcbL_aGCAAATTCCGATGCACACACCPcfbuG genepcbLoaGCAAATTCCGCTGCCTAATGPcfbuG genepcbLoaTAGCGACCGGGTCTGGCTGAAGGAPcrsdD genepc23g00420_revTAGGACACGGGCTCATGCACCACCPc2300420 genepc23g00420_revCATCCAGCGGGATATTTCPc23g01420 genepc23g00420_revCTCAGCACGGGGTAAGGAPc1bG genepc23g01420_revCCCCGCGCACGGGTCTAGGCACCACCPc23g0140 genepc23g01420_revCCCCGCGCCAAGGGCTCAAGGPc1bG genepc12g12190_revACGCCCGGTCTAGGCACACCPc3bg genepc12g12190_revACGCCCGGCTCAAGGGCTCAATGPc1bG genepc12g12190_revCCTGCGCCACGGCAAATGGAPc1bC genepc13g04920_forTGAGCAACGAGGCTCAATGGAPcbAB genepcbAB-RT-aGCCGCCCTCCCGCAAGCApcbAB genepcbAB-RT-aGCTGCCCGACGAGAACCAGACpcbAB	PclA_anti	ACAATTCGTGCCTCGACTCC	pclA (Pc22g14900) gene
Chry4AGCCAATTCCATCGCTCGPc21g16000 genePcpenDE_sCTGCCACCAAGAGATGATCCPcpenDEgenePcpenDE_aCTGCCACCAAGGCCAAGCCTPcpenDEgenepcbC_sCACCCATGGCTTCCACCCCCAAGGCCAATGPcphC genepcbC_aGTGCCATGGCTGCCGCGTCTTGTGTGATTAGACPcfluG genePcfluG-sCCAACGCCATGACCCATAACCTAT TGAAPcfluG genepcbLsGCCAATGCCATAACCTAT TGAAPcfluG genepcbLsGCCAATGCCATGACCATCACCACPcfluG geneflbB_forGCCAATGCCATCAACCACPcfluG geneflbB_revTGACCAGGCTTGCCCTAATGPcfluG genensdD_forTGACGAGGCTTGCCCTAATGPcfluG genepc23g00420_forTGAGCACCGGTGCGGAAGPc300420 genePc23g00420_forGCATCCAGGCTGCGGAACPc23g00420 genePc24g01940_revCTCAGCAGCGCTATGGCTAGCGPc24g01940 genePc24g01940_revCTCAGCACGCGTAGGCCAATGPc24g01940 genePc24g01940_revCTCAGCACGCGTAGGCAAGCPc24g01940 genePc24g01940_revCTCAGCACGCGTAGCCAATGPc1bC genePc12g12190_forGCCTCCCAGCTAGCCAAGGPc1bC genePc12g12190_forTGAGCACCAGCCCTCAGGAAGPc1bC genePc13g04920_forTGAGCACCAGCCCTAGGAAGAPc1bC genePc13g04920_forTGGCAAGGGAGAACCAGCCPc3bA genePcbAB-RT-aTGCTGAGCAGACCAGCCPc3bA genePcbAB-RT-aTGCTGAGCAGACCAGCCPc3bA genePcbAB-RT-aTGCTGAGCAGACCAGCCPc3bA genePcbAB-RT-aTGCTGAGCAGACGCAGACPcbA genePcbAB-RT-aTGCTGAGCAGAGCTGGAAGCAGACPcbA gene <td>Chry1</td> <td>GAGTTTGACTCGGGTCTTCG</td> <td><i>Pc21g16000</i> gene</td>	Chry1	GAGTTTGACTCGGGTCTTCG	<i>Pc21g16000</i> gene
PcpenDE_sCTGCCACCAAAGGATGATCCPcpenDEgenePcpenDE_aCCTGCCATGGCTGCGCCGACCTPcpenDEgenepcbC_sCACCCATGGCTTGCGCCGACCCCAAGGCCAATGPcpcbC genepcbC_aGTGCCATGGCTGTCTGGCCGTTCTTGTGATTAGACPcpluG genePcFluG-sCCACCATGCCCATAACCTATGAAPcfluG genepcfluG-sCCCAATGCCTGCCGTAACAAACCAACPcfluG geneflbB_forGCCAATGCCTGCCTAAGGPcfluG genensdD_forTAGCGTGGCTGCCGAAGGPcfluG genensdD_revTAGACCACGGTGCCGAACPcrsdD genepc23g00420_revCATCAAGCGTGCCGAACPc2300420 genePc24g01940_forGTCACCACGCCTATAGACAPc24g01940 genePc24g01940_forGCCACAGGTGCCGGAACPc24g01940 genePc24g01940_revCATCCAAGCGTCCTAGGCAPc24g01940 genePc12g12190_revACCCCCAGGTTAGCGAAAGPcflbC genePc12g12190_revACCCCCAGGTCTAGCGAAAGPcflbC genePc13g04920_forTGGCACACCGCGCTCAAGGAAGAPcflbC genePc13g04920_forTGGCGAAGGAGAAGAAGAPcflbC genePc13g04920_forTGGCGAAGGTCACGCGCAAGGAPcflbC genePc13g04920_forGCCCCCCGGCGCAAGGAAGAPcflbC genePc13g04920_forTGGCGAAGGAGAACAGGCPcbAB genePcbAB-RT-sGCCTCCCGGTTGCCAAGCPcbAB genePcbAB-RT-sGCCTCCCGGTTGCCAAGCPcbC genePcbAB-RT-sGCCTCCCGGTGCGAAGGAAPcbC genePcbC-RT-sGCTGCCCGGAAGGAGAAGAGAAPcbC genePcbC-RT-sGCTGCCCGGAAGGAGAGAGAAGAGAPcbC genePcbC-RT-sGCTGCCCCGGCCGCGCAAGGAAGAGAA<	Chry4	AGCCAATTCCATCTGCTCTG	<i>Pc21g16000</i> gene
PcpenDE_aCCTGGGGTTGAGCGCAGACCTPcpenDEgenepcbC_sCACCCATGGCTTCACCCCCAGGGCCATGPcpcbC genepcbC_aGTGCCATGGCTGTGGCGGTTCTGTGGATAGACACPcfluG genePcfluG-sCCACCATGGCCATAACCAATGCAAPcfluG geneflbB_forGCAAATTCCGATACAAAACCAACPcfluB geneflbB_forGCACATGGCATGACCACTCPcfluB geneflbB_forGCACAGTGGCTGCCAGACACCCPcfluB genensdD_forTAGCGGGCTGCCGAAGGPcnsdD genensdD_forTAGGGGCGCGACCGACCGACPcnsdD genePc23g00420_forTAGAGACCAGGGCGAACPc2300420 genePc23g00420_revCATCAACGGGCTATAGACACPc2300420 genePc24g01940_forGTCACGACGGGTATGCCAACPc24g01940 genePc24g01940_revCTCACGACCGGGTATAGCACAPc24g01940 genePc24g01940_revCTCACGACCGGGTATAGCCACGPc24g01940 genePc24g01940_revCTCACGACCGGCTAATGCCACGPc1bC genePc12g12190_forGCCTCCAGCTATGCCTACGPc1bC genePc13g04920_forTGAGCAACCAGGCTCAATGPcbAB genePc13g04920_forTGAGCAACCAGGCTCAATGACACPcbAB genePc13g04920_forCTGCCCTAGTGCTCACCCCACGCPcbAB genePcbAB-RT-aGCGTGCAACGAGAACAGACpcbA genePcbC-RT-sCCTCCCGTTCTCCTCAATCpcbC genePcbC-RT-sGCGGAAGAGAACCAGACpcbC genePcbC-RT-sGCGCAGAGAGAACCAGACpcbC genePcbC-RT-sGCGAGAGAGAGCGGAAGGAAGAGApcbC genePcbC-RT-sGCGCCTCGTCTCCTCAATCpcbC genePcbC-RT-sGCGCCCTCGTCGTCGCAAGGAGAGAGAGApcnD	PcpenDE_s	CTGCCACCAAAGAGATGATCC	<i>PcpenDE</i> gene
pcbC_sCACCCATGGCTTCCACCCCCAAGGCCAATGPcpbC genepcbC_aGTGCCATGGCTGTCGGCGTTCTTGTTGATAGACPcpluG genePcFluG-aGCACATGCCCATACCTATTGAAPcfluG geneflbB_forGCCAATGCCATGCACACCPcfluG geneflbB_forGCCAATGCCATGCACCCCPcfluG geneflbB_revTGACCAAGTGCTGTCAAGAGPcfluG genemsdD_forTAGCGTGGCTTCGCCTAATGPcnsdD generevTAGAGCACGGGTGCCGGAACPc2300420 genePc23g00420_revCATTCAACCGGGTGCCGAACPc2300420 genePc24g01940_revCTCAACCACGGTGCCGAACPc24g01940 genePc24g01940_revCTCAACCACGGGTATGCCTACGPc24g01940 genePc24g01940_revCTCAACCACGGGTATGCCTACGPc24g01940 genePc24g01940_revCTCAACCACGGCGTATGCCTACGPc1bC genePc24g01940_revACGCCCAGGTCTAGCCAACGPc1bG genePc12g12190_revACGCCCAGGTCTAGCGAAAGPc1bG genePc13g04920_forTGACCACGCCCTAATGCAACGPc1bG genePc13g04920_forTGACGACACGCCCTCAATGGAPc1bA genePc13g04920_forTGGCCAAGGCAGACCAGACPcbAB genePcbAB-RT-sGCCCTCCCGTTCTCCTCCPc5AB genePcbAB-RT-sCCCTCCGTTCTTCGTCAATCpcbAB genePcbC-RT-sCCTCCCGTTCTTGTCAATCGpcbC genePcbC-RT-sGAATCATCGGGAAGGAGApcbC genePcbC-RT-sGCTCCCCGTTGTCCTCAGApenDE genePcbC-RT-sGCTCCCCTTGTCCAGApcbC genePcbC-RT-sGCTCCCCTTGTCCTCAGAPcDpg1 genePcDF-RT-sGCTCCCCCTTGTCCTCAGAPcDpg1 geneP	PcpenDE_a	CCTGGCGTTGAGCGCAGACCT	<i>PcpenDE</i> gene
pcbC_aGTGCCATGGCTGTCTGGCCGTTCTTGTGATTAGACPcpuCbC genePcFluG-sCCACCATGGCCATAACCTAATTGAAPcfluG genePcFluG-aGCAAATTCCGGATACAAAACCAACPcfluG geneflbB_forGCCAATGGCATGGACACCACCPcflbB geneflbB_revTGACCAAGTGCTGTCAAGAGPcflbB genensdD_forTAGCGTGGCTTCGCCTAATGPcnsdD genensdD_revTAGAGACCGAGTGCGCGAACPc2300420 genePc23g00420_revCATTCAAGGGTGCTGACACCPc2300420 genePc24g01940_forGTCACCACGGTGCTAAGACCPc24g01940 genePc24g01940_revCTCAGCAACCGGGATATTCCPc24g01940 genePc24g01940_revCTCAGCAACCGGGATATTCCPc24g01940 genePc12g12190_forGCCTTCAGCTATGCCTAAGPcflbC genePc13g04920_forTGGCACCCGGGATATTCCPc24g01940 genePc13g04920_forCTCGCCTAGCGTAGCGAAGPcflbC genePc13g04920_forCTGGCACCCGGCTCAAGGPcflbC genePc13g04920_forCTGGCACCAGGGCTCAAGGPcbAB genePc13g04920_forCTGCGCCTAGTCCTCCCPcstuA genePcbAB-RT-aGCGTCAACGAGATATTGGApcbAB genePcbAB-RT-aCGCTCCCGTTCGCAATGpcbAB genePcbC-RT-aCTGCAGATACGGAAACCAGACpcbAB genePcbC-RT-aCTGCAGCATATTGGApcbC genepenDE-RT-aTGATAGGCCTGGAAGGAGAACCAGACpcbC genepenDE-RT-aCTGCAGCTGGAAGGAGAGAGAGApcnDE genepenDE-RT-aCTGTGCCCTTGCTCAAGAPcppJ genePcbC-RT-aCCTGCCCTGTGCTCTCAGAPcppJ genePcDC-RT-ACCTGCCCTGGGAAGGAGAGAGAGAGAGAGAGA	pcbC_s	CACCCATGGCTTCCACCCCCAAGGCCAATG	PcpcbC gene
PcFluG-sCCACCATGCCCATACCCTATTGAAPcfluG genePcFluG-aGCAATTTCCGATACAAACCCAACPcfluB geneflbB_forGCCAATGGCATGGACCACTCPcfluB geneflbB_revTGACCAAGTGCTGTCAAGAGPcflbB genensdD_forTAGCGTGGCTTCGCCTAATGPcnsdD genensdD_revTAGAGCACCGGGTGCGAACPc2300420 genePc23g00420_forTAGAGACCACGGTGCCGAACPc2300420 genePc23g00420_revCATCAAGCGCGTATGGCAGACPc2300420 genePc24g01940_forGTCAGCACGCGTATGACCPc24g01940 genePc24g01940_revCTCAGCAACCGGGATATTTCPc24g01940 genePc12g12190_forGCCTTCCAGCTATGCTAGAGPcflbC genePc13g04920_forTGAGCACCGCGTATGCCTACGPcflbC genePc13g04920_forCTGCGCTAGTGCTAGGAAGPcflbC genePc13g04920_forGCGCCCAGGCTCAAGGPcstuA genePc13g04920_forCTGCGCTAGTCTCCTCCPcstuA genePc3094920_forCTGCGCTAGCGAACCAGACpcbA genePc3094920_forCTGCGCTAGCGAACCAGACpcbA genePcbAB-RT-sGCCGCAACGAGAACCAGACpcbA genePcbAB-RT-sCCTCCCGTTCTTCGTCATGCpcbA genePcbAB-RT-sCCTCCCGTTCTGCCAACGACpcbC genePcbC-RT-sCTGCGAAGGAGACCAGACpcbC genePcbC-RT-sGATACTGCGGAAGGTTGGApcnDE genePcbC-RT-sGATACTGCGGAAGGATGGApcnDE genePcbC-RT-sGCTTCCCCTTCGTGCATGGAPcpp1 genePcpp1 RT-sGCTTCCCCTTCGTCCTCCAGAPcpp1 genePcpp1 RT-sGCTTCCCCTTCGTCCTCCAGAPcpp1 genePcpp1 RT-	pcbC_a	GTGCCATGGCTGTCTGGCCGTTCTTGTTGATTAGAC	PcpcbC gene
PcFluG-aGCAAATTTCCGATACAAAACCAACPcfluG geneflbB_forGCCAATGGCATGGACCACTCPcflbB geneflbB_revTGACCAAGTGCTGTCAAGAGPcflbB genensdD_forTAGCGTGGCTTGCCCTAATGPcnsdD genensdD_revTAGAGCACCGGTGCCGAACPcrsdD genePc23g00420_forTAGAGACCACGGTGCCGAACPc2300420 genePc23g00420_revCATCAAGCGGTGCTAGATCCPc2300420 genePc24g01940_forGTCAGCACGGGCTAGATCCPc24g01940 genePc24g01940_forGCCACGCCTATAGCACACPc24g01940 genePc24g01940_revCTCAGCAACGGGGATATTTCPc24g01940 genePc12g12190_revACGCCCAGGTTAGCGAAGPcflbC genePc12g12190_revACGCCCAGGTCTAGCGAAGPcflbC genePc12g12190_rovCCCGCCAGGTCTAGCGAAGAPcflbC genePc13g04920_forTGGGGAACCAGGGCTCAATGPcstuA genePc13g04920_forTGGGGAACGAGGAACCAGGApcbAB genePcbAB_RT-aGCGTCCAGGTATGCCCAAGApcbAB genePcbAB_RT-aCGCGCCAGGAACCAGGApcbC genePcbC-RT-aCTCCCGTTCTCGCGAAGApcbC genePcbC-RT-aGAATCATCGGGAAGGAGAGApcbC genePcbC-RT-aGAATCATCGCGAAGGAGAGAGApcbC genePcbC-RT-aGAATCATCGGGAAGGAGAGApcbC genePcbC-RT-aGCTCCCCTTGCCTAGGAAGGAGApcbC genePcbC-RT-aGCTGCCCTTGGCAAGGAGAGAGApcbC genePcbC-RT-aGCTGCCCTTGCCTAGGAAGGAGApcbC genePcbC-RT-aGCTGCCCTGGGAAGGAGAGAGAGApcbC genePcbC-RT-aGCTGCCCCTGCCCTACGApcbC genePcDF_R	PcFluG-s	CCACCATGCCCATAACCTATTGAA	<i>PcfluG</i> gene
flbB_forGCCAATGGCATGGACCACTCPcflbB geneflbB_revTGACCAAGTGCTGTCAAGAGPcflbB genensdD_forTAGCGTGGCTTCGCCTAATGPcnsdD genensdD_revTAGGCACCGGAGTAGGGAAGPcrasdD genePc23g00420_forTAGGCACCGGGTGCTGGCGAACPc2300420 genePc24g01940_forGTCAGCACCGGCTATAGCCACPc2300420 genePc24g01940_forGTCAGCACCGCGTATAGACACPc24g01940 genePc24g01940_revCTCAGCAACCGGGATATTTCPc24g01940 genePc12g12190_forGCCTTCCAGCTATGCCTACGPcflbC genePc12g12190_revACGCCCAGGTCTAGCGAAGPcflbC genePc13g04920_forTGAGCAACCAGCGCTCAATGPcstuA genePc13g04920_forTGAGCAACCAGCGCTCAATGGAPcstuA genePc13g04920_forTGGGAACGAGAACCAGACpcbAB genePcbAB-RT-aTGGTGGACGGAGAACCAGACpcbAB genePcbAB-RT-aTGGTGAACGAGAACCAGACpcbAB genePcbC-RT-sCCCTCCCGTTCTGCTCAATCpcbC genePcbC-RT-aTGGCAGATAGTGCCCGTACGApcbC genePcbC-RT-aCTGCAGATAGTGGCCGTACGApcbC genePenDE-RT-sGAATCATCGGGAAGGTGGApcDE genePenDE-RT-sGAATCATCGGGAAGGTGGApcDE genePenDE-RT-sGAATCATCGGGAAGGTGGAPcppJ genePcpp1-RT_sGCTTGCCCCTTGCCCTTCGCAACPcppJ genePcpp1-RT_sCCTTGCCCCTTGCCCTTCGCAACPcppJ gene	PcFluG-a	GCAAATTTCCGATACAAAACCAAC	<i>PcfluG</i> gene
flbB_revTGACCAAGTGCTGTCAAGAGPcflbB genensdD_forTAGGGGGCTTGCCCTAATGPcnsdD genensdD_revTAGAGCACCGGGTAGGGAAGPc2300420 genePc23g00420_forTAGAGCCAGGTGCCGAACPc2300420 genePc23g00420_revCATTCAAGCGTGCTAGATCCPc2300420 genePc24g01940_forGTCAGCACCGGGATATTCCPc24g01940 genePc24g01940_revCTCAGCAACCGGGATATTCCPc24g01940 genePc12g12190_forGCCTTCCAGCTATGCCTACGPc1bC genePc13g04920_forTGAGCACCAGGCTCTAGCGAAAGPcflbC genePc13g04920_forTGAGCAACCAGGCCTCAATGPcstuA genePc13g04920_forTGAGCAACCAGGCTCTACTCCTCCPcstuA genePc13g04920_forTGAGCAACGAGAATATTGGAPcbA genePcbAB-RT-sGCCGTCAACGAGAACCAGACpcbA genePcbAB-RT-sGCCGTCAACGAGAACCAGACpcbA genePcbC-RT-sCCCTCCCGTTCTTCGTCAATCpcbC genePcbC-RT-sGAATCATCGGAAAGTTGGApcbC genePcbC-RT-sGAATCATCGGGAAGGTTGGApcbC genePcbC-RT-sGAATCATCGGGAAGGTTGGApcbC genePcbC-RT-sGAATCATCGGGAAGGTTGGApcbC genePcbC-RT-sGAATCATCGGGAAGGTTGGApcbC genePcbC-RT-sGATCATCGGGAAGGTGGApcbC genePcb-RT-sGATCATCGGGAAGGTGGApcbC genePcb-RT-sGATCATCGGGAAGGTGGApcbC genePcb-RT-sGATCATCGGGAAGGAGApenDE genePcp01-RT-sGCTTGCCCCTTGCCTCCAAPcpp1 genePcp01-RT-sGCTTGCCCCTTGCCTCAAPcpp1 genePcp01-RT-sGCTTGCCCCTTG	flbB_for	GCCAATGGCATGGACCACTC	<i>PcflbB</i> gene
nsdD_forTAGCGTGGCTTCGCCTAATGPcnsdD genensdD_revTAGAGCACCGAGTAGGGAAGPcnsdD genePc23g00420_forTAGAGACCACGGTGCCGAACPc2300420 genePc23g00420_revCATTCAAGCGTGCTAGATCCPc2300420 genePc24g01940_revCCTCAGCACGCCTATAGACACPc24g01940 genePc24g01940_revCTCAGCACGCGCTATAGACACPc24g01940 genePc24g01940_revCTCAGCACCGGGATATTCCPc24g01940 genePc12g12190_forGCCTTCCAGCTATGCCTACGPc1bC genePc12g12190_revACGCCCAGGTCTAGCGAAAGPcflbC genePc13g04920_forTGAGCAACCAGCGTCAATGPcstuA genePc13g04920_forCTGCGCCTAGTTCTCCTCCPcstuA genePcbAB-RT-sGCCGTCAACGAGATATTGGApcbAB genePcbAB-RT-aTGGTGAACGAGAACCAGACpcbAB genePcbC-RT-sCCCTCCCGTTCTTCGTCAATCpcbC genePcbC-RT-sGCCGTCCGGAAGGTTGGApcbC genePcbC-RT-sGAATCATCGGGAAGGTTGGApenDE genePcnDE-RT-sGAATCATCGGAAGGATGGApenDE genePcpg1-RT-sGCTTGCCCTTCGTCCTCAACPcpg1 genePcpp1-RT-sGCTTGCCCTTGCCTTCAGAPcpg1 genePcpp1-RT-sGCTTGCCCTTGCCTTCAGAPcpg1 genePcpp1-RT-sGCTTGCCCTTGCCTTCAGAPcpg1 genePcpp1-RT-sGCTTGCCCTTGCCTTCAGAPcpg1 genePcpp1-RT-sGCTTGCCCTTGCCTTCAGAPcpg1 genePcpp1-RT-sGCTTGCCCTTGCCTTCAGAPcpg1 genePcpp1-RT-sGCTTGCCTTCCCTCAACPcppg1 genePcpp1-RT-sGCTTGCCTTGCCTTCAGAPcppg1 genePcpp1-RT-s </th <th>flbB_rev</th> <th>TGACCAAGTGCTGTCAAGAG</th> <th><i>PcflbB</i> gene</th>	flbB_rev	TGACCAAGTGCTGTCAAGAG	<i>PcflbB</i> gene
nsdD_revTAGAGCACCGAGTAGGGAAGPcnsdD genePc23g00420_forTAGAGACCACGGTGCCGAACPc2300420 genePc23g00420_revCATTCAAGCGTGCTAGATCCPc2300420 genePc24g01940_forGTCAGCACCGCCTATAGACACPc24g01940 genePc24g01940_revCTCAGCAACCGGGATATTTCPc24g01940 genePc12g12190_forGCCTTCCAGCTATGCCTACGPcflbC genePc12g12190_revACGCCCAGCTATGCCTACGPcflbC genePc13g04920_forTGAGCAACCAGCGCTCAATGPcstuA genePc13g04920_forCTTCGCGCTAGTTCTCCTCCPcstuA genePcbAB-RT-sGCCGTCAACGAGATATTGGApcbAB genePcbAB-RT-aTGGTGAACGGAGAACCAGACpcbAB genePcbC-RT-sCCCTCCCGTTCTTCGTCAATCpcbC genePcbC-RT-aCTGCAGATAGTCGCCGTACGApcbC genePcbC-RT-aTCATAGGCCTGGAAGAGApenDE genePenDE-RT-aTCATAGGCCTGGAAGGAGApenDE genePcpg1-RT-sGCTTGCCCTTTCTCTCCAGAPcpg1 genePcpg1-RT-sGCTTGCCCTTGTCCTTCAGAPcpg1 genePcpg1-RT-sGCTTGCCCTTGTCCTTCAGAPcpg1 genePcpg1-RT-sGCTTGCCCTTGTCCTTCAGAPcpg1 genePcpg1-RT-sGCTTGCCCTTGTCCTTCAGAPcpg1 genePcpg1-RT-sGCTTGCCCTTGTCCTTCAGAPcpg1 genePcpg1-RT-sPcpCTGCTTGTGCACAGAPcpg1 genePcpg1-RT-sPcpCTGCTTGTGCAGAGAGAGAPcpg1 genePcpg1-RT-sPcpCTGCTTGTGCAGAGAGAGAGAPcpg1 genePcpg1-RT-sPcpCTGCCTTGTGCCTTGCCTTCAGAPcpg1 genePcpg1-RT-sPccCTTGCCCTTGTGCCTTGCAGAGAGAGAGAGAGAGAPcpg1 g	nsdD_for	TAGCGTGGCTTCGCCTAATG	PcnsdD gene
Pc23g00420_forTAGAGACCACGGTGCCGAACPc2300420 genePc23g00420_revCATTCAAGCGTGCTAGATCCPc2300420 genePc24g01940_forGTCAGCACGCCTATAGACACPc24g01940 genePc24g01940_revCTCAGCAACCGGGATATTTCPc24g01940 genePc12g12190_forGCCTTCCAGCTATGCCTACGPcflbC genePc12g12190_revACGCCCAGGTCTAGCGAAGPcflbC genePc13g04920_forTGAGCAACCAGCGCTCAATGPcstuA genePc13g04920_forCTTGCGCCTAGTTCTCCTCCPcstuA genePcbAB-RT-sGCCGTCAACGAGATATTGGApcbAB genePcbAB-RT-aTGGTGAACGAGAACCAGACpcbAB genePcbC-RT-sCCCTCCCGTTCTCGTCAATCpcbC genePcbC-RT-aCTGCAGATAGTCGCGTACGApcbC genePcbC-RT-aCTGCAGATAGTCGCGTACGApcbC genePcbC-RT-aCTGCAGATAGTCGCGTACGApcbC genePcbC-RT-aGAATCATCGGGAAGGTGGApcbC genePcDF-RT-aTCATAGGCCTGGGAAGGAGApcbC genePcpp1-RT-sGCTTGCCCTTGTCCTTCAGAPcnp01 genePcpp1-RT-sGCTTGCCCTTGTCCTCAGAPcnp01 genePcmond-BT_aCCCCCTTGCCCTTGCCTCAGAPcnp01 gene	nsdD_rev	TAGAGCACCGAGTAGGGAAG	PcnsdD gene
Pc23g00420_revCATTCAAGCGTGCTAGATCCPc2300420 genePc24g01940_forGTCAGCACGCCTATAGACACPc24g01940 genePc24g01940_revCTCAGCAACCGGGATATTTCPc24g01940 genePc12g12190_forGCCTTCCAGCTATGCCTACGPcflbC genePc12g12190_revACGCCCAGGTCTAGCGAAAGPcflbC genePc13g04920_forTGAGCAACCAGCGCTCAATGPcstuA genePc13g04920_forCTTGCGCCTAGTTCTCCTCCPcstuA genePcbAB-RT-sGCCGTCAACGAGAACCAGACpcbAB genePcbC-RT-aTGGTGAACGAGAACCAGACpcbAB genePcbC-RT-aCTGCAGATAGTCGCCGTACGApcbC genePcbC-RT-aCTGCAGATAGTGGCGTAGAApcbC genePcbC-RT-aGAATCATCGGGAAGGTTGGApcbC genePcnDE-RT-aTCATAGGCCTGGGAAGGAGApcbC genePcnDF-RT-aTCATAGGCCTGGGAAGGAGApcnDE genePcpg1-RT-sGCTTGCCCTTCGTCAAGAPcppg1 genePcpg1-RT-sGCTTGCCCCTTGTCCTCAGAPcppg1 genePcnDF-RT-sGCTGGCCCTTGGCAACGCCTAGAPcppg1 genePcnDF RT-sGCTGGCCCTTGCCCTTCAGAPcppg1 genePcnDF RT-sGCTGGCCCTTGCCTTCAGAPcppg1 genePcnDF RT-sGCTGGCCCTTGCGCAACGCCTTGAGAPcnDF genePcnDF RT-sGCTGGCCCTTGCCCTTGCAACGCCTTCAGAPcnDF genePcnDF RT-sGCTGGCCCTTGCCCTTGCAACGCCTTGCAACGCCTTGCAACGCCCTTGCCTTCAGAPcnDF genePcnDF RT-sGCTGGCCCTTGCCCTGCAACGCCTTGCAACGCCTTGCAACGCCCTTGCCTTCAGAPcnDF genePcnDF RT-sGCTGGCCCTTGCCCTTGCAACGCCTTGCAACGCCTTGCAACGCCTTGCAACGCCTTGCAACGCCTTGCAACGCCTTGCAACGCCTTGCAACGCCTTGCAACGCCCTTGCACGCCTTGCAACGCCTTGCAACGC	Pc23g00420_for	TAGAGACCACGGTGCCGAAC	<i>Pc2300420</i> gene
Pc24g01940_forGTCAGCACGCCTATAGACACPc24g01940 genePc24g01940_revCTCAGCAACCGGGATATTTCPc24g01940 genePc12g12190_forGCCTTCCAGCTATGCCTACGPcflbC genePc12g12190_revACGCCCAGGTCTAGCGAAAGPcflbC genePc13g04920_forTGAGCAACCAGCGCTCAATGPcstuA genePc13g04920_forCTTGCGCCTAGTTCTCCTCCPcstuA genePcbAB-RT-sGCCGTCAACGAGATATTGGApcbAB genePcbAB-RT-aTGGTGAACGAGAACCAGACpcbAB genePcbC-RT-sCCCTCCCGTTCTTCGTCAATCpcbC genePcbC-RT-aCTGCAGATAGTCGCCGTACGApcbC genePcbC-RT-aGAATCATCGGGAAGGTTGGApcbC genepenDE-RT-aTCATAGGCCTGGGAAGGAGApcbC genePchDF-RT-aTCATAGGCCTGGGAAGGAGApcbC genePchDF-RT-aTCATAGGCCTGGGAAGGAGApcbC genePchDF-RT-aTCATGCGCTGGGAAGGAGApcDC genePchDF-RT-aTCATAGGCCTGGGAAGGAGApcDC genePchDF-RT-aTCATAGGCCTGGGAAGGAGApcDF genePchDF-RT-aTCATGCCCTTGTCCTTCAGAPcpp1 genePcpp1-RT-sGCTTGCCCCTTGTCCTTCAGAPcpp1 genePcrostPcrostPcrostPcrostPcrostPcrostPcrostPcrostPcrostPcrostPcrostPcrostPcrostPcrostPcrostPcrostPcondPcrostPcrostPcrostPcondPcrostPcrostPcrostPcondPcrostPcrostPcrostPcondPcrostPcrostPcrostPcond<	Pc23g00420_rev	CATTCAAGCGTGCTAGATCC	<i>Pc2300420</i> gene
Pc24g01940_revCTCAGCAACCGGGATATTTCPc24g01940 genePc12g12190_forGCCTTCCAGCTATGCCTACGPcflbC genePc12g12190_revACGCCCAGGTCTAGCGAAAGPcflbC genePc13g04920_forTGAGCAACCAGCGCTCAATGPcstuA genePc13g04920_forCTTGCGCCTAGTTCTCCTCCPcstuA genePcbAB-RT-sGCCGTCAACGAGATATTGGApcbAB genePcbAB-RT-aTGGTGAACGAGAACCAGACpcbAB genePcbC-RT-sCCCTCCCGTTCTTCGTCAATCpcbC genePcbC-RT-sCTGCAGATAGTCGCCGTACGApcbC genePcbC-RT-aCTGCAGATAGTCGCCGTACGApcbC genePenDE-RT-sGAATCATCGGGAAGGTTGGApenDE genePenDE-RT-aTCATAGGCCTGGGAAGGAGApenDE genePcpg1-RT-sGCTTGCCCTTCGTCAAGAPcpg1 genePcpg1-RT-sGCTTGCCCTTGGCCGTACGAPcppg1 genePcrupal PL aCCCCCTTGCCCTTCAGCCGTACGAPcppg1 gene	Pc24g01940_for	GTCAGCACGCCTATAGACAC	<i>Pc24g01940</i> gene
Pc12g12190_torGCCTTCCAGCTATGCCTACGPct/bC genePc12g12190_revACGCCCAGGTCTAGCGAAAGPcf/bC genePc13g04920_forTGAGCAACCAGCGCTCAATGPcstuA genePc13g04920_forCTTGCGCCTAGTTCTCCTCCPcstuA genePcbAB-RT-sGCCGTCAACGAGATATTGGApcbAB genePcbAB-RT-aTGGTGAACGAGAACCAGACpcbAB genePcbC-RT-sCCCTCCCGTTCTTCGTCAATCpcbC genePcbC-RT-aCTGCAGATAGTCGCCGTACGApcbC genePcbC-RT-aCTGCAGATAGTCGCCGTACGApcbC genePenDE-RT-aTCATAGGCCTGGGAAGGAGApenDE genePenDE-RT-aTCATAGGCCTGGGAAGGAGApenDE genePcpg1-RT-aTCATAGGCCTGGGAAGGAGAPcppg1 genePcpg1-RT-sGCTTGCCCCTTCGTCAACGAPcppg1 genePcpg1-RT-sGCTTGCCCCTTGGCCAGAGGAGAPcppg1 genePcpg1-RT-sGCTTGCCCCTTGGCCGTACGAPcppg1 genePcpg1-RT-sGCTTGCCCCTTGGCCAGAGGAGAPcppg1 gene	Pc24g01940_rev	CTCAGCAACCGGGATATTTC	<i>Pc24g01940</i> gene
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Pc13g04920_torTGAGCAACCAGCGCTCAATGPcstuA genePc13g04920_forCTTGCGGCCTAGTTCTCCTCCPcstuA genePcbAB-RT-sGCCGTCAACGAGATATTGGApcbAB genePcbAB-RT-aTGGTGAACGAGAACCAGACpcbAB genePcbC-RT-sCCCCCCGTTCTTCGTCAATCpcbC genePcbC-RT-aCTGCAGATAGTCGCCGTACGApcbC genePcbC-RT-sGAATCATCGGGAAGGTTGGApcbC genepenDE-RT-sGAATCATCGGGAAGGTTGGApenDE genePcpp1-RT-sGCTTGCCCTTGGTCCTACGApcpg1 genePcpp1-RT-sGCTTGCCCCTTGTCCTTCAGCAPcppg1 genePcpp1-RT-sGCTTGCCCCTTGGCCAGACPcppg1 genePcpp1-RT-sGCTTGCCCCTTGGCCGTACGAPcppg1 genePcpp1-RT-sGCTTGCCCCTTGGCCGTACGAPcppg1 gene	Pc12g12190_rev	ACGCCCAGGTCTAGCGAAAG	Pcf/bC gene
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PcbAB-R1-sGCCGTCAACGAGATATTGGApcbAB genePcbAB-RT-aTGGTGAACGGAGAACCAGACpcbAB genePcbC-RT-sCCCCCCCGTTCTTCGTCAATCpcbC genePcbC-RT-aCTGCAGATAGTCGCCGTACGApcbC genepenDE-RT-sGAATCATCGGGAAGGTTGGApenDE genepenDE-RT-aTCATAGGCCTGGGAAGGAGAGpenDE genePcppg1-RT-sGCTTGCCCCTTGTCCTCAGAAPcppg1 genePcppg1-RT-sGCCTGCCCTTGGCCAGAPcppg1 gene	PCI3g04920_TOP		Postua gene
PcbAB-RT-aIGGTGAACGAGAACCAGACpcbAB-genePcbC-RT-sCCCTCCCGTTCTTCGTCAATCpcbC genePcbC-RT-aCTGCAGATAGTCGCCGTACGApcbC genepenDE-RT-sGAATCATCGGGAAGGTTGGApenDE genepenDE-RT-aTCATAGGCCTGGGAAGGAGApenDE genePcppg1-RT-sGCTGCCCTTGTCCTCTCAGAPcppg1 genePcnpc1-RT-sGCTGCCCTTGGCCGTACGGAPcppg1 gene			pcbAB gene
Proberties CTGCCGGTAGGTCGGGCGTACGA problegene PenDE-RT-a CTGCCGGTAGGGAGGGTGGGA penDE gene penDE-RT-a TCATAGGCCTGGGAAGGAGA penDE gene Pcppg1-RT-s GCTTGCCCCTTGTGCCTTCAGA Pcppg1 gene Pcropg1-RT-s GCTGCCCCTTGGCGCGTACGA Pcppg1 gene			pcbAb gene
PerpedExtra ClackGalasticGecerracia penDE penDE-RT-s GAATCATCGGGAAGGAGA penDE gene penDE-RT-a TCATAGGCCTGGGAAGGAGA penDE gene Pcppg1-RT-s GCTTGCCCCTTGTGCCTTCAGA Pcppg1 gene	PCDC-RT-S		pcbC gene
penDE-RT-a CATAGGCCTGGGAAGGAGA penDE gene Pcppg1-RT-s GCTTGCCCCTTGTCCTCAGA Pcppg1 gene Pcnpc1 gene Pcppc1 gene Pcppc1 gene			per gene
Properties GCTTGGGCCCTTGGTACGAGA Properties Properties GCTTGGCCCTTGGTACGAGA Properties	penDE-RT-3		penDE gene
	Pennal-RT-s	GCTTGCCCCCTTGTCCTTCAGA	Propal gene
	Pcppg1-RT-a	CGCTGGTACGCTTGACCTCA	Propal gene
Propertation Contract Contra	Pcpre1-RT-s	TGGGACACTGCTGGATGATCT	Pcpre1 gene
Prore1-RT-a GCTAATAACCTGCCGCACATG Prore1 gene	Pcpre1-RT-a	GCTAATAACCTGCCGCACATG	Pcpre1 gene
Pcpre2-RT-s CATGGTGTGGTCCGAGTAGCA Pcpre2 gene	Pcpre2-RT-s	CATGGTGTGGTCCGAGTAGCA	Pcpre2 gene
Pcpre2-RT-a CGGCGGTGCTGAAAGTCTACT Pcpre2 gene	Pcpre2-RT-a	CGGCGGTGCTGAAAGTCTACT	Pcpre2 gene
NcSSU1 ATCCAAGGAAGGCAGGC small subunit ribosomal RNA	NcSSU1	ATCCAAGGAAGGCAGCAGGC	small subunit ribosomal RNA
NcSSU2 TGGAGCTGGAATTACCGCG small subunit ribosomal RNA	NcSSU2	TGGAGCTGGAATTACCGCG	small subunit ribosomal RNA
Pre2-hom-f GTAATTATCTACTTTTTACAACAAATATATGGCGACATCATCTCCAATTC Pcpre2	Pre2-hom-f	GTAATTATCTACTTTTTACAACAAATATATGGCGACATCATCTCCAATTC	Pcpre2
Pre2-hom-r ATTGATCTATCGATTTCAATTCAATTCAACACGATTGAATTGTTCCTT Pcpre2	Pre2-hom-r	ATTGATCTATCGATTTCAATTCAATTCATCACGATTGAATTGTTCCTT	Pcpre2